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subspecies: the North African *A.m. intermissa* and the western European *A. m. mellifera*. The whole mtDNA patterns were compared with those obtained with the intergenic tRNA^{leu}-cox2 region. As expected, a concordant northeastern-southwestern cline formed by the two highly divergent lineages A and M was observed. However, the previously grouping of haplotypes into the three African sublineages is not supported by the entire coding portion of the mitochondrial molecule. This finding suggests that the tRNA^{leu}-cox2 region is still a good marker for understanding the big picture of variation patterns.

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Genome-wide detection of signatures of selection in non-synonymous positions of Iberian honey bee (*Apis mellifera iberiensis*)

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Maternal and biparental genetic surveys of the Iberian honey bee (*Apis mellifera iberiensis*) populations have revealed complex and incongruent patterns of variation which have yet to be completely understood. Complex patterns are expected in regions like the Iberian Peninsula because (1) it comprises a diverse range of habitats and climates, (2) it has served as a glacial refugium during the Pleistocene, and (3) it has functioned as a bridge for populations migrating between Africa and Europe. While the demographic history played an important role in shaping the genome of the Iberian honey bee, selection is an evolutionary force that cannot be discarded. In this study we used Illumina technology to sequence the whole genomes of 87 Iberian honey bees collected across three longitudinal transects in the Iberian Peninsula. The whole-genome dataset was scanned for signatures of selection using two genetic-environment association methods (LFMM and *Samβada*). A total of 828 SNPs, spanning 308 genes, were detected by both methods. Of the 308 genes, 25 have SNPs in non-synonymous positions which were analyzed for positive selection using eight codon-substitution models (four neutral and four under selection) implemented by PAML and

Selectonsoftwares. Of the 25 genes, 13 out show signals of positive selection. Functional annotation indicates that these genes are involved in various biological processes such as sensory perception of smell (2 genes), oxidation-reduction (2 genes), neurogenesis (1 gene) and cellular response to starvation (1 gene). This study represents an important first step into understanding local adaptation of Iberian honey bees.

Selecting highly informative SNP panels for honey bee conservation management

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The native honey bee subspecies of Northern Europe, *Apis mellifera mellifera*, is threatened by introgression from introduced conspecifics. To limit introgression, conservation efforts have been implemented across Europe either using wing morphology or microsatellites to detect and remove hybrids. Here, we aim to characterize the honeybee population structure in Switzerland and the French Alps using whole-genome sequencing and to test whether a limited number of informative SNPs is able to separate and estimate admixture between native and introduced honeybees.

We re-sequenced haploid drones sampled throughout Switzerland and France including *A. m. mellifera* (N=103), *A. m. carnica* (N=34) and Buckfast bees (N=14). To infer fine-scale population structures, we incorporated ancestry proportions inferred by the program Admixture together with a network-based clustering approach (NetView). Based on the network topology, all subspecies can clearly be distinguished from each other. Furthermore, we detected fine-scale population substructures within *A. m. mellifera* suggesting isolation by distance or local ecotypes.