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Friday, April 24, 2026

12:00-1:00 pm

Morgridge Hall Seminar Room 2516

Zoom Meeting: 966 3372 9112

<https://uwmadison.zoom.us/j/96633729112?pwd=tHFc9i1dAAqmXe05uWtw8wXBIQZxGB.1>

Passcode: 621125

Evolution of plant genome architecture with integer data

Abstract: Polyploidy is an important mechanism in plant evolution. It can drive speciation in some lineages, provide the genetic basis for key innovations, and provide a path to niche diversification and climate change resilience. While more prevalent in some lineages, such as grasses, than others, the genomes of all angiosperms carry the signatures of at least one ancient whole-genome duplication. Much of the foundational work on ancient whole-genome duplications was enabled with the first plant genomes, but the increasing accessibility of chromosome-level assemblies for diploids and polyploids across the Tree of Life creates new opportunities to revisit classic hypotheses of genome evolution after polyploidization with syntenic cluster data. I will cover how syntenic data can be represented as integers with phylogenetic profiles and investigated with birth-death models. Some method development on inferring ploidy from sequence data and its application to the evolution of grassy biomes will also be covered.

Bio: I am an evolutionary biologist that primarily works on plant evolution and polyploidy. I am especially interested in grasses as a model for polyploid evolution because of their importance to agriculture and ecosystems. I started as an Assistant Professor at North Carolina State University in August of 2025. Prior to that, I was a Marie Curie Fellow at the Royal Botanic Gardens Kew and a postdoctoral scientist at Duke University. I completed a PhD on computational phylogenetics at the University of Florida in 2017. Most of my empirical work has focused on Madagascar, where I apply evolutionary biology to conservation issues about grassy ecosystems and the genetics of climate change resilience. Most of my research questions are from an organismal perspective, but I also enjoy developing bioinformatic tools and teaching materials that remove computational barriers to biodiversity science. My lab currently works on phylogenetic networks, polyploid population genomics, and gene duplication and loss across plants.



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