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understanding of the distribution, genetic diversity and population structure of *A. mellifera* sp in the SWIO islands, we analysed the genetic diversity of two mitochondrial regions (COI-COII and ND2) and at 15 microsatellites nuclear loci on samples from the Mascarene (n = 2941), Seychelles (n = 209) and Comoros archipelagos (n = 90). Potential population of origins such as Madagascar (n = 855), continental Africa (n = 84) and Europe (n = 76) were implemented in the analysis to better apprehend the genetic diversity of SWIO populations. Both sequencing of COI-COII and ND2 regions revealed a new mitochondrial African subgroup in the SWIO islands. Mitochondrial diversity patterns supported ancient colonization followed by diversification of *A. m. unicolor* in 10 islands out of the 11 studied. Nuclear analysis showed that SWIO populations were genetically closer to Madagascar than any other African populations and also exposed to recent European introductions in the Mascarene, yet well differentiated between island or continental populations, suggesting the indigenous status of *A. m. unicolor* in the area.

Patterns of Iberian honey bee variation inferred from the coding regions of whole mtDNA genomes: comparison with the popular intergenic tRNA^{leu}-cox2 region

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Iberian honey bees (*Apis mellifera iberiensis*) are well-known for their complex patterns of variation, which have been extensively reported by PCR-RFLP data of the intergenic tRNA^{leu}-cox2 region of the mitochondrial DNA. This mtDNA marker has revealed a highly structured and diverse subspecies characterized by the presence of western European (M) and African (A) haplotypes belonging to three African sublineages (A_I, A_{II}, A_{III}) forming a cline possibly originated from secondary contact. While the African-derived haplotypes occur in the southwestern half of Iberia, with sublineage A_{III} mostly present in the northern Atlantic coast, the

northeastern half of Iberia is occupied by haplotypes of M ancestry. Here we report on the diversity patterns inferred from the coding portion of 87 mitochondrial whole genomes of Iberian honey bees and 20 of two reference 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