

OR393

Analysis of a complete high-density recombination map of Apis mellifera

Katelyn Miller, Olav Rueppell, Corbin Jones, Caitlin Ross

The Western honeybee (*Apis mellifera*) is well known among social insects and other model organisms to have an exceptionally high recombination rate. Although recombination maps have been in existence since the mid 1990s our understanding of the high recombination in honeybees and other social insects is incomplete. A population of 192 brother drones was analyzed by multiplexed Illumina HiSeq 2000 re-sequencing. Single nucleotide polymorphisms (SNPs) were identified by alignment with BWA and variant calling with SAMtools. Informative SNPs will be selected and analyzed to construct a high-density, genome-wide map of recombination events. This map will be examined for putative hotspots and specific recombination events will be correlated with sequence motifs and structural properties of the genome. Our results will be compared to several other recent studies to contribute to our understanding of recombination patterns in *A. mellifera* and the evolution of high recombination rates in general.