



HAL
open science

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

Kamila Canale-Tabet, Giovanna Salvatore, Amira Chibani Bahi Amar, Bahi Amar, Riad Fridi, Nacera Tabet Aoul, Soumia Saci, Emmanuelle Labarthe, Valentino Palombo, Mariasilvia d'Andrea, et al.

► To cite this version:

Kamila Canale-Tabet, Giovanna Salvatore, Amira Chibani Bahi Amar, Bahi Amar, Riad Fridi, et al.. Genetic characterization of two Algerian honey bees *Apis mellifera intermissa* and *sahariensis* populations by whole genome sequencing. 48 International Apicultural Congress APIMONDIA, Sep 2023, Santiago (Chile), Chile. hal-04891785

HAL Id: hal-04891785

<https://hal.inrae.fr/hal-04891785v1>

Submitted on 16 Jan 2025

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Kamila Canale-Tabet¹, Giovanna Salvatore², Amira Chibani Bahi Amar³, Riad Fridi³, Nacera Tabet Aoul^{3,4}, Soumia Saci⁵, Emmanuelle Labarthe¹, Valentino Palombo², Mariasilvia D'Andrea², Alain Vignal¹, Pierre Faux¹

¹GenPhySE, Université de Toulouse, INRAE, INPT, INP-ENVT, 31326, Castanet-Tolosan, France

²Department of Agricultural, Environmental and Food Sciences, University of Molise, Via De Sanctis snc, 86100 Campobasso, Italy

³Laboratoire de Génétique Moléculaire et Cellulaire (LGMC), Département de Génétique Moléculaire Appliquée, Université des Sciences et de la Technologie d'Oran Mohamed Boudiaf, USTOMB, BP 1505, El M'naouer, 31000 Oran, Algérie

⁴Department of Biotechnology, Faculty SNV, University of Oran1 Ahmed BENBELLA, Oran, Algeria

⁵National Institute of Agronomic Research of Algeria (INRAA), El Harrach, Alger, Algeria

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*