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Spatial patterns of single nucleotide polymorphisms (SNPs) support a scenario of secondary contact in Iberian honey bees *(Apis mellifera iberiensis)*

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Dissecting diversity patterns of organisms endemic to Iberia has been truly challenging for a variety of plant and animal taxa, and the Iberian honey bee *(A. m. iberiensis)* is no exception. Surveys of genetic variation in the Iberian honey bee are among the most extensive for any honey bee subspecies. From these, differential and complex patterns of diversity have emerged, which have yet to be fully resolved. Here we used a genome-wide data set of 309 neutrally-tested SNPs, scattered across the 16 honey bee chromosomes, which were genotyped in 711 honey bee haploid males. These SNPs were analyzed along with an intergenic locus of the mtDNA to reveal historical patterns of population structure across the entire range of the Iberian honey bee. Overall, the patterns of population structure inferred from nuclear loci by the spatial principal component analysis (sPCA) were consistent with two major clusters bisecting Iberia along a northeastern-southwestern axis, a pattern that closely parallels that of the mtDNA. These findings support a scenario of secondary contact that probably results from expansions out of Pleistocene Iberian refugia. This study highlights the complexity of the Iberian honey bee patterns and reinforces the importance of Iberia as a reservoir of Apis mellifera diversity.