ENBE 2025

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BOOK OF ABSTRACTS

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TALK 26| HUMAN-MEDIATED RAPID EVOLUTIONARY CHANGE IN EUROPEAN HONEY BEES

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Abstract

In its vast distributional range, spanning Africa, Europe, the Middle East, and western Asia, the honey bee *Apis mellifera* diversified into 30 subspecies grouped into four major evolutionary lineages. Two of these lineages, M (western/northern European) and C (southeastern European), are parapatric in Europe. However, increasingly intensified queen trading is likely eroding the natural genetic boundaries and altering the continent's diversity patterns. To evaluate the impact of this recent human-mediated gene flow, we conducted an unprecedented survey spanning 33 countries and sampling more than 1,300 colonies, including 139 from conservation apiaries of the M-lineage subspecies *A. m. mellifera*. We used a dual-marker approach combining the hypervariable mitochondrial tRNA^{Leu}–cox2 intergenic region with nuclear genome-wide single-nucleotide polymorphisms (SNPs). Both markers were highly concordant at the lineage level and European scale, showing that in the native area of M-lineage, which covers western and northern Europe, C-lineage ancestry is now predominant. This pattern is congruent with widespread commercial dissemination of C-lineage subspecies (*A. m. carnica*, *A. m. ligustica*), which is leading to introgressive hybridisation and, in many regions, to almost complete replacement of native subspecies. The exceptions to this trend are the Iberian Peninsula, Ireland, and conservation apiaries, which retain almost exclusively native M-lineage ancestry. Remarkably, even within the native C-lineage range in the Mediterranean and southeastern Europe, the Italian subspecies *A. m. ligustica*, the most widely favoured subspecies worldwide, shows worrying levels of introgression from its C-lineage neighbour *A. m. carnica*. Equally striking is the widespread presence of African-lineage mitotypes, whose routes of introduction remain unclear. Altogether, these findings raise serious concerns about the genetic integrity of native subspecies and the consequences of admixture for adaptation in a rapidly changing environment shaped by climate change and emerging parasites and pathogens. Further, these changes may affect the gene pools of wild *A. mellifera* populations, recently classified as Endangered by the IUCN.

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