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## Genetic characterization of two Algerian honey bees *Apis mellifera intermissa* and *sahariensis* populations by whole genome sequencing

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The original geographical distribution of the honey bees *Apis mellifera* in Africa, Europe, and Western Asia, has been extended worldwide through human beekeeping activities. Despite, many studies carried out in order to better understand the genetic diversity of *Apis mellifera* genetic diversity, the genetic composition of some African subspecies is still poorly described. Within the frame of the TSARA initiative, we initiated the study of the Algerian honey bee population, composed of two described subspecies *A. m. intermissa* in the north and *A. m. sahariensis* in the south. Genetic differentiation is expected to match phenotypic specificities and adaptation to heat and drought in *A. m. sahariensis*. Contamination by imported bees is also possible. To shed light on the structure of this population and to integrate these two subspecies in the growing dataset of available haploid drone sequences, we performed whole genome sequencing of 151 haploid drones. Integrated analyses with a dataset of drone sequences from European reference populations did not detect any significant admixture in the Algerian honey bees. Interestingly, most of the genetic variation was not found between the *A. m. intermissa* and *A. m. sahariensis* subspecies and instead, two main genetic clusters were found along an East-West axis. We found that the correlation between genetic and geographic distances was higher in the Western cluster and that close-family relationships were mostly detected in the Eastern cluster, sometimes at long distance. The differences between the two main genetic clusters suggest differential breeding management between Eastern and Western Algeria, with a higher exchange of genetic material over long distances in the East. The lack of detected admixture events suggests that, unlike what is seen in many places worldwide, imports of queens from foreign countries does not seem to have occurred at a large scale in Algeria, a finding of relevance for conservation purposes. The outcomes of our study should be considered in local honey bee biodiversity improvement and conservation initiatives. In the future, we would like to specifically sample and analyse *A. m. sahariensis*, to initiate conservation strategies based on whole genomic data.

Keywords: genetic diversity, sequencing, *Apis mellifera*