

18th Annual Graduate Student Symposium

Saturday, February 13th, 2016



Organized by the Graduate Students in Ecology and Evolutionary Biology (GEEEB)

Sponsored by the Program in Ecology, Evolution and Conservation Biology (PEEC), and the Departments of Animal Biology, Entomology, Plant Biology and Natural Resources and Environmental Sciences (NRES).

Program Contents

General Information	2
What is GEEB?	3
Acknowledgements	4
Schedule of Talks	6
Abstracts for Oral Presentations	8
Poster Titles and Abstracts	17
Sample Evaluation Form for Oral Presentations	22
Map of Symposium	23

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18th Annual Graduate Student Symposium

The 18th Annual Graduate Student Symposium will take place on Saturday, February 13, 2016. Talks will begin at 9:00 a.m. in B102, Chemical and Life Sciences Laboratories (CLSL), at the University of Illinois at Urbana-Champaign. All of the talks will be given by University of Illinois graduate students, whose research is related to ecology, evolutionary biology, or related fields. The talks will end at 4:15 p.m., with a reception immediately following at 4:30 p.m. at the Concourse Café Space in IGB (maps provided on page 25). All participants, attendants, faculty, and staff are cordially invited to the reception.

Goals

The goals of the symposium are twofold:

1. The symposium is an opportunity for students and faculty to gain exposure to graduate student research in ecology, evolution, and related fields. Participation and attendance is encouraged from anyone working in ecology, evolutionary biology, behavior, conservation, environmental sciences, fisheries and wildlife biology, systematics, biogeography, modeling and other related fields.
2. The symposium is an opportunity for graduate students to gain experience presenting research ideas and results to peers in a formal setting and to receive constructive feedback on oral presentations.

Awards

Awards will be presented in three categories:

1. Best Overall Talk
2. Best Talk by a PhD Candidate (post-preliminary exams)
3. Best Talk by a PhD/MS Student (pre-preliminary exams)

Announcement of awards will be made at the reception following the symposium.

See page 24 for criteria used to evaluate oral presentations.

Graduate Students in Ecology and Evolutionary Biology

The symposium is organized by Graduate Students in Ecology and Evolutionary Biology (GEEB). GEEB is a registered student organization (RSO) at the University of Illinois consisting of graduate students conducting research related to the disciplines of ecology and evolutionary biology. The fundamental goal of this organization is to coordinate and unite graduate students from various departments through their interests in ecology and evolutionary biology. Members of GEEB include students from a wide diversity of campus units; we encourage and welcome students from any campus department to participate in GEEB social and academic activities.

In addition to organizing this annual symposium, other GEEB activities include:

1. Workshops and discussions with invited speakers on issues of interest to GEEB members (e.g. NSF/EPA grant writing skills, job preparation, mentoring)
2. Weekly research presentation and discussions (“Ecolunch”)
3. Archives of example grant applications to assist students in obtaining funding
4. Social activities such as happy hours, tailgating, field trips, charity events and a ‘new grad student welcome’ event in the fall to encourage inter-department camaraderie among students.

For more information and to receive email announcements about GEEB activities and news items, subscribe to our listserve at www.life.uiuc.edu/geeb.



Or follow us on twitter @GEEBatUIUC

GEEB officers for the 2015-16 academic year:

President	Kelsey Witt (kewitt2@illinois.edu)
Vice-President/Treasurer	Tyler Refsland (refslan2@illinois.edu)
Symposium Coordinator	Miles Bensky (bensky2@illinois.edu)
Ecolunch Coordinator	Rachel Moran (rmoran9@illinois.edu)
Outreach Coordinator	Ian Traniello (traniel2@illinois.edu)
Social Coordinator	Tara Stewart (tarastew@illinois.edu)
Webmaster	Selina Ruzi (ruzi2@illinois.edu)

Acknowledgments

Sponsorship

We thank the **Program in Ecology and Evolution and Conservation Biology (PEEC)** for their generosity in providing funding and resources for this event. PEEC is an interdisciplinary, campus-wide program designed to provide individualized training for graduate students for research and teaching careers in ecology and evolutionary biology and to produce scientists who are both technically competent and broadly educated in ecology, evolution and conservation biology. With approximately 60 faculty participants from 12 departments (in 5 colleges) and allied state agencies, there are many areas of concentration within the broad disciplines of ecology, conservation biology, evolution, and systematics. Students in PEEC can be found working at scales ranging from the molecular level to ecosystem responses to global change. PEEC is committed to supporting graduate education and research through summer research grants, travel grants, and an active seminar series.

We thank the **Department of Animal Biology** for their generous sponsorship of the GEEB symposium. There is a long tradition of departmental excellence stemming from Victor E. Shelford (faculty member from 1914 to 1947), who was instrumental in the development of the field of ecology in North America. His emphasis on empirical studies in both academic and research programs has continued to the present. The Department of Animal Biology's faculty teaches and conducts research in behavioral ecology, population & community biology, evolutionary ecology, evolution & development, molecular evolution, population genetics, conservation biology, and phylogenetics. Current research involves a wide range of organisms, from protozoans through mammals. The excellence of Animal Biology faculty is reflected in several recent awards including the Presidential Early Career Award for Scientists and Engineers (the highest honor bestowed by our Government on a young scientist), the Young Investigators Award from the American Society of Naturalists, the Helen Corley Petit Scholar award, and the Premio Internazionale 'Felice Ippolito' international prize for Antarctic research. Research facilities include laboratories well equipped for molecular biology, a modern avian behavior laboratory, greenhouses, and nearby research areas with mature forest, restored tall-grass prairies, and extensive areas for manipulative studies.

