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Spatial patterns of genetic variation in the Iberian honey bee hybrid zone: a comparison between mitochondrial and nuclear DNA

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The Iberian honey bee (*Apis mellifera iberiensis*) has been intensely surveyed for genetic variation with different markers ranging from morphology, allozymes, mitochondrial DNA (mt DNA), to microsatellites. Some of these markers have revealed non-concordant complex patterns of genetic variation, which led scientists to evoke competing hypotheses for the origin of Iberian honey bees. While complex patterns and underlying historical processes are typical of hybrid zones, the use of more powerful molecular and analytical tools and the fine-scale sampling promised to help dissecting the complexities of the Iberian hybrid zone. In this study, we conducted a genome-wide sampling by genotyping over 384 SNPs (single nucleotide polymorphisms) and sequenced an intergenic fragment of the mt DNA in 711 georeferenced honey bee samples collected across three North-South transects in the Iberian Peninsula. Both mt DNA and SNP datasets were analyzed using spatial tools to represent the structure generated by both types of molecular markers. We found concordant spatial patterns between markers which led to rejection of the standing hypothesis of recent human introductions and selection as the processes shaping Iberian honey bees patterns. This study shows that the fine-scale genomic and spatial analyses can reveal patterns which would otherwise had been undetected.

Key words: Iberian honey bee, *Apis mellifera iberiensis*, mitochondrial DNA, spatial analysis, landscape genetics.

Deriving indicators to assess historical effects of selective logging in oak pine forests of Western Mexico

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Unsustainable forest management is one of the major causes of forest degradation that is intended to be counteracted by the implementation of the REDD+ mechanisms (Reduced emissions from deforestation and forest degradation, carbon enhancement and conservation of carbon stocks). In this study, we investigated the relationship between spectral image components and forest degradation, with the objective to evaluate possible indicators derived from remote sensing that ultimately can serve to indirectly measure forest degradation. Spectral image components are derived after modifying multispectral or hyperspectral image data, to extract the percentage of the main materials found in each image pixel. In our case, after the processing of SPOT 5 data (2004, 2010) soil and green vegetation were identified as such components. The field data that was related with the image components were obtained through forest inventory performed in areas of oak-pine forest that have undergone intensive logging processes in the last 30 years, and areas without human intervention for more than 30 years, that serve as reference areas. A participatory mapping approach was used to locate such areas. Canopy cover, above ground biomass (AGB), forest height, basal area, and species richness obtained from field data were related with the percentage of soil and green vegetation components. The percentage of soil explained 61% of

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