



The 18<sup>th</sup> Annual Early Career Scientists Symposium

***Global Change and  
Its Consequences for  
Green Life***

March 31st, 2023, at the University of Michigan  
Matthaei Botanical Gardens

# ECSS 2023 SCHEDULE

- 9:30-10 AM — Registration @ Matthaei Botanical Gardens
- 10:00 - 10:05 AM — Welcome and introduction:  
Dr. David Michener, University of Michigan
- 10:05 – 10:50 AM — 1st Keynote presentation:  
Dr. Jen Lau,  
Indiana University
- 10:50-11:20 AM — Dr. James Santangelo,  
University of California Berkeley
- 11:20- 11:50 AM — Dr. Lindsey Kemmerling,  
University of Minnesota
- 11:50 AM – 12:30 PM — Lunch Break
- 12:30-1:00 PM — Dr. Meredith Zettlemoyer,  
University of Georgia
- 1:00-1:30 PM — Dr. Daniel Anstett,  
Michigan State University
- 1:30-1:45 PM — Break
- 1:45-2:15 PM — Dr. Carrie Tribble,  
University of Hawaiï at Mānoa and  
University of Kentucky
- 2:15-2:45 PM — Dr. Constance Bolte,  
Penn State University
- 2:45-3:30 PM — 2nd Keynote Presentation:  
Dr. Susana Wadgymar,  
Davidson College
- 3:30-4:30 PM — Poster Session
- 4:30-6:00 PM — Reception

# SPEAKERS

## **Jennifer Lau, Assistant Professor**

### ***The Cryptic Role of Microbes in Plant Ecological and Evolutionary Responses to Global Change***

Abstract: Soil microbial communities have tremendous taxonomic diversity, provide a large variety of ecosystem functions, can produce or simulate plant hormones, and are capable of rapid ecological and evolutionary change. For these reasons, diverse soil microbial communities have the capacity to buffer plants from environmental stress, manipulate plant phenotypes, and help maintain plant fitness in rapidly changing environments. In short, microbes are unseen players in terrestrial plant communities; yet they may play outsized roles. We aim to predict how, when, and why diverse microbial communities promote adaptive plant responses to stress (defined loosely, as any mechanism that maintains or increases plant fitness in a given environment, genetic or otherwise). We have demonstrated the potential for “microbe-mediated adaptation (i.e., that microbial communities shift in ways that promote plant fitness in a particular environment) and find that microbial responses to drought stress protect plants from the negative consequences of drought. These findings demonstrate that microbes can shift in ways that maintain plant fitness under environmental stress, our newer work aims to identify when such microbe-mediated adaptation should arise in nature.

## **James Santangelo, Postdoctoral fellow**

### ***Adaptation to the world's urban jungles in a cosmopolitan plant***

Abstract: Approximately 55% of the world's human population currently lives in urban environments, a figure that continues to increase annually. As cities grow, dense urban infrastructure results in substantial changes in abiotic and biotic ecological factors that can drive evolutionary responses in natural populations. Furthermore, because cities are constructed to suit the needs of humans, urban environments around the world are predicted to be more like one another than to their own surrounding non-urban habitat, which may drive parallel evolutionary responses to urbanization. We tested these predictions and leveraged large-scale, replicated urban environments to examine the extent of parallel evolution in the production of hydrogen cyanide (HCN)—an ecologically important antiherbivore defense that also affects tolerance to abiotic stressors (e.g., drought, frost)—in natural populations of white clover (*Trifolium repens*). By sampling over 110,000 plants from ~6,000 populations across 160 cities, we show that urban habitats around the world have converged to similar environmental features: cities are warmer, less vegetated, and contain more

impervious surfaces than surrounding non-urban habitats. These convergent urban environments have driven changes in the frequency of HCN in urban populations (i.e., urban-rural HCN clines) in 47% of the 160 cities sampled, and sequencing the whole genomes of 2,074 plants from 26 cities around the world has confirmed that clines are adaptive: urban and rural habitats consistently had equal amounts of genetic diversity, and we detected signatures of selection on the HCN phenotype and its underlying loci in cities with urban-rural clines. In addition, variation in the strength of clines could be predicted by urban-rural changes in the strength of drought and herbivory, factors also known to influence HCN frequencies at continental scales. Stepping back from HCN and focusing on a single city, ongoing work is identifying urban-rural differentiation and signatures of selection in numerous quantitative traits and genes that may be facilitating white clover's persistence in urban environments. My work has contributed to long-standing questions in evolutionary biology regarding the extent of parallelism in nature and provides fundamental insight into the drivers of evolution in one of the planet's fastest-growing and most environmentally destructive ecosystems—cities.

