

Talks – Session 1

Behavioral Ecology I (314A)

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| 10:30 | <p>Nocturnal folivores in the rainforest: might feeding at night have nutritive benefits?</p> <p>*Luke Zehr, Brian E. Sedio, May R. Berenbaum</p> <p>The chemically-mediated interplay between insect herbivores and their hostplants is a ubiquitous ecological pattern. Herbivores have multiple mechanisms for coping with deleterious plant compounds, from genetically encoded detoxification to selective feeding behavior. Behavioral adaptations of herbivores that serve to minimize exposure to or otherwise circumvent distasteful and harmful plant secondary metabolites may reduce the demand on costly biochemical detoxification pathways. I propose that feeding primarily or entirely at night, which I suggest may be a general pattern of most folivorous insects in the Neotropics, could serve to limit exposure to the harmful effects of some plant secondary metabolites. For several species of understory shrubs, I show that leaf area removal is significantly greater during the night. Additionally, for these same plant species, I provide evidence that the suite of putative defense compounds present in the leaves differs between the day and the night. If some plant defenses are less effective at night, nocturnal feeding rhythms of herbivores may have nutritive and performance advantages.</p> |
| 10:45 | <p>Modeling the sequential behaviors of simultaneous predator and prey patch use</p> <p>*Patrick W. Cain, William A. Mitchell</p> <p>Foragers tend to distribute themselves among habitat patches that provide the highest rates of return, given the presence of frequency-dependent competition and an absence of predation risk. This ideal free distribution, however, is highly susceptible to influence by predation risk. Models used to investigate predator-prey games often fix the behavior of one player while allowing the other to make patch use choices. Here, we use an adaptive dynamic approach to model changes in behavioral rates of a predator and prey, while explicitly allowing both prey and predators to make decisions simultaneously. Our model focuses on a two-patch situation. The prey is in one patch and can move between the open, which allows for energy intake but also predation risk, or a refuge with no possibility of energy intake or exposure to predation risk. The predator is able to move between that patch, where it can attack prey if in the open, and a patch containing a fixed return rate. An initial result from our model show that predators will quickly leave a patch after attacking a prey that escapes to a refuge, and the prey will spend little time in the refuge before moving back to the open.</p> |
| 11:00 | <p>Exploring the role of predation and sexual selection in a polymorphic species</p> <p>*Lynette Strickland, Don Windsor, Carla Caceres</p> <p>There are multiple ecological and environmental factors that come into play when investigating the presence of phenotypic variation within populations. Two of these</p> |

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| | <p>driving ecological factors are sexual selection and predation, both of which have been studied in a broad range of systems from different environments. Studying the role of sexual selection and predation is particularly relevant in polymorphic species where individuals of differing phenotypes co-occur and mate over an extended geographic range. Here, I investigate the role of sexual selection on color variation in a polymorphic Panamanian tortoise beetle, <i>Chelymorpha alternans</i>. This species displays four color polymorphisms differing strongly in head and wing coloration which have been shown to follow Mendelian inheritance. Using four invertebrate predators I observe whether phenotypes experience differential predation and/or if they elicit learned avoidance behaviors in predators. Additionally, I examine mate preference among color phenotypes using mating trials and the known mode of inheritance for color pattern in this species among progeny. These studies suggest that mating in this species is random and that predation may influence the presence of color variation within Panamanian populations of <i>C. alternans</i>.</p> |
| <p>11:15</p> | <p>Personality types in a genetically determined polymorphic species, the white-throated sparrow</p> <p>*Margarida Barcelo Serra, R.A. Gonser, E.M. Tuttle</p> <p>White-throated sparrows (<i>Zonotrichia albicollis</i>) are a polymorphic species exhibiting two morphologies (tan and white) that differ in plumage coloration, behavior, physiology and genetics. Morph is determined by the presence of alternate supergene alleles located on a rearrangement of chromosome two. Tan birds are homozygous for the ZAL2 supergene allele (i.e. ZAL2/ZAL2), whereas white birds are heterozygous for both supergene alleles (i.e. ZAL2m/ZAL2). During the breeding season white birds are found to be more aggressive and sing at higher rates than tan birds. Our research during the winter has demonstrated differences in response towards a novel object between morphs with white birds being more neophobic (less bold) than tan birds. These findings contradict the basic statement of animal personality, boldness should be correlated with aggression, and therefore less bold individuals should also be less aggressive. In this study we used a breeding population of white-throated sparrows to examine personality differences between morphs. We assessed aggression towards conspecifics, boldness towards a novel object and boldness towards a predator. Examining behavioral consistencies between genetic morphs of the white-throated sparrow across seasons will greatly expand our understanding of the evolutionary basis of animal personality.</p> |
| <p>11:30</p> | <p>The primacy effects of seasonal shifts on the foraging behavior of wild-caught woodland deer mice (<i>Peromyscus maniculatus gracilis</i>)</p> <p>*Dominic J. Acri, Michael J. Cramer</p> <p>This study explores the immediate shifts in foraging behavior of woodland deer mice (<i>Peromyscus maniculatus gracilis</i>) caused by sudden onset of fall weather. The immediate effects of a shift in seasonality include a significantly delayed onset of nocturnal activity, but do not include a shift in offset of nocturnal activity. A study on deer mice has shown the species-specific feeding preferences (Cramer 2014); our study found that such preferences are altered after experimental seasonal shifts. Under the stress of a shift in seasonality, <i>P. m. gracilis</i> show an increased preference for <i>Acer saccharum</i> seeds. Further analysis of foraging behavior, through an index which calculates the probability that uneaten seeds were handled,</p> |

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| | <p>suggests that <i>P. m. gracilis</i> are more likely to handle <i>A. saccharum</i> seeds under fall conditions. The shift in foraging behavior caused by the primacy effects of seasonal shifts supports the hypothesis that these foraging behaviors have an underlying seasonal rhythm.</p> |
| 11:45 | <p>Opposite effects of nonapeptide antagonists on paternal behavior in the teleost fish <i>Amphiprion ocellaris</i></p> <p>*Ross DeAngelis, Joseph Gogola, Logan Dodd, Justin Rhodes</p> <p>The nonapeptides isotocin (IT) and arginine vasotocin (AVT), along with their mammalian homologs oxytocin and arginine vasopressin, are well known regulators of social behaviors across vertebrate taxa. However, little is known about their involvement in paternal care. Here, we measured the effect of an IT and an AVT V1a receptor antagonist on paternal behaviors in the primarily paternal teleost <i>Amphiprion ocellaris</i>. We also measured effect of the IT receptor antagonist on aggression in dyadic contests between two non-reproductive fish to assess specificity of the effect on paternal behaviors. Individual differences in levels of paternal behaviors (nips, fanning the eggs, and proportion of the time in the nest) were consistent across spawning cycles when no treatments were administered. The IT receptor antagonist severely reduced paternal behaviors but had no effect on aggression, whereas the AVT V1a receptor antagonist increased paternal behaviors. These results support the idea that IT signaling is crucial for the expression of paternal behavior. Based on a previous study showing that the AVT V1a antagonist decreases aggression in dyadic contests, we hypothesize that the antagonist enhances paternal behavior indirectly by reducing vigilance and aggression, thereby alleviating effort directed towards other competing behaviors and allowing for the increased paternal behaviors.</p> |

Population & Community Ecology I (314B)

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| 10:30 | <p>Preliminary study of seasonal variation in morphological features of the small hive beetle, <i>Aethina tumida</i> Murray (Coleoptera: Nitidulidae)</p> <p>*William Montag</p> <p>The small hive beetle is a widespread exotic secondary pest of honey bees. In the past two decades, its distribution has expanded from its native sub-Saharan range to several new areas, including the temperate zone. I collected specimens during the summer and fall periods from UIUC hives to determine if seasonal morphological variation is present and if it differs between the sexes. Specimens were collected from hives maintained by the UIUC Bee Research Lab. I measured body length along the midline and body width at the rear edge of the pronotum. Unequal variance T-tests displayed a significant seasonal difference in our length and width measurements for female specimens only. Based on previous studies of small hive beetle longevity displaying greater female longevity, and overwintering studies showing increased overwintering capacity for larger beetles in the family Tenebrionidae, I expect future research into the seasonal patterns of small hive beetles to show increased female persistence in overwintering populations over males.</p> |
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| <p>10:45</p> | <p>Evaluation of Two Common Sugar Substitutes as Potential Pesticides Against the House Fly (<i>Musca domestica</i>)</p> <p>*Edwin R. Burgess IV, B. H. King</p> <p>The non-nutritive sugar alcohols erythritol and xylitol were assessed for their potential as insecticides against adults of the house fly <i>Musca domestica</i> L. (Diptera: Muscidae). Sugar is the common vehicle used to encourage house flies to eat insecticidal granular baits. Solutions of each sugar significantly decreased fly survival at ten and twenty days relative to a sucrose control; flies survived nearly twice as long with sucrose as with either non-nutritive sugar. When maintained on non-nutritive sugars, 50% of flies died in as few as 2 days. To confirm toxicity versus starvation as the insecticidal mode, a concentration response was done. Significant reduction in survival as concentration increased was observed in xylitol only. Finally, to determine if both non-nutritive sugars have acute toxic properties, flies were fed one of the two non-nutritive sugars for 24 h and then maintained on sucrose for 19 more days. As much as a 75% reduction in survival was observed by day 20. These results suggest that non-nutritive sugars possess insecticidal properties when house flies feed on them. Further testing would be worthwhile against other filth flies and how to deploy these sugars for pest control.</p> |
| <p>11:00</p> | <p>An experimental approach to understanding the impact of a size-structured top predator on trophic cascades</p> <p>*Robin Baker, Cy Mott, Coty Fields, Katelyn May, Howard Whiteman</p> <p>Trophic cascades are ubiquitous in natural systems and have widespread implications for natural resource management, conservation biology, and agriculture. Classic understanding of ecosystem dynamics, including trophic cascades, rarely incorporates variation at a finer scale than species. Investigating the influences of interspecific variation can further our understanding of these complex ecological interactions. In this project, we explore the impacts of body size variation in a top predator population on an aquatic ecosystem using mole salamanders (<i>Ambystoma talpoideum</i>) as a model species. We hypothesized that ecosystems which contained <i>A. talpoideum</i> populations with greater variation of body sizes would exhibit weaker trophic cascades due to cannibalism and more diffuse predation pressure. To test these questions, we constructed 54 artificial, identical pond ecosystems, or mesocosms, which were populated with one of three salamander size-structure treatments. We monitored changes in the ecosystems through a suite of abiotic and biotic parameters over a period of six months. Preliminary results show that there may be an effect of salamander presence on primary production. Further analyses on zooplankton and invertebrate community populations are currently in progress to confirm the presence of a trophic cascade and understand the impact of size variation on the strength of any cascades present.</p> |
| <p>11:15</p> | <p>Reproductive Trade-Offs in a Mast Seeding Species</p> <p>*Abigail C. Leeper, Jalene M. LaMontagne</p> <p>Individuals have limited resources, typically leading to trade-offs in the size and number of offspring produced. However, evolutionary pressures may alter this relationship. For instance, many perennial plant species exhibit a reproductive</p> |

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| | <p>pattern known as mast seeding (the synchronous but highly temporally sporadic production of large seed crops). During mast seeding events, individuals produce very large seed crops and it is hypothesized to be a result of increased pollination efficiency, whereby there is expected to be higher reproductive success during mast conditions. Thus during a mast event, this trade-off may not exist. Using white spruce (<i>Picea glauca</i>) as a focal species, we investigated the relationship between mast seeding and the offspring size and number trade-off. Between 2012 and 2016, ~40 cones were collected from 38 trees at a field site in northern Michigan. We found that the relationship between cone length (hence seed number) and the total number of cones produced varied across years. Understanding this relationship can provide insight into the phenomenon of mast seeding influences life-history traits for reproduction.</p> |
| <p>11:30</p> | <p>Effectiveness of Boat Electrofishing Settings Within a Large Mesotrophic Reservoir</p> <p>*Bradley Hartman, Timothy Spier</p> <p>Globally, aquatic ecosystems are negatively affected by a variety of mechanisms including habitat destruction, fish overharvesting, climate change, and the introduction of invasive species. Long term monitoring of entire fish communities, including abiotic and biotic factors, is crucial in establishing effective management strategies. While there are existing fish community monitoring programs across the United States, a long term monitoring program that includes non-game and non-commercial fish community dynamics has not been established within Kentucky Lake in Western Kentucky. The purpose of this research is two-fold: To determine which boat electroshocking settings provide the highest catch per unit effort and species diversity and the widest range of total lengths, and to develop a standardized fish community sampling protocol using the most effective boat electroshocking settings. Four centrally located embayments within Kentucky Lake were sampled and within each embayment, 6 separate electrofishing samples were obtained from randomly chosen 500-meter shoreline segments. Each sample utilized 1 of 6 different randomly selected electroshocking wave forms. Concurrently with Hancock Biological Station's water quality/plankton surveys, this sampling protocol will be used for a long-term fish monitoring program that will track catch per unit effort, body condition, and species diversity of fish communities within Kentucky Lake.</p> |
| <p>11:45</p> | <p>How do resource use and the resource spectrum determine the structure of competitive communities?</p> <p>*Ravi Ranjan, Christopher Klausmeier</p> <p>Community assembly is determined by two processes, interspecific competition and environmental filtering, which are assumed to result in contrasting trait distributions. Interspecific competition is thought to result in over-dispersion of traits due to competitive exclusion of similar species, while environmental filtering is assumed to result in clustered trait distributions. Here, we examine these assumptions by modeling a community of competing species with a trait-based Lotka Volterra model. We assume that carrying capacity and competition strength (modeled as a competition kernel) are functions of the species' trait. We examine two carrying capacity functions (unimodal and bimodal) to mimic two different environments. We also vary the width of the competition kernel relative to the width of the carrying</p> |

capacity function. We focus on the long-term outcome by numerically solving for un-invasible communities (evolutionary stable state [ESS]). We found that as the width of the competition kernel decreases, the number of coexisting species increases. We also found that trait distributions are generated by an interplay between competition and environmental filtering. Particularly, extremely local competition can result in evenly spaced traits even with environmental filtering. Thus, future empirical work needs to consider the role of localization of competition while making inferences from trait distributions.

Conservation Biology & Invasion Ecology I (407)

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| <p>10:30</p> | <p>Effects of habitat variation and functional groups on local extinction rates</p> <p>*Meredith Zettlemoyer, Jennifer Lau</p> <p>Anthropogenic disturbance and land alteration driven by urbanization and agriculture produce high local extinction rates and are a primary cause of decreasing biological diversity. Examination of a large sample of species can reveal the traits that influence the distribution of taxa across habitats and inform their vulnerability to local extinction. I use historical data from Kalamazoo County, MI, to investigate habitat-specific patterns of plant diversity decline and examine what functional groups may be most at risk of local extinction. Certain habitats, namely prairies and wetlands, experience high rates of extinction. This result suggests that management should focus on spatially differentiated patterns of diversity loss. Extinction also varies across families, suggesting that evolutionary history and traits may influence extinction. To investigate this, we examined extinction rates for several functional groups, and found that native species, forbs, and species with limited niches or at the edge of their range are more vulnerable to local extinction. This nonrandom pattern of extinction reflects the idea that certain species attributes are beneficial or detrimental in the face of anthropogenic change. Understanding spatial and taxonomic patterns of local extinctions will aid in identification of species and habitats most in need of conservation attention.</p> |
| <p>10:45</p> | <p>Distribution, Abundance, and Pattern of Wavyleaf Basketgrass Invasion</p> <p>*Anna K. M. Bowen, M. H. H. Stevens</p> <p>One of the largest threats to natural communities and ecosystem processes is the spread of exotic species. <i>Oplismenus undulatifolius</i> (Ard.) Roem. & Schult (wavyleaf basketgrass) (WBG) is a relatively new invasive grass species that was introduced to the United States in 1996 near Baltimore, Maryland. Although many organizations have observed the large mats that this species forms in the understories of forests in Maryland and Virginia, it is unclear if this species is a significant threat to eastern deciduous forests. The objective of this study was to describe the distribution, abundance, and pattern of WBG invasion in Shenandoah National Park. We did a stratified survey with 160 transects throughout the park and collected patch metrics as well as abiotic and biotic information in each patch that we encountered. We identified 227 patches of WBG, all of which were unknown to the park staff, but were all nearby previously identified patches. Patches were found on a variety of sites, but most were in low elevation areas with basaltic parent rock. Patch size, WBG stem density, and cover were generally low,</p> |

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| | <p>and we found evidence that suggests that WBG is inhibiting the growth or establishment of forbs and tree seedlings.</p> |
| <p>11:00</p> | <p>Using genetics and life history knowledge to design effective sampling for ex situ conservation seed collections</p> <p>*Sean Hoban</p> <p>In the face of ongoing environmental change, conservation and natural resource agencies are initiating or expanding ex situ seed collections from natural plant populations. In all cases it is advisable to capture as much phenotypic and genetic diversity from the natural populations as possible. In this talk, I will explain and demonstrate a new approach to optimize sampling protocols for a conservation seed collection. I use spatial, demographic and genetic data from three species, as well as simulated data under an individual-based model, to lead to tailored collections that maximize diversity while minimizing collection size. I find that characteristics of plant reproduction and dispersal, as well as logistical factors, significantly influence the genetic diversity captured in seed collections. As one example, a highly self-pollinating, low dispersal species needs sample sizes five times larger than current guidelines. Results show that minimum collection protocols should be customized for the target species, rather than commonly implemented “rules of thumb.” It is possible to improve the value of seed collections by quantitatively integrating current knowledge of plant biology, spatial distribution and genetics into collection design.</p> |
| <p>11:15</p> | <p>Defining the consequences of anthropogenic change: impacts of plant invasions and land conversion on grassland bird reproduction</p> <p>*Scott B. Nelson, Jaime J. Coon, James R. Miller</p> <p>Land conversion, habitat fragmentation, and exotic plant invasions have dramatically changed the structure and composition of wildlife habitats. From 2013-2016, we investigated the impacts of anthropogenic habitat change on crop conversion, road construction, woody encroachment, and other plant invasions on breeding dickcissels (<i>Spiza americana</i>); specifically, how these changes impact dickcissel nest survival and brood parasitism by brown-headed cowbirds (<i>Molothrus ater</i>). Nests in microsites heavily invaded by the invasive grass tall fescue (<i>Schedonorus phoenix</i>) experienced high rates of predation and parasitism, but exotic legume cover decreased parasitism. The effects of woody encroachment on parasitism differed across spatial scales: parasitism risk decreased as woodland cover within 500m of nests increased, but increased with woody cover near nests. Row-crop agriculture in the landscape slightly reduced nest survival, but road construction affected neither predation nor parasitism. Parasitized nests experienced high predation risk during the nestling phase. The impacts of anthropogenic changes on wildlife habitat quality are clearly non-uniform. Landscape conversion appears to have limited effects on nest predation, though broad-scale woody encroachment influences parasitism. In contrast, biological invasions have strong effects at fine spatial scales. This level of detailed understanding will enable practitioners to identify management goals that mitigate negative impacts of anthropogenic change.</p> |

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| <p>11:30</p> | <p>Plant community impacts of reintroduced bison in a restored tallgrass prairie</p> <p>*Ryan Blackburn, Holly Jones</p> <p>Bison (<i>Bison bison</i>) were almost hunted to extinction but they are now recovering and have recently been reintroduced to restored prairies for their ecosystem-engineering roles. The effects bison have on remnant (never-plowed) prairie vegetation are well documented. However, there is little known about how bison will affect vegetation assembly and productivity in restored prairies. The goals of this study were to measure the impacts of bison reintroduction and restoration age on plant communities for both restored and remnant tallgrass prairie at Nachusa Grasslands. We conducted plant surveys and collected aboveground biomass (AGB) at randomly selected sites. We found that bison did not have an immediate impact on plant diversity or abundance. However, these measures were different across restoration age. We also found that plant species richness and AGB declined from younger to older restorations and remnant sites were similar to older restorations. In addition, we found that the presence of bison decreased AGB, especially in younger restorations. These findings suggest that plant communities are changing with restoration age and that bison may have a larger impact on productivity in younger restorations.</p> |
| <p>11:45</p> | <p>Habitat indicators of a federally listed glacial relict plant species restricted to cliffs in the Northern U.S.</p> <p>*K.Z. Mattingly, D.J. Leopold</p> <p><i>Rhodiola integrifolia</i> subsp. <i>leedyi</i> (Leedy's roseroot, Crassulaceae) is a rare cliff-dwelling subspecies federally listed as threatened in the U.S. Thought to be a glacial relict, all seven known populations of Leedy's roseroot are endemic to cliffs, likely in large part due to the specific environmental factors at these cliffs. This study took place at Glenora Cliffs, New York, the largest population of this subspecies in the world. We identified habitat factors associated with Leedy's roseroot occurrence by comparing areas where Leedy's roseroot was present to adjacent areas where Leedy's roseroot was absent. Leedy's roseroot occurrence was associated with increased light, lower height on the cliff, geologic features of the cliff including greater degree of water seeping from crevices, higher plant species richness, and higher mean temperatures, with temperature trends varying over the growing season. Analysis of the Glenora Cliffs plant species community suggested Leedy's roseroot co-occurs with other cliff-dwelling species that may serve as indicators of Leedy's roseroot habitat. Our characterization of habitat factors associated with Leedy's roseroot supports its glacial relict status, suggests global climate change may impact it differently than most plant species, and informs management and potential ex situ conservation of this rare subspecies.</p> |

Genetics & Evolution I (210)

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| <p>10:30</p> | <p>The Molecular Interdependence of Plant Resistance and Tolerance</p> <p>*J. Miles Mesa, Daniel R. Scholes, Ken N. Paige</p> <p>Plants have numerous mechanisms to cope with the negative effects of herbivory, including plant resistance, structural and chemical traits that reduce damage, and</p> |
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| | <p>plant tolerance, the ability to compensate for tissues lost. It has been argued that resistance and tolerance represent alternate strategies and thus there should be a tradeoff between resistance and tolerance. However, resistance and tolerance are controlled via the same molecular pathway, the Oxidative Pentose-Phosphate Pathway and the process of endoreduplication. Endoreduplication is the replication of the genome without mitosis, which leads to an increase in cellular chromosome number. Increasing chromosome number and therefore gene copy number provides a means of increasing gene expression that has been shown to enhance compensation following herbivory. By measuring glucosinolate levels and seed production following the removal of apical dominance in ecotypes of <i>Arabidopsis thaliana</i> we show that there is a positive association between tolerance and induced chemical defense. Similarly, the direct association between compensation and resistance is demonstrated by genetically manipulating the endoreduplication pathway. By overexpressing ILP1, a positive regulator of endoreduplication, and thus compensation, we experimentally increased glucosinolate production and compensation in the Col-0 genotype.</p> |
| <p>10:45</p> | <p>The effect of relaxed selection and gene interactions on the evolution of antibiotic resistance in a long-term experiment with <i>Escherichia coli</i></p> <p>*Kyle Card, Jasper Gomez, Richard Lenski</p> <p>Antibiotic resistance traits that are favored in an environment containing an antibiotic may be detrimental in the antibiotic's absence. Moreover, epistatic interactions between a resistance mutation and its genetic background may determine its fitness effect. Both phenomena may play key roles in the evolution of antibiotic resistance. We examined these phenomena using strains of <i>Escherichia coli</i> that have evolved for 20 years in antibiotic-free conditions during a Long-Term Evolution Experiment. Using antibiotic selection experiments with ampicillin and tetracycline, we compared antibiotic susceptibility in the ancestral strain and evolved clones from four populations to determine if susceptibility has increased over time. We also examined the evolvability of antibiotic resistance in the different backgrounds. Our preliminary results show that all evolved strains are more sensitive to these antibiotics than the ancestor. We also found that evolved strains gain different degrees of resistance than the ancestor. These results confirm that resistance traits are not maintained in an antibiotic-free environment and that genetic background affects the evolution of antibiotic resistance. We will follow up these experiments by determining the genetic changes that affect antibiotic susceptibility and evolvability under this relaxed selection.</p> |
| <p>11:00</p> | <p>Plants that switch sex! Synchronous dichogamy in <i>Canella winterana</i></p> <p>*Patrick Garrett</p> <p>The factors that drive the evolution of specialized pollination systems are considered a central tenant of future research in the field of pollination ecology. We seek to bring further understanding to a poorly understood but taxonomically widespread specialized pollination system. Synchronous dichogamy, the synchronized temporal separation of sexual function, is found in <i>Canella winterana</i>, a woody tree species native to the West Indies and southern Florida. In this system all flowers within a plant bloom synchronously as functional females and after 24 hours they synchronously switch to functional males. In this way, pollen is dispersed away from the plant to other individuals in the environment. Theoretically,</p> |

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| | <p>synchronous dichogamy should reduce the amount of self-pollination in these plants, thus promoting the deposition of congeneric pollen via animal-mediated pollen dispersal. However, there is little empirical evidence for synchronous dichogamy as a specialized pollination syndrome and little is known about how this affects the genetic structure of populations. The aim of this study is to bring further understanding to how this specialized pollination system promotes gene flow in populations of <i>Canella</i> by assessing the genetic structure of populations found in the Bahamas and southern Florida.</p> |
| <p>11:15</p> | <p>Evolution in the Constant Cold: Varied Loss of the Cellular Response to Heat Stress Among Antarctic Notothenioid Fishes</p> <p>*Kevin T. Bilyk and CHC Cheng</p> <p>Confined within the freezing Southern Ocean, the Antarctic notothenioid fishes have evolved to become highly cold-specialized, including an apparent loss of the classic heat shock response (HSR). However, it remains unclear whether this HSR loss pervades the suborder and the extent to which such losses extend into the broader transcriptional responses to heat stress. Understanding these losses is crucial in evaluating the adaptability of this stenothermal taxon that now faces escalating climate change. In this study, we used RNA-Seq to assess the evolutionary status of cellular responses to heat stress in three select notothenioid lineages: the basal temperate <i>Eleginops maclovinus</i>, the nearest non-Antarctic sister species; the cryopelagic <i>Pagothenia borchgrevinki</i>, which inhabits Antarctica's iciest waters; and the highly derived <i>Chionodraco rastrospinosus</i>, one of the hemoglobin-lacking Antarctic icefishes. <i>E. maclovinus</i> exhibited a robust heat shock response, supporting the HSR as a plesiomorphy that preceded the Antarctic notothenioid radiation. <i>C. rastrospinosus</i> maintained a robust response but lacked the classic HSR, while the <i>P. borchgrevinki</i> response was extraordinarily muted. These disparate transcriptional responses to heat stress suggest that the evolution of cold-specialization has progressed to differing extents among Antarctic notothenioid lineages, which may impact their ability to adapt to a warming world.</p> |
| <p>11:30</p> | <p>A High-Resolution Marker Panel for Elucidating Red Fox Patriline</p> <p>*Halie Rando, Jeremy T. Stutchman, Estelle R. Bastounes, Jennifer L. Johnson, Carlos A. Driscoll, Christina S. Barr, Lyudmila N. Trut, Benjamin N. Sacks, Anna V. Kukekova</p> <p>A lack of Y-chromosome sequence for the red fox (<i>Vulpes vulpes</i>) has hindered the inclusion of male lineages in analyses of population diversity. These analyses, primarily with mitochondrial DNA, have found that some wild North American fox populations have geographically heterogeneous origins, most likely due to admixture with European and farm-raised red foxes. Now that the genome of a male red fox has been sequenced and assembled, sequence from the Y-chromosome was identified and scanned for repeated motifs. From the 194 putative sites identified, eleven novel male-specific microsatellites markers were developed. Markers were genotyped in male red foxes from a farmed population as well as three wild populations: eastern Canada, eastern USA, and Great Britain. Genotype analysis identified 22 Y-chromosome haplotypes. The haplotypes clustered primarily according to continent but also suggested introgression from feral and European foxes into the eastern USA population. The development of these markers has greatly increased the resolution at which red fox Y-diversity can be</p> |

