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Abstract book



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Welcome

It is our sincere pleasure to welcome you on the EurBee 10 Congress in Tallinn, Estonia! The Congress is organized by the Estonian University of Life Sciences with assistance by Publicon OÜ.

EurBee is the event, where old and new friends get together to exchange the knowledge of novel scientific findings, associated with honeybees and other pollinators.

We encourage young researchers to meet the leading scientists on their field. Establishing networking and creating new connections is extremely important for sustainable bee research.

The City of Tallinn is the capital of Estonia. Tallinn's Hanseatic old town and nowadays modern architecture is a great mixture for every taste. We recommend you to discover the great Estonian flavors and the interesting culture that Tallinn offers you in abundance on every corner.

Looking further, Estonian nature with its forests, bogs and swamps is unique in the world – all the EurBee guests have the opportunity to experience its magic!

Experience magic – experience Estonia!

Sincerely Yours,

Risto Raimets

President of EurBee 10



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EXPLORING POPULATION STRUCTURE AND ADAPTATION IN HONEY BEE SUBSPECIES FROM SOUTHERN GLACIAL REFUGIA: *A. M. IBERIENSIS* AND *A. M. LIGUSTICA*

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Abstract

Glacial refugia harbor populations with complex diversity patterns. In honey bees, the Iberian and Italian Peninsulas served as two of the most important glacial refugia in Europe. Here, we analyzed whole genomes generated from drones to infer population structure, genetic diversity, and the molecular basis of the local adaptation for the two native subspecies of these Peninsulas: *A. m. iberiensis* (N=86; M-lineage) and *A. m. ligustica* (N=225; C-lineage). For *A. m. iberiensis*, Admixture analysis revealed a strong cline between two genetic backgrounds from Southwest to Northeast and no C-lineage introgression was detected. For *A. m. ligustica*, introgression with *A. m. carnica* occurred in Central and Southern Italy (median q-value_{carnica}=0.069; IQR=0.187), away from the natural hybridization zone in Northeastern Italy where higher admixture proportions were detected (median q-value_{carnica}=0.229; IQR=0.262). *A. m. mellifera* introgression was detected especially in the Northwest (median q-value_{mellifera} 0.053; IQR=0.030), and with lower values in Central and Southern Italy (median q-value_{mellifera} 0.014; IQR=0.041). *A. m. iberiensis* showed higher diversity when compared to *A. m. ligustica*. Θ ($\Theta_{iberiensis}$ =0.325, $\Theta_{ligustica}$ = 0.245, p-value<0.001); H_e ($H_{e,iberiensis}$ =0.319, $H_{e,ligustica}$ =0.319; p-value<0.001) but lower relatedness (IBD kinship_{iberiensis}=0.002, IBD kinship_{ligustica}=0.014; p-value<0.001). Selection signatures were detected and cross-validated using PCAdapt, SAMBADA, and RDA. SNPs with q-adjusted p-values < 0.01 detected by at least two methods were considered strong candidates. For *A. m. ligustica*, 133 candidate SNPs annotated to 125 genes were detected by all three methods, including dnaJ homolog subfamily C member 9, nephrin, and the diuretic hormone receptor, and these were correlated with precipitation. For *A. m. iberiensis*, 528 SNPs annotated to 527 genes were detected, and these included proteins related to heat-shock response, such as Cyp40 and rrp45. While no common candidate SNPs were detected

between both subspecies, 20 common genes containing candidate SNPs were detected, such as 4-coumarate-CoA ligase 1, CPR9, and alpha-mannosidase 2.

GENOMIC INSIGHTS INTO MIDDLE EASTERN HONEY BEE SUBSPECIES: POPULATION STRUCTURE AND GENETIC INTEGRITY

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Abstract

The genetic patterns of Middle Eastern *A. mellifera* subspecies have been understudied, hindering a comprehensive understanding of honey bee evolutionary history. Here, we studied the genetic integrity of five Middle Eastern subspecies across a broad geographical range: Turkey (*A. m. anatoliaca*, N=97; *A. m. caucasica*, N=75; *A. m. syriaca*, N=18), Jordan and Lebanon (*A. m. syriaca*, N=238 and N=29), Iran (*A. m. meda*, N=75), Oman, and the UAE (*A. m. jemenitica*, N=13 and N=10). ADMIXTURE and PCA analyses were conducted on SNPs detected from whole-genomes. Our findings reveal concerning conservation statuses for many populations/subspecies. In *A. m. caucasica* and *A. m. anatoliaca*, only 10 and 28 samples, respectively, were pure (introgression < 90%). In the *A. m. caucasica* range, 60 samples were hybrids of *A. m. caucasica*, *A. m. syriaca*, and *A.*