We appreciate the generous support of the **Department of Plant Biology**. The Department of Plant Biology at the University of Illinois has enjoyed a long tradition of identifying, training, and graduating many of the world's top plant biologists. Plant Biology is home department to some of the world's most highly cited researchers and boasts world class facilities for work in the areas of physiology & development, ecology & climate change, systematics & evolution, and biochemistry & genetics. Investigations in plant biology extend from studies of the behavior of subatomic particles in photosynthetic reaction centers to the dynamics and complexity of Paleozoic ecosystems. Researchers and students in this department address many of society's most pressing challenges: managing and conserving our natural resources, assessing effects of climate change on crop yields and ecosystem function, and developing new sources of renewable energy.

We appreciate the generous support of the **Department of Natural Resources and Environmental Sciences (NRES)**. The Department of Natural Resources and Environmental Sciences (NRES) is an interdisciplinary unit in applied sciences that brings biological, physical, and social scientists together to understand, teach, and work towards increasing the sustainability of urban, managed, and natural ecosystems from the local to global scale. All NRES educational and research programs center on science, applied ecology, and conservation in a variety of aquatic, terrestrial and human dominated ecosystems. Within that framework, our faculty, staff, and students study a wide variety of ecological systems with emphases on soil, water, people and social systems, forests, plants, animals, and microbes. Much of our research focuses on natural and social processes, such as habitat fragmentation, regulation, dispersal, disturbance, invasion, bioactivity, and decision-making.

We also appreciate the generous support of the **Department of Entomology**. The Department of Entomology was organized in 1909, beginning with S.A. Forbes as its first department head, establishing high standards for research and teaching that have characterized the department ever since. In 2005, the department was rated the top in the nation by the Faculty Scholarly Productivity Index and boasts two faculty members who belong to the National Academy of Sciences. Research is conducted as interdisciplinary collaborations with multiple departments and organizations. Additionally, the department participates in many outreach activities in the surrounding community.

Logistical Support

Many thanks to all the individuals who contributed to planning the GEEB Symposium and related activities, without whom this eventful weekend could not exist: Todd Johnson, Tyler Refsland, Dora Cohen, Tara Stewart, Kelsey Witt, Jennifer Jones, Amanda Owings, and Philippe Doucet Beaupré. Many thanks also to the many unlisted individuals in GEEB who donated their time, especially our moderators and speakers listed elsewhere in the program.

Thank you to Lisa Smith (Animal Biology), Kim Leigh (PEEC), Lezli Cline (NRES), Karen Claus (NRES), Rayme Dorsey (Plant Biology), Marty Forrest (School of Integrative Biology), Penny Broga and Staci Sears (School of Integrative Biology) and Angela Kent (PEEC) for taking on the massive task of arranging a stimulating weekend for all of the prospective students.

Judges

Finally, we thank the faculty, post docs, and graduate students (not listed to maintain anonymity) who generously volunteered their time to provide student-presenters with valuable feedback on their presentations and to help us in selecting the award-winning presentations.

Morning Schedule*

- 8:15 – 9:00 Morning Refreshments
- 9:00 – 9:15 Welcoming Remarks – Miles Bensky
- Moderator: Janice Kelly*
- 9:15 – 9:30 **Brian Zalay:** Zooplankton response to Asian carp harvesting in Illinois River backwaters
- 9:30 – 9:45 **Tara Stewart:** Diving into Daphnia defenses: how a waterflea kills its parasitic invaders
- 9:45 – 10:00 **Christina Ruiz-Rodriguez:** A non-synonymous polymorphism in Toll-like receptor 2 is associated with reduced somatic cell count in the milk of dairy goats (*Capra hircus*)
- 10:00 – 10:15 **Lorena Ríos-Acosta:** Genotypic diversity in yield and grain quality responses to elevated ozone of diverse inbred and hybrid maize
- 10:15 – 10:30 **Halie Rando:** Assembly of the Red Fox Chromosomes
- 10:30 - 10:45 Break
- Moderator: Andrew Sweet*
- 10:45 – 11:00 **Miles Mesa:** Plant tolerance and resistance: Alternative defense responses to herbivory?
- 11:00 – 11:15 **Linnea Meier:** Species-specific blends of shared pheromone components minimize interspecific attraction among cerambycid beetles in the subfamily Lamiinae
- 11:15 – 11:30 **Xander Hazel:** Palynological analysis of frass from adult long-horned beetles
- 11:30 – 11:45 **Todd Jones:** Nestling body condition and wing development predict juvenile post-fledging survival in a neotropical migratory songbird
- 11:45 – 12:00 **Samniqueka Halsey:** A community modeling approach to understanding the ecology of Lyme disease
- 12:00 – 1:15 Lunch