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| | analyzed and will allow future studies to analyze both patrilineal and matrilineal contributions to red fox diversity and phylogeography. |
| 11:45 | <p>Leveraging genomic data to develop diagnostic markers for a cryptic agricultural pest</p> <p>*Meredith M Doellman, Glen R Hood, Charles CY Xu, Jeffrey L Feder</p> <p>The apple maggot fly, <i>Rhagoletis pomonella</i>, is a damaging agricultural pest threatening the Pacific Northwest's \$2.25 billion apple industry. Historically native to hawthorn (<i>Crataegus</i> sp.) in the eastern United States, <i>R. pomonella</i> colonized domestic apples (<i>Malus domestica</i>) ~160 years ago, was introduced to Portland, OR ~50 years ago, and has recently spread north and west, posing an imminent threat to central Washington's apple industry. Monitoring and control of this spread are critical, but field identification is complicated by the ubiquity of <i>R. zephyria</i>, an innocuous but morphologically indistinguishable sympatric congener that infests the non-commercial snowberry fruit (<i>Symphoricarpos</i> spp). In this study, we leverage RAD-seq data to identify diagnostic genetic differences between <i>R. pomonella</i> and <i>R. zephyria</i>. First, we examine genome-wide differentiation between species at a sympatric site in the Columbia River Valley (WA), corroborating previously reported pronounced genetic differences. Second, we identify SNPs that are nearly fixed between the two species and confirm that these unambiguously discriminate all <i>R. pomonella</i> and <i>R. zephyria</i> individuals from an independently sampled sympatric site. Future work will mine these SNPs to generate an easily implemented diagnostic panel, for use by the USDA to rapidly and accurately identify individuals during the annual apple maggot survey.</p> |

Talks – Session 2

Behavioral Ecology II (314A)

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| 3:00 | <p>Behavior of animals in wild populations within urban vs suburban habitats</p> <p>*Jesse Hacker, Lydia Hopper, Seth Magle, Jalene M. LaMontagne</p> <p>Urbanization is associated with fragmented habitats, human-associated food sources, noise, and an increase in novel objects. Despite this, some species are highly adapted to urban areas and are found in large numbers. We investigated the impact of urbanization on behavior around a novel object and assess relative levels of neophobia in populations living in urban vs suburban environments. Wooden boxes containing food rewards were placed in five urban areas within Chicago and five exurban areas outside the city. Activity at these sites was monitored for four weeks: two weeks with food absent from the box's surface, followed by two weeks with food present, using a motion-triggered camera, taking 1-min duration videos. A total of 1624 videos were taken in exurban sites and 1603 videos in urban sites. Fifteen species interacted with the boxes, the most common being eastern gray squirrels (<i>Sciurus carolinensis</i>) and raccoons (<i>Procyon lotor</i>). Interactions with the boxes increased in frequency and duration when food was available, and data from one of the sites in each habitat will be discussed. Understanding how animals react</p> |
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| | <p>to the presence of a novel object can help us understand what makes some animal species successful in highly urban areas.</p> |
| 3:15 | <p>Fish fortune favors the angry: Behaviorally submissive and sociable bluegill sunfish are more likely to be caught by anglers</p> <p>*Michael Louison, Jennifer Jeffrey, Cory Suski, Jeffrey Stein</p> <p>Research has shown that many animal taxa display consistent behavioral tendencies, often referred to as “personalities.” In the case of sportfish species, fitness can be radically altered by personality if certain personality types are more likely to be captured by anglers. While behaviors such as boldness have been studied in this context, social tendency has not been examined though it may play a key role in driving catchability. To examine this, we conducted a study which evaluated catchability, social tendency, and dominance in bluegill sunfish, <i>Lepomis macrochirus</i>. 150 bluegills were subjected to experimental angling, and a subset of 19 captured and 19 non-captured fish were then tested twice for shoaling behavior and once for dominance in a dyadic trial. Results showed a role for social behavior in driving catchability, with captured fish spending significantly more time near conspecifics compared to non-captured fish. In addition, dominant individuals in dyadic trials were less likely to be captured, as were individuals which showed less between-trial flexibility in behavior in the shoaling test. Collectively, these data show that social individuals may be more vulnerable to capture, demonstrating an example of how personality may influence fitness outcomes in interactions between animals and humans.</p> |
| 3:30 | <p>Characterizing ant odor plumes in a tropical forest</p> <p>*Rachel L. Wells, Christopher Frost, Stephen P. Yanoviak</p> <p>Many organisms release odorous chemicals into their environment when threatened, and species "eavesdrop" on these signals. Ants are masters of chemical communication, but little is known about the ecological importance of eavesdropping on ant pheromones by non-ants. <i>Azteca trigona</i>, a common arboreal Neotropical ant, produces a pungent and distinctive alarm pheromone that is detectable several meters away. The goal of this study was to characterize the odors surrounding <i>A. trigona</i> nests in terms of chemical concentration and composition. We collected multiple open-air samples 0.02-5m away from <i>A. trigona</i> nests, artificial nests, and sites with no <i>A. trigona</i> presence in Panama. We also sampled individual worker odors using the headspace sampling technique. Gas chromatography/mass spectrometry revealed that 2-heptanone, a key component of the alarm pheromone of <i>A. trigona</i>, is present in open air at concentrations up to 391 ng/hr at least 5m from the nests. In the individual samples, 2-heptanone was found at a concentration of up to 4370 ng/hr. These results suggest that organisms near <i>A. trigona</i> nests could detect their presence based on odor alone, thus avoiding direct encounters with this aggressive species.</p> |
| 3:45 | <p>Parasite-related trait modifications of intermediate host (<i>Caecidotea intermedius</i>) and their effects on transmission to definitive host (<i>Lepomis cyanellus</i>)</p> <p>*Jordan Johnson, Timothy Sparkes</p> |

The acanthocephalan parasite *Acanthocephalus dirus* is a trophically-transmitted parasite that uses fresh-water isopods as intermediate hosts and fish as definitive hosts. Infected isopods undergo modification of behavioral and physiological traits (e.g. behavior, activity and body pigmentation) and some evidence suggest that these changes increase predation by the definitive host as part of a manipulation strategy by the parasite. There are numerous examples of changes to individual traits, however, less is known about the simultaneous change of multiple traits and their underlying mechanism. Using laboratory experiments, we examined if multiple parasite-related modifications to the intermediate host (*Caecidotea intermedius*) are associated with an increase in the transmission of *A. dirus* to its definitive host (*Lepomis cyanellus*). Infected isopods were less active and exhibited a suppressed escaping behavior when exposed to a predatory attack than uninfected isopods. Infected isopods also were more likely to be experience an attempt at predation by the intermediate host. We propose that parasite-related modifications in intermediate host behavior, activity and body pigmentation increase the trophic transmission of the parasite to the definitive host. Furthermore, we propose that changes to the intermediate host behavior and activity may be due to multiple mechanisms (e.g. parasitic manipulation, pathological effects and/or host-counter adaptation).

Microbial Ecology (314B)

Consequences of Domestication on the Maize Microbiome

*Alonso Favela, Martin Bohn, Angela Kent

3:00

For the past 9,000 years, humans have directed the evolutionary trajectory of *Zea mays* by selecting desirable traits. Domestication results in loss of complex characteristics that were once crucial to survival, but are made redundant by the domesticator. Recent research has shown that microbial communities associated with plant roots behave like gene-controlled phenotypic traits. As a consequence, anthropogenic selection could have unintentionally shaped plant-microbe interactions. Determining if microbiome contributions to ecosystem services have been interrupted is crucial in efforts to improve modern maize's nutrient availability, and sustainability. Here, we conducted a greenhouse experiment to examine at the effects of host genotype and domestication. Using Illumina sequencing, we characterized the rhizosphere microbial communities of 3 subspecies of *Zea mays* across 34 genotypes. Further, we surveyed the abundance of nitrogen cycling functional genes present in the microbiome to see if functional group selection has been shaped in domestication. Contrary to previous results, we found that domesticated plants had more diverse microbial communities, but functional genes at lower abundances. These findings suggest that domestication has resulted in the diversification of the maize microbiome; with modern cultivars being less selective when compared to ancestral relatives. Our results demonstrate that plant shape the composition and abundance of nitrogen cycling microbes in the rhizosphere. Understanding the link between host genetics and microbial assemblage of nitrogen cycling microbes is key to improving nutrient use efficiency and sustainability in all crops.

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| <p>3:15</p> | <p>Distribution of <i>Pseudomonas aeruginosa</i> in household drains</p> <p>*Aubrey Mojesky, Susanna Remold, Jeffrey Bara</p> <p><i>Pseudomonas aeruginosa</i> is an opportunistic pathogen and a leading cause of morbidity in individuals with cystic fibrosis (CF). Understanding where individuals with CF may come into contact with <i>P. aeruginosa</i> is important because infections are commonly acquired from environmental sources. Although <i>P. aeruginosa</i> is often stated to be ubiquitous, a systematic longitudinal sampling of 15 houses by our lab found that with exception of household drains, <i>P. aeruginosa</i> was rarely recovered. In this study, we conducted an in-depth follow-up study to better understand the distribution of <i>P. aeruginosa</i> within bathroom and kitchen sink drains.</p> <p>We hypothesized that <i>P. aeruginosa</i> will not significantly differ in its recovery between bathroom and kitchen sink drains. We collected 100 kitchen and bathroom sink drain samples from 48 homes in the Kentucky area. Drain samples were processed with the use of selective media and a species specific PCR reaction. We found a 50% recovery rate of <i>P. aeruginosa</i> in drains with no significant difference among the relative rates of recovery between bathroom and kitchen sink drains. This study will increase our understanding of <i>P. aeruginosa</i> distribution in the human home and help to pinpoint the potential household sources of these chronic infections.</p> |
| <p>3:30</p> | <p>Foliar microbiome community assembly driven by phylogenetic relatedness of Asteraceae hosts in a common garden</p> <p>*Briana K. Whitaker, Natalie Christian, Chai Qing, Keith Clay</p> <p>Foliar fungal endophytes form a ubiquitous, yet asymptomatic microbiome within all plant species studied to date, but many questions remain about how these communities assemble across hosts in nature. Phylogenetic distance between host species could represent a useful proxy for host traits that act as biotic filters on fungal endophyte colonization and persistence within leaf tissues. In this study, we tested whether host phylogenetic distance drives fungal endophyte community assembly using a novel common garden approach. Eighteen host species from the plant family Asteraceae and one outgroup species (<i>Lobelia cardinalis</i>) were planted in a common garden and exposed to natural inoculum for three months. Endophyte communities were characterized using metabarcoding techniques. We found that more phylogenetically related host species shared more similar fungal endophyte communities than more phylogenetically distant hosts. Similarly, host individuals that were more spatially proximate in the common garden shared more similar fungal endophyte communities than more spatially distant hosts, though the magnitude of the spatial effect was weaker than for host phylogenetic effect. These results demonstrate an important role for biotic filters and host evolutionary relationships in shaping the endophyte microbiome, even when controlling for other mechanistic drivers, such as host age and regional environmental variation.</p> |
| <p>3:45</p> | <p>Comparison of the oral, rectal, and vaginal microbiomes in four primate species</p> <p>*Abigail E. Asangba, Lawrence Mugisha, Karen E. Nelson, Steven R. Leigh, Brenda A. Wilson, Bryan A. White, Rebecca M. Stumpf</p> |

The study of the primate microbiomes has served as a critical tool in understanding the impact of bacterial communities on the health of both non-human primates and humans. These bacterial communities have been found to play several significant roles in the host organism. These include providing the necessary metabolic pathways for the breakdown of fibers, supplying gut lining with nutrients and serving as a source of proteins as well as protection from hostile competitors. They have also been found to be associated with several metabolic, auto-immune, and infectious human diseases. In this study, we collected and analyzed matched oral, rectal and vaginal swabs from 36 semi-captive chimpanzees (*Pan troglodytes schweinfurthii*) from the Ngamba Island of Uganda, 23 wild lemurs (*Propithecus verreauxi*) from Madagascar, 26 captive sooty mangabey (*Cercocebus atys*) and 45 captive titi monkeys. Using 16S rRNA sequencing, we compared the bacterial community composition and structure of all samples. Samples clustered mainly by body site with the least variability observed in the oral samples and most variability in the vaginal samples. Generally, within sample diversity was lower than between sample diversity.

Disease Ecology (407)

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| 3:00 | <p>Meta-analysis of viral infection on honey bee gene expression</p> <p>*Ian Traniello</p> <p>Understanding the decline in pollinator health is limited by a lack of knowledge of molecular response to viral infection. In particular, the Western honey bee <i>Apis mellifera</i> is commonly infected with numerous viral pathogens that have been shown to replicate in the brain and impart behavioral abnormalities, suggesting a link between infection and neuromolecular programs, but the technology for examining these effects has only recently become available. I present a meta-analysis of published honey bee transcriptomic data with a focus on the impact of several prevalent picornaviruses on gene expression profiles in the brain. My results suggest molecular signatures of viral infection are both virus-specific and region-specific, as I take advantage of data generated from different parts of the honey bee brain. I find both classic markers of inflammatory processes as well as changes in the expression profiles of several RNA-interference genes, suggesting a potential link between viral infection and a “hijacking” of RNA-silencing machinery. These results may be used to assist viral management efforts and serve as a cautionary tale in the application of sequencing technologies to wild populations of animals.</p> |
| 3:15 | <p>Ecological and Evolutionary Drivers of Disease in Freshwater Zooplankton</p> <p>*Ilona A. Menel, P. Lee, C.J. Holmes, M.A. Duffy, S.R. Hall, C.E. Caceres</p> <p>To test hypotheses about ecological and evolutionary causes and consequences of epidemics, we coupled field surveys with laboratory assays of the fungal pathogen <i>Metschnikowia bicuspidata</i> in the host <i>Daphnia dentifera</i>. The host overwinters as sexually produced diapausing eggs and annually recolonizes the water column from the egg bank. Parasite epidemics occur in fall and vary in magnitude among lakes and year. We collected <i>Daphnia</i> from five populations in July and November, genotyped them at six microsatellite loci, and established 15 clonal lines per lake from the July 2014 collection for laboratory assays. We found</p> |

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| | <p>significant differences in diversity, both in terms of the number of unique multi-locus genotypes collected in field samples before and after epidemics, the genetic diversity among the five lakes, and in the phenotypic diversity collected from life-tables. These laboratory and field results will shed light on the role that parasite-mediated selection and other ecological interactions can play in the dynamics of host populations.</p> |
| <p>3:30</p> | <p>Parasite transmission strategies: egg fibrils, site attachment, and host feeding behavior</p> <p>*Alaina C. Pfenning, Timothy C. Sparkes</p> <p>Parasites often utilize multiple hosts in their life cycle, which requires parasites to thrive in multiple habitats. Given the array of different host types, parasites utilize a variety of transmission strategies, which are a response to the target host's ecology. <i>Acanthocephalus dirus</i> (Phylum: Acanthocephala) infects a stream-dwelling isopod as its intermediate host and a fish as its definitive host. Infection of the isopod occurs when <i>A. dirus</i> eggs are consumed along with food located on the sediment. Eggs of <i>A. dirus</i> exhibit fibrils, which have been proposed to aid in transmission of eggs to the intermediate host. We examined the role of fibrils from an evolutionary and ecological approach. To understand the evolution of fibrils, a phylogenetic tree of the Acanthocephala was created with 18S rDNA and then fibrils were mapped on, which indicated that fibrils are a homoplasy. We studied ecological factors that may influence the evolution of egg fibrils. We examined the timing of fibril release and fibrils' ability to attach to sediment, which indicated that <i>A. dirus</i> exhibit a delay in fibril release and eggs with fibrils do not move with water currents. We examined the role of fibril attachment in transmission, which suggested that fibrils increase the prevalence of infection and overall parasite number. The presence of fibrils and the timing of their release is a mechanism that evolved in response to host ecology.</p> |
| <p>3:45</p> | <p>Parasite-induced host compensatory feeding in the <i>Drosophila-Macrocheles</i> mite system</p> <p>* Lauren Titus, Michal Polak</p> <p>Parasites and pathogens are ubiquitous, and they often represent potent agents of natural selection. Hosts have evolved a wide range of well-documented adaptations to resist parasites and combat disease, yet little is known about how hosts may mitigate parasitic stress through behavioral tolerance mechanisms, such as compensatory feeding. Previous studies suggest that organisms may be able alleviate some parasitic symptoms and fitness consequences by altering the amount and/or nutrient balance of food consumed. Using a naturally occurring <i>Drosophila-Macrocheles</i> mite system, we tested the compensatory feeding hypothesis. Female <i>D. nigrospiracula</i> were allowed to feed on two liquid diets, one of yeast (protein) and one of sucrose (carbohydrate) simultaneously. Overall, infected females (1-5 mites) consumed significantly more protein than uninfected females, but the same amount of carbohydrate. Additionally, fecundity was maintained in infected individuals. The data support the hypothesis that infected females over-consume protein in order to mitigate resource loss due to infection.</p> |

Genetics & Evolution II (210)

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| <p>3:00</p> | <p>Untangling the evolutionary interactions between New World ground-doves and their parasitic body lice using genomic data</p> <p>*Andrew D. Sweet, Kevin P. Johnson</p> <p>Parasites and their associated host organisms form relationships that can be difficult to understand within an evolutionary framework. However, genomic sequencing can help untangle these interactions by providing large amounts of data for phylogenetic and population genetic analyses. In this study, we developed a novel pipeline to assemble ~1,000 nuclear loci and call genome-wide SNPs for parasitic body lice (<i>Physoconelloides</i>) from New World ground-doves. From these data, we estimated the phylogenetic relationships of the lice and compared it to an existing host phylogeny. We also estimated population genetic structure of the lice. Phylogenetic analysis estimated a well-supported louse tree, and also indicated several possible cryptic species. Population genetic analysis indicated similar patterns of cryptic diversity. The host and parasite phylogenies were very congruent, which indicates high levels of cospeciation between these organisms. However, there were also some incongruent relationships. The overall congruence is perhaps due to the inability of body lice to switch hosts by grasping to winged hippoboscid flies, a tactic utilized by other types of dove lice. However, there is evidence of some host-switching, which suggest that other factors, such as geography or host ecology, play important roles in shaping this host-parasite relationship.</p> |
| <p>3:15</p> | <p>An intact stress axis is required for normal growth, development and survival during the larval period in the frog <i>Xenopus tropicalis</i></p> <p>*Leena H. Shewade, Daniel R. Buchholz</p> <p>Thyroid hormone (TH) is necessary and sufficient to initiate amphibian metamorphosis. Corticosterone (CORT, a vertebrate stress hormone) is known to potentiate the effects of TH by increasing tissue sensitivity to TH or super-induction of common response genes, thereby accelerating metamorphic progression. In mammals, CORT is essential for normal maturation of lungs and brain, but little is known about the independent actions of CORT during amphibian development. We used TALENs in <i>Xenopus tropicalis</i> to disrupt adrenocorticotrophic hormone (ACTH)- the pituitary hormone required to stimulate CORT production from the interrenal glands. Mosaic founders were crossed to generate F1 homozygous knockouts at a frequency of 25-90%. ACTH knockout tadpoles die just after metamorphic climax (NF stage 64), and the lethal phenotype was rescued with continuous CORT, but not TH, treatment. Also, ACTH knockout tadpoles had impaired growth and development, where they lagged behind the controls by 2-3 stages and had a significantly lower body size. Physiological analyses revealed higher amount of fat bodies and reduced blood glucose in the knockouts which is consistent with the metabolic effects of CORT. These results indicate that endogenous CORT plays roles independent of TH in normal amphibian growth and development and is required for completion of metamorphosis.</p> |

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| 3:30 | <p>Evolutionary genetics of variation in breeding and mating systems in a wild tomato species</p> <p>*Andrew Raduski, Boris Igic</p> <p>Self-incompatibility (SI) is a widespread mechanism used by angiosperms to enforce outcrossing. One SI system, S-RNase SI, is ancestral to most eudicots and is associated with higher species diversification rates within the Nightshade family. Despite the long-term benefits of SI, it is often lost and rarely, if ever, regained. Theoretical population genetic models of the loss of SI predict that a small number of factors influence the likelihood of complete loss of SI in a population. Here, we identify variation in the SI response across individuals in natural populations, a potential first step in the eventual loss of SI, and describe its effect on outcrossing rates. We also discuss results of controlled greenhouse crosses that further illuminate the nature of the genetic mutation(s) underlying variation in SI.</p> |
| 3:45 | <p>Caste-biased gene expression in a facultatively eusocial bee suggests a role for genetic accommodation in the evolution of eusociality</p> <p>*Beryl M. Jones, Callum J. Kingwell, William T. Wcislo, Gene E. Robinson</p> <p>Developmental plasticity may accelerate the evolution of phenotypic novelty through genetic accommodation, but studies of genetic accommodation often lack knowledge of the ancestral state to place selected traits in an evolutionary context. A promising approach for assessing genetic accommodation involves using a comparative framework to ask whether ancestral plasticity is related to the evolution of a particular trait. Bees are an excellent group for such comparisons because caste-based societies (eusociality) have evolved multiple times independently and extant species exhibit different modes of eusociality. We measured brain and abdominal gene expression in a facultatively eusocial bee, <i>Megalopta genalis</i>, and assessed whether plasticity in this species is functionally linked to eusocial traits in other bee lineages. Caste-biased abdominal genes in <i>M. genalis</i> overlapped significantly with caste-biased genes in obligately eusocial bees. Moreover, caste-biased genes in <i>M. genalis</i> overlapped significantly with genes shown to be rapidly evolving in multiple studies of 10 bee species, particularly for genes in the glycolysis pathway and other genes involved in metabolism. These results provide support for the idea that eusociality can evolve via genetic accommodation, with plasticity in facultatively eusocial species like <i>M. genalis</i> providing a substrate for selection during the evolution of caste in obligately eusocial lineages.</p> |

Talks – Session 3

Behavioral Ecology III (314A)

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| 4:15 | <p>Why so blue? Environment-dependent sexual selection on color polymorphisms in bluefin killifish (<i>Lucania goodei</i>)</p> <p>*Lisa Mitchem, Becky Fuller</p> |
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| | <p>The interaction between visual behaviors and lighting environment can create drastic differences in body coloration between populations. Visual communication relies of signals that are maximally conspicuous in a given environment; however, light availability is often heterogeneous within a species range. The best signal in one locality isn't always efficient in another. In this study, bluefin killifish (<i>Lucania goodei</i>) are used as a system to test the affects of lighting environment on visual communication. Male <i>L. goodei</i> exhibit a striking distribution of color polymorphisms. Males with blue anal fins are highly abundant in tannin-stained environments, while males with red and yellow fins dominate clear environments. The utility of this coloration was previously ill-defined. Here, we hypothesize that blue morphs are favored for sexual selection in tannin-stained environments due to maximized color contrast with background lighting. Mate choice and male competition assays were conducted to determine the utility of anal fin coloration. Blue morphs are significantly more dominant than red and yellow morphs in tannin-stained environments while all color morphs are equally dominant in clear environments. Results indicate that male dominance is a key selective force for <i>L. goodei</i> anal fin variation in different lighting environments.</p> |
| <p>4:30</p> | <p>Evolution of signaling behavior in predator-prey interactions using game theory</p> <p>*Divya Ramesh, William Mitchell</p> <p>Signaling by prey animals can draw the attention of a predator and delay escape, both potentially lethal costs. Hypotheses to explain the evolution of this behavior typically involve benefits due to kin selection or reciprocal altruism. We consider an alternative mechanism: the ability of a signal to reduce the value of the prey patch to a predator, relative to other patches in the landscape. We use evolutionary game theory and behavioral adaptive dynamics to identify signaling equilibria in a two-prey one-predator system. Our analysis reveals several interesting results. As the probability of detecting the predator increases, signaling is more likely to evolve if signal cost is sufficiently high. When signal cost is low, we find a non-signaling equilibrium where the predator always attacks. We find that mixed evolutionarily stable strategies exist for intermediate signal costs. Also, prey are more likely to signal upon detecting a predator when predators are more difficult to detect. This model provides a novel mechanism for the evolution of signaling behavior in group-living prey.</p> |
| <p>4:45</p> | <p>The effects of habitat on the courtship signal active space of two wolf spiders</p> <p>*Emily E. Pickett, George W. Uetz</p> <p>Habitats constrain effective communication. Two closely related species, <i>Schizocosa ocreata</i> and <i>S. rovneri</i>, are similar morphologically, yet reproductively isolated by courtship behavior and microhabitat. Male <i>S. ocreata</i> exhibit visual and vibratory courtship signals and occupy complex upland deciduous forest litter, whereas male <i>S. rovneri</i> use vibratory signals and reside in compressed floodplain litter. Courtship signal transmission was analyzed in mesocosms representing these native habitats by randomly assigning males to each mesocosm type. Females were paired with a conspecific male and restrained at one end of the mesocosm for an hour or until orientation towards the male. Female <i>S. rovneri</i> had longer latency and shorter orientation distance; however, no significant differences were found within species for orientation distance or latency between mesocosm types. A</p> |

