

P181*Comparative genomic linkage mapping in Apis***Olav Rueppell**, Katelyn Miller, Ryan Kuster, Mananya Phiancharoen, Salim Tingek, Nikolaus Koeniger

The exceptionally high genomic recombination rate of the Western honeybees, *Apis mellifera*, has attracted significant scientific attention. A recent linkage map in the closely related *A. cerana* has found similarly high recombination rates and the same conclusion was reached for the more distantly related *A. florea*, based on limited data from two chromosomes. Here, we report on two complete linkage maps in this genus, extending existing genome-wide linkage maps to all three major honeybees clades. Based on genotyped SNPs identified by RAD-tag sequencing in single-family mapping populations, we will present genome-wide recombination maps of *A. florea* and *A. dorsata*. We will compare our results to the published findings in *A. mellifera* and *A. cerana*. Together with the emerging genome sequences of these two species the recombination maps will also be used to assess genomic synteny, recombination rate distribution, and genome correlates of local recombination rate. The combined results will improve our understanding of the evolution of very high genomic recombination rates and genome organization of the advanced eusocial insects.