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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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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.*

m. ligustica. In the *A. m. anatoliaca* range, 69 samples showed high hybridization degrees with *A. m. syriaca*, and *A. m. caucasia*. Only six samples in the Turkish range of the *A. m. syriaca* range were identified as pure, while the rest were also hybrids. All samples from Jordan and Lebanon showed variable *A. m. ligustica* introgression. In Iran, 23 samples were classified as pure *A. m. meda*. The rest showed introgression primarily due to *A. m. ligustica* and *A. m. caucasia*. In the UAE, two main groups were identified: the first comprised hybrids of *A. m. jemenitica*, *A. m. lamarckii* and *A. m. ligustica*, and the second group mainly consisted of hybrids of *A. m. lamarckii* and *A. m. ligustica*. Oman stands out as the sole location where all samples were identified as pure *A. m. jemenitica*. This study indicates widespread hybridization across various regions and underscores the urgent need for targeted conservation efforts for Middle Eastern subspecies.

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