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Candidate loci for selection in Iberian honeybees: a genome-wide scan using SNP genotyping.

Pinto MA*, Chávez-Galarza J, Henriques D, Muñoz I, De la Rúa R, Azevedo J, Patton JC, Johnston JS

Email: apinto@ipb.pt

Over the last 20 years Iberian honeybees (IHB) have been scrutinised with a variety of genetic markers including morphology, allozymes, mtDNA, and microsatellites. The complex patterns and processes revealed have yet to be fully understood. While mtDNA is useful to reveal the maternal component, biparental markers capture genome-wide effects (admixture, expansions, and contractions) and locus-specific effects (selection). Accordingly, we expect to dissect out, through genome-wide scans, neutral and selection effects. In this study, the Illumina GoldenGate Assay was used to genotype SNPs across the complete genome of IHBs. The SNP data set was analysed for evidence of selection using a frequentist, FDIST, and a Bayesian method, BayeScan. Additionally, a spatial analysis method (MatSAM) was used to test for associations between SNPs and climatic variables. With these approaches we detected eight loci with a strong signal of directional selection. The genome positions and putative gene functions, given in the HB genomic resources, suggest that these putatively selected loci are strong candidates for selection. The spatial representation of these same loci reveals a clinal pattern of variation, further supporting selection. Our approach allows for a rigorous consideration of selection as the underlying cause of observed patterns of diversity and contrast with previous studies where evocation of selection was merely speculative.

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SNP (Single Nucleotide Polymorphism) analysis on the honeybees of Turkey.

Tunca RI, Kence M, Galindo A, Giray T, Kence A*

Email: aykut@metu.edu.tr

Ruttner has said that Anatolian bees were present in Thrace and they were separated from the rest of the honeybees of Europe along the borders of Turkey. He also stated that it's hard to explain this observation. We have studied 50 samples from Turkey at 994 SNP loci to answer this question. After structure analysis of 50 samples we have recognised Thracian honeybees and Anatolian honeybees with different genetic combinations. Besides according to our previous microsatellite analysis between Thracian and Anatolian honeybee populations there were minimum gene flow. A phylogenetic tree was constructed using distance matrix based on SNP results also revealed that Thracian honeybees of Edirne and Kirklareli region form a separate cluster compared to samples from other Anatolia regions. Therefore Thracian honeybees are completely different from Anatolian honeybees and they must be closer to European honeybees.