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| | <p>subsequent field study found the average vanishing point of <i>S. rovnerei</i> vibratory signals in the floodplain was greater than the average vanishing point of male <i>S. ocreata</i> in the upland, deciduous forest habitat as described by previous studies. Taken together, the shorter vanishing point of <i>S. ocreata</i> vibratory signals, yet greater female orientation distance regardless of mesocosm, suggests that the visual component of the multimodal signal of <i>S. ocreata</i> acts to increase courtship active space.</p> |
| 5:00 | <p>Impacts of unionized ammonia on righting behavior in two species of freshwater snails</p> <p>*Megan DeVries, James E. Alexander</p> <p>Unionized ammonia (NH₃) is a common water pollutant toxic to freshwater animals. To date, only one study has assessed the effect of NH₃ on snail behavior; the results suggested that it affects movement, which in turn affects behaviors integral to fitness, such as foraging and avoiding predators. This laboratory study examined if NH₃ affects the righting time (RT) of two freshwater snails, <i>Lithasia obovata</i> (Say 1829) and <i>Elimia semicarinata</i> (Say 1829). RT is the time it takes an upturned snail to right itself. RT was determined for each snail before exposure and after 24 hours exposure to a range of NH₃ concentrations. Concentration of NH₃ affected change in RT for <i>L. obovata</i>, with a significant increase in righting time at 2.38 mg/L (p=0.034). NH₃ did not significantly impact change in RT for <i>E. semicarinata</i> over the range of concentrations tested (0.00 mg/L - 3.61 mg/L). An increase in RT could negatively impact snail fitness via increased predation risk and reduction in feeding time. As NH₃ levels continue to rise in aquatic systems due to increased anthropogenic inputs and elevated water temperatures, determining the sublethal impacts of NH₃ on aquatic organisms becomes increasingly important.</p> |

Eco-evolutionary Dynamics (314B)

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| 4:15 | <p>Spatial distribution of <i>Striatopollis catatumbus</i> through the Cenozoic.</p> <p>*Ingrid Romero, Michael A. Urban, Carlos Jaramillo, Francisca Oboh-Ikuenobe, Surangi W. Punyasena</p> <p>The analysis of taxonomic groups at levels higher than species is essential for identifying ecological characteristics caused by shared evolutionary history. <i>Striatopollis catatumbus</i>, a pantropical fossil pollen grain has been associated to four genera of the Fabaceae family, which are <i>Anthonotha</i>, <i>Crudia</i>, <i>Isoberlinia</i> and <i>Macrolobium</i>. This fossil pollen has been identified in the fossil record from the late Cretaceous to the Quaternary (65-0.01Ma) and has been associated with fluvio-deltaic environments within warm climatic periods. In the Neotropical fossil record, its highest abundances are registered during the Early Eocene Climate Optimum (EECO) and the Middle Miocene Climate Optimum (MMCO). Studies have suggested that Fabaceae abundance is affected by changes in temperature, being more abundant in warm environments. In this study, we attempt to narrow the taxonomic affinity of <i>S. catatumbus</i> within Fabaceae, by comparing superresolution confocal images of the fossil to that of the modern specimens. We also want to assess the relation between the abundance variation of <i>S. catatumbus</i> and shifts in temperature during the Cenozoic. Moreover, the biogeographic history</p> |
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| | <p>of <i>S. catatumbus</i> will provides a snapshot into the evolution of modern Neotropical flora.</p> |
| 4:30 | <p>Divergence before the host shift? Prezygotic reproductive isolation among three varieties of a specialist fly on a single host plant</p> <p>*Alaine C. Hippee, Maren E. Elnes, Jarod S. Armenta, Marty A. Condon, Andrew A. Forbes</p> <p>Ecological interactions can play an important role in reducing gene flow between diverging lineages during speciation. Many pre- and post-zygotic ecological barriers to gene flow are known to be important in speciation, but the specific barriers associated with the initiation of speciation are often unknown. Specialist sunflower maggot flies (<i>Strauzia longipennis</i>) are an excellent study system for evaluating the impacts of specific barriers to reproduction because there is evidence of several recent divergence events within the species. This work aims to measure the impacts of three pre-zygotic ecological barriers to gene flow between the recently diverged <i>S. longipennis</i> varieties. We evaluated the presence and strength of habitat isolation, allochronic isolation, and pre-copulatory sexual isolation between the varieties using microsatellites, no choice mating experiments, studies of allochronic isolation, and field collection data. We find that allochronic and pre-copulatory sexual isolation both contribute to reduced gene flow between <i>S. longipennis</i> varieties. While host shifting and subsequent habitat isolation is generally associated with speciation events in specialist insects, we find no evidence of a host shift among varieties of <i>S. longipennis</i>, suggesting that other reproductive barriers may arise prior to and facilitate host shifts.</p> |
| 4:45 | <p>Characterization of <i>A. thaliana</i> growth and regrowth patterns suggests a tradeoff between fitness and damage tolerance</p> <p>*Erika N. Rasnick, Daniel R. Scholes, Ken N. Paige</p> <p>Herbivory is a fundamental plant-animal interaction that presents selection pressure on plants to replace lost tissues and prevent subsequent losses in fitness. Apical herbivory, which entails removal or damage to the apical meristem, causes changes in plant architecture by disrupting hormone production by the apical meristem. For an annual semelparous plant, the ability to preserve fitness following damage is dependent on the plant's patterns of regrowth and resource allocation following damage. We assessed 28 traits of undamaged and damaged plants of 33 <i>Arabidopsis thaliana</i> genotypes ranging in architecture, undamaged fitness, and damage tolerance. We report an evolutionary bet-hedging strategy to maximize fitness under herbivory-genotypes with the greatest seed production when undamaged exhibited a significant reduction in seed yield when damaged, while genotypes with low undamaged seed production were the only genotypes whose seed yield increased when damaged. Patterns of endopolyploidy paralleled those of seed production, such that the increase in whole-plant ploidy by genome re-replication during growth/regrowth may contribute to undamaged fitness, damage tolerance, and their tradeoff. This study provides the first large-scale characterization of <i>A. thaliana</i> architectures and suggests that investment into fitness and endopolyploidy when undamaged comes at a cost to fitness once damaged.</p> |

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| 5:00 | <p>Evolution and divergence of inquiline wasps associated with North American cynipid gall-forming wasps</p> <p>*Anna K.G. Ward, Andrew A. Forbes, William Carr</p> <p>Cynipid gall-forming wasps associated with North American oaks are attacked by a wide range of natural enemies that include parasitoids, inquilines and hyperparasitoids. Inquiline wasps of several genera exploit the tissue of the gall at the expense of the gall-former. Because gall formers and their inquilines are both diverse and at least partly specialized on particular hosts, we can ask how they have evolved in relation to one another, their oak tree hosts, and geography. For this study, we are interested in measuring diversity of inquiline wasps and using host associations and phylogeny to infer how patterns of inquiline wasp divergence. In order to study the diversity and evolution of oak gall-associated inquilines, I have collected galls of various species of cynipid wasps and reared inquiline wasps from these galls. The inquilines belong to three primary genera (<i>Ceroptres</i>, <i>Euceroptres</i> and <i>Synergus</i>), with up to four different species emerging from any single gall type. Using mitochondrial COI sequences and a 4% divergence cutoff, I organize collections into molecular operational taxonomic units (MOTUs). Based on molecular species definitions, which may underestimate total diversity, patterns suggest that inquiline speciation is often correlated with gall traits such as morphology, location and time of appearance.</p> |
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Evolution & Development (210)

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| 4:15 | <p>Hormone and melanocyte signaling in development of a social feather ornament</p> <p>*Mikus Abolins-Abols, Hannah D. Kassab, Ellen D. Ketterson.</p> <p>Bird feathers are one of the most striking examples of diversity in nature. Variation in feather ornaments often signals the status or quality of an individual. To understand why and how particular ornaments are used as social signals, we must understand the factors that regulate their development. Here we used a combination of in vitro studies, protein and gene expression assays, and experimental manipulations to investigate the development of a melanin-based ornament used in attracting mates and signaling status- the white tail feathers of Dark-eyed junco- and test if it is regulated by testosterone, a hormone which has been shown to regulate sex differences in feather color. Our results show that melanocytes from white feathers produce pigment in vitro, and that the amount of white in developing feathers correlates positively with expression of melanocortin-1 receptor, and agouti signaling peptide. Developing feathers expressed androgen receptors, but experimental manipulation of testosterone signaling did not affect feather color. Our results show that color of this social ornament is regulated locally, but that its development is not sensitive to testosterone.</p> |
| 4:30 | <p>Analysis of <i>D. melanogaster</i> Viability of Different Dietary Sterols</p> <p>*Andrew Beiter, Grace Lyndsey, Lisa Nelson, Robert Grebenok, Andrew Stewart</p> <p>Ecdysone is essential for larval development and pupation in most insects and must be synthesized, in most cases, from sterols that insects receive in their diet. One</p> |

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| | <p>such insect is <i>D. melanogaster</i>, which has been used extensively as a model system for studying hormone-mediated development. Previous research suggests that cholesterol is the optimum sterol for ecdysone synthesis in <i>D. melanogaster</i>, however, this is seemingly at odds with their life history. Cholesterol, a sterol only found in animal products, is not typically found in the diet of wild or lab reared fruit flies. Therefore, it makes little sense that these organisms would preferentially utilize cholesterol over plant sterols, such as β-sitosterol, that can also serve as the base for ecdysone. To test whether cholesterol or plant sterols are more easily utilized, we reared <i>D. melanogaster</i> on a series of defined diets, with the only differences being the type and concentration of sterol that they contained: β-sitosterol or cholesterol. In contrast to previous studies, our data indicate that, regardless of concentration, plant sterols are more readily utilized than cholesterol for ecdysone synthesis. However, within each treatment, developmental success was maximized at different concentrations.</p> |
| <p>4:45</p> | <p>Cranial asymmetry arises later in the life history of the blind Mexican cavefish</p> <p>*Amanda K. Powers, Erin M. Davis, Shane A. Kaplan, Joshua B. Gross</p> <p>As a consequence of adaptation to the subterranean environment, the blind Mexican cavefish, <i>Astyanax mexicanus</i>, has undergone several extreme morphological changes, such as pigmentation regression, eye loss, and alterations to the skull. Extant surface-dwelling morphs enable powerful comparisons between ancestral and derived (cave-adapted) morphologies. In addition to the cranial alterations that impact the size, shape and positioning of cranial bones, cavefish also manifest lateral asymmetries. These bony fragmentations and fusions frequently occur on only one side of the face. We implemented a geometric morphometric approach to evaluate shape variation of the chondrocranium and osteocranium across life history in surface fish and two cavefish populations. Interestingly, measures of cartilaginous skull in juveniles were bilaterally symmetric and shape was conserved across all three populations. In contrast, osteocranial shape segregated into significantly distinct groups in adults. Cavefish demonstrated significant asymmetry for bones surrounding the collapsed eye orbit, and the opercle bone posterior to the orbit. Interestingly, we discovered that cavefish exhibit directional asymmetry of skull shape, which was biased to the left. In sum, this work reveals dynamic changes to the craniofacial complex over the course of cavefish life history, which has evolved in response to extreme environmental pressures of the cave.</p> |
| <p>5:00</p> | <p>Relative Body-Size Scaling in <i>D. melanogaster</i></p> <p>*Kyle Samson, Andrew Stewart</p> <p>In any organism body-size is a fundamental trait, affecting the outcomes of both natural & sexual selection. Moreover, since body size is a trait controlled by hundreds, if not thousands, of gene loci, there is virtually limitless potential phenotypic variation. While body-size is often studied in an evolutionary context, it is largely unknown whether all components of body size change at the same rate (i.e. isometric vs. allometric), while under uniform selection pressure. In <i>Drosophila melanogaster</i>, main body-size components include: head, thorax, abdomen, wings, & legs. Currently in the lab of Dr. Andrew Stewart, a long term (10+ years) selection experiment has been running, where lines of flies have been constantly selected to be smaller, larger, or disruptively selected (large males & small females). This study</p> |

utilized these lines to address the question of body-size scaling, in terms of thorax, femur and wing size, using the differentially selected flies. Our results support strong linear relationships between thorax, wing size, and femur length, indicating changes in body-size is largely isometric while under uniform selection.

Talks – Session 4

Behavioral Ecology IV (314A)

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| 10:30 | <p>Male-driven reproductive and agonistic character displacement in darters</p> <p>*Rachel L. Moran, Rebecca C. Fuller]</p> <p>Reinforcement can play a critical role in completing the speciation process after secondary contact by directly selecting for an increase in prezygotic isolation in response to maladaptive hybridization. The classic signature of reinforcement is reproductive character displacement (RCD), in which reproductive traits (signals and/or signal recognition) are show increased divergence between species in sympatry compared to allopatry. Recent studies have shown that maladaptive competitive interactions between species in sympatry can also lead to character displacement in traits associated with competition, termed agonistic character displacement (ACD). We examined whether RCD and ACD were present between the orangethroat darter <i>Etheostoma spectabile</i> and the rainbow darter (<i>Etheostoma caeruleum</i>). To test for RCD, we examined whether there was an increase in male <i>E. spectabile</i> preference for conspecific females in sympatry. To test for ACD, we examined whether there was an increase in (1) male <i>E. spectabile</i> recognition of conspecific male rivals in sympatry, and (2) male <i>E. spectabile</i> color pattern distance from male <i>E. caeruleum</i> in sympatry. We found a pattern consistent with RCD and ACD in sympatry. Together, this data provides strong evidence that selection against maladaptive heterospecific mating and fighting are both driving behavioral isolation between <i>Ceasia</i> and <i>E. caeruleum</i>.</p> |
| 10:45 | <p>ERα expression and monogamy: an experimental field study</p> <p>*Connor T. Lambert, Brian Keane, Bruce S. Cushing, Nancy G. Solomon</p> <p>Understanding the evolution of monogamous mating systems requires examining both ultimate and proximate mechanisms of monogamous behavior in natural conditions. While laboratory experiments have demonstrated that relatively low expression of estrogen receptor alpha (ERα) in the medial amygdala (MA) of the brain is linked to behaviors indicative of social monogamy in male prairie voles (<i>Microtus ochrogaster</i>), this relationship has not been experimentally examined in a field setting. We tested the hypothesis that ERα expression in the MA influences the monogamous behavior of male prairie voles in an ecologically relevant setting. We created semi-natural populations of prairie voles by releasing 8 females and 8 males bred for high ERα expression into each of eight 0.1 ha enclosures in summer 2016. ERα expression was inhibited using RNAi in four males of each enclosure prior to release. Voles were trapped and radiotracked for 15 weeks to examine space use and social associations. Preliminary analyses detected no differences in</p> |

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| | <p>monogamous behaviors between males due to ERα levels. Both low- and high-ERα males often formed monogamous pairs and did not differ in their number of mates. Our experiment demonstrates the necessity of examining proximate mechanisms in natural conditions to understand the evolution of complex behaviors.</p> |
| <p>11:00</p> | <p>Using a common ELISA to detect pesticide residues in a burrowing insect of economic importance</p> <p>*Aspen Kremer, Edwin R. Burgess, Sherine Elsawa, Bethia H. King</p> <p><i>Spalangia endius</i> is a parasitoid wasp that oviposits in the pupal stage of flies, killing the flies in the process. Its fly hosts include economic pests in livestock systems, and it is sold commercially as a biocontrol. Parasitoids may encounter the commonly used pesticide, imidacloprid, while burrowing for hosts in contaminated sites. In a previous experiment, <i>S. endius</i> was exposed to imidacloprid at a sublethal level, and an effect on parasitization ability was seen when wasps were given hosts without wet, organic media, but not when wasps burrowed for hosts through media. A follow-up experiment using a competitive ELISA kit tested whether burrowing washed off pesticide residue. Parasitoids were exposed to imidacloprid and placed with hosts in the presence or absence of decaying organic matter. These wasps were then homogenized in solvent and subjected to an Envirologix Quantiplate for detecting imidacloprid to quantify residues in the supernatant. The results showed significantly more imidacloprid in the no media treatment, suggesting that burrowing does have an effect on the imidacloprid present on parasitoids. This demonstrates a novel way of quantifying imidacloprid residue in insects using an ELISA kit, and the importance of testing the effect of pesticides in a range of environments.</p> |
| <p>11:15</p> | <p>Swimming ability of the bigeye thresher shark, <i>Alopias superciliosus</i>, inferred from geometric morphometrics of placoid scales in lamniform sharks</p> <p>* Joseph A. Frumkin, Windsor Aguirre, Kenshu Shimada</p> <p>The genus <i>Alopias</i> (Alopiidae: thresher sharks) is a group of lamniform sharks characterized by a highly elongate caudal fin with three known extant species: <i>A. pelagicus</i>, <i>A. superciliosus</i>, and <i>A. vulpinus</i>. <i>Alopias pelagicus</i> and <i>A. vulpinus</i> are known as strong swimmers and use their caudal fin to hunt for small fish prey by stunning them, but the exact feeding behavior and swimming ability of <i>A. superciliosus</i> remains unknown. To better infer the biology of <i>A. superciliosus</i>, we examined placoid scale morphology of the three <i>Alopias</i> species and four additional lamniform taxa (<i>Mitsukurina</i> [goblin shark], <i>Psuedocarcharias</i> [crocodile shark], <i>Megachasma</i> [megamouth shark], and <i>Lamna</i> [salmon shark]) using geometric morphometrics because scale morphologies usually give insights into hydrodynamic efficiency in sharks. For each individual (preserved museum specimen), scale patches were sampled from the mid-section of the body as well as from three positions in each caudal fin. A conical variate analysis clearly shows that <i>A. pelagicus</i> and <i>A. vulpinus</i> are clustered closely with <i>Lamna</i> (salmon shark) known as a fast-swimming shark. In contrast, <i>A. superciliosus</i> is clustered with slow-swimming taxa: <i>Mitsukurina</i>, <i>Psuedocarcharias</i>, and most closely with <i>Megachasma</i>. Therefore, our placoid scale-based study at least suggests that <i>A. superciliosus</i> is a slow swimmer.</p> |

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| <p>11:30</p> | <p>Loafing: the wild turkey's guide to the nap</p> <p>*Christine Parker, Jeff Hoover, T.J. Benson, Wendy Schelsky, Paul Shelton</p> <p>Habitat selection throughout the annual life cycle of wild turkeys has been well studied. Turkeys are generally thought of as forest birds, yet use a variety of habitats in addition to forest that reflect changes in behavior and associated habitat requirements throughout the annual cycle. Loafing, or the resting time between foraging periods remains an elusive aspect of turkey behavior and habitat use. During 2015 - 2016, we monitored 62 wild turkey hens in central Illinois using microGPS units equipped with accelerometers. GPS units logged locations every two hours during daylight and average acceleration rates every five minutes. We used location and acceleration data to determine the average time per day turkeys were engaged in loafing and the predominate landscape cover where loafing occurred. We then developed logistic regression models to evaluate how season and temperature influenced loafing behavior and location.</p> |
| <p>11:45</p> | <p>Courtship Communication in the Wolf Spider, <i>Gladicosa bellamyi</i></p> <p>*Madeline M. Lallo, George W. Uetz</p> <p>Spider communication is critical for species recognition and mating success (and reduction of sexual cannibalism). Communication often involves multiple sensory channels, and sometimes two or more of these sensory channels are combined simultaneously into multimodal signals. Wolf spiders (Lycosidae) communicate using multiple sensory modes, including vibratory signals, visual displays, and chemical signals. While many lycosid species communicate with primarily vibratory signals, some species utilize multimodal communication. A species recently discovered in S.W. Ohio, <i>Gladicosa bellamyi</i>, exhibits the potential for multimodal communication. Male <i>G. bellamyi</i> possess leg pigmentation, suggesting the hypothesis that they utilize visual displays as well as vibration in multimodal courtship signals. Using a laser Doppler Vibrometer and video camera, we characterized the vibratory and visual courtship signals of male <i>G. bellamyi</i>. Males court females with two unique visual displays and produce a vibratory signal made of three components. Visual signals of male <i>G. bellamyi</i> were similar to those used by other lycosid species. Female <i>G. bellamyi</i> show no apparent vibratory signals, but possess visual receptivity displays. We conclude that male <i>G. bellamyi</i> simultaneously exhibits complex vibratory signals and visual displays, supporting our hypothesis that <i>G. bellamyi</i> uses multimodal courtship communication.</p> |

Population & Community Ecology II (314B)

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| <p>10:30</p> | <p>Modeling Complex Ecosystems from Incomplete Data</p> <p>*Nicholas LaRacunte, James O'Dwyer</p> <p>Ecological systems often involve more interacting variables than are practical to measure directly. These include abiotic resources, dark taxa, life stages of individuals in populations, and a wide variety of other potential influences. Finding the right form of theoretical model to fit these systems can be difficult, especially in the face of such hidden aspects. We address these challenges with a new method inspired by recent developments in equation-free forecasting and sparse</p> |
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| | <p>regression. Our approach shows improved short-term forecasting accuracy compared with previous tools and is able to explicitly distinguish the effects of unmeasured factors from pure noise. We begin to address limitations of previous techniques, including generalization to non-stationary processes. In addition to making short-term predictions, we discuss how equation-free forecasting can reveal mechanistic aspects of the system and inform construction of a more traditional equation-based model.</p> |
| <p>10:45</p> | <p>Effects of Size and Size Structure on Top-Down Control by an Omnivore</p> <p>*Donald J. Benkendorf, Howard H. Whiteman</p> <p>Intraspecific predator size variation has been posited as a major determinant of a species' ability to control lower trophic levels. The importance of predator feeding strategy (e.g. omnivory) and changes with body size may also be important factors controlling the pervasiveness of top-down control. We sought to identify the effects of size and size structure on top-down control by omnivorous Speckled Dace, <i>Rhinichthys osculus</i>, and how these effects scaled with density. Within our study system, <i>R. osculus</i> inhabit small isolated beaver ponds, the conditions of which we replicated in 1000L cattle tanks. Size, size structure, and density of <i>R. osculus</i> were then manipulated within these tanks and resulting changes in invertebrate and algal communities were monitored over 8 weeks. Benthic algal biomass was significantly lower in the fishless control and lowest fish density treatment, indicating that <i>R. osculus</i> may have caused a trophic cascade that varied in intensity by treatment. Invertebrate samples are currently being processed and should provide insight into the specific pathways of this potential trophic cascade. Once completed, this research will contribute to a growing body of knowledge regarding the importance of intraspecific variation in maintaining the full suite of complex interactions that constitute healthy ecosystems.</p> |
| <p>11:00</p> | <p>Urban habitats: Tree cavity availability in cemeteries and city parks</p> <p>*Ryan A. Bovyn, Michael C. Lordon, Abigail Leeper, Kattie Morris, Heather Anderson, Jalene M. LaMontagne</p> <p>Tree cavities provide shelter, nesting sites, and food storage for many species of birds, mammals, and insects. Most prior tree cavity research has been conducted in forests, with fewer studies in urban areas. City parks and cemeteries may provide adequate habitat space for cavity-nesters, especially in urban areas where cavities are limiting. While these habitats have some similarities (e.g., lawn, tree maintenance) there are differences (e.g., types and levels of human activity). Our research objective was to determine if parks and cemeteries are comparable habitat types. We sampled 1000 trees across 10 cemeteries and 10 large parks throughout Cook County, IL for excavated and natural cavities. Trees in cemeteries tended to be larger and more decayed than in parks, and trees with cavities (natural or excavated) were larger and more decayed than control trees without cavities. There were slightly more natural cavities per tree in parks, but 3.5 times as many woodpecker excavated cavities per tree in cemeteries. Cavity availability was variable and related to tree maintenance (branch pruning), particularly in cemeteries. This research shows the potential for cemetery and park management to promote cavity excavators and nesters.</p> |

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| <p>11:15</p> | <p>Insect Pest and Natural Enemy Responses to Structural Diversity in a Production Agroforestry System</p> <p>*Adam Kranz, Kevin Wolz</p> <p>Production agroforestry systems rely on ecosystem services that benefit farmers. Conservation biological control is one service of particular importance in crops with low tolerance for pest damage and chemical control. While natural enemies have been shown to benefit from increased woody plant structural diversity and alley cropping, these techniques have never been tested together, and reductions in pest damage have been inconsistent. I sampled insect communities in a production agroforestry system with three components--alley-planted hay with rows of shrub crops interspersed with tree crops--and tested hypotheses about how these vegetation components affect insect communities. Since mowing hay disrupts insect community in alleys, predators and herbivores were predicted to move to alternate habitats, including shrubs and trees. My results showed insect abundance in each tree and shrub crop increased after mowing and declined thereafter. I also hypothesized that shrub species composition affects insect communities in adjacent tree crops both in their equilibrium abundance and in their response to mowing. However, preliminary results do not support any effect of neighboring shrub composition on tree insects. I will be testing each hypothesis for economically important pests and their natural enemies to inform planting and management decisions to maximize pest control.</p> |
| <p>11:30</p> | <p>Single-Camera Trap Survey Designs Miss Detections: Impacts on Estimates of Occupancy and Community Metrics</p> <p>*Brent S. Pease, Clayton K. Nielsen, Eric J. Holzmüller</p> <p>Camera traps are a common tool in wildlife ecology. However, few have considered how the number of detections of wildlife differ depending upon the number of camera traps placed at camera-sites, and how this impacts estimates of occupancy and community composition. During December 2015-February 2016, we deployed four camera traps per camera-site, separated into treatment groups of one, two, and four camera traps, in southern Illinois to compare whether estimates of wildlife community metrics and occupancy probabilities differed among survey methods. The four-camera survey method detected 1.25 additional species per camera-site than the one-camera survey method, and was the only survey method to completely detect the ground-dwelling silvicolous community. The four-camera survey method recorded individual species at 3.57 additional camera-sites ($P=0.003$) and nearly doubled the number of camera-sites where white-tailed deer (<i>Odocoileus virginianus</i>). We also compared occupancy rates estimated by survey methods; as the number of cameras deployed per camera-site increased, CI for occupancy estimates decreased, detection probabilities increased and associated estimation error decreased. Having multiple camera traps per site revealed significant shortcomings with the common one-camera trap survey method. We suggest increasing effort to at least two camera traps facing opposite directions per camera-site in habitat association studies.</p> |

Conservation Biology & Invasion Ecology II (407)