## **Lindsey Kemmerling, Postdoctoral Associate**

### ***Restored prairie strips support biodiversity and ecosystem services in row crop farms***

Abstract: Agricultural landscapes can be managed to protect biodiversity and maintain ecosystem services. One approach to achieve this is to restore native perennial vegetation within croplands. Where row crops have displaced prairie, as in the US Midwest, restoration can align with crops in so called “prairie strips”. We tested the effect of prairie strips in addition to other management practices on a variety of taxa and on a suite of ecosystem services. We worked within a 33-year-old experiment that varied methods of agricultural management across a gradient of land use intensity. In the two lowest intensity crop management treatments, we introduced prairie strips occupying 5% of crop area. We asked: What are the effects of newly established prairie strips on the spillover of biodiversity and ecosystem services into cropland?, and: What are the tradeoffs and synergies among biodiversity conservation, ecosystem services, and crop yield across a land use intensity gradient?

Within prairie strip treatments, where sampling effort occurred within and at increasing distance from strips, dung beetle abundance, spider abundance and richness, active carbon, decomposition, and pollination decreased with distance from prairie strips, and this effect increased between the first and second year. Across the entire land use intensity gradient, treatments with prairie strips and reduced chemical inputs had higher butterfly abundance, spider abundance, and pollination services. In addition, soil organic carbon,

butterfly richness, and spider richness increased with a decrease in land use intensity. Crop yield in one treatment with prairie strips was equal to that of the highest intensity management, even while including the area taken out of production. Our results show that, even in early establishment, prairie strips and lower land use intensity can contribute to the conservation of biodiversity and ecosystem services without a disproportionate loss of crop yield.

**Meredith Ann Zettlemoyer, *Postdoctoral Researcher***  
***Consequences of phenological shifts for performance across biological scales***

Abstract: Species' vulnerability to anthropogenic change is largely determined by traits that influence their sensitivity and ability to adapt to novel conditions. For instance, rising temperatures have dramatically accelerated the phenology of many species, but we still have limited evidence of whether variation in phenological responses really influences population dynamics or macroecological patterns of extinction and spread. Since phenology's potential benefits for species success are common motivations for documenting phenological shifts, we need to consider mechanisms underlying how phenology influences performance across biological scales. My work links phenological shifts to performance at three scales: individuals, populations, and macroecology. I first leverage a long-term dataset on climate, phenology, and demography in an alpine plant to quantify individual variability in phenological responses to climate. I then assess the adaptive value of phenological plasticity by quantifying the environmental sensitivity of selection on phenology at the population level. Third, I use a combination of herbarium records and experimental warming to examine how phenological plasticity to rising temperatures affects patterns of invasion and extirpation in tallgrass prairies. Altogether, we need to consider how phenology might affect performance across biological scales for phenology to truly serve as an indicator of species' success under climate change.

**Daniel Anstett, *Research Associate***

***Using landscape genomics to study adaptation to climate change***

Abstract: Climate change is threatening global plant biodiversity. As extreme climate events become more common, populations risk decline due to increasing maladaptation. Evolution may be able to rescue populations undergoing demographic decline through rapid evolution; however, this requires sufficient adaptive genetic variation. Genetic offset, a metric of genomic vulnerability to climate change, has been used to predict which populations may be maladapted to climate change. The promise of this algorithm is considerable, but its accuracy at predicting population decline has not been well established. Here, I leverage whole-genome sequencing on 55 populations across the range

of scarlet monkeyflower (*Mimulus cardinalis*) to study genomic vulnerability to extreme drought in California and Oregon. I identify 294 SNPs that were most highly associated with climate and use these to calculate genetic offset, which I then use to explain rate of change in population growth seen across 11 populations throughout extreme drought. Populations with greater genetic offset also had greater population declines, implying that these populations are likely at greater risk of extinction because of a deficit of adaptive genetic variation. Through temporal genomic sequencing, I follow the change in climate-associated SNPs in these 11 populations through a period of severe drought. I show that rapid evolution occurs broadly, but is insufficient to counter demographic decline in most populations.

