



SIGNATURES OF SELECTION IN THE IBERIAN HONEY BEE: A GENOME WIDE APPROACH USING SINGLE NUCLEOTIDE POLYMORPHISMS (SNPS)

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Dissecting genome-wide (expansions, contractions, admixture) from genome-specific effects (selection) is a goal of central importance in evolutionary biology because it leads to more robust inferences of demographic history and to identification of adaptive divergence. The publication of the honey bee genome and the development of high-density SNPs genotyping, provide us with powerful tools, allowing us to identify signatures of selection in the honey bee genome. These signatures will be an important first step towards understanding the transition of genotype into phenotype and the basis of adaptive divergence. The Iberian Peninsula harbours the greatest honey bee genetic diversity and complexity in Europe. The challenge of deciphering the mechanisms underlying such complexity has led to numerous morphological and molecular marker-based surveys of the Iberian honey bee. Yet, in spite of the numerous studies, the evolutionary processes underlying patterns of Iberian honey bee genetic diversity remain poorly understood. The evolutionary process in the Iberian Peninsula has been dynamic and the genetic consequences are too complex to be addressed piecemeal, using few markers with unknown or poorly known linkage relationships. Accordingly, in 2010 more than 650 honey bee colonies were sampled across latitudinal and longitudinal clines in the Iberian Peninsula. The 650 honey bee samples were genotyped for 1536 SNPs – all equally distributed across the honey bee genome and all with known linkage relationships, based on the latest honey bee genome assembly. Herein we show the preliminary results of this genotyping, focusing on an Iberian honey bee genome inquiry on recent selective sweeps. We provide new insights into the evolutionary processes shaping the Iberian honey bee patterns.