Afternoon Schedule*

- 1:15 – 1:30 Afternoon Remarks – Kelsey Witt
Moderator: Tara Stewart
- 1:30 – 1:45 **Rachel Moran:** Rapid evolution of male-driven behavioral isolation among allopatric species in a dichromatic fish clade
- 1:45 – 2:00 **Kai Zhao:** A web application for identifying the provenance of African elephant ivory samples using mitochondrial DNA.
- 2:00 – 2:15 **Daniel Urban:** An earful of jaw, then and now: insights from evolutionary developmental biology
- 2:15 – 2:30 **Andrew Sweet:** Cophylogenetic patterns between small New World ground-doves and their parasitic wing lice (Phthiraptera: Columbicola)
- 2:30 – 2:45 **Henry Pollock:** Seasonal flexibility in avian thermoneutral zone breadth across latitude: implications for climate change
- 2:45 – 3:00 Break
Moderator: Luke Zehr
- 3:00 – 3:15 **Elizabeth Mallot:** Dietary correlates of gut microbe composition in white-faced capuchins (*Cebus capucinus*)
- 3:15 – 3:30 **Beryl Jones:** Molecular Determinants of Behavioral Plasticity in a Facultatively Eusocial Bee, *Megalopta genalis*
- 3:30 – 3:45 **Jessica Brandt:** Genetic analysis of Sumatran rhinoceros (*Dicerorhinus sumatrensis*) specimens reveals pattern of structuring and reduced diversity in modern population
- 3:45 – 4:00 **John Crawford:** Intraspecific variation in sensitivity to resource quality in *Daphnia pulex*
- 4:00 – 4:15 **Mary Rogers:** CYP19A1 methylation and timing of menarche in a rural Polish population
- 4:30 – 6:30 **Reception and Poster Session:** Posters will be on display in the Concourse Café space on the first floor of IGB (see map on the last page).

*Note: All talks in B102 Chemical and Life Sciences Lab B. (See map on page 25.)

Abstracts for Oral Presentations

1. Brian Zalay

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ZOOPLANKTON RESPONSE TO ASIAN CARP HARVESTING IN ILLINOIS RIVER BACKWATERS

Since Asian carp (*Hypophthalmichthys nobilis* and *Hypophthalmichthys molitrix*) have arrived in the Illinois River, they appear to have a major negative impact on zooplankton. In an effort to keep the Asian carp population low, the Illinois DNR has been contracting ten commercial fishing crews. The objectives of this study are to understand the zooplankton ecological response to the reduction of Asian carp and determine the effectiveness of Asian carp harvesting for ecosystem recovery. The fishing crews harvested bimonthly at select backwaters of the upper reaches of the Illinois River. As a major food source for Asian carp and other fish, the idea is that zooplankton may respond positively to the harvesting. Zooplankton samples were collected over four months at ten backwaters during the summer of 2015. I will compare the zooplankton community structure between a spectrum of Illinois River backwaters with harvesting of Asian carp at different frequencies and intensities.

2. Tara Stewart

PhD student, Program in Ecology, Evolution, and Conservation Biology, tarastew@illinois.edu

DIVING INTO *DAPHNIA* DEFENSES: HOW A WATERFLEA KILLS ITS PARASITIC INVADERS

Hosts have evolved a series of traits to defend against parasites. Hosts can avoid encountering parasites, resist parasite invasion using barriers, or eliminate parasites with immunity. In host populations, the strength of and variation in defenses can influence parasite transmission, and a critical question in disease ecology is what maintains this variation. *Daphnia dentifera* and its fungal parasite, *Metschnikowia bicuspidata*, provide an ideal system for addressing variation in defense traits. *Daphnia* feeding rate (exposure) has been linked to susceptibility with *Metschnikowia*, but the role of barriers and immune defenses in limiting infections is unknown. I performed an observational time-series of the *Metschnikowia* infection process, and evaluated transition rates across infection stages for ten *Daphnia* genotypes. Genotypes vary in the strength of their barriers, killing of fungal spores, and killing of fungal hyphae. This variation arises from tradeoffs between defenses and tradeoffs with investment in reproduction.

3. Christina T. Ruiz-Rodriguez, Jessica R. Brandt, Ryan Oliverio, Yasuko Ishida, Noa Guedj, Gila Kahila Bar-Gal, Nikolas Nikolaidis, Felipe C. Cardoso, and Alfred L. Roca

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A NON-SYNONYMOUS POLYMORPHISM IN TOLL-LIKE RECEPTOR 2 IS ASSOCIATED WITH REDUCED SOMATIC CELL COUNT IN THE MILK OF DAIRY GOATS (*CAPRA HIRCUS*)

Mastitis is inflammation of the mammary gland, often due to infection by Gram-positive bacteria, and often characterized by higher somatic cell counts (SCCs) in milk. Since Toll-like receptor 2 (TLR2) of the goat innate immune system recognizes Gram-positive bacteria, we looked for an association between TLR2 genotype and the SCC of milk in dairy goats (*Capra hircus*). Milk and blood samples were obtained from 40 domestic goats at a single farm. Three single nucleotide polymorphisms (SNPs) were identified in the sequence of *TLR2* in the goats, of which 2 were synonymous. The non-synonymous mutation resulted in a Valine (Val) to Isoleucine (Ile) amino acid substitution. Goats heterozygous for the non-synonymous mutation had significantly ($p < 0.02$) lower SCCs than the homozygous goats. The findings of this study could potentially help the dairy goat industry genetically improve the health of goats and increase milk production.

4. Lorena Ríos-Acosta, Gorka Erice, Matt Kendzior, Mark Lewis, Jessica Mulcrone, Inés Resano-Goizueta, Ben Thompson, Tiago Tomaz, Ilse Barrios-Perez, Crystal Sorgini, Jessica Wedow, Patrick J. Brown, Lauren McIntyre, Elizabeth A. Ainsworth, and Andrew D.B. Leakey

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GENOTYPIC DIVERSITY IN YIELD AND GRAIN QUALITY RESPONSES TO ELEVATED OZONE OF DIVERSE INBRED AND HYBRID MAIZE

Oxidative stress from exposure to tropospheric ozone currently causes significant yield losses (~\$14 to \$26 billion) in the world's major crops. However, little is known about the genetic and genomic basis for yield loss to oxidative stress in any crop, but especially C4 crops like maize. The yield and grain quality of maize were compared under ambient and elevated ozone concentrations over two growing seasons at the FACE site in Champaign, IL. Ear mass was, on average, significantly lower in inbred (-7%) and hybrid (-9%) lines. But, some lines were sensitive to yield loss (up to -76% in inbreds and -26% in hybrids) while others were highly tolerant of growth at elevated O₃. Yield loss was primarily driven by decreased kernel number on inbreds versus decreased individual kernel mass in hybrids. Current analyses are evaluating kernel growth rate and grain-filling period to assess whether reduced photoassimilate supply or a shorter grain filling period causes yield loss.

