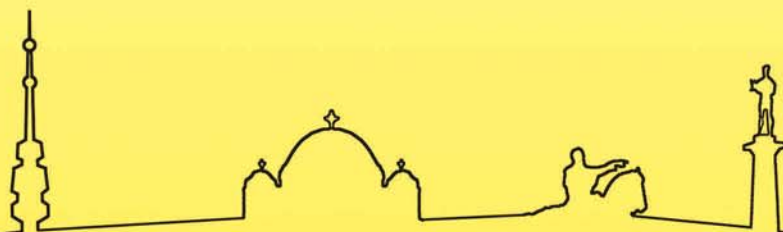




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MOLECULAR DIVERSITY AND SELECTIVE SWEEPS IN IBERIAN HONEY BEE

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Deciphering the genetic basis of the process of adaptation of organisms has been and remains one of the fundamental goals of evolutionary biology. Genomes contain information related to the history of natural populations. The Iberian honey bee (*Apis mellifera iberiensis* Engel 1999) exhibits a complex genetic diversity pattern of clinal variation shaped not only by evolutionarily neutral processes but also by selection. Unravelling the variation of subgenomic regions in this subspecies not only allows us to better understand the complexity of clinal patterning, but also the identification of genetic variation involved in local adaptation.

Several regions related to vision, xenobiotic detoxification, and immune response have shown signals of selection in *A. m. iberiensis*. In this study, analyses of sequence variation around candidate subgenomic regions (~100 kpb) have been carried out. The aims of this work are to provide further evidence of positive selection in the Iberian honey bee, to localize at a much finer scale the direct points of such selection, and to find the underlying source of the beneficial alleles or variants.

Keywords: Genomic conservation, Introgression, *Apis mellifera iberiensis*

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