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| <p>10:30</p> | <p>Chronic contact exposure to realistic soil concentrations of a neonicotinoid pesticide during development has important sublethal effects on solitary bees</p> <p>*Nicholas Anderson, Alexandra Harmon-Threatt</p> <p>The non-target effects of pesticides, such as those related to systemic neonicotinoid insecticides, are an area of growing concern, particularly for ecologically and economically important organisms such as bees. Previous work on the effects of neonicotinoids on bees has focused predominantly on the consumption of contaminated pollen and nectar by a limited number of eusocial species. However, neonicotinoids are known to accumulate and persist in soils at levels higher than in food resources and most bees nest in the ground - suggesting a potentially important, and under-explored, route of exposure. The aim of this study was to assess the effect of chronic contact exposure to realistic soil concentrations of imidacloprid - the most widely used neonicotinoid - on bee development speed, body mass, and longevity. Cohorts of <i>Osmia lignaria</i> and <i>Megachile rotundata</i> were used as proxies for ground nesting species. A number of sublethal effects were detected in response to imidacloprid treatment including: reduced development speed at low and intermediate concentrations, increased conservation of pollen provision mass, and changes to immature and adult longevity. These results suggest that chronic exposure to nesting substrates contaminated with neonicotinoids represents an important route of exposure that could have significant physiological and ecological consequences for bee conservation.</p> |
| <p>10:45</p> | <p>Intra-specific variation in early growth traits of invasive <i>Miscanthus sinensis</i></p> <p>*Destiny J. Palik, A.A. Snow</p> <p>A continuing challenge to managing biological invasions is a lack of knowledge about the nature and distribution of intraspecific variation in the introduced range. Patterns in variation can arise from a number of things, including local adaptation to distinct habitats, high phenotypic plasticity maintaining fitness under a range of conditions, or high-performance genotypes. Knowledge about intraspecific variation is an important step towards understanding future invasive potential. In this study the perennial grass <i>Miscanthus sinensis</i> was used to investigate possible mechanisms underlying patterns of an ongoing invasion. <i>M. sinensis</i> has invaded under a wide range of environmental conditions and appears to show variation in invasiveness. Greenhouse and field common garden experiments were performed using seeds from nine feral populations over three regions. Biomass, height, and tillering were assessed as an indication of potential for colonization success. High levels of variation were detected within populations, moderate levels among populations, and negligible variation among regions. This suggests that local adaptation may be weak in the traits measured. This result could also reflect survival of widely-adapted genotypes, a type of filtering that happens during colonization. Without evidence of local adaptation it may be that patterns of spread are driven by changes in propagule pressure.</p> |

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| <p>11:00</p> | <p>Landscapes of fear on the prairie: Bison wallowing impacts on seed predation in a restored grassland</p> <p>*Maria Weston, Holly Jones, Nick Barber</p> <p>Small mammals and invertebrates contribute to seed removal and dispersal, which can shape ecosystem functioning, especially in grasslands. Many prairie restorations have begun to reintroduce bison (<i>Bison bison</i>), but it is unknown how this will impact seed predation. Bison wallow, which eliminates vegetation and creates large bare ground areas. This could create “landscapes of fear” where wallowed patches are less frequented by seed predators due to fear of predation. We experimentally manipulated seed availability and seed size in 50 sites with three treatments: 1) accessible to all seed predators, 2) accessible to invertebrate seed predators, and 3) excluding all seed predators (control). Using general linear models, we compared how seed removal changed in wallows vs. in vegetation and based on seed size. Our preliminary analysis shows that more seeds were removed when open to all seed predators. However, we found little impact of bison wallows on seed predators, indicating that newly-reintroduced bison wallowing does not impact the behavior of seed predators in our study system. We are currently exploring the mechanisms behind seed removal, including the role of moonlight and precipitation, and how that may alter the behavior of seed predators.</p> |
| <p>11:15</p> | <p>Impact of Roundup and honeysuckle leaf litter on crayfish (<i>Procambrus clarkii</i>) foraging and growth</p> <p>*Sydney Richards, Amber Burgett</p> <p>Freshwater crayfish play an integral role in their ecosystems, particularly in regards to food-web interactions. Some crayfish species are on the decline, with agricultural runoff and increased urban development contributing greatly to this plight. Other species i.e. <i>Orconectes rusticus</i> (an invasive species in Ohio), appear to be thriving in certain freshwater habitats. As omnivores, crayfish consume macro- invertebrates as well as plants, leaf litter, and algae. Many crayfish species in much of the Eastern United States experience pulses of agricultural runoff. Depending on the levels of runoff crayfish are exposed to, it may influence their growth, survival, or food availability in their habitat. Given their omnivorous diet, crayfish have an ability to alter the structure and function of the stream ecosystem. It is important, then, to understand how contaminants may impact foraging patterns. Additionally, invasive Amur honeysuckle, <i>Lonicera mackaii</i>, grow in large numbers along streams, which further alters conditions of the stream ecosystem. Management strategies of honeysuckle along streams often involves the removal of the trees and the application of roundup to the remaining stumps. Therefore, we sought to determine how sublethal glyphosate concentrations in freshwater habitats affects food availability and how the native (Eastern Red Bud) versus non-native (Honeysuckle) plant availability affects weight gain of crayfish. Twenty-four crayfish, <i>Procambarus clarkia</i>, were randomly divided into four experimental groups. A two by two factorial design was executed to examine how Roundup presence and food source impacted their growth. The presence of roundup had no impact on overall growth, and the crayfish grew similarly on a diet of native or invasive food sources. However, there appears to be a strong trend towards an interaction between honeysuckle and roundup. This indicates that while agricultural contaminants may not influence the overall growth of crayfish, it may alter their food availability, interact with roundup in</p> |

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| | <p>the crayfish system, and significantly change biotic and abiotic conditions in the stream ecosystem.</p> |
| 11:30 | <p>Safeguarding Ex Situ Plant Collections- how much sampling is enough?</p> <p>*Emma Spence, Patrick Griffith, Sean Hoban</p> <p><i>Ex situ</i> seed collections from natural populations are an important conservation strategy that provides the foundation for restoration, research and plant breeding. A major goal of ex situ plant collections is to maximize phenotypic and genetic diversity as found in natural populations while minimizing costs (e.g. number of individuals collected). Many seed collections for ex situ conservation work are performed using the theoretical guideline of 50 individuals/site. However, recent work has found that the number of individuals needed to maximize genetic diversity may differ by species and may be linked to species' life history traits (i.e., animal/wind pollinated, small/large range, etc.). We will describe a new project using 12 plant species (having a variety of life histories) to determine if optimal sampling strategies can be based on life history traits, thus helping inform future sampling strategies. We will genotype (using microsatellites) samples from in situ and ex situ populations to determine how well ex situ collections represent the genetic diversity in situ. Plans for sampling, genotyping and quantitative methods for the project will be discussed, demonstrating how this project synthesizes ecological and evolutionary approaches to achieve conservation of woody plant species.</p> |
| 11:45 | <p>White-tailed deer browse preference for invasive shrub, Amur honeysuckle, among other common woody plant in SW Ohio</p> <p>*Gabrielle Wright, David L. Gorchov</p> <p>Selectivity by overabundant, generalist herbivore populations leads to intensive browsing on more palatable species. A concern of this selectivity is white-tailed deer's preference for native species over introduced which may allow invasive species to flourish. Recent work from our lab indicated that <i>L. maackii</i> constitutes a large proportion of deer diet in Miami University Natural Areas, but low frequencies of alternative browse prevents assessment of deer preference for this invasive species. This leads to two competing hypotheses: (1) White-tailed deer prefer to browse on <i>L. maackii</i> versus other woody plants that are within their browsing height range, or (2) <i>L. maackii</i> is not a preferred source of browse, but is consumed when alternative foods are depleted. We assessed preference level by measuring browse proportions of <i>L. maackii</i> and other woody plants across 8 sites in SW Ohio and calculate in an electivity index which ranges from -1.00 (avoided) to +1.00 (preferred). Study results have shown a wide range of electivity (-0.66 - + 0.57). Regressions revealed strong, negative linear effects of <i>L. maackii</i> twig abundance/total twigs at the site (($r^2=0.92$, $p<0.001$) and a positive relationship between abundance of less preferred species/m² ($r^2=0.85$, $p=0.001$). Deer density estimations are currently underway.</p> |

Ecosystem Ecology (210)

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| <p>10:30</p> | <p>An ecoinformatic analysis on the seasonal and long-term flowering phenology of two lowland Neotropical forests using aerial pollen trap and climatic data</p> <p>*Derek S. Haselhorst, David K. Tcheng, J. Enrique Moreno, Surangi W. Punyasena</p> <p>The influence of seasonal and inter-annual variation in temperature, rainfall, and solar irradiance on the phenological behavior of plant species is poorly resolved in tropical habitats. Relative to temperate latitudes, reduced variability in observed inter- and intra-annual climatic conditions and a lack of empirical long-term phenological datasets has limited the capacity to detect biological responses to environmental fluctuations. To address the statistical constraints imposed by tropical datasets, we developed a series of predictive models using multivariate linear regression and a slope correlation analysis to model the reproductive response of each individual taxon to seasonal and annual changes in temperature, rainfall, and sunlight. This analysis was applied to two seasonally sampled aerial pollen records collected between 1996-2006 from two Panamanian forest sites characterized by differences in seasonality and annual climate: Barro Colorado Island and Parque Nacional San Lorenzo. Using aerial pollen influx data as a proxy for flowering productivity, our results support previous analyses of long-term flower data indicating that flowering productivity is suppressed during periods of increased rainfall across habitats and enhanced under warmer temperatures in more seasonal environments. Long-term monitoring of pollen data can be expanded to different ecosystems better understand ongoing responses to climatic changes.</p> |
| <p>10:45</p> | <p>Evaluating Interactive Effects of Temperature and Phosphorus Supply on Stream Ecosystem Structure and Function</p> <p>*Lyndsie Collis, James Hood, Jonathan Benstead, Alex Huryn, Philip Johnson, Wyatt Cross, Gisli Gislason, Jon Olafson</p> <p>Climate warming and phosphorus (P) enrichment are both major anthropogenic stressors of aquatic ecosystems. Recent work has described the influence of these stressors in isolation; however, we lack understanding of how temperature and P interact to shape ecosystem structure and function. We conducted a stream-side channel experiment that simultaneously manipulated temperature and P and evaluated metabolic response (Gross Primary Production (GPP) and Ecosystem Respiration (ER)). A previous experiment demonstrated that the temperature dependencies of GPP and ER were stronger than predicted by metabolic theory due to the strong temperature dependence of nitrogen-fixation. Here, we predicted that P enrichment would alleviate limitation to nitrogen-fixation, particularly at high temperatures, thus amplifying the temperature dependencies of GPP and ER. Unexpectedly, P did not promote nitrogen-fixation, and thus did not influence the temperature dependence of metabolic processes in our study system. This was likely due to alternative limitation by trace elements such as iron or molybdenum, which can also limit nitrogen fixation in aquatic ecosystems. These results suggest that temperature-nutrient interactions in ecosystems are complex, and may lead to increased variability in metabolic responses to future climate change and eutrophication scenarios.</p> |

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| <p>11:00</p> | <p>Plant response-effect trait linkages along a resource gradient in fire-managed forests: implications for soil carbon stocks</p> <p>*Tyler Refsland, Jennifer Fraterrigo</p> <p>Researchers have identified a coordinated ‘trait-space’ of plant functional traits that respond to environmental conditions as well as affect ecosystem function. Although a useful framework, we lack empirical evidence on how disturbance mediates the influence of abiotic conditions on trait assembly and in turn, ecosystem processes. We investigated how repeated low-intensity fires along a resource gradient affect understory and canopy trait composition and soil organic carbon (SOC) stocks. We tested the following hypotheses: the disturbance-resource gradient affects SOC stocks through (1) mass-ratio, by influencing trait abundance; (2) through non-additive effects, by influencing the functional diversity (FD) of plant communities; or (3) directly, through either combustion or environmental controls on SOC stocks.</p> <p>Leaf economic trait distributions were determined by environmental filtering and limiting similarity associated with abiotic constraints and not fire disturbance. Although fire disturbance had limited influence on trait distributions, our results suggest that fire reversed the effect of understory FD in maximum height on SOC stocks from negative to positive. Fire was associated with a significant positive and negative effect on fast-cycling and slow-cycling SOC stocks, respectively, resulting in no net effect of fire on total mineral SOC stocks. We conclude that canopy community-aggregated traits and understory FD acted as both ‘response traits’ to a disturbance-resource gradient and ‘effect traits’, but only those traits influenced by abiotic constraints were associated with changes to SOC stocks. Determining response-effect trait linkages for predicting forest soil C stocks will thus require careful consideration of how disturbance and resource gradients interact.</p> |
| <p>11:15</p> | <p>Foragers Alter Resource Distribution of the Environment, and With It, Their Strategy Efficacy</p> <p>*Samantha E. Cohen, Logan Holmes, Peter M. Todd</p> <p>A number of works have examined how the efficacy of strategies change with the environment and under competition. However, few have examined how searching changes the environment itself. Using an agent-based foraging simulation in a patchy environment, we examine the qualitative and quantitative differences made to the distribution of resources by agents using three different strategies under competition. Our work suggests that foraging in such a repeated environment can alter the success of a strategy, and the usefulness of optimal foraging theory.</p> |
| <p>11:30</p> | <p>Effects of Burn Timing on Bee Communities</p> <p>*Brenna Decker</p> <p>Tallgrass prairies of the Midwest have recently been undergoing extensive restoration in response to pollinator declines. Most Illinois prairies are restored from agricultural lands, and only a few remnant prairies remain. One management strategy for both prairies types is to conduct prescribed burns, adding disturbance to the habitat. Two burn types have been employed on Illinois prairies; dormant season burns are conducted when vegetation is dormant over the winter months,</p> |

and growing season burns are conducted in late fall while vegetation is still growing. It is unknown if the timing of such burns affects the following year's bee community. Bees that construct nests above ground in stems (cavity-nesters) are more likely to be negatively impacted by dormant season burns compared to bees that are sheltered in below ground nests (ground-nesters). In 2016, bees were collected from four prairie sites in south-central Illinois using active netting, pan traps and vane traps. The abundances and species richness of cavity- and ground-nesting bee communities between burn treatments at each site were not significantly different. Many factors other than in-site nesting, such as the matrix habitat, may maintain a balanced bee community in terms of nesting guild simply by providing refuge habitat.

Posters

Behavioral Ecology

Poster 1 – 22

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| 1 | <p>Kin recognition in two species of cellar spiders, (Pholcidae), and its effects on inter- and cross-intra-specific predation of spiderlings</p> <p>*Alexander Berry, Ann Rypstra</p> <p>Cannibalistic species must have a mechanism to identify offspring and potential mates and suppresses predatory behaviors toward them. A similar process may facilitate reduced competition and enhanced fitness when introduced to new environments by selectively killing and consuming the offspring of others. This intense predation on the young of heterospecific competitors may be one way that an invasive species can take over a habitat from a well-established population. We tested this hypothesis using two non-native species of pholcid spiders in Ohio, the larger, well established <i>Pholcus phalangioides</i> and the smaller, newly invasive <i>Pholcus manueli</i>. In the laboratory, we allowed females of both species to produce clutches. Once hatched, the spiderlings were separated from their mother, for 1 hour, and then introduced to the mother, a conspecific, or a heterospecific adult female. The number preyed upon was recorded. Our results showed that <i>P. phalangioides</i> predation patterns were consistent across species, but that <i>P. manueli</i> feed on <i>P. phalangioides</i> young at 3x the rate of young conspecifics. Further mothers did not prey on their own young. This means that these species can selectively repress cannibalism and that <i>P. manueli</i> can gain an advantage by selectively preying on the young of other species.</p> |
| 2 | <p>Patterns and Implications of the Microbiota of Eastern Bluebird Eggs</p> <p>*Patricia Bollinger, Eric K. Bollinger, Steven Daniel, Rusty Gonser, Elaina Tuttle</p> <p>As part of a study on the effect of incubation onset on eggshell microbial loads and egg viability in Eastern Bluebirds (<i>Sialia sialis</i>), we sampled eggshell microbiota on 147 eggs on the day of laying. Microbial loads were relatively high and members of the bacterial family Enterobacteriaceae, often found in rotten eggs, were common. These results are similar to those reported for passerine eggs in the tropics but less</p> |

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| | <p>similar to those from other temperate-zone studies. Eggs averaged 157 CFU (colony-forming units) on the day of laying, with a median of 50 CFU/egg; 100% of eggs tested with nonselective growth media showed bacterial contamination. All genera of bacteria identified have been recorded elsewhere in rotten eggs or as pathogenic in adult birds. Fungi, poorly documented on wild bird eggs, were found on 59% of eggshells and included several genera capable of toxin production or proteolysis. Experiments showed that incubation onset prior to clutch completion reduced eggshell microbial loads and that viability was greater for eggs incubated naturally than for those experiencing incubation delay. In sum, our results indicate that even in temperate environments eggshell microbes may be an important factor influencing the timing of clutch initiation.</p> |
| <p>3</p> | <p>Experimental Study of Juvenile American Alligator Responses to Conspecific Vocalizations</p> <p>*Todd Bollinger</p> <p>Crocodylians are known for their ability to vocalize throughout their lives in a variety of social and ecological contexts, particularly during their vulnerable juvenile life stage. However, few studies have analyzed juvenile calls in laboratory settings, fewer still have analyzed them across large sample sizes or with respect to sex and body size, and no studies to date have analyzed crocodylian vocalizations with respect to human conditioning in captivity or animal personality profiles. This study tests juvenile American alligator's (<i>Alligator mississippiensis</i>) ability to respond via movement and callback vocalizations to pre-recorded conspecific contact calls across a large sample size (n=36), and tests for correlation between response rates and juvenile body size and sex. Juveniles responded overwhelmingly via movement toward the source of pre-recorded vocalizations, and 75% of juveniles who vocalized in return did so only to contact calls rather than controls (though the latter difference was not significant given the number of callbacks); there was also no significant difference in movement toward recorded vocalizations across size or sex. However, one particularly vocal individual whose upbringing in captivity was known was identified as a possible unique personality profile given its propensity for callback vocalizations in comparison to its fellow study subjects.</p> |
| <p>4</p> | <p>Study of pair retention and divorce rates in the polymorphic white-throated sparrow (<i>Zonotrichia albicollis</i>)</p> <p>*Morgan Chaney, M. Barcelo-Serra, R. Gonser, E. Tuttle</p> <p>Bird mating systems are often characterized as monogamous, creating prolonged bonds between pairs for the purposes of increasing fitness. The term monogamous implies that individuals will pair with only one member of the opposite sex, but does not infer that these pair bonds are for life. When individuals begin a new breeding season they face the option of choosing a new partner or remaining with their past partner. Using individual marking, researchers have studied divorce rates in primarily monogamous bird species but it is not clear what factors are influencing divorce. We used a long-term data set from a white-throated sparrow (<i>Zonotrichia albicollis</i>; WTSP) population to help determine factors behind divorce in social pairs. WTSPs are unique because they have two morphs (white and tan) that differ in plumage coloration, behavior, and genetics. Morph is determined by the presence of alternate supergene alleles located on a rearrangement of chromosome two. These morphs are maintained in the population through disassortative mating (W</p> |

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| | <p>males with T females and T males with W females). We found that divorce is as prominent as pair retention. Also, divorce rate is not affected by fitness, but could be influenced by population density and habitat.</p> |
| <p>5</p> | <p>Large brain evolution generates energetic and behavioral constraints across and within highly encephalized species of weakly electric mormyrid fishes</p> <p>*Megan Freiler, Kimberley Sukhum, Bruce Carlson</p> <p>Mormyrids, weakly electric African fishes, have complex brains for processing electrocommunication signals. Interestingly, certain species evolved an especially large brain relative to body mass. Energetic expenses for costly brain tissue could be met through trade-offs in other organ sizes or increased metabolic rate. It is unclear whether diversifying selection within species drove variation across lineages, or if large brain size and its costs evolved after divergence. By comparing patterns of inter- and intraspecific variation in oxygen consumption and hypoxia tolerance in species of mormyrids with varying brain sizes, I determine how selection within species impacts brain size across species. Given mormyrid brain size is uncorrelated with other organ sizes, large brain evolution likely necessitates increased metabolism. As predicted, large-brained species have increased oxygen consumption rates and reduced hypoxia tolerance. Intraspecifically, if increased brain size generates energetic costs before divergence, relatively large-brained individuals should exhibit greater metabolic requirements. Within large-brained species, relative brain size appears to be positively correlated with metabolic rate and negatively correlated with hypoxia tolerance, while the trend is less defined within smaller-brained species. Species-specific differences suggest metabolic costs of large brain evolution constrain extreme encephalization in mormyrids, but may not create strong selective pressures within smaller-brained lineages.</p> |
| <p>6</p> | <p>Invertebrate Prey Selection by Speckled Dace, <i>Rhinichthys osculus</i>: Potential Impacts on Omnivorous Trophic Cascades</p> <p>*Abigail Glass, Donald J. Benkendorf, Howard H. Whiteman</p> <p>The Speckled Dace, <i>Rhinichthys osculus</i>, is a small native cyprinid in Kimball Creek, Colorado. We conducted a mesocosm experiment in order to determine if <i>R. osculus</i> was capable of causing a trophic cascade. To better understand the consumptive interactions taking place in the mesocosms, we also performed a prey preference experiment. We set up three treatments in 15 small aquaria: 5 replicates of a single small <i>R. osculus</i>, 5 replicates of a single large <i>R. osculus</i>, and 5 replicates of a fishless control treatment. We added six different types of invertebrate prey to each aquarium to determine if there were differences in prey preference between the large and small <i>R. osculus</i>. We found that there were certain prey items that were completely avoided by <i>R. osculus</i> and other prey items that were eaten frequently. However, we did not find any significant differences in prey preference or electivity among taxa that were consumed. Additionally, no significant differences were found between large and small <i>R. osculus</i>. This information has provided a better understanding of the consumptive interactions taking place within our mesocosm experiments and how these interactions may affect a trophic cascade.</p> |

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| <p>7</p> | <p>Developmental Effects of Early Life Sleep Disruption in an Ecologically-Relevant Model</p> <p>*Shawn Gompa, Cathleen Rodda, and Jeffrey Alberts</p> <p>Infant mammals spend a large portion of their overall time budget sleeping; of sleep time, active sleep (AS) is the dominate sleep state. Infant mice spend over 80% of overall sleep time engaged in AS. The high amount of AS which characterize infant sleep is theorized to promote brain maturation. Investigations into the importance of infant AS are typically conducted using pharmacological means to accomplish total AS deprivation and/or older animals (8 days or older). In order to disrupt the AS of mouse pups starting on postnatal day (PND) 2 and ending on PND 12 we implemented a technique called 'gentle handling'. The AS of pups was disrupted for three 30 minute sessions a day over the course of 11 days. We then tested mice for social/emotional development in the pre-weaning period (PND 17-19), the post-weaning period (PND 25-30), and as adults (PND 55-60). Post-weaning and adult mice were tested for deficits in learning/memory, depression-like and anxiety-like behaviors, and social behavior, as measured by elevated plus-maze discriminative avoidance task, a two choice bottle test for anhedonia (sucrose vs. water), open-field behavior, and a social interaction test with an unfamiliar animal of the same age, sex, and weight. Our results demonstrate long term deficits in social/emotional behavior that persist into adulthood, suggesting the homeostatic mechanisms of sleep pressure and rebound do not completely mitigate the effects of early post-natal AS disruptions. Currently, we are exploring play behavior as a measure of social/emotional development following AS disruptions in pre-weaning mice.</p> |
| <p>8</p> | <p>Springers do Jerry Springer: Paternity testing in jumping spiders to assess mating frequency</p> <p>*Emily Hamel, Michael Henshaw</p> <p>The sexes have differing strategies to maximize mating success. Male gametes are easily produced, and in many species males mate with multiple partners to produce successful offspring. Female gametes require much more energy to make. In many species, this leads to females being more selective and choosing fewer partners. However, females also benefit from mating multiply, for example by producing offspring with better, or more diverse genes. <i>Phidippus audax</i> is a common jumping spider found throughout North America. Jumping spiders have been a common model organism for studies of sexual selection because they have elaborate mating strategies such as dances and female defense. Lab studies have shown that females may not be receptive to multiple mating, although behavior in an artificial environment may differ from that in the field. This is the first genetic test of paternity in naturally-mated <i>P. audax</i>. We genotyped 6 females and their offspring at 7 microsatellite markers to sort offspring into putative sibling groups to determine whether females mate more than once. If the offspring from one brood contain more than 4 alleles at a locus, then we can infer multiple fathers.</p> |
| <p>9</p> | <p>Connecting the dots on eggshell pigmentation: do male house wrens use color to determine their level of nestling provisioning?</p> <p>*Kara E. Hodges, Charles F. Thompson, Scott K. Sakaluk</p> |

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| | <p>Eggshell pigmentation varies widely among birds, and explanations range from serving a camouflage function to providing structural support. One proposed hypothesis is the sexually selected eggshell coloration hypothesis, which proposes that pigmentation acts as a signal of female or offspring quality, and that males use this information to adjust their investment in offspring. In species with brown-maculated eggshells whether the degree of pigmentation provides a reliable indicator of female or nestling superiority remains unresolved, and so too are the effects of these differences on male investment.</p> <p>Using a cross-fostering experiment in house wrens (<i>Troglodytes aedon</i>), I will investigate the significance of variation in maculation of eggshells in this cavity-nesting species. Eggs will be scored to classify clutches into light and dark categories. In addition, to decouple expected nestling quality and actual nestling quality, I will perform a second switch and return nestlings to their original nests to determine if male investment is associated with the extent of maculation of the eggs their mate incubated. Provisioning by both male and female parents will be quantified at different stages of the nesting cycle, and effects on nestling growth and development will also be assessed.</p> |
| <p>10</p> | <p>A Closer Look at the Age when Rhesus Macaque Females Develop a Red Face Preference</p> <p>*Shreya Jaiswal, Sean Coyne, Dario Maestriperi</p> <p>Red skin coloration has been important in primate sexual selection since they evolved trichromacy. In rhesus macaques (<i>Macaca mullata</i>), researchers have found that adult females prefer dark red faced males as opposed to pale pink faced males as mates. Surprisingly, red pigmentation of the face is not correlated with dominance rank in males. This preference makes females more likely to solicit dark red faced males, irrespective of rank. However, juvenile individuals (18 month olds) did not display the same bias, so the present study investigated when the bias develops to determine the role of the red face/red face preference in sexual selection. We conducted a looking-time experiment in which individuals of both sexes (male, female) and different ages (2, 3, 4 years) were simultaneously presented with two male faces (one dark red and one pale pink). Analyses show no significant looking time preference for either face in any age of sex class. The results of this study may indicate that the bias seen in previous studies is driven by older females, perhaps those who have had several mating seasons' experience, or pregnancy.</p> |
| <p>11</p> | <p>A Behavioral Study of <i>Phidippus audax</i>: Preference for Height, Connected Location, and Grid Location</p> <p>*Alex Kayfish, *Emily Noordyke, Stephen Martin, Michael Henshaw</p> <p>Jumping spiders are cursorial hunters that stalk their prey using sophisticated eyesight and spatial skills. As a result, they have the ability to learn and to navigate complex environments. We placed individual <i>Phidippus audax</i> (Bold Jumping Spider) spiders in a 4x4 grid of 44 cm tall dowels that were connected to each other by randomly placed paper bridges at 37 cm height. We assessed whether certain grid positions were more attractive than others to the spiders. We assessed <i>P.</i></p> |