5. Halie Rando

PhD student, Department of Animal Sciences, rando2@illinois.edu

ASSEMBLY OF THE RED FOX CHROMOSOMES

Through the Genome 10K Project, the genomes of vertebrate species are being sequenced and assembled at a previously unimaginable pace. Though this rapid advance has been made possible by Next-Generation Sequencing (NGS) technologies, genomes assembled using NGS are prone to certain limitations. The Red Fox genome is one such assembly for which a large number of scaffolds and a lack of chromosome information impeded the use of the genome in areas of ongoing research. A computational pipeline based around the program Reference Assisted Chromosome Assembly allowed for the construction of 42 fox chromosomal fragments from the 676,878 scaffolds. In addition to producing the large chromosomal fragments, this approach also provided a higher-resolution look at the chromosomal evolutionary history of the canids.

6. Miles Mesa

PhD student, Department of Animal Biology, jmmsa2@illinois.edu

PLANT TOLERANCE AND RESISTANCE: ALTERNATIVE DEFENSE RESPONSES TO HERBIVORY?

Plants have a variety of evolved mechanisms to cope with the negative effects of herbivory, including plant resistance, structural and chemical traits that reduce tissue damage and plant tolerance, the ability to compensate for tissue loss. It has been argued that resistance and tolerance represented two alternative and redundant strategies and therefore should be negatively correlated. However, plant resistance and tolerance appear to be controlled via the same molecular pathway, the Oxidative Pentose-Phosphate Pathway. Here, we take the first step in showing that the two strategies are positively correlated rather than negatively. Specifically, using HPLC, we measured glucosinolate levels following the removal of apical dominance (simulating natural herbivory) in two ecotypes of *Arabidopsis thaliana*: an undercompensator, Landsberg *erecta*, and an overcompensator, Columbia. Furthermore, utilizing RILs from a cross between Columbia and Landsberg *erecta* demonstrates a general positive relationship between resistance and fitness compensation.

7. Linnea Meier

PhD student, Department of Entomology, lrmeier2@illinois.edu

SPECIES-SPECIFIC BLENDS OF SHARED PHEROMONE COMPONENTS MINIMIZE INTERSPECIFIC ATTRACTION AMONG CERAMBYCID BEETLES IN THE SUBFAMILY LAMIINAE

Research over the last decade has revealed extensive pheromonal parsimony within the large beetle family Cerambycidae, with many species producing the same, or very similar aggregation-sex pheromones. Interspecific attraction may be minimized among species in the subfamily Cerambycinae by temporal segregation, or by minor pheromone components that strongly synergize attraction of conspecifics, or inhibit attraction of heterospecifics to the dominant

components. Less is known about pheromones of species in the largest subfamily, the Lamiinae. Adults of most lamiine species of eastern North America are nocturnally active during the summer, suggesting that they are less likely to be segregated temporally. Here, the identification of species-specific pheromone blends for three lamiine species with very similar activity periods supports the hypothesis that interspecific attraction is minimized by differences between species in pheromone composition.

8. Xander Hazel

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PALYNOLOGICAL ANALYSIS OF FRASS FROM ADULT LONG-HORNED BEETLES

This presentation analyzes the frequency of pollen feeding by adult long-horned beetles in the Cerambycinae subfamily (Coleoptera: Cerambycidae). Pollen was extracted from the frass, or egested waste, from 14 cerambycines collected in east central Illinois from 2013 to 2015. Several pollen types were present in the frass from 4 of the cerambycines used in this study. Almost all of the cerambycines that consumed pollen were among the first species to emerge as adults in the spring, which overlaps with the flowering periods of many trees. To date, there have been no previous reports of pollen feeding by 3 of the 4 species. This project is qualitative in its current form and ongoing. Further investigations will be conducted on intraspecific, phenological, and geographic variation of pollen feeding.

9. Todd M. Jones, Michael P. Ward, Thomas J. Benson, and Jeffrey D. Brawn

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NESTLING BODY CONDITION AND WING DEVELOPMENT PREDICT JUVENILE POST-FLEDGING SURVIVAL IN A NEOTROPICAL MIGRATORY SONGBIRD

Phenotypic traits acquired in one life history stage can carryover and affect survival in subsequent stages. For songbirds, trait carryover effects from the pre- to post-fledging period may be crucial for survival but are poorly understood. We assessed whether juvenile phenotypic traits at fledging carryover and influence survival during the post-fledging period in the Dickcissel (*Spiza americana*). We found pre- to post-fledging carryover effects of body condition and wing development at fledging, in which traits were positively associated with survival during the early part of the post-fledging period, but each effect was conditional on cause-specific mortality; body condition conferred a greater advantage in resisting mortality due to exposure while wing development was more beneficial for avoiding mortality due to predation. Our findings suggest that cause-specific mortality of fledglings may drive growth strategies of nestling birds, whereby nestlings prioritize growth of particular phenotypic traits in response to primary sources of post-fledging mortality.

