

OR386*Genomic signatures of social evolution in bees***Karen Kapheim**, Cai Li, Hailin Pan, Guojie Zhang, Gene Robinson

Variation in social behavior among bees provides a unique opportunity for understanding the molecular basis of social diversity within an evolutionary framework. Eusociality has repeatedly evolved from a solitary lifestyle in two families of bees - Apidae and Halictidae. More elaborate forms of eusociality, characterized by colony-level reproduction and very large colony sizes, have independently evolved from basic forms of eusociality twice within the Apidae. We used comparative genomics to identify molecular targets of selection, investigate patterns of genomic plasticity through methylation and gene regulation, and describe patterns of gene family evolution, as they relate to this repeated evolution of multiple convergent phenotypes among bees. We compared whole genomes of ten species from three families of bees that vary in social organization, with both solitary and eusocial species represented in Apidae and Halictidae. This involved *de novo* whole genome sequencing of five species, the draft genomes of which we present here. We included an additional five species with independently sequenced genomes for a comprehensive study of sociogenomics. Our analyses identify genes for which evolutionary rate is associated with social complexity, and reveal some of the evolutionary mechanisms likely to be driving these changes, including natural selection, variation in pan-genome distribution of GC content, and changes in cis-regulation. We discuss resulting insights into the mechanisms underlying convergent eusocial evolution.