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European Honeybee Subspecies Genomes at the Individual and Population Levels

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W617: European Honeybee Subspecies Genomes at the Individual and Population Levels

Wednesday, January 15, 2020

01:30 PM - 01:50 PM

📍 Pacific Salon 4-5 (2nd Floor)

Throughout western Europe, the endemic honeybee subspecies *Apis mellifera mellifera*, the black bee, has gradually been replaced in many beekeeper operations by other subspecies and hybrids of *A. m. ligustica*, *A. m. carnica*, *A. m. caucasica*, (C-type bees) and *A. m. mellifera* (M-type bees), which were found to be more efficient producers of honey or royal jelly, and also to be less aggressive. In order to understand the impact of these practices on the genomes of bee populations we followed two complementary approaches. The first was to produce a high-continuity reference genome for M-type bees by PacBio sequencing, for comparison with the current Amel_HAV3.1 reference - a C-type bee. A single haploid drone from a closed population was selected for sequencing and the overall genome assembly obtained is 227 Mb for the 16 chromosomes. The longest contig obtained is 11.6 Mb, the N50 contig size is 5.1 Mb and chromosome 16 was obtained as a single 7.2 Mb contig. Contigs were ordered along chromosomes by minimizing genetic recombination. Comparison with Amel_HAV3.1 allowed the high confidence detection of inversions between the two reference genomes. Long-read sequencing also allowed the discovery of new highly repeated elements. The second approach is the sequencing of several hundred haploid drones from separate colonies, which includes black bee conservatories, French queen breeders (honey and royal jelly production) as well as out-groups from various European regions from where genetic stock is imported for breeding purposes. Varying degrees of admixture between the M- and C-type bees are observed, often reflecting different breeding practices. Regions of high differentiation between the two genetic types are also detected.

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