10. Samniqueka Halsey and James R. Miller

PhD student, Program in Ecology, Evolution, and Conservation Biology, shals3@illinois.edu

A COMMUNITY MODELING APPROACH TO UNDERSTANDING THE ECOLOGY OF LYME DISEASE

In the past 40 years, numerous research has been conducted to understand the ecological mechanisms that have resulted in the emergence of Lyme disease. The causative agent of this zoonosis is the pathogen *Borrelia burgdorferi*, transmitted via the black-legged tick *Ixodes scapularis*. The tick has multiple hosts, some of which are reservoirs for *B. burgdorferi* resulting in pathogen transmission. Due to the complexity of this system, much is still unknown. My approach involves using a community modeling approach using an individual-based modeling (IBM) framework to understand tick-host-pathogen dynamics. The first step is to duplicate the interactions between *I. scapularis*, its hosts and the environment in the model. In doing so, this model will simulate tick phenology and tick density both on and off-host that is comparable to real-world data. Future modeling efforts have the potential to identify the significant components involved in the invasion of the tick and establishment of the pathogen.

11. Rachel Moran

PhD candidate, Program in Ecology, Evolution, and Conservation Biology, rmoran9@illinois.edu

RAPID EVOLUTION OF MALE-DRIVEN BEHAVIORAL ISOLATION AMONG ALLOPATRIC SPECIES IN A DICHROMATIC FISH CLADE

Most studies of speciation via sexual selection have focused on divergent female mating preferences leading to male trait diversification. However, recent research has indicated that male mate choice and male competition can also cause behavioral isolation and speciation. We examined behavioral isolation among four recently diverged allopatric darter species in the orangethroat clade (*Etheostoma:Ceasia*) that vary in male coloration and genetic sequence. We asked (1) what are the relative contributions of female and male behavior to behavioral isolation, and (2) does color distance (i.e. selection) or genetic distance (i.e. genetic drift) best predict isolation between species? We conducted free spawning behavioral assays to measure behavioral isolation between species. Color distance between species was determined using digital photography and color analyzing software. We used RAD-Seq to generate genome-wide estimates of F_{ST} among species. Results indicate that male mate choice and male competition are important in driving behavioral isolation and male trait diversification.

12. Kai Zhao, Yasuko Ishida, Nicholas Georgiadis, and Alfred L. Roca

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A WEB APPLICATION FOR IDENTIFYING THE PROVENANCE OF AFRICAN ELEPHANT IVORY SAMPLES USING MITOCHONDRIAL DNA

Molecular markers can trace the provenance of wildlife products by comparing their genotypes to those of voucher specimens of known geographic origin. Among African elephants, only males disperse from their natal core social group or “herd”. Since female elephants do not

typically migrate between herds, mitochondrial DNA (mtDNA) haplotypes are quite limited in their geographic extent. We developed a web-based tool that identifies the provenance of elephants using mitochondrial sequences as input. The tool compares the input sequence to a curated database of mitochondrial sequences from elephants of known origin. The method relies on a global sequence alignment and comparison to segregating sites in known haplotypes. Regions where haplotypes identical or similar to the input sequence are shown using Google Maps. The software may facilitate identification of the geographic origins of seized ivory, enabling law enforcement to target poaching “hot spots”.

13. Daniel Urban

PhD candidate, Department of Animal Biology, djurban2@illinois.edu

AN EARFUL OF JAW, THEN AND NOW: INSIGHTS FROM EVOLUTIONARY DEVELOPMENTAL BIOLOGY

During synapsid evolution, postdentary elements in the reptilian jaw transitioned into the middle ear of mammals. Though this astounding change is well documented in the fossil record, questions regarding the developmental sequence that drove the ossicular transition still remain. At birth, modern marsupials possess a reptilian jaw joint with functional articulation between the articular and quadrate. These elements will later become the malleus and incus of the middle ear. This entire transition occurs postnatally, and represents a natural system for comparison with the fossil record. We utilized extant marsupials and traced the development of ossicular structures as they separate from the jaw and fully incorporate into the middle ear. Micro-CT scans taken throughout development and three-dimensional reconstructions compared marsupial developmental stages with the known fossil record of early mammals. Additional analyses employed immunohistochemistry, tissue laser capture and RNA sequencing to determine the cellular and molecular basis of middle ear separation.

14. Andrew D. Sweet and Kevin P. Johnson

PhD candidate, Program in Ecology, Evolution, and Conservation Biology, adsweet2@illinois.edu

COPHYLOGENETIC PATTERNS BETWEEN SMALL NEW WORLD GROUND-DOVES AND THEIR PARASITIC WING LICE (PHTHIRAPTERA: *COLUMBICOLA*)

Due to their high level of host specificity, parasitic lice of pigeons and doves (Aves: Columbidae) are an excellent system for understanding patterns of host-parasite coevolution. Additionally, doves harbor two types of lice, wing lice and body lice, which can act as “ecological replicates.” Past work has indicated that the two lineages of lice have different cophylogenetic patterns with their hosts. In this study, we targeted the parasitic wing lice (Pthiraptera: *Columbicola*) of small New World ground-doves, a monophyletic clade within Columbidae. Using molecular data, we inferred a phylogenetic tree for the dove lice and compared our results to the host phylogeny to test for patterns of cospeciation. Our cophylogenetic analyses indicated some cospeciation, but the two phylogenies were not overwhelmingly congruent. However, host biogeography can perhaps explain patterns of diversification in the wing louse phylogeny. These results provide valuable insight into factors contributing to host-parasite diversification patterns.