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| | <p><i>audax</i> preferences 1) for certain heights on the dowels 2) for dowels that were well connected to others vs. isolated ones and 3) for regions within the grid irrespective of connectedness (edges, center, front, back). We determined preference by the frequency with which the spider appeared in a specified location during a six hour trial. They frequently used the paper bridges and were most often found at 37 or 43 cm. Analyses of preferences for certain kinds of locations within the grid will also be presented.</p> |
| <p>12</p> | <p>Examining male mates of unpaired female prairie voles (<i>Microtus ochrogaster</i>) using microsatellite markers</p> <p>*James Lichter, Connor Lambert, Brian Keane, Nancy G. Solomon</p> <p>While monogamous mating systems were previously considered to explain both social bonding and mating exclusivity, it is now apparent that socially monogamous animals often mate outside the pair bond. Previous work with prairie voles hypothesized that single-living females were most likely mating with unpaired wanderer males because resident males were already paired with another female, researchers did not have access to parentage data at the time. We tested female prairie voles living in semi-natural field enclosures in summer 2015 to evaluate this hypothesis and determine whether there is a difference between female mating with wanderer versus resident males. We divided the field season into four trapping periods to account for the fact that males and females may change status within a field season. Within the second and third, females mated with significantly more resident males than wandering males although most resident males did not have a female social partner at their nest. These 2015 results will be combined with field data from 2016 to examine whether or not this result is consistent.</p> |
| <p>13</p> | <p>The effects of Roundup on crayfish growth, behavioral response to predators, and territoriality towards conspecifics</p> <p>*Jessica Mertus, Amber Burgett</p> <p>Agricultural runoff brings contaminants such as fertilizers, pesticides, and herbicides into aquatic habitats, which can impact the aquatic community. One of the largest chemicals seen in our local runoff is Roundup. Freshwater crayfish serve an important role within the aquatic ecosystem as omnivores and are able to structure the aquatic community. Roundup has been shown to cause changes in the behaviors of several organisms, including amphibians and shrimp. Therefore, we studied the impacts of Roundup on the territoriality, behavioral response after predator exposure, and the growth of invasive rusty crayfish with conspecifics through laboratory microcosm experiments and behavioral trials. Results showed no impact of roundup on overall territoriality or aggression of crayfish towards conspecifics, however the presence of Roundup did alter the behavior of crayfish in response to the presence of a predator. Crayfish spent more time in their territory when exposed to a predator, however, roundup treated crayfish spent proportionately less time in their territory when a bluegill sunfish caged predator was introduced. Although it has been shown that Roundup impacts the chemo reception of amphibian larvae, our work demonstrates that Roundup likely influences the ability of crayfish to perceive chemical cues as well.</p> |

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| 14 | <p>Influence of Aging on Ovipositional Behavior of <i>P. rapae</i></p> <p>*Malcolm S. Mikkelsen, Tracy L.E. Wagner, Rodrigo J. Mercader</p> <p>Ovipositional behavior is considered to play a key role in determining host range evolution in plant feeding insects. Identifying the factors that influence host-selection behavior will therefore help gain a mechanistic understanding how associations between plants and plant feeding insects evolve. Due to its effect on the time available for host selection and learning, butterfly age is expected to have a significant effect on host selection. Here we examine the influence of aging on behaviors associated with host acceptance by <i>P. rapae</i>. <i>P. rapae</i> is a synovigenic insect species for which the ability to learn has been demonstrated. Therefore, as adult females age they are expected to become less selective as they become time limited, but also have the potential to be more efficient foragers due to prior experience. To test this, <i>P. rapae</i> were reared in laboratory conditions and female ovipositional behavior recorded 4, 8, and 12 days after emergence and subsequently behavioral sequences were analyzed. Females were recorded with three host options, a preferred n host, a lower quality host, and a non-host. Preliminary results suggest that in effect <i>P. rapae</i> do exhibit less selectiveness as they age and decrease the time required to recognize a proper host.</p> |
| 15 | <p>Effects of Vegetation Characteristics on Nest Site Selection and Reproduction of Female Prairie Voles (<i>Microtus ochrogaster</i>)</p> <p>*Malory Owen, Connor Lambert, Brian Keane, Nancy Solomon</p> <p>Nest site location can be an important determinant of female reproductive success. Identifying the habitat characteristics of nest sites and if these characteristics influence reproductive success is important to understanding the evolution of nest site selection. In our study, we examined the nest sites of prairie voles (<i>Microtus ochrogaster</i>) maintained in enclosures located in old fields dominated by grasses and forbs. The goals of our study were to determine if 1) there was a significant difference in vegetative characteristics at nests sites compared to random sites, and 2) if vegetative characteristics at nest sites predict reproductive success or offspring survival. We recorded vegetative characteristics focusing on those that reflected preferred food availability and refuge from predators. Nest sites had significantly more thorny and woody cover than random sites. Using AIC model selection, we found that vegetation height was the best predictor of female reproductive success. Our results suggest that voles tend to select nest sites that may protect them from aerial or ground predation, a strong selective pressure.</p> |
| 16 | <p>Plasticity and Reproductive Investment: A comparative study of reproductive morphs of three field cricket species</p> <p>*Brandi Pessman, John Kreckman, Marguerite Ernst, Chandreyee Mitra</p> <p>Phenotypic plasticity is the ability of one genotype to produce different phenotypes in different environments. Some field cricket species are plastic for several traits related to flight and reproduction. Plasticity varies amongst species - some species are highly plastic while others are completely fixed as one morph. This raises the question- Does plasticity have fitness costs? Here we present the results of a preliminary comparative study correlating levels of plasticity to reproductive investment in three cricket species: <i>Gryllus lineaticeps</i>, <i>G. veletis</i> and <i>G.</i></p> |

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| | <p><i>pennsylvanicus</i>. We hypothesized that the more plastic the species would have lower reproductive investment. We found that <i>G. veletis</i> and <i>G. pennsylvanicus</i>, both species with majority one morph (low plasticity), invest more of their body mass in reproduction than the highly plastic <i>G. lineaticeps</i>. This results in the direction we predicted. However, we need more data on more species to fully explore our hypothesis.</p> |
| <p>17</p> | <p>Effects of territory quality on reproductive allocation in female house wrens (<i>Troglodytes aedon</i>)</p> <p>*Dylan Poorboy, Charles F. Thompson, Scott K. Sakaluk</p> <p>In territorial birds, both parental and territory quality vary and influence resource allocation to offspring. In our study population of house wrens, evidence of such heterogeneity, its temporal consistency, and its fitness consequences, comes from the historic record of reproductive success at fixed-site nestboxes. To assess the potential effects of habitat heterogeneity independent of parental quality, we tested the hypothesis that territory quality influences female reproductive allocation in house wrens. Territories were categorized into low-, intermediate-, and high-quality based on fledging success the previous 5 years. Entrance size was increased in nestboxes (wrens prefer small entrances) on high-quality territories and on randomly-selected intermediate-quality territories to alter site attractiveness, thereby disrupting any covariation between territory quality and individual quality. Eggs were measured and cross-fostered in pairings between nests on high- or low-quality territories and intermediate-quality territories, to disentangle prenatal and postnatal effects of variation in territory quality. We found that territory quality had minimal effect on measures of parental resource allocation both prenatally and postnatally; however, a strong relationship between current nest success and territory quality persisted. Therefore, other factors of territory quality, such as predation risk, play important roles in determining reproductive success.</p> |
| <p>18</p> | <p>The effect of estrogen receptor alpha expression in the medial amygdala of males on female social preference in prairie voles (<i>Microtus ochrogaster</i>)</p> <p>*Kyle B. Smith, Alexis R. Gronda, Brian Keane, Nancy G. Solomon</p> <p>In socially monogamous species, females can optimize their reproductive success by selecting male social partners that form strong pair-bonds with them. Laboratory experiments have shown that behaviors associated with social monogamy (e.g., pair-bonding, paternal care) in rodents are influenced by neural estrogen receptor alpha (ERa) expression in the medial amygdala (MeA). Prairie voles are socially monogamous rodents and in laboratory studies, males with lower ERa expression in the MeA form stronger pair-bonds with females. Since male social partners with low ERa expression could increase female reproductive success, we conducted a female preference experiment to test the hypothesis that females, when given a choice between males with low versus high ERa expression, would exhibit a social preference for males with low ERa expression. Counter to expectations, females spent significantly more time with males with high ERa expression during the third day of 72-hour trials. These results may have been affected by female preference for chambers on the outside away from other voles being tested in separate arenas at the same time. Future research is necessary to verify that such a preference did</p> |

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| | <p>not influence female social preference and whether this study provides evidence that male ERa expression influences female social preference.</p> |
| <p>19</p> | <p>Determinants of site preference in the gill parasite <i>Naobranchia lizae</i> (Copepoda): relative effects of habitat availability and intraspecific competition</p> <p>*Sara Teemer , Isaure de Buron, Timothy C. Sparkes</p> <p>The copepod <i>Naobranchia lizae</i> is a common parasite on the gills of striped mullet (<i>Mugil cephalus</i>) in the Charleston Harbor Estuarine System (South Carolina). Settlement of <i>N. lizae</i> on the gills is non-random with preference occurring among and within gill arches. We collected 297 <i>N. lizae</i> from the gills of 60 <i>M. cephalus</i> in order to examine the relative importance of habitat availability and intraspecific competition to this pattern of settlement. We divided each gill arch into 16 potentially habitable regions, yielding 128 sites per fish (four gill arches, two sides). For each fish, we recorded the number and location of each copepod, along with five measures of their body size. The copepod number per fish ranged from 1-25, which we then divided into three groups of intensity (low=1-5, medium=6-10, high=11+). We compared habitat occupancy and body size of adult copepods among intensity groups and found that habitat occupancy was independent of copepod intensity, and body size did not differ among groups. This suggests that intraspecific competition does not appear to influence copepod distribution or size, and we propose that variation in habitat quality likely contributes to the distribution of individuals of <i>N. lizae</i> on the gills of striped mullet.</p> |
| <p>20</p> | <p>Pheromonal role of excreta in assembly for aggregation, defense, habitat suitability and environmental persistence in the terrestrial velvet mite</p> <p>*Greyden Yoder, Garrin J. Bachinski, Andre L. Lorenz, Jay A. Yoder</p> <p>Terrestrial red mites (<i>Balaustium murorum</i>) are natural regulators of plant pests, scale insects, spider mites, and aphids. These small, conspicuous bright red mites are seen scurrying about on various surfaces in early summer. During resting periods and low activity hours, they form aggregations consisting of thousands of individuals under bark. Based on short range attraction bioassays, we could mimic this aggregation response by using extracts of mite excreta that had been collected on filter paper where mites had previously crawled. A major component of mite excreta, guanine, similarly caused the mites to aggregate. Other related excretory purines, hypoxanthine, uric acid, and xanthine, also had arrestment properties, but not as pronounced as guanine. Individual mites in aggregations retained water more effectively (lower water loss rate) that resulted in an increase in survival compared to non-aggregated, mobile mites, as a physiological consequence of the reduced activity (decrease in respiratory water loss). Thus, excreta modifies behavior that concentrates mites in select habitats for oviposition, overwintering, protection against desiccation, and access to prey, that enables these mites to persist in the environment after they have become established. We conclude that excreta contains an assembly pheromone, and guanine is the active component of this pheromone.</p> |

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| 21 | <p>Carnivore competition shaped initial human dispersal to Australia</p> <p>*Alexandra J. Zachwieja, Laura L. Shackelford</p> <p>In extant predator communities in Southeast Asia, high competition has been shown to cause migration in lower ranked carnivores. Predator-prey communities in Southeast Asia have maintained similar dynamics for the past 80,000 years. We suggest that humans may have experienced competition with carnivores during initial human dispersal to Australia and that this may have directed and reinforced rapid dispersal patterns in conjunction with climatic pressures. We calculate exploitative competition between humans and carnivores using a Competition Index (CI) for six Pleistocene human occupation sites in Laos and Vietnam. This method is based on mass reliant prey choice and prey preference that has been previously established for Southeast Asian predator communities.</p> <p>Data shows that humans would have overlapped with hyenas, leopards, and tigers from a perspective of mass based prey choice. Addition of hunting method (pack vs. ambush) shows humans would have primarily competed with hyenas, the only carnivore species now extinct in Asia. Because prey choice overlap is high, competition intensity is also high across species. In habitats where easily attainable plant resources were low, it is likely spatial partitioning was used by humans, causing movement towards the fringes of the habitat or complete migration, potentially reinforcing dispersal.</p> |
| 22 | <p>Developmental Effects of Ecologically-Relevant Sleep Disruption in Mice</p> <p>*Shawn Gomba</p> |

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Conservation Biology

Poster 23 - 29

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| 23 | <p>Effectiveness of two herbivory deterrent treatments on survival of <i>Asclepias</i> species in restored tallgrass prairie</p> <p>*Amanda C. Bressoud, *S. Jane Jordan</p> <p>Plants of the <i>Asclepias</i> genus, commonly known as milkweed, serve an important role as the larval host of the monarch butterfly (<i>Danaus plexippus</i>). In this study, we examined the effectiveness of two herbivory deterrents on the survival of four <i>Asclepias</i> species (<i>A. syriaca</i>, <i>A. tuberosa</i>, <i>A. verticillata</i>, and <i>A. incarnata</i>) in four plots of restored Iowa tallgrass prairie, each differing in aspect and plant community. <i>A. syriaca</i> ultimately experienced the heaviest herbivory. The chicken wire fence was most effective at preventing herbivory, which was lowest overall in the least speciose plot. Our findings suggest that future conservation efforts for both <i>Asclepias</i> and <i>D. plexippus</i> should utilize fencing as an herbivory deterrent, and balance the habitat needs of both species.</p> |
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| <p>24</p> | <p>Lethal and Sub-Lethal Effects of Neonicotinoid Pesticides on Bee and Fly Taxa of the North American Tallgrass Prairie</p> <p>*Alexander Hajek</p> <p>Domesticated and wild bee populations are in decline due to a variety of interconnected factors such as disease, parasites, habitat loss and fragmentation, and pesticide contamination (Teeters et al., 2012, Abbott et al. 2008). In particular, neonicotinoid pesticides used in horticulture and agriculture have a high potential to contaminate and impact bee species (Abbott et al., 2008, Vaughan et al., 2014, Teeters et al., 2012). While the effects of neonicotinoids on honeybees (<i>Apis mellifera</i>) have been well documented, the effects of these pesticides is poorly characterized for most native bees and other insect pollinators. This study examined the lethal and sub-lethal impacts of contamination by the neonicotinoid imidacloprid on four different bee taxa (<i>Apis</i>, <i>Bombus</i>, <i>Melissodes</i>, and <i>Augochlorella</i>) and one taxon of bee-mimicking flies (<i>Eristalis</i>) common to the Tallgrass Prairie of North America. The pollinators were separated into dose groups and contaminated with different concentrations of imidacloprid. Mortality and motor function were assessed at 24 hours and 48 hours. There were significant differences between taxa in both the mortality and motor function experiments. There were also some differences in mortality and motor function between the control dose groups (0ppb) and the experimental dose groups (625ppb, 1250ppb, 2500ppb, 5000ppb) at both 24 hours and 48 hours. Knowing the effects of neonicotinoid pesticides on bees and flies enhances understanding of how bee populations and species are disappearing, and how impaired pollination services may affect plant communities, ecosystems, and landscapes.</p> |
| <p>25</p> | <p>From the visible to the invisible: Patterns of parasitism in Illinois birds</p> <p>*Krti Tallam, Tara Stewart, Loren Merrill, T.J. Benson</p> <p>Populations of many bird species have been declining throughout North America, although the causes of decline are often unclear. Rapidly changing environments present novel stressors that may be driving these declines by negatively impacting the health of birds. Therefore, we assessed how avian health is affected by environmental stressors along an urban to natural gradient. One potential indicator of bird health is infection with parasites and pathogens. In order to understand how environmental factors impact infection levels, we have to establish a baseline for measures of parasite diversity and abundance. For this project, we conducted a literature survey of articles from the past century documenting parasites and pathogens in seven common shrubland birds: the American Robin, Brown-headed Cowbird, Eastern Towhee, Field Sparrow, Gray Catbird, Brown Thrasher, and Northern Cardinal. We provide parasite species lists for each host, examine shared infections among hosts, and provide a map of the geographic range of observations. Parasites of many hosts are understudied, and we explore how detection bias may limit our understanding of parasite diversity and abundance.</p> |

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| <p>26</p> | <p>Diatom algae and sediment organic content reveal long-term presence of Sphagnum mat in Volo Bog Nature Preserve</p> <p>*Michael Vujanovic, Jennifer Slate</p> <p>As the only quaking bog in Illinois with a floating mat of Sphagnum moss, Volo Bog Nature Preserve is unique due to the low level of nutrients and naturally acidic water. Sphagnum moss sequesters nutrients from water and increases acidity by releasing hydrogen ions into its environment. Radiocarbon data revealed that the sediment was deposited over the past 6,300 years. We determined percent organic content through the use of loss on ignition by drying the sediment and then burning the organic matter at 550 °C. We determined the abundance of diatom algae by examining diatoms that were preserved over time due to having siliceous cell walls. Some diatom algae are able to thrive in acidic conditions and others are not. The percent organic content below 7.5 m was low, with an average of 36%. Above 7.5 m, the percent organic content increased to an average of 77%. Acidophilic diatoms (e.g. Eunotia) were more common above 7.5 m and alkaliphilic diatoms (e.g. Fragilariaceae) were more common below 7.5 m. This change from alkaliphilic to acidophilic diatoms, along with the increase in organic content in the sediment, suggests that the Sphagnum moss has been present for approximately 5,300 years.</p> |
| <p>27</p> | <p>Phenology and Citizen Science: Two projects on the North Central College Campus</p> <p>*Veronica Wagner, Austin Wheatley, Chandreyee Mitra</p> <p>Phenology is the study of seasonal changes in plants and animals (e.g., when plants bud, flowers bloom, butterflies emerge, etc.). It is increasingly being used for scientific public outreach as a way to widely gather data while getting people interested in their environment. On the North Central College campus, we plan to partner with: (1) Project Budburst (NEON, Boulder, CO), and (2) USA National Phenology Network, to develop a local phenology project. In working towards this, last summer we documented native plants on campus and their general biology, and selected a set of plants that will underlie our program. Next summer, we will set up these projects on campus and work on engaging the community to document phenological changes such as date of budding, first leaves, flowers, fruits, etc. The aim of these projects is to add to a long term dataset that can be used to infer larger, global patterns like the ecological effects of climate change, from observations of local, phenotypic changes.</p> |
| <p>28</p> | <p>Quantifying the Ecosystem Services of Dung Beetles in a Restored Tallgrass Prairie</p> <p>*Peyton Whiston, Holly Jones, Nick Barber</p> <p>Humans are highly dependent upon functional ecosystems for a wide variety of goods and services, known as ecosystem services. Through the decomposition of dung, dung beetles provide an ecosystem service valued at US\$380 million per year in the United States. The decomposition of dung also aids in the cycling of nutrients, dispersal of seeds, and control of parasites in tallgrass prairies. The tallgrass prairies of North America are among the most threatened ecosystems in the world. The reinstatement of disturbance regimes, including bison grazing, are a key facet in the active management of restored and remnant tallgrass prairies, and</p> |

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| | <p>the effects of these disturbances on both flora and fauna have been well studied. However, the effect of bison grazing and time since restoration on the ecosystem service of dung decomposition has not been studied in tallgrass prairies. At Nachusa Grasslands in Northern Illinois, we studied dung decomposition rates in six restoration sites with varying time since restoration and bison presence. Dung decomposition rates were unaffected by the age (time since restoration) of sites. Dung beetles were more abundant in bison-grazed sites, but this did not result in differences in dung decomposition between grazed and non-grazed sites. Further research will be able to determine the proportional role of individual beetle species in this critical ecosystem service.</p> |
| 29 | <p>White-Winged Wood Duck Water Quality Monitoring and Management at Hiram College's James H. Barrow Field Station</p> <p>*Taylor Yamamoto, James Kercher</p> <p>White-winged wood ducks are native to Southeast Asia. The population has undergone a rapid decline, and only 1000 individuals are currently estimated to be living in the wild. Hiram College's James H. Barrow Field Station is home to 12 white winged wood ducks. The ducks are bred in captivity. Decline in duck populations could be due to avian tuberculosis (<i>Mycobacterium avium</i>) and the occurrence of free-living pathogenic amoeba. Chemical conditions also contribute to the quality of the water; mycobacterium avium favors lower pH levels. The existing biological filters were remodeled to better the living conditions of the ducks and to help filter bacteria out of the water. A variety of native and nonnative plants were added to the filters to compare their ability to purify the water, thus applying the idea of hydroponics. It was found that the filter for Pool 9 was the best at removing mycobacteria and regulating chemical conditions in comparison to other pools.</p> |

Invasion Ecology

Poster 30 – 37

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| 30 | <p>Potential Indirect Effects of an Outbreak of a Native Herbivore Specialist Following the Removal of Honeysuckle</p> <p>*Logan R. Appenfeller, Rodrigo J. Mercader</p> <p>Invasive plant species abatement often involves rapid removal of the invasive often leading to rapid uneven growth of native plant species. This condition may lead to rapid expansion of one plant species creating a large resource concentration that may lead to local herbivore outbreaks. At a site in Shawnee Co., KS during the summer of 2012, an outbreak of the locally monophagous herbivore of the common paw-paw, <i>Asimina triloba</i>, the asimina webworm moth, <i>Omphalocera munroei</i>, was observed. This outbreak initiated in locations of rapid increase of understory growth of <i>A. triloba</i> following the removal of Amur Honeysuckle, <i>Lonicera maackii</i>. Defoliation levels peaked in 2013 reaching near complete defoliation. The outbreak also led to an apparent increase in predator numbers and parasitism rates as suggested by a departure from expected defoliation patterns, and higher parasitism</p> |
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| | <p>rates observed in larvae collected in 2016 compared to 2014. This suggests a strong potential for increased predation and parasitism of other native species, particularly because <i>O. munroei</i> has a single generation emerging late in the summer likely leading predators emerging the following year to feed on other species, and the primary parasitoid observed, <i>Itopectis conquisitor</i>, is a generalist with multiple generations.</p> |
| <p>31</p> | <p>Establishing plots to test the potential for low intensity honeysuckle abatement as a habitat improvement tool in urban and suburban environments</p> <p>*Paul E. Bergeron, R.J. Mercader, D.J. Emry</p> <p><i>Lonicera maackii</i> rapidly out competes native understory plants and can disturb regeneration pattern of canopy species. Honeysuckle abatement can be prohibitively labor intensive or unfeasible. To determine if small scale removal of <i>L. maackii</i> would allow for the creation of stable small native patches that may serve as future sources of native plants for an incremental abatement effort 20 small plots with dense <i>L. maackii</i> in Shawnee County, KS were selected. Half were cleared of <i>L. maackii</i> and half left untouched. Plant cover was surveyed and <i>L. maackii</i> age determined by counting tree rings immediately following abatement efforts. Plant cover was reassessed in late summer and soil samples collected to estimate the available seed bank. Mean plot age was 18 yrs old with the oldest plot containing a 35 years old <i>L. maackii</i>. Mean coverage by species other than <i>L. maackii</i> of 18.8% and no significant increase detected in late summer. Results also indicate low levels of viable seeds present in soils. These results suggest low diversity in these plots, providing a good baseline to test the possibility of using low intensity management to create small patches that may serve as sources of native plants for future restoration efforts.</p> |
| <p>32</p> | <p>Immediate Microhabitat Changes Following Buckthorn Removal on a Minnesotan Bog Edge</p> <p>*Alyson Jacobs</p> <p>Bog habitats are unique, fragile wetland ecosystems that have interesting microhabitat conditions and support a variety of endemic vegetation. Contributing to their uniqueness, bogs are becoming increasingly rare. Anthropogenic actions have caused the number of bogs to decline, including the introduction and spread of invasive species. However, there has been little investigation into the impact that invasive species, and their removal, have on remaining bogs. My study aimed to determine the abiotic and biotic effects of removing buckthorn, an invasive shrub, from a bog edge in Minnesota. Buckthorn was removed at the end of June, and at the beginning of August, I collected data on pH, canopy cover, ground cover, soil moisture, soil litter, native species, temperature, and humidity. I also collected earthworms to determine whether earthworm-buckthorn co-facilitation occurred. My results suggest that pH and canopy cover change immediately after removal of buckthorn, suggesting that microhabitat can change quickly after invasive species removal towards natural bog conditions. My research shows that after one month of buckthorn removal, bogs may be more resilient to disturbance than previously thought.</p> |

