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GENOME-WIDE SCANS DETECTED SIGNATURES OF SELECTION IN GENES RELATED WITH VISION, XENOBIOTIC METABOLISM, AND IMMUNITY IN THE IBERIAN HONEY BEE GENOME

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Genome-wide scan approaches to detect signatures of selection have become popular tools to study local adaptation at the molecular level and single nucleotide polymorphisms (SNPs) are seemingly the most appropriate marker for that endeavor. SNPs (i) provide a genome-wide coverage, (ii) generate high quality data, (iii) are suitable for automated high throughput technologies allowing genotyping of hundreds to thousands of loci in many individuals, and (iv) are commonly observed in functional genes. In this work, a total of 711 individuals of *A. m. iberiensis* were collected in 23 sites across three north-south transepts in the Iberian Peninsula. This collection was genotyped for 383 SNPs using the GoldenGate assay of Illumina. Then, the SNP dataset was examined in search for the footprints of selection with the following five different methods: (i) coalescence - LOSITAN and ARLEQUIN, (ii) Bayesian - BAYESFST and BAYESCAN, and (iii) Spatial Analysis - matSAM. These methods identified 10 loci exhibiting strong selection signal. The 10 loci were then located in the honey bee genome and their putative functions were determined using the honey bee genomic resources. The 10 loci were mapped to putative genes with diverse biological functions, which included vision, detoxification metabolism, and immunity.