15. Henry S. Pollock, Jeffrey D. Brawn, and Zachary A. Cheviron

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**SEASONAL FLEXIBILITY IN AVIAN THERMONEUTRAL ZONE BREADTH ACROSS
LATITUDE: IMPLICATIONS FOR CLIMATE CHANGE**

Phenotypic flexibility, or the ability to make reversible phenotypic adjustments to varying environmental conditions, is essential for organisms to cope with environmental change. An emerging framework for understanding variation in phenotypic flexibility is the Climate Variability Hypothesis (CVH), which predicts that flexibility should increase with climatic variability. We used flow-through respirometry to measure seasonal variation in thermoneutral zone (TNZ) breadth in suites of temperate-zone and tropical bird species to test whether seasonal flexibility in TNZ breadth increases with latitude as predicted by the CVH. We found that both tropical and temperate-zone species exhibited seasonal variation in TNZ breadth, but that the magnitude of flexibility was greater in temperate-zone species, supporting the CVH and suggesting that tropical birds may have reduced ability to cope with environmental change compared to temperate-zone counterparts.

16. Elizabeth K. Mallott, Paul A. Garber, and Ripan S. Malhi

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**DIETARY CORRELATES OF GUT MICROBE COMPOSITION IN WHITE-FACED
CAPUCHINS (*CEBUS CAPUCINUS*)**

This study examines the response of white-faced capuchin gut microbial community structure and function to changes in food availability and diet. A group of wild white-faced capuchins was followed for 12 months. Information on behavior and diet were collected, and food availability was assessed at 2-week intervals. The v3-v5 region of 16S rRNA was amplified from 170 fecal samples and sequenced on the Illumina MiSeq platform. White-faced capuchin gut bacterial communities were characterized primarily by Firmicutes (41.6%) and Proteobacteria (39.2%). There was a significant effect of fruit availability on gut microbe community composition; however, there was no significant effect of invertebrate availability. Several plant and invertebrate taxa were significantly correlated with the number of operational taxonomic units assigned to predicted metabolic functions. These results increase our understanding of how primate gut microbiomes are related to diet composition and may buffer seasonal differences in food availability.

17. Beryl M. Jones, Callum J. Kingwell, William T. Wcislo, and Gene E. Robinson

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MOLECULAR DETERMINANTS OF BEHAVIORAL PLASTICITY IN A FACULTATIVELY
EUSOCIAL BEE, *MEGALOPTA GENALIS*

One remarkable feature of eusociality is reproductive division of labor. A single genotype can generate both queens and workers, and this striking phenotypic plasticity is regulated by environmental influences during development. While mechanisms of queen-worker differentiation in highly eusocial insects are well understood, we know less about the origins of castes. Bees exhibit rich social diversity and several origins of eusociality, providing opportunities to utilize genomic approaches for evolutionary analyses. Some bees, including *Megalopta genalis*, are facultatively eusocial and may represent transition points in eusocial evolution. Here, we present differences in brain and abdominal gene expression associated with caste and shifts in reproductive behavior of *M. genalis*. We report on genes putatively involved in the regulation of foraging, reproduction, and social interactions. We compare our findings to those from other eusocial lineages to discover possible overlap in the mechanisms underlying reproductive division of labor across independent evolutionary origins of eusociality.

18. Jessica R. Brandt, Peter J. Van Coeverden de Groot, Oliver A. Ryder, and Alfred L. Roca

PhD candidate, Department of Animal Sciences, jrbrandt@illinois.edu

GENETIC ANALYSIS OF SUMATRAN RHINOCEROS (*DICERORHINUS SUMATRENSIS*)
SPECIMENS REVEALS PATTERN OF STRUCTURING AND REDUCED DIVERSITY IN
MODERN POPULATION

The Sumatran rhinoceros (*Dicerorhinus sumatrensis*), once widespread across Southeast Asia, now consists of ca. 100 individuals in three isolated populations on the island of Sumatra. Here we use mitochondrial DNA from modern (N = 16) and museum (N = 25) samples to assess genetic diversity and structure. A total of seventeen mitochondrial control region haplotypes, forming geographic clusters, were identified. The cluster containing all individuals known to originate from Sumatra was comprised of 10 haplotypes. Haplotype diversity within this cluster was higher in the museum specimens ($H = 0.88$) than in the modern samples ($H = 0.63$); thus suggesting a potential loss of diversity over time. Microsatellite data from the modern samples showed the presence of structuring within the current Sumatran population. This study provides information essential to the conservation of the remaining populations of Sumatran rhinos.

19. John W. Crawford, Matthew Schrader, Spencer R. Hall, and Carla E. Cáceres

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INTRASPECIFIC VARIATION IN SENSITIVITY TO RESOURCE QUALITY IN *DAPHNIA PULICARIA*

Populations maintain a high degree of genetic diversity in many ecologically important traits including the acquisition and allocation of resources. Growth on available resources is a physiological response to changing food quality in which highly sensitive individuals grow well on rich-quality resources and poorly on poor-quality resources. This is contrasted with low sensitivity individuals who are able to maintain growth in both resource quality environments. Using the keystone zooplankton *Daphnia pulicaria* from 6 populations, we tested numerous genotypes for sensitivity to resource quality. We found high amounts of variation in sensitivity to resource quality. Mean sensitivity is higher in the spring when resource quality is richer. Population mean sensitivity declined in the summer when resource quality also declined. We also found that whether a population persists year round or not also results in significantly different mean sensitivity to resource quality.

20. Mary Rogers

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CYP19A1 METHYLATION AND TIMING OF MENARCHE IN A RURAL POLISH POPULATION

Human reproductive ecology research has long examined the adaptive flexibility of reproduction in the face of variable environments. The timing of women's first menstruation, menarche, is variable between and within populations. Energetic stressors during childhood are correlated with variation in menarcheal age, yet few studies draw mechanistic connections between the two. Epigenetics, the study of covalent modifications of DNA, is one way by which the environment interacts with the genome. I investigate the relationship between farming in childhood (a measure of childhood energetics), methylation of a reproductive-related gene CYP19A1, and menarcheal age. Participants (N=50) included women of reproductive age in rural Poland. Women who farmed during childhood and had the highest degree of CYP19A1 promoter methylation also had the latest ages at menarche ($p=0.0015$, $R^2 = 0.28$). This mechanistically-grounded relationship suggests that there are long-term epigenetic effects of early life stressors that correlate with menarcheal timing.

