Dr. Meixia Zhao is an Assistant Professor of Plant Science in the Department of Microbiology and Cell Science at the University of Florida. Her research laboratory uses a combination of computational and functional genomic, genetic, and epigenetic approaches to study the mechanisms underlying genome evolution, transposon silencing, and epigenetic regulation of meiotic recombination in maize. Meiotic recombination is essential for plant breeding to map quantitative traits and introduce desirable traits into elite breeding lines. The process is regulated by both genetic and epigenetic factors. While a great deal is known about genetic factors, relatively little is known about epigenetic factors. Dr. Zhao's laboratory addresses this gap by delving into the investigation of recombination frequency, particularly in mutants deficient in DNA methylation. Additionally, her group has been using the parental inbreds of the maize nested association mapping population to compare whether meiotic recombination differs between males and females at both global and local scales, and whether local DNA sequences and chromatin structures play important roles in the distinction between male and female recombination. Her team also investigates variations in meiotic recombination among distinct maize lines during the process of maize domestication. This talk will focus on genetic and epigenetic regulation of meiotic recombination in maize populations, shedding light on the intricate interplay between these factors in shaping the maize genome and potentially facilitating maize breeding.