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| 33 | <p>Failure To Launch: The Threespine Stickleback of Lake Michigan</p> <p>*Franklin Joaquin</p> <p>In 1984 threespine stickle back (<i>Gasterosteus aculeatus</i>) were first recorded as having successfully established a population in the greater Lake Michigan area. For this study, we borrowed preserved specimens (n=281) from museums and performed geometric morphometric assays and took linear body measurements for armor traits of Lake Michigan, Lake Ontario, Atlantic, and Pacific stickleback populations. A discriminate function analysis was performed which showed strong divergence among groups based on collection area. Rates ranged from 73.4% in L. Ontario to 90% in Pacific samples. 84.5% of L. Michigan fish were classified correctly based on body shape alone. Linear measurements showed a different pattern; L. Michigan fish showed higher similarity to Atlantic fish than Lake Ontario fish and were homogenous for 6 of 8 measures and 5 of 6 armor traits. Lake Ontario fish showed a reduction if armor traits and differed significantly for 4 of 6 armor traits from Atlantic fish. Body shape and linear measurements suggest Lake Michigan fish may have been in the process of adapting to the open waters of Lake Michigan which favors slender bodies for hydrodynamic efficiency and larger armor structures for defense against predators in open waters.</p> |
| 34 | <p>Invasive grass colonization by arbuscular mycorrhizal fungi increased with lower inorganic N and P availability</p> <p>*Robin A. Johnson, Laura Y. Podzikowski, Richard P. Phillips</p> <p>The ability of invasive plants to form flexible relationships with mycorrhizal fungi is hypothesized to be a key trait allowing plants to achieve high productivity in a variety of habitats. Yet, the extent to which environmental factors influence the mycorrhizal colonization of invasive plant roots remains poorly investigated. Previous greenhouse studies suggest that the invasive grass, <i>Microstegium vimineum</i> (M.v.), associates with arbuscular mycorrhizal fungi (AMF) to enhance nutrient uptake. In this study, we sought to determine how AMF colonization of M.v. roots varies across a natural nutrient gradient. To do this, we quantified AMF colonization, soil nitrogen (N) and phosphorus (P) availability, and M.v. traits in nine paired invaded and uninvaded plots in a southern Indiana forest. Across all plots, we observed high AMF colonization of M.v. (64-95% colonization). AMF colonization was inversely related to soil P ($r^2=0.61$, $p=0.01$) and soil nitrate ($r^2=0.56$, $p=0.02$), suggesting that high AMF colonization allows M.v. to cope with nutrient scarcity. Higher AMF colonization yielded significantly wider plant tissue C:N (roots: $r^2=0.61$, $p=0.01$; leaves: $r^2=0.45$, $p=0.048$). However, M.v. biomass did not vary across the nutrient gradient, suggesting that flexibility in mycorrhizal associations may enable invasive plants to achieve high productivity in nutrient-poor soils.</p> |
| 35 | <p>Facilitative effects of dead honeysuckle shrubs on native tree seedling growth and survival</p> <p>*Kevin D. Lash, David L. Gorchov</p> <p>In the fragmented forests of Ohio, native tree recruitment has been substantially reduced by abundant white-tailed deer and invasion of Amur honeysuckle (<i>Lonicera maackii</i>). In areas of high deer densities, there is a substantial amount of seedling</p> |

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| | <p>mortality due to browse and deer tend to suppress growth and recruitment of palatable native species. Honeysuckle tends to form dense monocultures in the shrub layer and because of its broad canopy it blocks a substantial amount of light from reaching plants growing in the understory. Though honeysuckle competes with native tree seedlings for light and water, it may facilitate seedling growth in the presence of high levels of deer browse by providing refugia for seedlings. Currently, a popular method for honeysuckle removal involves cutting and removing stems, leaving the understory open and vulnerable to deer browse. I will be investigating whether or not dead honeysuckle shrubs, if left in place, act as refugia for native tree seedlings and if this information can be used to inform best practices for honeysuckle management with regard to promoting native tree recruitment. I hypothesize that dead honeysuckle shrubs will provide protection to native tree seedlings, promoting growth and survival relative to open-grown seedlings.</p> |
| <p>36</p> | <p>Response of adult Asian longhorned beetles to isothiocyanates in laboratory bioassays</p> <p>*MacKenzie L. O’Kane, Scott Gula, Emily Franzen, Ann M. Ray</p> <p><i>Anoplophora glabripennis</i> (Motschulsky), commonly known as the Asian longhorned beetle (ALB), is a destructive invasive pest. ALB is native to China, and a population of ALB has established in Claremont County, OH. Beetle larvae most likely entered Ohio in solid wood packing material from a shipment from China. Monitoring for adult ALB is difficult because pheromone-baited traps are not very effective in the field. The discovery of a chemical attractant for adult ALB to traps would improve monitoring for ALB in and around quarantine areas. Thus, we assessed the response of ALB adults to isothiocyanates, a class of previously unstudied potential attractants that are the breakdown products of glucosinolates. Some insect species, like cabbage aphids, sequester glucosinolates from their host plants. If aphids are attacked, sequestered glucosinolates react with endogenously produced myrosinase to produce isothiocyanates (ITCs), which act as an alarm pheromone. Genes for the myrosinase enzyme were found in the genome of ALB. However, ALB do not feed on plants that produce glucosinolates, nor do ALB sequester glucosinolates. We hypothesized that ITCs may therefore play a role in chemical communication in adults of ALB, and might act as attractants. We tested the response of both virgin and mated male and female adults of three ITCs in a Y-tube choice bioassay. Adults of neither sex were significantly attracted to any ITCs tested in this experiment.</p> |
| <p>37</p> | <p>Dendrochronology study on the Ohio infestation of Asian longhorned beetle (<i>Anoplophora glabripennis</i>)</p> <p>*Stephen Todd, Emily Franzen, Scott Gula, Bill Panagakos, Annie Ray</p> <p>In June of 2011, a population of Asian longhorned beetles (ALB, <i>Anoplophora glabripennis</i> [Motschulsky]), was detected in Clermont County, OH. ALB poses a serious threat to natural and managed forests in the United States. If new populations of ALB establish or if existing populations expand, the costs of the resulting damage could exceed \$669 billion, and could lead to the mortality of 30% of trees in North American hardwood forests. Although the status of the infestation in Ohio has been closely tracked by state and federal surveys, it is unclear how quickly the invasion was detected. Using tree ring analysis, we seek to conclusively determine when ALB first established in Ohio. We determined the date that a tree</p> |

was first infested by dissecting and sanding infested sections of trees, marking oviposition sites and exit holes, and counting growth response rings. Our data will be used to help delineate quarantine boundaries for existing infestations and to inform trapping and survey efforts for new infestations.

Landscape Ecology

Poster 38 - 40

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| 38 | <p>Grassland Management Potential for Improving Shrubland Bird Habitat: Research Proposal</p> <p>*Jane Capozzelli, Jim Miller</p> <p>Grassland afforestation by native and non-native trees and shrubs, a phenomenon termed woody encroachment, threatens grasslands by inducing grassland to shrubland conversion. To control woody encroachment, prescribed fire and grazing management strategies are applied on grasslands across the United States. But the performance of paired fire-grazing has not been adequately tested in tallgrass prairie systems. To address this knowledge gap, I will explore how prescribed fire and cattle grazing affect the structure, composition, and extent of woody encroachment in a 70,000-ha grassland region in Southern Iowa-Northern Missouri. Prairie conservation efforts often target woody encroachment in order to restore herbaceous habitat for grassland obligate birds. However, invading woody vegetation may provide important habitat for shrubland birds, a community of regional and national conservation concern. Therefore, I will study avian community composition, abundance, and foraging activity in woody vegetation of shrubland species such as Field sparrows, Common yellowthroats, Loggerhead shrikes, Black-billed cuckoos, and others. Foraging activity will illuminate differences in food availability that may arise from vegetative characteristics and fire-grazing treatments. Collectively, this project evaluates the ability of ubiquitous management strategies to achieve conservation goals, but also questions the wisdom of eradicating a habitat type that may be beneficial to threatened taxa.</p> |
| 39 | <p>Vegetation community structures and avian diversity in three Chicago parks.</p> <p>*Omar Morales, Edder Antunez</p> <p>Eight restoration and eight recreational areas were analyzed and compared in Jackson, Horner, and West Pullman park in Chicago for vegetation structure and their relationship with avian diversity. Bird point count plots were overlaid with tree and vegetation plots to accrue avian species count, tree species count, diameter at breast height (DBH), and percent vegetation coverage respectively. There was a significant difference between the number of avian species seen between natural and traditional areas in Jackson and Horner park but not in West Pullman park. Tall woody plants and tall grasses over 1.5m tall made up over 50% of the vegetation coverage in all natural areas. Our observations indicate that avian diversity may be correlated with the aforementioned vegetation structures as well as to the size of a park or habitat. Future research will consider bird abundance and collecting data on a larger scale.</p> |

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| 40 | <p>Soils and rainfall drive changes in the diversity and functional composition of tree communities in lower montane tropical forest *Cecilia M. Prada, Ben L. Turner, Jim W. Dalling</p> <p>Understanding which factors influence species composition in lower montane tropical forests is critical to their conservation. We examined the diversity and composition of trees in 12 one-hectare plots at Fortuna in western Panama. We recorded all trees > 5 cm diameter at breast height (d.b.h), measured soil properties (0-10 cm depth), and measured rainfall over several years. We found that alpha diversity was high and varied markedly among plots. Turnover reflected distinct community types developed on different parent materials. Although non-metric multidimensional scaling (NMDS) ordination showed that seasonality of rainfall was significantly correlated with species turnover, large compositional differences among sites < 2 km apart were attributable to differences in soils. At Fortuna, steep soil and moisture gradients drive differences in richness, taxonomic and functional composition of tree communities. Understanding how local edaphic conditions structure montane forests will be critical to predicting how tree communities will respond to climate change.</p> |
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Ecosystem Ecology

Poster 41 - 46

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| 41 | <p>Effects of stream quality on insect-gut associated denitrifying bacteria abundance *Allison Beckwith, Paul Ayayee, Laura Leff</p> <p>Gut bacteria in macroinvertebrates in streams and rivers contribute to nitrous oxide (N₂O) emissions from these systems through partial denitrification. Denitrification is an anaerobic microbial process which converts nitrates (NO₃⁻) to dinitrogen (N₂), removing excess nitrogen from these ecosystems. Poor stream quality negatively impacts the diversity and abundance of certain macroinvertebrate taxa, such as stoneflies, mayflies and caddisflies. The objective of this project was to quantify the abundance of gut-associated denitrifying bacteria in insects from freshwater bodies that differ in quality (Tinker's Creek, TC and West Branch of the Mahoning River, WBM) and determine if stream quality impacts both insect taxa, as well as gut-associated denitrifying bacteria. Samples of insects, water, and biofilms from debris were collected from these streams. Four insect families, Chironomidae, Elmidae, Hydropsychidae and Cambaridae were common in both streams. The insect family Lestidae was only found in TC and Baetidae, Perlidae and Empididae were only found in WB. Bacterial 16S rDNA, and the denitrification genes nirK and nosZ were detected in all samples. Impact of stream quality of the abundances of these bacterial genes are currently being investigated via quantitative PCR (qPCR).</p> |
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| <p>42</p> | <p>Historic changes in species composition and stand structure influence transpiration in the northern Great Lakes Region</p> <p>*Bethany Blakely, Jason McLachlan, Adrian Rocha</p> <p>In the northern Great Lakes Region, forests have been recovering from historic land use for a century or more. However, second growth forests remain more deciduous than historic forests, and consist of younger, smaller trees. These differences in species composition and stand structure affect transpiration, a critical bioclimatic process linking energy exchange and water balance. We investigated the effect of historic land use on transpiration by monitoring sap flux in an old-growth and mature second growth forest in the northern Great Lakes Region. We expect old growth forest to transpire less than second growth forest due to lower evergreen sap flow rates and reduced sapwood efficiency in older trees. At the stand level, total transpiration was lesser in old growth forest despite greater basal area. Sap flux velocity was lower in evergreen trees than in deciduous trees, and sap flow differences were twice as strong for transpiration per sapwood area, suggesting that old growth trees may utilize their sapwood more conservatively than second growth trees. Our findings indicate that historic land use likely increased transpiration in the northern Great Lakes Region. Understanding this and other long term effects of land use is critical for understanding the future of Midwestern landscapes</p> |
| <p>43</p> | <p>Getting to the Root of it: Variations in Root Morphology and Biological Nitrogen-Fixation among Switchgrass Varieties</p> <p>*Tayler Chicoine, Sarah S. Roley, G. Philip Roberston, Lisa Tiemann, Maren Friesen, Sarah Evans</p> <p>Switchgrass (<i>Panicum virgatum</i>) is a C4 perennial grass being explored for its promise as a low-input bioenergy crop. Switchgrass has unique nitrogen (N) conservation strategies, such as associating with free-living N-fixers (diazotrophs) that help it survive in N-limited, degraded soils. A recent study found that a higher yielding switchgrass variety associated with a larger community of diazotrophs than a lower-yielding variety, though it is unknown what drives these differences in their diazotrophs. Root morphology, also shown to vary among switchgrass varieties, is known to influence root exudation rates, which directly impact the amount of carbon (C) available to energetically-demanding N-fixation processes. We are investigating the relationship between specific root length (SRL) and the N-fixing potential of the microbial communities across 12 switchgrass varieties, at Kellogg Biological Station in southwest Michigan. We predict that N-fixation rates and gene abundance (nifH) differ among the varieties and that this is driven by differences in root morphology. Specifically, if thinner root systems (higher SRL) provide more C through exudation, we expect to find higher N-fixation potential. Discerning what plant characteristics support diazotrophic communities has important implications for the development of low-input agricultural systems. Funding: Great Lakes Bioenergy Research Center (US DOE Office of Science: DE-FCO2-07ER64494 and Office of Energy Efficiency and Renewable Energy: E-ACO5-76RL01830) and Department of Energy BER Genomics Program.</p> |

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| 44 | <p>The Plant Cuticle in Arid Land Decomposition: Interactions with Sunlight and Non-Rainfall Moisture</p> <p>*Robert Logan, Kathryn Jacobson, Peter Jacobson , Sarah E. Evans</p> <p>Current decomposition models underestimate mass loss and carbon emissions from arid lands suggesting novel mechanisms may be at play; these include the interaction of photodegradation, unique microbial communities, and plant litter chemistry, which can influence decomposition rates. Recent research has shown that non-rainfall moisture (fog, dew, and high humidity) can also lead to significant decomposition of aboveground standing litter by facilitating microbial decomposition, even in the absence of rain. We propose a new mechanism by which photodegradation of the outer cuticle on dead standing litter acts as a threshold process permitting microbial colonization and growth only after the outer water-resistant layer has been removed. This suggests new interactions between non-rainfall moisture and plant litter physical properties are important factors in dryland decomposition.</p> |
| 45 | <p>How does cover crop composition affect the soil nitrogen environment?</p> <p>*Eleanor E. Lucadamo, Ashley A. Holmes, Sam E. Wortman, Anthony C. Yannarell</p> <p>Cover crops can provide numerous benefits to agroecosystems. When planted in mixtures, cover crop residues decompose at varying rates, supplying plant-available nitrogen over a broad range of time. However, it is not yet understood how cover crop composition affects the rate of plant-available nitrogen release. The present study aims to explore how cover crop mixtures alter the soil nitrogen environment (nitrate, ammonium and potentially mineralizable nitrogen) on two organic farms in Illinois. Soils were collected at multiple days after termination to measure the change in nitrogen pools over time. Results from 2015 show that, across all cover crop treatments, ammonium levels are highest within the first 7 days after termination in plots with high cover crop biomass. Nitrate levels are highest within first 12 days after termination, though results varied by site. Potentially mineralizable nitrogen was most influenced by biomass and site. While site-specific microbial communities may be responsible for differences between the farms, nitrogen levels were generally correlated with cover crop biomass, and no variety of cover crop or mixture generated significantly higher soil nitrogen levels than any other. Our results suggest that cover crops that produce high biomass provide greater plant-available nitrogen to the soil.</p> |
| 46 | <p>Vegetation response to prescribed fire in an oak-hickory forest invaded with <i>Rhamnus cathartica</i> (European buckthorn)</p> <p>*Bret Powers, Abigail Hughes, Alice McNamara, Molly McNicoll</p> <p>Understory vegetation can be altered by fire suppression in Midwestern oak woodlands. Re-introduction of low intensity prescribed burns may have the added benefit of reducing invasive species, such as European Buckthorn (<i>Rhamnus cathartica</i>), although this interaction has not been fully investigated experimentally. We examined the effects of a single prescribed burn in permanent vegetation plots in <i>R. cathartica</i>-invaded and non-invaded areas in an oak-hickory forest. In non-invaded areas of the forest, average herbaceous species richness and percent cover were greater in plots with prescribed fire than without. In areas invaded with</p> |

R. cathartica, average species richness and cover were lower in burned than unburned plots. Average percent cover of *R. cathartica* was lower in burned than unburned plots, although most commonly this reflected top-kill of *R. cathartica*, rather than outright death of the invasive. In non-invaded areas, forest floor vegetation may have the capacity to respond more quickly after fire, whereas that capacity may be suppressed or absent in areas with a history of *R. cathartica* invasion. It is likely that reduction of *R. cathartica* and response from native understory vegetation will likely be stronger after multiple prescribed fires.

Disease Ecology

Poster 47 - 50

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| <p>47</p> | <p>Prairie Dependent Small Mammals Represent Potential Reservoir of <i>Bartonella</i> spp.</p> <p>*Malcolm Engelbrecht, Sean Beckmann</p> <p><i>Bartonella</i> is a genus of gram negative, blood borne, parasitic bacteria; that includes several species known to cause of disease, including Cat Scratch Fever and endocarditis. These bacteria are transmitted via the bite of arthropod vectors that have already fed on infected animals. However, little is known about which animals serve as reservoirs of the pathogen. This study sought to determine if prairie dependent small mammals serve as potential reservoirs of <i>Bartonella</i> in Northern Illinois. Over the course of two years, over 400 small mammals were captured and identified to species on a prairie restoration n Boone County, IL. Tissue samples were collected and tested for the presence of <i>Bartonella</i> spp via PCR. Infection rates were calculated and compared between years to look for any significant changes in the prevalence of <i>Bartonella</i>. <i>Bartonella</i> was present in all mammal populations tested, with an overall infection rate of approximately thirty percent. There was no significant difference in infection rate across years. These findings suggest that small mammals may represent reservoirs of <i>Bartonella</i> spp. in northern Illinois prairie ecosystems.</p> |
| <p>48</p> | <p>Bouts of Dehydration Prompt Phenotypic Alterations and Increase Blood Feeding Propensity in Mosquitoes</p> <p>*Christopher J. Holmes, Richard W. Hagan, Elise M. Szuter, Andrew E. Rosselet, Samantha C. Siler, Andrew J. Rosendale, Jacob M. Hendershot, Kiaira S.B. Elliot, Emily C. Jennings, Alex E. Rizlallah, Yanyu Xiao, Jason L. Rasgon, Miki Watanbe, Lindsey E. Romick-Rosendale, Joshua B. Benoit</p> <p>Mosquitoes are a major factor in the transmission of arthropod-borne disease. Despite extensive focus on the relationship between mosquitoes, environment, and disease transmission, the effects of dehydration on mosquito biology is vastly understudied when compared to temperature. In this study, <i>Culex pipiens</i> were exposed to short bouts of dehydration and phenotype changes were analyzed with metabolomics, RNA-seq, and behavioral monitoring. Metabolomics and RNA-seq revealed altered trehalose to glucose conversion but yielded negligible alterations in major nutrient reserve levels. Targeting trehalase with RNA interference suppressed trehalose breakdown and decreased dehydration-associated phenotypes. To</p> |

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| | <p>differentiate between the effects of exposure to desiccation conditions and actual water loss, groups were subjected to dehydration conditions with and without access to free water, or were permitted a rehydration opportunity. The groups with access to free water or following rehydration displayed no behavioral changes, while activity monitoring and landing assays suggested an increased propensity for blood feeding in dehydrated <i>C. pipiens</i>. Complementary results were noted in <i>Aedes aegypti</i> and <i>Anopheles quadrimaculatus</i>. These results suggest dehydration-induced phenotypes prompt mosquitoes to seek a bloodmeal as a rehydration mechanism. This elevated propensity to blood feed is predicted to increase transmission of West Nile virus by <i>C. pipiens</i>.</p> |
| <p>49</p> | <p>Investigation of Viral Suppression of RNA interference in the Honey Bee <i>Apis mellifera</i></p> <p>*Allyson M. Ray, Adam R. Hamilton, Gene E. Robinson</p> <p>Honey bees have exhibited a persistent global decline in health and population during the last several decades, and it is strongly suggested that pathogens, including RNA-based viruses, are a contributor to this phenomenon. RNA interference (RNAi) is a critical component of the insect immune response against these RNA-based viruses. Recently, evidence of viral suppressors of RNAi has been described within two <i>Drosophila melanogaster</i> viruses, Drosophila C virus and cricket paralysis virus. These pathogens belong to the same order as many viruses targeting honey bees, suggesting a potentially similar factor of increased potency of these viruses. This suggests that viral levels could be related to the efficacy of treatments employed by researchers to utilize the RNAi system to manipulate gene expression in a targeted manner. Here we show that colony level viral load of multiple honey bee viruses quantified via RT-qPCR in relation to decreased efficacy of experimental genetic knockdown via RNAi. These results suggest that viral suppression of RNAi may be an important factor limiting RNAi efficacy in targeted experiments as well as contributing to the decline in honey bee health.</p> |
| <p>50</p> | <p>Do prairie dependent small mammals serve as reservoirs of <i>Borrelia burgdorferi</i>?</p> <p>*Taggart A.E. Venegas, *Rhonda J. Freund, Sean M. Beckmann</p> <p>Rodent species, particularly members of the genus <i>Peromyscus</i>, serve as reservoirs for tick borne diseases such as Lyme disease. Over the last twenty years, cases of Lyme disease in humans have markedly increased. In particular northern Illinois and southern Wisconsin are hotbeds of Lyme diagnoses. This area is also home to many tallgrass prairie restorations. This study sought to identify rodent reservoirs of Lyme disease in prairie habitats. During the summer of 2016, tissues samples were collected from rodents on a prairie restoration in Boone County, Illinois. Five species of rodents were captured: <i>Spermophilus tridecemlineatus</i>, <i>Microtus pennsylvanicus</i>, <i>Microtus ochrogaster</i>, <i>Peromyscus maniculatus</i>, and <i>Zapus hudsonius</i>. <i>Zapus hudsonius</i> was the most abundant and <i>Microtus ochrogaster</i> was the least. <i>Borrelia burgdorferi</i>, the causative agent of Lyme, was found in all five species via PCR amplification of Flagellin B using <i>Borrelia</i> specific primers. Approximately 35% of rodents sampled were positive with infection rates ranging from ~20% in <i>P. maniculatus</i> to greater than 50% in <i>M. pennsylvanicus</i>. Engorged and questing ticks were also collected, with a large percentage of those testing positive for Lyme. Data indicate that prairie restorations</p> |

may harbor substantial amounts of Lyme disease and that several non-Peromyscine species may represent disease reservoirs.