Abstracts for Poster Presentations

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GRASSLAND BIRD COMMUNITY RESPONSE TO AN INVASIVE GRASS AND MANAGEMENT USING HERBICIDE

Grasslands are threatened by exotic grass invasion, but despite the salience for conservation, the impact of invasive grasses on songbirds is seldom explored. Nevertheless, because invasive plants often have detrimental economic impacts, invasive management is often implemented without testing wildlife response. I therefore studied the response of the grassland birds to invasive grass tall fescue (*Schedonorus phoenix*) in the context of a removal experiment using herbicide. My objectives were to determine (1) how fescue impacted the bird community over nine years and (2) how fescue removal using herbicide impacted the bird community one-year post spray. We found that herbicide significantly decreases fescue cover when compared to controls. However, avian response to herbicide is mixed. Dickcissels (*Spiza americana*) increased in response to herbicide, while grasshopper sparrows (*Ammodramus savannarum*) decreased ($p < 0.05$). This indicates that in the short term, herbicide application may reduce the density of some grassland birds and benefit others.

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COMPARATIVE FUNCTIONAL MORPHOLOGY AND KINEMATICS OF MINIATURE TRAP-JAW ANT (*STRUMIGENYS* SPP.) MANDIBLE STRIKES

High-speed appendages for prey capture or defense are common in nature. In ants, power-amplified trap-jaws have evolved independently at least four times, yet only one radiation of trap-jaw ants has been studied in detail. We examined morphology and kinematics of miniature trap-jaw ants (genus *Strumigenys*). Mandible shape and size vary greatly within this genus, and it remains unclear which species have power-amplified trap-jaws and which do not. We measured the kinematics of *S. eggersi* and *S. louisiana* mandible strikes using high-speed videography, and investigated the muscle morphology of various *Strumigenys* species using microCT. We found that *S. eggersi* and *S. louisiana* have snaps that occur an order of magnitude quicker than other trap-jaw ants. Maximum radial velocity for *S. eggersi* and *S. louisiana* was 69 m/s and 64 m/s, respectively. Both muscle morphology and labrum position show predictive potential for future studies aimed at predicting kinematics from morphology alone.

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THE IMPORTANCE OF WOOD NUTRIENT STORAGE IN TROPICAL FOREST NUTRIENT CYCLES: INSIGHTS FROM A SAPLING DEFOLIATION EXPERIMENT IN PANAMA

The availability of soil nutrients limits productivity and influences tree species distribution in tropical forests. Given the scarcity of soil resources, trees in tropical forests should be under selection to store nutrients for periods when nutrient demand exceeds supply. However, little is known about the capacity of trees to remobilize nutrients from long-lived woody biomass in tropical forests. We evaluated nitrogen (N) and phosphorus (P) remobilization from woody biomass via experimental defoliation of saplings from four widely distributed genera of tropical trees in Panama. In three of four genera studied, wood P concentrations declined after refoliation at both elevations, and the proportion of wood P remobilized was greater on low fertility compared to high fertility sites. In contrast, significant N remobilization was restricted to the low fertility montane site. These findings provide evidence that a significant fraction of N and P in woody biomass is can be remobilized in response to asymmetry in nutrient supply and demand.

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DENSITY DEPENDENT EFFECTS ON CONSPECIFIC CUE USE FOR HABITAT SELECTION AND REPRODUCTIVE SUCCESS IN YELLOW WARBLERS (*SETOPHAGA PETECHIA*)

Theoretical models of habitat selection are closely tied to negative density dependence. However, conspecific attraction, where animals settle near members of their species when selecting habitat is common among songbirds and could lead to positive density-dependent effects that outweigh the negative. Using playback experiments, we investigated if the Yellow Warbler (*Setophaga petechia*), a territorial songbird, experience negative density dependent effects on habitat selection in response to conspecific cues. Preliminary data from our research show that when experimental playbacks manipulate conspecific density to be high, Yellow Warblers treat the habitat as low quality by establishing larger territories, a pattern that commonly occurs in birds when actual habitat quality is low (e.g., less food or vegetation cover). Despite this negative density dependent effect, Yellow Warblers still cluster closer to high-density playbacks compared to low-density playbacks and silent controls. We conclude that apparent conspecific density from conspecific cues influences habitat selection process.

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TIMESCALE SEPARATION AND FUNCTIONAL RESPONSE IN CONSUMER-RESOURCE DYNAMICS

Given the large number of variables and inherent complexity of biological systems, even deciding the correct functional form presents a challenge in modeling. Many standard biological models assume that growth and interaction rates only affect the amplitude of parameters. We show how large differences in the timescales of dynamics between different species or abiotic variables may change the functional form of the effective model describing such species. We begin to determine what functional forms may result from Lotka-Volterra interactions with timescale separation and abiotic resources. Such variations present a possible answer to questions about the emergence of stability in functional forms that would at first glance appear unstable. Ultimately, we aim to show how complicated functional forms could emerge from simpler models, replacing the qualitative “which model” decision with a more quantitative and automated scale comparison.