### **Carrie Tribble, NSF Postdoctoral Fellow**

#### ***Macroevolutionary consequences of going underground: How belowground structures allow plants to thrive in seasonal climates***

Abstract: The study of systematics integrates diverse fields of biology, including taxonomy, computational biology, genomics, and natural history collections. My research uses these approaches to address fundamental questions about the evolution of tropical plants. In this seminar, I will discuss one of my major research questions: Are seemingly convergent morphologies produced through similar anatomical and molecular modifications and do they perform similar functions? Geophytes are plants that resprout from belowground buds, allowing these plants to go dormant underground seasonally or during periods of stress. Geophytes use underground storage organs to fuel renewed aboveground growth following dormancy. Using a novel phylogenetic comparative approach, I found that geophytes' underground storage organs have different developmental origins and that these differences mediate distinct organismal relationships to the environment. Finally, I will discuss new tools I am developing to identify macroevolutionary processes that drive convergence across levels of biological organization.

### **Constance E. Bolte, Postdoctoral Scholar**

#### ***Finding hope through hybrid zones: Adaptive introgression facilitates rapid evolutionary responses to climate change***

Abstract: Hybridization was once considered an evolutionary dead-end but is now recognized as an important mechanism that can influence speciation trajectory and biodiversity in several ways. Across forest trees, hybridization appears to be exceedingly common, yet few studies have explored the mechanisms that promote, inhibit, or result from interspecific gene flow within this group. While their long generation times and sessile nature challenges sufficient tracking of climate through dispersal and migration, introgression of

genetic variation via hybridization may be a more general mechanism trees rely on for adaptation to rapidly changing climate. Indeed, higher genetic diversity is linked to higher adaptive potential. Here, I present findings from two forest tree systems that illustrate how historical climate and introgression contributed to divergence and adaptation. First, I describe the demographic history of two pine species, *Pinus rigida* and *Pinus pungens*, with no active hybrid zone at present but a long history of introgression along the Appalachian Mountains in eastern North America. Second, I describe an active hybrid zone formed from secondary contact of two poplar species, *Populus trichocarpa* and *Populus balsamifera*, along the Rocky Mountains in northwestern North America. In both cases, a multidisciplinary approach (e.g., distribution modeling, demographic inference, redundancy analysis, and estimated effective migration surfaces) was used to quantify contributions of climate, geography, and gene flow to divergence. I relate these findings to other examples in the literature, contextualize hybridization extent and dynamics under future climate projections, and emphasize the importance of natural hybrid zones to conservation and management.

## **Susana Wadgyamar, Assistant Professor of Biology**

### ***Forecasting the migratory potential and range-wide population dynamics of species experiencing climate change***

Abstract: Under contemporary rapid climate change, natural populations are confronting new suites of abiotic conditions and biotic interactions to which they might not be adapted. Populations likely differ in their capacity to persist these accelerating environmental changes, yet we lack a comprehensive understanding of which populations are most vulnerable to climate change because forecasts of range shifts often fail to account for population-level variation in plasticity and genetic variation. Our inability to make mechanistic predictions of range-wide dynamics under climate change also limits the ability of conservation practitioners to design effective management strategies for threatened populations. In this talk, I will describe prior work on the annual legume *Chamaecrista fasciculata* that demonstrates limitations to the success of assisted gene flow and assisted migration programs beyond the current range boundary. I'll also share evidence that climate change has already introduced local maladaptation across the elevational range of the perennial mustard *Boechnera stricta*. Lastly, I'll outline upcoming efforts to integrate eco-evolutionary models of range-wide genomic variation, rates of gene flow, plasticity, and additive genetic variation in traits and fitness to forecast population persistence across the range of *Chamaecrista fasciculata* under rapid environmental change.



***Special thanks to our co-sponsor,  
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