Microbial Ecology

Poster 51 - 58

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| 51 | <p>Evaluation of Mycorrhizae as a Determinant of Chestnut Success</p> <p>*Pabitra Aryal, Scott J. Meiners</p> <p>Although agriculture focuses on row crops throughout much of the Midwest, chestnut appears to be an agroforestry crop well suited as a sustainable alternative in the region. As ectomycorrhizal (ECM) colonization is often crucial for tree establishment and production, we addressed the importance of ECM colonization on chestnut performance by assessing 1) natural ECM colonization in an established chestnut orchard and 2) the effect of ECM inoculation on seedling establishment and drought response in a greenhouse. We selected 50 Chinese-American hybrid chestnuts (Dunstan) trees in a commercial orchard and assessed their level of mycorrhizal colonization in relation to environmental factors. In the green house, we grew 80 seedlings from this orchard with and without mycorrhizal inoculation. Half were harvested to assess inoculation success and biomass, the remainder were subjected to experimental water stress and evaluated with chlorophyll fluorescence. In the orchard, ECM colonization was low and decreased with distance from adjacent oak forest. Inoculation increased above ground biomass significantly and reduced stomatal area, length and width. Inoculated seedlings recovered significantly faster from water stress. Our study clearly indicates that ectomycorrhizal colonization can be limiting in orchards and can help chestnut trees in their early growth and further establishment.</p> |
| 52 | <p>Search for a high efficiency strain that allows the organic production of soy in the north of Spain</p> <p>*Aran Del-Canto, A. Sanz-Sáez, B. Tellechea, A. Moreno, J. Miranda, A. Yoldi, A. Ortiz-Barredo, J. B. Relloso, M. Lacuesta</p> <p>In Spain, soybean planted area is very limited but its consumption has increased in recent years, being the first importer of the EU. For this reason, the local cultivation of organic soybean can be an interesting alternative not only for consumers and farmers but also for the environment. However, because it is not a traditional crop, its productivity is low due to lack of adapted cultivars and the absence of native strains in the soil.</p> <p>This study evaluated the production of soybean in organic and traditional managements in the north of Spain, either in the absence or presence of different <i>Bradyrhizobium japonicum</i> strains (SFJ14-36, SFJ4-24 and USDA110). During growth, plant physiological status was evaluated by estimating the leaf nitrogen concentration, plant height, and seed yield and quality.</p> |

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| | <p>In general, production of soybean was higher in inoculated plants, although the efficiency varied with the different strains tested. The high field effectiveness of the USDA110 strain was favored by the absence of native soybean <i>Bradyrhizobium</i> in the soil. In addition, there were no differences in production between both management practices, supporting the idea that organic soybean cultivation may be an interesting option for productive and sustainable agriculture in Spain.</p> |
| <p>53</p> | <p>Does the apple fall far from the tree? Intrauterine development and microbial inheritance in a live-bearing cockroach</p> <p>*Emily C. Jennings, Trinity L. Hamilton, Joshua B. Benoit</p> <p>Animals share their bodies with a diverse suite of microorganisms known as the microbiome. These microbes, especially those found in the gut, have been found to play important roles in a variety of processes, from nutrient metabolism to immune development. Extensive and complex interactions between mother and offspring during gestation and birth allow maternal experiences to affect progeny health. One mechanism is vertical transmission of microbes from mother to offspring. The importance of the microbiome composition and transmission in development is not limited to humans. In fact, invertebrate systems offer opportunities to conduct studies on microbiome-development dynamics. One such invertebrate is the cockroach, <i>Diploptera punctata</i>. Female <i>D. punctata</i> carry embryos in their brood sac, which acts as the functional equivalent of the uterus and placenta. 16S rRNA sequencing was used to characterize maternal and embryonic microbiomes, identifying 28 phyla and 161 families overall. Bacteroidetes and Firmicutes are the most abundant phyla in mothers, while Bacteroidetes was the only phylum identified in embryos, with Blattabacteria being the only genus having significant representation (99.4% of reads from embryos map to this genus). This suggests that <i>D. punctata</i> offspring, like humans, likely acquire additional endosymbionts for an adult microbiome during and after birth</p> |
| <p>54</p> | <p><i>Lespedeza cuneata</i> impacts nitrogen cycling at John English Prairie</p> <p>*Sarah E. Kania, Alyssa M. Beck, Victoria A. Borowicz, Anthony C. Yannarell</p> <p><i>Lespedeza cuneata</i>, a problematic grassland invader, is known to alter plant and microbial community composition at invasion sites. <i>L. cuneata</i> was first recorded in John English Prairie, McLean County, Illinois in 2006. The goal of this study was to examine how <i>L. cuneata</i> biomass, soil nitrogen availability, and the potential for microbial nitrogen cycling have changed over time at this site. From 59 permanent 1m² plots, we collected aboveground <i>L. cuneata</i> biomass in 2006, 2009, 2010, 2011, and 2016, and soil samples in 2011, 2014, and 2016. We used soil samples to conduct potential mineralization and nitrification assays and to determine soil nitrate and ammonium concentrations. <i>L. cuneata</i> biomass increased dramatically between 2011 and 2016. Soil nitrate and ammonium concentrations decreased during this time. 2016 <i>L. cuneata</i> biomass was positively correlated with soil ammonium concentration and negatively correlated with potential nitrification, but was not correlated with either soil nitrate or potential mineralization. These results suggest that <i>L. cuneata</i> may reduce the ability of the soil microbial community to perform nitrification processes, and thereby lead to increased soil ammonium concentrations. This study shows that <i>L. cuneata</i> invasion may have substantial impacts on soil properties and communities at John English Prairie.</p> |

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| 55 | <p>Horizontal Gene Transfer in Soil Microbial Communities</p> <p>*Heather Kittredge, Kevin Dougherty, Sarah Evans</p> <p>Horizontal gene transfer (HGT) or the movement of genetic components between bacterial species is often cited as a central force in microbial evolution. In soil, pools of extracellular DNA (eDNA) build up as cells lyse, providing the materials needed for HGT, but other properties of soil are also likely to influence rates of HGT. For example, the spatial heterogeneity of soil can prevent eDNA from coming into contact with bacteria. While model systems for bacterial evolution have extensively studied the mechanisms of HGT at the cellular level, little is known about the rate of HGT in natural environments and the role this process has played in the evolutionary history of bacterial populations. Using gas reporters instead of traditional visual reporters (i.e. GFP) allows us to track HGT directly in soil. This system imposes a direct correlation between HGT events and production of a volatile methyl halide gas that can be measured using gas chromatography-mass spectrometry (GC-MS). Quantifying rates of HGT using gas reporters in complex environments informs our understanding of how HGT may have facilitated microbial diversification and can inform predictions on the extent that microbial communities can adapt to rapid environmental change.</p> |
| 56 | <p>Restoration ecology in the honey bee by tree hive colonies that promote probiotic fungi</p> <p>*Andre Lorenz</p> <p>Tree hollows above the ground are natural habitat for honey bees, <i>Apis mellifera</i>. By mounting hive boxes in trees, it has been noted that bees have greater access to a larger diversity of food, more overwinter successfully, and less are impacted from predation by raccoons, yellow jackets, and skunks. Lynn Royce (http://treehivebees.com) devised this concept of returning bees to trees with hopes of strengthening the colony in response to colony collapse disorder. Beneficial colony fungi that act as probiotics were the subject of this study. Fungi were cultured, enumerated and identified from bee bread, the fungal fermentation product of stored pollen that is fed to bee larvae, to determine whether the mycoflora profile differs between tree versus ground colonies that are in the same habitat. <i>Aspergillus</i>, <i>Penicillium</i>, <i>Cladosporium</i>, and <i>Rhizopus</i> were major isolates in bee bread, and tree colonies contained about two-times more fungi than the ground colonies. When tested in competition bioassays, these fungi, alone and in combination, slowed or inhibited growth of the agents of chalkbrood (<i>Ascosphaera apis</i>) and stonebrood (<i>Aspergillus flavus</i>) diseases. Inhibition of these pathogens by more concentrated beneficial fungi from tree colonies was more rapid. Our conclusion is that tree colonies are more resistant against disease.</p> |
| 57 | <p>The Effect of Intercropping White Clover on Aspects of the Microbial Soil Ecosystem in Small Scale Market Gardens</p> <p>*Michael Michalski, *Jennifer Winther</p> <p>Little is known about soil ecosystem function in agricultural systems and how agricultural practices impact organisms within soils. Intercropping a living mulch is a sustainable agricultural practice that potentially decreases input requirements by promoting soil ecosystem functions and suppressing weed growth. This last</p> |

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| | <p>summer's Global Agricultural Sustainability Class (BIO 319) established and maintained an experimental plots containing vegetable crops with (Experimental) and without (Control) intercropped white clover living mulch. This project documents the effects of the treatment on the soil ecosystem. Microbial DNA extracted from soils sampled before planting and after crop establishment (but before clover intercropping) suggests more than 5,000 microbial species were initially present. Microbial metabolic activity measured as soil respiration suggests high soil microbial activity was present. Analysis of the results is ongoing, and current findings are presented.</p> |
| 58 | <p>Host symbiont feedbacks in the legume rhizobia mutualism</p> <p>*Taylor Weathers, Emily Davis, Katy Heath, Mike Grillo</p> <p>The mutualistic relationship between legumes and the microbe rhizobia is one of the most important mutualisms observed in nature. In this mutualism rhizobia fixes the atmospheric nitrogen into ammonium in the soil, that the plants can readily use. In this experiment we aim to look closer at this mutualism and see whether there is a feedback response associated with different species of <i>Trifolium</i> being planted on soils trained by another species(i.e. <i>Trifolium repens</i> planted on soil trained on <i>Trifolium hybridum</i>). We inoculate all of the soils with a three strain mix(1:1:1 ratio) of rhizobia and plant each species and genotype on their own soil for three training generations. Once we have finished training and testing the different species on different soils, we aim to ask three questions: will planting a species on soil that has been trained by a different species result in success for that species?, Will certain plant genotypes preferentially chose a strain in which to form a symbiosis?, and Does the composition of soil microbe communities actually affect the composition of plant communities (in this case clover)? We predict that plants that have been successful in the past based on previous studies will continue to be successful and that the plants will preferentially choose a specific rhizobia strain based on how closely the mutualism is mimicked in nature.</p> |

Population and Community Ecology

Poster 59 – 78

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| 59 | <p>Fetal data reveal reproductive trends in white-tailed deer (<i>Odocoileus virginianus</i>)</p> <p>*Mario A. Barenas, Michelle L. Green, Nohra E. Mateus-Pinilla, Jan E. Novakofski</p> <p>White-tailed deer (<i>Odocoileus virginianus</i>) have the highest economic value and the largest population size of the <i>Odocoileus</i> genus. Management of large populations requires knowledge of reproductive characteristics to inform practices. We analyzed fetal sex ratio, fetal growth, pregnancy rate, and litter size in Illinois white-tailed deer to understand current population dynamics.</p> <p>Female age class (fawn, yearling, adult) and location were known. Fetuses were collected by the state disease management program. We weighed fetuses, measured the crown-rump length, recorded the sex, noted litter size, and collected</p> |
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| | <p>tissue from the semimembranosus muscle for further analysis. We used length to estimate conception date and BMI to assess body size.</p> <p>We analyzed 3,884 females with 4,781 fetuses. We found pregnancy rate, litter size, and fetal size increased with maternal age. On average, 65.5% (\pm 31.4) of females were pregnant and carrying average litters of 1.9 (\pm 0.54) fetuses. Sex ratio was 1:1 and male fetuses were larger than their female counterpart.</p> <p>Resource availability, in particular nutrition, is a major contributor to reproduction in wild animals likely because nutrition is linked to body condition. As females age, they likely gain body size and improve reproductive output, thus affecting population size and herd health.</p> |
| <p>60</p> | <p>Territoriality of The Chestnut-Sided Warbler (<i>Setophaga pensylvanica</i>) in a Dynamic Landscape</p> <p>*Mary Benjamin, Sarah Mabey</p> <p>Chestnut-sided warblers (CSWA) are neotropical migrants that commonly breed in second-growth forest habitats of Northeast North America. During summer of 2016, individuals were detected at the James H. Barrow Field Station (JHBFS), not previously known to provide habitat for CSWA. In this study, song playback was used to map CSWA territories and determine method of habitat selection. Fifteen territories were mapped within second-growth and old-growth forest. Potential vegetation cues were measured by assessing the following variables within territories and paired random sites: canopy cover, ground cover, canopy height, vegetation density, presence of shrub species, woody species composition, and woody species size. No significant difference was detected for any vegetation variable in second-growth forest (all $P > 0.05$), suggesting that vegetation is homogenous. Territories showed a clumped distribution, indicating conspecific cues produce social neighborhoods. There was significant difference in the old-growth forest in two variables, suggesting that vegetation is heterogenous. Territories were further apart than those at the successional forest indicating significance of vegetation cues. Due to limited samples, few confident conclusions can be drawn; however trends can give a possible interpretation. It appears that CSWAs follow a hierarchy of cues in habitat selection and are possibly distributed according to dominance.</p> |
| <p>61</p> | <p>Effects of global warming on multiple mutualist interactions</p> <p>*Logan E.G. Brissette, Kane R. Keller, Mark Hammond, Jennifer A. Lau</p> <p>Climate change is changing the way organisms interact with their environments, and is even impacting inter-organism interactions. For mutualistic species these changes may alter host fitness by impacting symbioses and interactions within communities. In this experiment, we full-factorially manipulate two mutualisms associated with the legume <i>Chamaecrista fasciculata</i>, nitrogen fixing soil bacteria (<i>Rhizobia</i> spp) and protective ants. Our experimental treatments were temperature (ambient or elevated by 3°F), rhizobia inoculation (presence or absence), and ants (with or without, using Tanglefoot). The experiment was regularly censused by counting the number of ants per plant, measuring plant phenology, and plant fitness was measured at the end of season by counting fruits and seeds. Increased temperature resulted in more flowers blooming earlier and ant presence increased</p> |

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| | <p>plant fitness. Increased fitness is likely due to ant defense reducing herbivory. However, interestingly, rhizobia inoculation decreased fitness under ambient temperature, but increased fitness at elevated temperatures. Results indicate there may be a carbon trade-off for <i>C. fasciculata</i> between ants and rhizobia in ambient temperatures. Yet, rhizobia availability under elevated temperatures does not significantly influence ant abundance. Overall, spatiotemporal variation in herbivory and nutrient limitation may influence plant fitness from these two mutualisms over time.</p> |
| <p>62</p> | <p>Increased root-knot nematode suppression in endosymbiotic vs non-symbiotic morning glory roots</p> <p>*Lekeah Durden, Dong Wang, Keith Clay</p> <p>Some species of morning glories (Convolvulaceae) form endosymbiotic relationships with seed-transmitted fungal symbionts that colonize only above-ground tissues. These fungi produce ergot-alkaloids, which may contribute to plant-fungal defensive mutualisms. A previous study focused on alkaloid allocation in <i>Ipomoea tricolor</i>, found that these alkaloids are distributed to the roots. The root-knot nematode, <i>Meloidogyne incognita</i>, prefers to colonize young roots, causing systemic damage to the plant and often resulting in crop losses. The aim of this study was to determine whether the fungal endosymbiont suppresses nematode colonization, thereby enhancing host fitness. We hypothesized that symbiotic <i>I. tricolor</i> plants (E+) will have fewer nematodes colonizing roots than non-symbiotic plants (E-). To test this hypothesis, E+ or E- seeds either were germinated in the greenhouse. One-week old seedlings were then exposed to soil infested with either high nematode densities or no nematodes. After 3 weeks we quantified root colonization and plant biomass. We found that E+ plants decreased nematode infection by 50%, but there were no significant differences in plant biomass. Our results demonstrate fungal endosymbiosis within the plant can reduce below-ground biotic stressors. Applying these results could create safer environmental practices for nematode management.</p> |
| <p>63</p> | <p>Exploring a possible link between urban gardens and wild remnant plant populations</p> <p>*Andrea Feters, Tia-Lynn Ashman</p> <p>Urbanization reduces plant and pollinator biodiversity, as well as the plant-pollinator interactions that provide necessary ecosystem services (i.e. pollination). To mitigate these losses, cities have implemented urban garden initiatives that aim to preserve plant and pollinator biodiversity. Although such practices have been successful, there are several effects of human-mediated plant introductions on the surrounding landscape that remain unstudied. Therefore, I hypothesized that a planted species (<i>Heliopsis helianthoides</i>) and wild remnant species (<i>Impatiens pallida</i>, <i>Impatiens capensis</i>) interact via shared pollinators, that the planted species competes with the wild remnant species for pollinators, and that the presence of the planted species changes the pollinator community composition of wild remnant populations. Pollinator observations in Pittsburgh showed that the focal species share pollinators, that pollinators spend less time on either <i>Impatiens</i> when <i>H. helianthoides</i> is present, and that the composition of the pollinator community of either <i>Impatiens</i> is altered with the presence of <i>H. helianthoides</i>. The planted species gave pollinators more foraging choices, which places importance on</p> |

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| | <p>species-specific evolution of floral characteristics to allow the coexistence of several co-flowering species. Broader studies along an urban gradient, along with experiments that explore the fitness impacts on wild remnant species, could inform comprehensive management practices.</p> |
| <p>64</p> | <p>Snake species diversity and abundance in unmanaged successional grasslands of different ages</p> <p>*Meredith Fitschen-Brown, Matt Sorrick, Jennifer Clark</p> <p>Habitat destruction/fragmentation of grassland biomes has led to decreased biodiversity of vertebrate taxa. Of these vertebrate taxa, however, little is known about the persistence of snake communities. During the summer of 2016, we assessed snake species diversity and abundance in three ages of unmanaged successional grasslands: four years old (Eagle Creek Restoration Site [ECRS]), 12 years old (Stavenger), and 50+ years old (Black Walnut Grove [BWG]) (Hiram, OH). Ten corrugated metal and ten plywood cover boards were used at each site and both morning and evening surveys were conducted. A total of 87 snakes were caught and four species were identified (Northern brown snake, red-belly snake, Eastern garter snake, and Eastern milk snake). Species richness and abundance were significantly higher at ECRS than Stavenger and BWG (ANOVA, both $P < 0.0001$; Tukey's, $P < 0.05$) with Stavenger and BWG showing similar species richness and abundance (Tukey's, $P > 0.05$). There was also a significant effect of board type with higher species richness (ANOVA, $P = 0.0030$) and abundance (ANOVA, $P = 0.0009$) under plywood boards. However, there was no significant effect of time of day on species richness or abundance (ANOVA, both $P > 0.05$). These results suggest that northeast Ohio grassland snake populations prefer younger successional grasslands and plywood cover boards.</p> |
| <p>65</p> | <p>Drought occurrence, topography, and soils predict the geographic distribution of an arid-land annual plant, <i>Clarkia xantiana</i> ssp. <i>xantiana</i></p> <p>*Aidan Healey, Vincent M. Eckhart</p> <p>Species' geographic distributions are largely defined by their tolerance of varying environmental conditions. In its semi-arid environment, the distribution of the annual plant <i>Clarkia xantiana</i> ssp. <i>xantiana</i> responds to water availability, and variables relating to water availability have been used to model its distribution. In this study, I apply general linear modeling techniques to update previous models using longer-term climate data, and I incorporate both high and low extreme seasonal precipitation values into these models. Models built on longer-term climate data provided a better fit than models built on shorter-term data, and extreme precipitation values representing extended drought periods further improve the fit; higher overall and drought-period precipitation, igneous soil, and south-facing azimuth increased the probability of <i>C. xantiana</i> presence. These GLMs showed high habitat suitability at higher elevations near the range center, with decreasing suitability along the eastern range edge. High elevation areas of the current range, where abiotic environmental conditions are less limiting than at low elevations, may become future refuges. Habitat suitability models created using Maxent corroborated these predictions.</p> |

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| <p>66</p> | <p>Habitat quality and macroinvertebrate communities within streams of the Mill Creek Watershed, Cincinnati, Ohio</p> <p>*Kyle Madoni, Sophie Racey, Mollie McIntosh</p> <p>The Mill Creek Watershed has been exposed to urbanization and suffered from resulting runoff, sewage, and channelization as it flows through the Greater Cincinnati area into the Ohio River. The main objective of this study was to obtain baseline data on habitat quality and macroinvertebrate communities within the Mill Creek Watershed. Single assessments were conducted at a total of nine sites found within four streams of the watershed from July 11-16, 2016. Habitat metrics were assessed using the Ohio Qualitative Habitat Evaluation Index (QHEI) protocol that inferred habitat and stream quality. At each site, three quantitative macroinvertebrate kick samples were collected in separate riffle habitats and one qualitative macroinvertebrate sample was combined from all stream habitats present (riffle, run, pool, glide, and margins). All macroinvertebrates were then identified to family level. Habitat quality was highly variable across all sites, both within and among streams, with QHEI scores ranging from very poor to excellent. A total of 6,951 macroinvertebrates were identified, representing 50 distinct families, and were dominated by the Chironomidae, Hydropsychidae and Baetidae. Macroinvertebrate metrics were also highly variable across the nine sites probably due to the combined effects of multiple, variable stressors present throughout the watershed.</p> |
| <p>67</p> | <p>Germination and Community Dynamics of Parasitic Plants</p> <p>*Drake Mullett, Jeremie Fant</p> <p>Although it is thought that parasites increase diversity and promote species evenness within a community by suppressing dominate species, when looking at the impact of parasites on a host species, there have been conflicting observations. In some instances the parasite was found to decreases the biomass of the host but in other instances the host biomass is unchanged and even increased biomass in some species. These conflicting observations suggest this relationship, can range from parasitic, to commensalistic and even potentially mutualistic. More importantly, it raises the questions of what can drive the switch from negative to positive relationship. Some potential drivers could be nutrient availability or it could be an herbivory compensatory response. Also, is biomass the best indicator of host fitness? What is the response of parasite on host reproductive output? And how do other environmental stresses impacts the relationship. Investigating how a parasitized host responds to the stress of parasitism and how that affects their fitness and biomass in more or less stressful conditions can help us understand the role of parasites within a community. Therefore, for this study, I will investigate how different parasites impact their host plants fitness and how the nature of this relationship changes under a variety of different conditions, particularly under less stressful situations (more nutrients) and additional stress (herbivory). I will make this comparison using different types of parasites, stem versus root.</p> |

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| <p>68</p> | <p>A survival mechanism (anhydrobiosis) in a branchiobdellid worm that facilitates symbiosis for improving health of crayfish</p> <p>*Blake W. Nelson, Andre L. Lorenz, Jay A. Yoder</p> <p>We report that the freshwater branchiobdellid <i>Cambarincola mesochoreus</i> is anhydrobiotic. This worm reverses freely and multiple times between an active crawling state (hydrated) and an immobile, coiled, desiccation-resistant state (dehydrated) by the removal and addition of water. The coiled state is modified for enhanced water conservation and survival, losing water at about three-times the rate as the active crawling form. Adding a drop of water re-activates the worm, and this causes a water loss rate increase that coincides with increase crawling activity. This worm displayed a requirement for contact with a wet surface in attraction bioassays using agar films having a high water activity. The worms use crayfish as a site for reproduction, in turn, keep the gill chambers and body of the crayfish free of debris. Upon emersion, worms migrate to spaces on the crayfish where water collects. Further drying initiates the water-conserving, coiled form of the worm, which reverses into the crawling form once the crayfish returns to water in a pool or burrow. We conclude that this cleaning symbiosis with crayfish is favored in temporary streams by this worm's capacity for facultative quiescence.</p> |
| <p>69</p> | <p>Vegetation Preferences for Two Different Species of Closely Related Mice</p> <p>*Jeremy Papuga, Susan Hoffman</p> <p>The competitive exclusion principal states that no two species can exist in the same habitat and occupy exactly the same niche. Therefore, for species to coexist they must partition their resources in order to both survive. Otherwise, the better competitor will drive the other to local extinction. Two species of mice, <i>Peromyscus leucopus noveboracensis</i> (PLN) and <i>Peromyscus maniculatus gracilis</i> (PMG) are closely related and cohabitate in much of the southern Great Lakes Region. They are similar ecologically and can often be found in the same patch of forest. However, the two species are normally found in different relative proportions. I hypothesize that despite their similar ecology, the two species prefer different vegetative properties, which allows them to coexist. I trapped 6 different sites of varying compositions, two high PMG, two equal proportions, and two high PLN. I also categorized different aspects of vegetation that would be relevant to both species. I found that the high PMG sites tended to have higher average diameter downed wood, lower percent canopy closure, lower percent cover of leaf litter, and higher percent cover of shrubs compared to the high PLN sites. This difference in vegetation preference may be enough niche differentiation to allow cohabitation.</p> |
| <p>70</p> | <p>Temporal patterns of small mammal communities in a prairie restoration</p> <p>Sean Beckmann, *Nicholas Naber, *Casey Pettit</p> <p>Anthropogenic destruction for agricultural, residential, and commercial purposes has caused tallgrass prairies to become one of the most endangered habitat types in the world. Restoration efforts have successfully reestablished native plant populations through methods such as seeding and controlled burns. However, it is necessary to assess the effects of these efforts on animal communities as well. This study focused on the community dynamics of small mammals in a small prairie restoration over the course of four years. Animals were trapped in two prairie</p> |

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| | <p>patches in different stages of ecological succession from 2013-2016. <i>Spermophilus tridecemlineatus</i>, <i>Microtus ochrogaster</i>, <i>Microtus pennsylvanicus</i>, <i>Peromyscus maniculatus</i>, and <i>Zapus hudsonius</i> were captured and the abundances of each were compared. Species richness, Simpson's diversity index (D), Shannon's diversity index (H), species evenness, and Peterson's homogeneity index were calculated for each patch for each year and comparisons were made between the patches. Vole populations experienced a decrease during the study. Other species have shown large population increases. Diversity also increased over the course of the study. Additional monitoring is necessary to understand long term population trends in small prairie patches such as this.</p> |
| <p>71</p> | <p>Canopy ant communities along an urban-rural gradient</p> <p>*Daniella C. Prince, Benjamin J. Adams, Chloe Lash, and Stephen P. Yanoviak</p> <p>Ant communities of tropical forest canopies are relatively well described, but few studies have examined ant communities in temperate forest canopies. Likewise, the effects of urbanization on arboreal ant community structure remain unexplored. We examined the structure of arboreal ant communities at two sites along an urban-rural gradient in metropolitan Louisville, Kentucky. We surveyed ants on 99 trees at the Horner Wildlife Sanctuary, a suburban forest, and 43 trees on the urban University of Louisville campus. We collected a total of 24 ant species across the two sites. Ant species richness increased with increasing tree size in the urban campus site, and trees with vines had marginally more ant species. The two most common ant species in the forest were the carpenter ants <i>Camponotus pennsylvanicus</i> and <i>C. subbarbatus</i>, which occurred in 27% of the trees. The cornfield ant, <i>Lasius alienus</i>, was found in 58% of the trees in the urban site. We found that three ant species in the forest contributed to distinctive community composition between tree species: <i>Camponotus subbarbatus</i> was most common in oaks (<i>Quercus</i>) and maples (<i>Acer</i>), <i>Formica subsericea</i> occurred most frequently in oaks, and <i>Crematogaster ashmeadi</i> was generally found in American Linden (<i>Tilia</i>). These results contribute to our knowledge of ant diversity in Kentucky, and further our understanding of the effects of urbanization on arboreal ant communities.</p> |
| <p>72</p> | <p>Larval Mosquito Abundance and West Nile Virus Positivity in wetlands of Southwestern Ohio</p> <p>*Alexander Reitz, Seth Buchholz, Calvin Larson, Sophie Racey, Dottie Engle, Jennifer Robbins, Mollie McIntosh</p> <p>West Nile Virus (WNV) is transmitted horizontally between adult mosquitoes and birds; however, evidence suggests that WNV may also be vertically transmitted, from adult mosquito to offspring. Once infected, adult mosquitoes can then transmit the virus to humans, with over 42,694 human cases being reported in the United States since the introduction of WNV in 1999. Vertical transmission of WNV has been demonstrated in a laboratory setting with little evidence of this collected in nature. The objective of this study was to assess larval mosquito populations overtime and to test for the presence of WNV in these wild populations. Samples were collected from May through October 2014-2016 at four wetland sites from the Cincinnati, Ohio region. Larval mosquito samples were collected from shallow-water edge habitats along the perimeter of each wetland to assess mosquito population abundance and test for WNV presence via PCR testing. At each site larval populations were dominated by <i>Aedes</i>, <i>Culex</i>, and <i>Anopheles</i> mosquitoes with</p> |

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| | <p>variable abundance observed overtime. Positive WNV larval mosquito populations were identified at all sites at variable times of the year in 2014 and 2015, with no positive populations identified in 2016.</p> |
| 73 | <p>Fire and Reproduction in <i>Liatris aspera</i></p> <p>*Lea Richardson</p> <p>Periodic fire in prairie remnants and restorations has been associated with increased flowering of native forbs. A common assumption is that these changes following fire can all be attributed to changing resource availability and competitive interactions between plants. However, previous studies with <i>Echinacea angustifolia</i> have suggested fire may improve female reproduction (seed set) by increasing temporal synchrony of flowering and spatial density of flowers. In this study, I assess whether similar mechanisms are at work in another common prairie species in the composite family, <i>Liatris aspera</i>. Throughout summer 2016, I monitored 90 randomly chosen <i>Liatris aspera</i> individuals, half in a burned unit and half in an unburned unit of Staffanson Prairie Preserve in Douglas County, MN. I recorded flowering phenology, gps data, and collected seed at the end of the season for each individual. Spatial density of flowering individuals, mean seed set, flowering duration, and number of inflorescences per individual was higher in the burned unit compared to the unburned unit, however flowering synchrony was similar in both units. Thus, there is evidence that burn treatments are associated with increased reproductive success in this <i>Liatris aspera</i> population.</p> |
| 74 | <p>Short-term responses in fish community structure and habitat following stream restoration</p> <p>*Andrew D. Runyon, *Neil B. Zook, Meredith S. Fitschen-Brown, Jennifer M. Clark</p> <p>In order to improve stream health, restoration efforts are common across the U.S. with more than \$1 billion spent annually. Long-term monitoring to assess the success of stream restoration, however, is limited with only 10% of streams monitored post-restoration. During the summer of 2013, a section of Eagle Creek (Hiram, OH) was restored and long-term monitoring efforts are in place to survey changes in abiotic parameters and habitat characteristics with an emphasis on their impact on fish communities. Electrofishing and habitat surveys were completed one year prior to restoration (2013), one-year post-restoration (2014), and three-years post-restoration (2016). Fish community structure was correlated to habitat variables with average fish size decreasing with decreasing canopy cover, substrate size, and water depth (Pearson's correlation, all $P < 0.03$); all significantly lower in new channel sites than other sites throughout Eagle Creek (ANOVA, all $P < 0.05$) and showing an overall trend towards less adult fishes in the system; particularly in the new channel. Although the short-term consequences on fish communities appear to be negative, long-term surveys are necessary to determine future recovery.</p> |
| 75 | <p>Alpha-Melanocyte Stimulating and Steroid Hormone correlates in lizard populations that vary in melanization</p> <p>*Ryan J. Seddon, Diana K. Hews</p> <p>A growing area of behavioral ecology examines how mechanisms underlying production of pigments can affect traits other than body coloration. Regulation of</p> |