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THERMAL CHALLENGES OF OVERWINTERING EASTERN BOX TURTLES (*TERRAPENE C. CAROLINA*) IN EASTERN ILLINOIS

Ectotherms must evolve to withstand the many challenges presented by winter in temperate ecosystems. The Eastern Box Turtle (*Terrapene c. carolina*) combats sub-zero temperatures by mobilizing glucose in the bloodstream. To determine the extent to which Eastern Box Turtles tolerate freezing in the wild, we collected temperature data adjacent to 24 over-wintering box turtles from November 2009 to April 2010 in Vermillion County, Illinois. We placed temperature probes in substrate near each individual brumating turtle at the depth of each form and removed them after the turtles had emerged. Twenty-three turtles survived the winter and one was lost due to transmitter failure. Seven turtles were exposed to below-freezing temperatures for several days, and two experienced multiple freezing episodes.

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THE POST-GLACIAL SPECIES VELOCITY OF *PICEA GLAUCA* FOLLOWING THE LAST GLACIAL MAXIMUM IN ALASKA.

Anthropogenic climate change is leading to dramatic fluctuations to Earth’s biodiversity that has not been observed since past interglacial periods. The paleorecord provides information on past species distributions in relation to climate change, which can illuminate the patterns of potential future distributions of species. In this study, we assessed the change in the distributions of white spruce (*Picea glauca*) from the Last Glacial Maxima (LGM) to present-day

for the entire state of Alaska. To accomplish this, we created species distribution models (SDMs) calibrated from modern vegetation data and high-resolution, downscaled climate surfaces at 60m. These SDMs were applied to downscaled modern and paleoclimate surfaces to produce estimated ranges of white spruce during the LGM and today. Our results indicate the importance of topographic complexity in buffering the effects of climate change, particularly near the edges of the species' range.

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A SYSTEMATIC REVIEW OF THE IMPACTS OF INVASIVE PLANTS ON AVIAN ECOLOGY

Understanding how invasive plants impact wildlife is a crucial conservation need. Birds may be particularly responsive to invasion because they use vegetation cues to select habitat, and vegetation affects food and predation. We reviewed 122 studies assessing the impacts of invasive plants on birds. Although pluralities of studies suggest that invasive plants do not affect avian abundance and nest survival, many studies report significant effects. Abundance of individual bird species decreased in 17.5% of tests and increased in 16.7%. Richness responded directionally, decreasing in 29.5% of tests and conditionally decreasing in 22.7%. Birds preferred to nest in invasive substrates in 54.2% of cases. However, equal numbers of tests showed positive and negative impacts on nest survival—13.6%. Overall, impacts of invasive plants are non-uniform, and invasive plants influence some factors more strongly than others. We advocate for more mechanistic work to improve the foundation for conservation in an invaded world.

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THE EVOLUTION AND PHYLOGEOGRAPHY OF AFRICAN ELEPHANT MITOCHONDRIAL GENOMES

Mitochondrial genomes are inherited maternally and ideal for examining the evolutionary history, ancient migrations, and ancient hybridization patterns of African elephants. However, because only male elephants disperse, and females remain with their natal herd, mitochondrial DNA (mtDNA) is a poor marker of population structure or species boundaries. Savanna and forest elephants comprise two distinct species. Sequences of 4kb of mtDNA from 653 elephants have been used to divide African elephant mitogenomes into eight distinct subclades, with more than 100 distinct haplotypes identified. Almost all subclades and haplotypes have a limited geographic distribution due to limited female dispersal. Mitochondrial genomes of African elephants, mammoths, and Asian elephants have been used to calculate that the divergence date between the forest and savanna elephant was in the Late Miocene. We will sequence additional mitogenomes for further insights into the evolutionary history of African elephants.

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EFFECTS OF PRAIRIE MANAGEMENT ON SOIL CHARACTERISTICS AND BEES

This research involves four prairie management types: burning, haying, and patch burn grazing (new/old). These management types have the potential to affect certain soil characteristics such as bulk density, pH, and soil type. Our goal was to determine whether these management types affected these soil characteristics between each management type and between top and bottom soils within each type. This study was a part of a larger project which also examined whether prairie management affected bee abundance in these areas. We found significant differences between management types and between top and bottom soils within each type in terms of both bulk density and pH. Despite the fact that 80% of bee species nest in the soil, this topic is under-researched. Although our results regarding bee abundance in prairies employing these management types were not significant, they may provide insight into certain trends for these ground-nesting bees.

Sample Evaluation Form for Oral Presentations

Presenter: _____

****This form will be returned to the student presenter after judging. Please make your comments as constructive and supportive as possible.****

Presentations are to be judged in six categories. Each category should be evaluated as on a 5 pt scale where a 5 is excellent and a 1 is poor.

Evaluation of presentation

Significance and broad context..... _____
Defined research question/hypothesis..... _____
Quality of methodology _____
Results clearly described..... _____
Validity of conclusions drawn from results..... _____
Presentation (poise, clarity, coherence, competence with A/V)..... _____

TOTAL SCORE: _____

Comments on scientific content (effectiveness of putting project in general theoretical framework, creativity of ideas, focused research question, quality of methodology, validity of conclusions etc.).

Comments on presentation style (effectiveness at communicating ideas, poise, clarity, competence with A/V, creativity, etc.)

Judge's estimate of own ability to evaluate talk. High _____ Medium _____ Low _____

Symposium presentations will be held in B102, Chemical and Life Sciences Laboratories at 602 S. Goodwin, indicated by the black oval below. The reception will be held on the bottom floor of IGB in the Concourse Café Space (i.e. Array Café) indicated by a star below. Entrance to the Café Space will be through the gatehouse outside of the IGB (marked with a star on the map below). Once inside the gatehouse, proceed downstairs and the reception will be straight ahead.

