

THE IBERIAN HONEY BEE (*Apis mellifera iberiensis*): COMPLEX NEUTRAL AND SELECTIVE PATTERNS REVEALED BY MATERNAL AND BIPARENTAL MARKERS

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The Iberian Peninsula has been recognized as a hot spot of diversity and endemisms for numerous plant and animal species, and the honey bee is no exception. Honey bees occur naturally in Europe, Africa, western Asia, and the Middle East. In this vast range of habitats, adaptation to diverse ecological conditions has led to evolution of over 31 subspecies, which have been grouped into four main evolutionary lineages. The Iberian Peninsula harbours two of such lineages (African, A, and western European, M) and the greatest genetic diversity and complexity across Europe. Unravelling the evolutionary forces underlying such complex patterns of diversity has been a major goal of numerous studies and an increasingly important undertaking given the escalating threats to the honey bee populations (e.g. exotic diseases and parasites, pesticides, land use change and climate change). Here, I will present our main findings on the Iberian honey diversity patterns obtained from mtDNA, wings geometric morphometrics, nuclear SNPs and whole-genome data. Notwithstanding current intense honey bee management, a complex pattern of clinal variation that has been shaped by neutral and selective forces was revealed by the wide array of markers and approaches. Our data highlights the complexity of the Iberian honey bee patterns and reinforces the importance of Iberia as a reservoir of *Apis mellifera* diversity.

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