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| | <p>melanin, which involves the melanocortin system, can directly and indirectly affect other phenotypic traits, such as aggression or physiology. Selection on one trait within a hormone-mediated suite of traits may lead to changes in the hormone signal, causing either beneficial or detrimental changes in correlated traits. These associations have been studied mainly in birds and mammals, but less so in reptiles. We studied correlation of melanization with these other traits, comparing between-population differences of adult male western fence lizards, <i>Sceloporus occidentalis</i>. We compared population in California where individuals are increasingly darker at higher elevations. We measured and confirmed that the higher elevation populations were more melanized. We measured baseline peptide and steroid hormones to compare hormone and melanization relationship across populations. While we did not find any significant differences in baseline levels of MSH, we found a positive relationship with baseline plasma testosterone and a negative correlation with baseline corticosterone. We describe potential differences in selective regimes that could produce these different patterns across vertebrates. These data suggest that hormonal pleiotropy does not constrain phenotypic variation.</p> |
| <p>76</p> | <p>White-tailed Deer Hunting and Habitat Use in Allerton Park</p> <p>*Noelle E. Thompson, Michelle L. Green, Michael G. Buhnerkempe, Marilyn O. Ruiz, Nohra E. Mateus-Pinilla, Jan E. Novakofski</p> <p>To help managers identify potential refuge sites and congregation among deer as a result of hunting pressure, we visualized changes in deer habitat use in Robert Allerton Park (RAP). The University of Illinois' RAP offers 1,500 acres of diverse habitat situated within east-central Illinois' predominantly-agricultural landscape. Since the 1980's, RAP has maintained a white-tailed deer research program. Before 2004, hunting was prohibited within RAP and it was seen as a refuge area for deer. Hunting began in 2004 to reduce population numbers and has continued each subsequent year.</p> <p>Since 1981, yearly aerial counts have been conducted following the hunting season. Using both RAP's deer data and the Illinois Natural Areas Inventory's vegetation data, our aim was to evaluate changes in deer habitat use influenced by hunting and to identify further changes in habitat use between years with and without culling in addition to their recreational hunting program.</p> <p>Preliminary spatial analysis using Global Moran's I and Getis-Ord General G spatial statistic tools indicates that a decrease in deer clustering has been observed within RAP after the implementation of hunting. These results could be due to hunting's behavioral effect on deer or due to the decrease in total deer on the landscape.</p> |
| <p>77</p> | <p>Effects of spatial temperature disparity on growth of <i>Picea glauca</i> near Lake Superior</p> <p>*Michael W. Wade, Jalene M. LaMontagne</p> <p>Many species are responding to climate change by adjusting their spatial distribution and altering their growth patterns. Populations near range boundaries are more susceptible to impact. Conifer species, such as white spruce (<i>Picea glauca</i>) have been studied near their northern range limit, but less work has been done in the south. We studied white spruce populations in Michigan along the</p> |

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| | <p>southern shore of Lake Superior. We also took advantage of a lake effect in the area, where inland areas can be up to 2°C warmer than the lakefront during the growing season. To record historical growth rates of <i>P. glauca</i> populations, core samples were collected from the three largest trees at six sites (3 near the lake, 3 inland) and ring width increments were measured. Trends in growth were compared to mean temperature differences across each site. We demonstrate the use of regional weather patterns, influenced at local scales by topographical features (e.g., the presence of large water bodies), to study the effects of climate change.</p> |
| 78 | <p>Con- and heterospecific leaf litter induces negative feedback in <i>Asteraceae</i> species</p> <p>*Max M. Zaret, Briana K. Whitaker, Keith Clay, Jonathan T. Bauer</p> <p>The plant-soil feedback framework has provided an effective model for understanding plant species coexistence. However, aboveground microbial communities can colonize plant seedlings via persistent leaf litter. Thus, there is potential to incorporate aboveground microbiota into the plant-soil feedback framework. In this experiment, we investigated how seedling establishment is affected by con- and heterospecific litter microbiota. Using a full-factorial experimental design, ten native <i>Asteraceae</i> species were exposed to con- and heterospecific leaf litter under controlled greenhouse conditions. After three weeks, seedlings were harvested and measured for plant biomass. Using the statistical framework developed for studies of plant-soil interactions, average pairwise feedback was calculated for each species. We found that four out of ten species experienced reduced growth when exposed to conspecific leaf litter relative to heterospecific leaf litter. These findings indicate that negative feedbacks can arise through plant species interactions with aboveground microbiota, and these interactions have the potential to stabilize species coexistence. These negative feedback effects could also be key factors in spatial patterns of seedling establishment, and mimic results from previous plant-soil feedback studies. In a larger ecological context, litter microbiota may be an underappreciated mechanism driving plant community diversity in natural systems.</p> |

Eco-Evolutionary Dynamics

Poster 77 - 79

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| 79 | <p>The influence of social cues on oviposition decisions in the mosquito <i>Aedes aegypti</i></p> <p>*Ashwini Ramesh, M. Sharma, K. Isvaran</p> <p>Animals use a variety of social and non-social cues in evaluating the habitat quality of a patch. Incorporating this information into future decisions can translate into important fitness consequences. Particularly, social cues like adult-density can play a crucial role in affecting maternal decisions like oviposition site-selection that can set-off a cascade of responses in parent and offspring. Using <i>Aedes aegypti</i> as a model-system we investigated the influence of adult-density on oviposition responses. Specifically, we measured oviposition responses of individual adult females to patches differing in quality when present singly, or in the presence</p> |
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| | <p>of non-breeding adult individuals. In a series of binary choice experiments, patch quality was represented by pools differing in larval predation or larval competition risk. Overall, the study indicates that individual adult females are able to assess the presence of other individuals and in response modify their behaviour during oviposition events. Adult-females responded to the presence of other females by adopting a bet-hedging strategy, sometimes withholding eggs perhaps to distribute eggs further across multiple pools while exhibiting preference for riskier patches. We suggest that adult-female density may favour a shift in preference of individual females towards seemingly riskier patches and discuss potential evolutionary explanations for this shift.</p> |
| <p>80</p> | <p>Evolutionary Branching in Disease Dynamics</p> <p>*Vanessa Rivera-Quiñones, Zoi Rapti, Carla Cáceres</p> <p>In many disease systems, it has been observed that focal host strains characterized by various life-history traits can coexist. These are often competing for resources and interacting with pathogens and predators. Our main goal is to study when coexistence is achieved due to evolutionary branching. As a motivating example, we focus on the zooplankter <i>Daphnia dentifera</i>, commonly known as “water flea”, which experiences epidemics of the fungus <i>Metschnikowia bicuspidata</i>. To integrate the role of <i>Daphnia</i> as consumers, competitors and hosts, we develop an ODE system and analyze its dynamics. We use the theory of adaptive dynamics to describe the long term evolution of the population by considering small mutations. We derived an expression for their growth rate using adaptive dynamics and determined conditions that allow polymorphisms to occur in our system.</p> |
| <p>81</p> | <p>Ecophysiology traits related to drought tolerance in the wild progenitors of rice</p> <p>*Yuting Qiu, Michael Grillo</p> <p>Climate change and the increasing demands of human population growth are serious threats to providing food security in the coming generations. A thorough understanding of resistance mechanisms to abiotic stress, such as drought, is crucial for meeting these demands. Through the domestication process, many crops have lost the ability to effectively cope with environmental stress. Wild crops relatives provide a unique opportunity for studying abiotic stress mechanisms that can be incorporated into breeding programs. Here we examine ecophysiology traits related to drought tolerance in the wild progenitors of rice, <i>Oryza rufipogon</i> and <i>O. nivara</i>, and look for associations with survival following a drought treatment. To accomplish this we generated a F₂ hybrid population between these species with the long term goal of mapping Quantitative Trait Loci (QTL). These wild species differ in their drought tolerance as well as stomata size and number, anthocyanins production, and carbon isotope discrimination. We find a tradeoff between stomata size and number, suggesting a shared genetic mechanism that controls these traits. In this study there is no association between survival during drought and stomata traits or anthocyanins. Experiments are underway to measure additional traits related to drought and to uncover their genetic basis.</p> |

Genetics and Evolution

Poster 82 - 89

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| 82 | <p>Analysis of three-dimensional bony metrics in blind cavefish using micro-computed tomography (micro-CT)</p> <p>*Daniel Berning, Amanda K. Powers, Joshua B. Gross</p> <p>The blind Mexican cavefish, <i>Astyanax mexicanus</i>, exhibits a variety of cranial abnormalities, including bony fusions and fragmentations. These alterations occur in the suborbital bones surrounding the collapsed orbit of the eye and are bilaterally asymmetric. Here, we examine the largest of the suborbital bones, the suborbital number 3 (SO3) bone, which is frequently fragmented into separate elements. Interestingly, prior research found that cavefish also have smaller SO3 bones. To evaluate this further, we explored three-dimensional SO3 using micro-computed tomography imaging. We performed software-assisted isolation and 3D volume rendering of SO3 bones to collect surface area (SA), volume, SO3 bony fragment number, and standard length from surface-dwelling fish and three distinct populations of cavefish. Surface fish have the largest SO3 bones and never exhibit bone fragmentation. Interestingly, Chica cavefish are similar to surface fish with respect to SA and volume, possibly due to introgressive hybridization with surface fish during periodic flooding events. Tinaja cavefish have the smallest SO3 bones, while Pachón cavefish exhibit more fragmentation than any other cave locality. This research illuminates the nature of cranial convergence in natural populations of cavefish, yet highlights population-specific differences in the nature of these skeletal changes in phylogenetically -distinct lineages.</p> |
| 83 | <p>Conservation genetics of an endangered, highly clonal oak species (<i>Quercus havardii</i>)</p> <p>*Drew Duckett, Ross McCauley, Mackenzie Coden, Chuck Cannon, Sean Hoban</p> <p><i>Quercus havardii</i> (Fagaceae) is unique because it primarily reproduces clonally and hybridizes readily with related species. This oak often persists on very poor, deep sandy soils in arid environments, adapting well to a very harsh habitat. Human disturbances in its southwestern American range are causing population declines. We have initiated a project to assess its conservation status, collect samples across its distribution, and gather observations about its basic biology. As a first step, we will examine the spatial and taxonomic distribution of genetic variation in the species, work to better understand its genetic delimitation and interaction with other sympatric oak species, and determine the most effective management options to prevent further population loss. Field collections have produced samples from ~600 ramets representing thirty-six different sites throughout the species range. Completed analyses include the examination of leaf preservation, tissue homogenization, and chemical extraction protocols to determine optimal DNA extraction procedures for producing high quantity and high quality DNA. Microsatellites developed in other white oak species are currently being tested for their utility in <i>Q. havardii</i>. Successfully amplified microsatellites will then be utilized for genetic analyses, which will include clonality, parentage, hybridization, and population structure.</p> |

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| 84 | <p>Parallel QTL mapping to find shared and unique loci for adaptation and reproductive isolation among <i>Solanum</i> species</p> <p>*Mathew J. Gibson, E.B. Josephs, L.C. Moyle</p> <p>Understanding the genetic basis and evolutionary accumulation of reproductive isolation is a crucial step in understanding the process of speciation. Because this accumulation unfolds over time, species must go through periods when loci contributing to reproductive barriers are polymorphic. We evaluated within species variation for loci causing interspecific reproductive isolation by simultaneously mapping QTL for reproductive isolation and other traits in two independent, interspecific mapping populations of wild tomato (<i>Solanum pimpinellifolium</i>). Loci that are shared between parental genotypes should colocalize to the same genomic location in both mapping populations. To do so, we are developing new approaches for performing comparative QTL analysis in populations that share a limited set of common markers, by leveraging genetic resources available in tomato. We identified several QTL for pollen fertility, seed set, floral morphology, and leaf physiology. The majority of QTL identified were limited to one of the two populations, suggesting few shared alleles between <i>S. pimpinellifolium</i> genotypes, although the power to detect QTL in these populations may not be equal. Indeed, the population in which we detect few QTL has an excess of missing genotypes. Nevertheless, our approach was successful at mapping QTL simultaneously in the two populations despite sharing limited marker sets.</p> |
| 85 | <p>The evolution of plumage sexual dichromatism in a globally-distributed avian genus, the true thrushes</p> <p>*Alec B. Luro, Mark E. Hauber</p> <p>Many species of birds exhibit striking feather colors and patterns which are used for both species-recognition by the animals themselves, and taxonomic delineation by researchers. The genus of the well-known American robin (<i>Turdus migratorius</i>), the true thrushes (<i>Turdus</i>), are an exceptionally diverse passerine genus with ~65 species distributed worldwide and exhibit striking diversity in melanin-based plumage coloration. Importantly, differences in plumage coloration between the sexes (i.e., sexual dichromatism) have yet to be investigated in this globally-distributed genus. Here, we examine the evolution of plumage coloration and sexual dichromatism in the diverse <i>Turdus</i> genus by mapping reflectance spectrophotometry measurements of five separate body regions onto a previously published molecular phylogeny.</p> |
| 86 | <p>Population Genetic Structure of the Prairie Vole (<i>Microtus ochrogaster</i>) at the Subspecies Level</p> <p>*Joshua Robinson, Nancy Solomon, Brian Keane</p> <p>Determining the geographic pattern of genetic variation across a species' range can be useful in understanding the current population structure of a species and its evolutionary history. The prairie vole (<i>Microtus ochrogaster</i>) is currently classified into seven putative subspecies based on morphological and geographical data. However, subsequent morphological analyses have failed to find consistent differences among subspecies. The only molecular phylogenetic study, using length polymorphisms at six microsatellite loci, indicated the presence of two</p> |

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| | <p>genetic clusters rather than the seven predicted clusters. The objective of my study was to characterize the genetic structure of prairie voles throughout its range using DNA sequence data from two neutral nuclear loci and the mitochondrial cytochrome-b locus. The sequence data provides greater resolving power for assessing population genetic structure and evaluating the validity of the subspecies classification. We are examining sequence data from museum specimens that represented all seven putative subspecies from 39 populations across the species range. Preliminary data from the cytochrome-b region suggest that three genetic clusters exist and does not support the current subspecies classification.</p> |
| <p>87</p> | <p>Str. 34945: A potential biomarker for stress</p> <p>*Katelin A. Schneider, Leena H. Shewade, Daniel R. Buchholz</p> <p>Stress experienced during early life causes higher basal stress hormone levels and predisposes individuals to later life cardiovascular, neural, and metabolic diseases, but mechanisms underlying the developmental origins of these chronic adult diseases have yet to be determined . Towards understanding how early stress brings about permanent effects on development, I characterized a stress-hormone response gene, <i>ush1g</i>, in the frog <i>Xenopus tropicalis</i>, a model organisms for the role of hormones in development. <i>Ush1g</i> was identified by mapping a transcribed locus, Str. 34945, to the 3' UTR of <i>ush1g</i> using gene expression studies and PCR-based genome analysis. To determine how and where Str. 34945 is expressed in the tadpole, we treated tadpoles with corticosterone (CORT, the frog stress hormone) and measured <i>ush1g</i> expression via quantitative PCR. <i>Ush1g</i> is induced by CORT in the tail, lungs, liver, and heart but not brain or kidney. Furthermore, <i>ush1g</i> shows a peak in expression at the climax of metamorphosis coinciding with the peak plasma CORT levels. <i>Ush1g</i> is the only known CORT-response element in tadpoles not also regulated by thyroid hormone and will be a valuable tool to study the role of stress hormones in development</p> |
| <p>88</p> | <p>Mitochondrial and Y-Chromosome Haplotypes Reveal Population History of North American Foxes</p> <p>*Jeremy T. Stutchman, H.M. Rando, J.L. Johnson, L.N. Trut, B.N. Sacks, A.V. Kukekova</p> <p>The red fox (<i>Vulpes vulpes</i>) is renowned for its adaptability, which has allowed it to become the most widespread carnivorous mammal, inhabiting regions of Europe, Asia, Africa, Australia, and North America. This adaptability also facilitated the farm-breeding of foxes, beginning in North America and spreading across the world. While many farmed foxes are known to have originated from North American stock, the relationship between farm and wild foxes in North America is not well characterized. Mitochondrial DNA (mtDNA) and Y-chromosome (Y) haplotypes were identified for wild foxes from Eastern Canada, Maryland, and Great Britain, as well as farmed foxes from the Midwestern United States and Novosibirsk, Russia. Simultaneous analysis of the mtDNA and Y-haplotypes was used to determine the population of the wild progenitors of the farmed foxes and to evaluate the rate of introgression of the farmed foxes into wild fox populations in the United States. Using markers to characterize both the matrilineal and patrilineal heritage of North American foxes offers new support for the complex phylogeographic history of the North American fox populations.</p> |

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| 89 | <p>Phylogeographic origins of rice rats (<i>Oryzomys</i>) in southern Illinois</p> <p>*Conrad Williams</p> <p>The marsh rice rat (<i>Oryzomys palustris</i>) is a semiaquatic rodent native to wetlands in the southeastern United States. While previously classified as a subspecies of <i>O. palustris</i>, recent analysis of the genetic divergence between rice rat populations in the eastern United States (<i>Oryzomys palustris palustris</i>) and the Texas rice rat (<i>Oryzomys texensis</i> or <i>Oryzomys palustris texensis</i>) suggest that the Texas rice rat should be recognized as a separate species. These two putative species appear to be the result of separate eastern and western glacial refugia during the last glacial period. The most current range maps for the <i>Oryzomys palustris</i> species complex show rice rats in southern Illinois as belonging to <i>O. palustris palustris</i>, but molecular evidence for this classification is lacking. In this study, I use DNA sequence data from two mitochondrial loci (Cytochrome B and the control region) along with existing sequence data from GenBank to show that rice rats in southern Illinois actually represent an expansion of the Texas rice rat. This study illustrates that molecular data can be an important tool for delineating the range of closely related species.</p> |
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Evolution and Development

Poster 90 – 95

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| 90 | <p>Effects of Temperature Variation on the Formation of Vertebral Anomalies in <i>Astyanax mexicanus</i></p> <p>*Melina Kanji, Windsor E. Aguirre</p> <p>Vertebrae are functionally important in fishes and vary with body form and ecological habits. Because fishes are ectotherms, they are vulnerable to changes in temperature during development. In this study, the frequency and type of vertebral anomalies of 313 fishes reared in four different temperatures were examined (20°C, 23°C, 25°C, and 28°C). Wild-caught individuals (218) from the same area were also examined for anomalies. The frequency of each type of anomaly was then examined in order to determine which temperature would increase or decrease the likeliness of each of the observed anomalies to appear. A vertebral anomaly guide was created based on Boglione et al., in order to classify the five anomalies seen. The results showed that more anomalies were seen at the extreme temperatures of 20°C and 28°C, with 28°C showing the most anomalies. It could also be observed that type 2 (incomplete fusion) was the most frequent anomaly in both extreme temperatures. Additional research can be done to analyze how these anomalies impact the fitness of the individuals and may give insight into what is ultimately being modified in the vertebral column of fish when reared at varying temperatures.</p> |
| 91 | <p>Investigation of Purple and Violet Feather Coloration</p> <p>*Nicholas M. Justyn, Matthew D. Shawkey</p> <p>Feather colors are created by the selective absorption of light by pigments, interactions of light with materials of differing refractive indices, or a combination of both pigmentary and structural mechanisms. Revealing the mechanisms of color production is essential to understanding the underlying functions and evolution of</p> |

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| | <p>the colors themselves. However, the mechanisms of production of purple and violet coloration in feathers are not well characterized, and the terms are frequently used incorrectly or interchangeably with one another. Violet is a true color characterized by a single peak in the visible spectrum between 380nm and 450nm, and purple is a highly variable secondary color created by the combination of two peaks typically in the violet-blue and red regions of the spectrum. Here we investigate over 20 different species across a wide range of avian taxa and characterize the methods by which they produce purple and violet colors. We think this study will encourage more accurate characterization of purple and violet feathers, and further investigation into the evolution of purple and violet coloration. This will contribute to a better understanding of the functions of purple and violet feathers within these species and further address the limitations of color production in birds.</p> |
| <p>92</p> | <p>A large actinopterygian bony fish skeleton from the Upper Cretaceous Eagle Ford Group of Texas, USA</p> <p>*Maxwell G. London, Michael J. Polcyn, Kenshu Shimada</p> <p>SMU 76938 is a fossil skeleton of a large, nearly complete actinopterygian bony fish housed in the Southern Methodist University in Dallas, Texas, USA. It was collected in the 1980s from the Tarrant Member (Upper Cenomanian) of the Upper Cretaceous Eagle Ford Group in Tarrant County, Texas, where it was under the North American Western Interior Seaway. The specimen presently exposes the left lateral side, and whereas parts of the skull and dorsal fin are damaged, the fish measures about 93 cm, 109 cm, and 119 cm in standard length, fork length, and total length, respectively, and about 17 cm in maximum body depth with a fusiform body plan. The vertebral column is nearly complete with a total count of at least 54 (no more than 58) centra, and the caudal fin is well preserved, including its soft tissue outline. Its dentition is villiform where each tooth is small measuring no more than 1.5 mm in height and is conical with a lingual curvature. The exact taxonomic identity is presently uncertain, but a unique combination of anatomical characters suggests that SMU 76938 may be a new taxon belonging to Crossognathiformes, possibly within Pachyrhizodontidae.</p> |
| <p>93</p> | <p>Male-Mediated Effects of Diet and Oxidative Stress on Post-Fertilization Fitness Outcomes</p> <p>*Margot Meredith, Michal Polak, Parker Young</p> <p>Embryo mortality contributes to reproductive failure within a range of animals. Whereas there are well-established casual relationships between maternal nutrition and embryo loss, environmental stresses operating through the father have been overlooked. Yet, ejaculate production can require significant resource distribution, and seminal plasma components are increasingly recognized to exert wide-ranging effects on females and offspring, so a link between paternal nutritional history and embryo health may be expected. Here, using <i>Drosophila melanogaster</i>, we test for effects on methodically varying levels of protein (P), carbohydrate (C), and caloric load in male diet on embryo mortality. P and C balance and total calories expressed significant effects, which depended on male mating order. Caloric restrictions placed on the father elevated embryo mortality within the offspring, but this effect was observed only in the males' second mates when mated consecutively with 2 females. Treatment with paraquat, a pharmacological agent known to induce oxidative stress (OS), did not interact statistically with diet to affect embryo</p> |

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| | <p>mortality, suggesting that the influence of paternal nutrition on embryo loss is not mediated via OS. Male exposure to paraquat at low levels produced embryos with elevated survivorship, indicating the discovery of a potential hermetic effect operating via the ejaculate. Conclusions of this intriguing finding, including for post-copulatory sexual selection, are addressed.</p> |
| <p>94</p> | <p>The Effects of Diet Quality on Mature Eggs in <i>Drosophila nigrospiracula</i></p> <p>*Ashley Moulton, Lauren Titus, Michal Polak</p> <p>Research was conducted, using female <i>Drosophila nigrospiracula</i>, studying the effects of diet quality of female reproductive potential. Specifically, we tested the effects of varying concentrations of protein and carbohydrate on female fecundity, measured as the number of mature eggs present within the ovaries. Utilizing the CAFE assay, where females were allowed to feed ad libitum on liquid diets varying in concentration of sucrose and protein (from yeast), consumption measurements were taken daily over the course of seven days. At the conclusion of the trials, the ovaries were dissected from the fly under a stereomicroscope, and the total mature eggs were counted. When given higher concentrations of food, total consumption decreased due to their ability to obtain desired nutrients in smaller liquid amounts. Ovaries dissected from flies that consumed more protein produced significantly more mature eggs given the increased availability of nutrients promoting egg growth and development. This study shows that female <i>D. nigrospiracula</i> are sensitive to, and able to alter their consumption when presented with diets of varying quality. In conclusion, the research demonstrated significant nutritional effects on body-size specific fecundity in <i>D. nigrospiracula</i> under controlled laboratory conditions using the CAFE assay.</p> |
| <p>95</p> | <p>Putative roles for pmela and tyrp1b in complex pigmentation development of <i>Astyanax mexicanus</i></p> <p>*Connor R. Sears, Bethany A. Stahl, Joshua B. Gross</p> <p>The blind Mexican cavefish, <i>Astyanax mexicanus</i>, is an emerging model system for regressive evolution. Across 29 recorded cave localities, the obligate cave dweller has independently evolved pigmentation loss compared to the ancestral surface morphotype, resulting in hypopigmentation or complete albinism. In cavefish, previous work has described the Mendelian phenotypes of albinism (<i>oca2</i>) and brown (<i>mc1r</i>). These monogenic traits fail to completely explain the spectrum of complex pigmentation regression. For instance, cavefish demonstrate reduced numbers of melanophores. A QTL analysis identified several loci associated with numerical variation in melanophores. Two loci were closely linked to the genes <i>pmela</i> and <i>tyrp1b</i>. Both genes have been implicated in melanophore migration and ultrastructure in other model systems. We tested the function of these genes in vivo using morpholino knockdown and embryonic whole-mount in situ hybridization in cave and surface morphotypes. Knockdown of <i>pmela</i> and <i>tyrp1b</i> results in a clustered and dispersed distribution of melanophores, respectively. Furthermore, <i>pmela</i> expression is substantially delayed in cavefish compared to surface embryos. Functional and quantitative analyses of these genes underscores the genetic and phenotypic complexity that underlies regressive pigmentation loss in natural cavefish populations. This work is supported by a grant from the National Science Foundation (DEB-1457630) to JBG.</p> |

