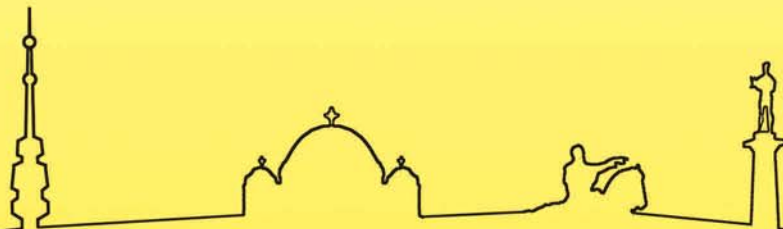**EurBee 9**
9th European Congress of Apidology
20-22 September 2022
Belgrade, Serbia

Abstract Book

MEDIBEES PROJECT: DISENTANGLING DIVERSITY PATTERNS AND PROCESSES OF MEDITERRANEAN HONEY BEE SUBSPECIES BY WHOLE-GENOME SEQUENCING

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Apis mellifera is represented by 31 presently acknowledged subspecies that are native to Asia, Africa, and Europe. Approximately 40% of that richness evolved in the Mediterranean region, as the result of adaptation to diverse environmental conditions. Understanding and preserving such diversity will help to promote the honey bee's resilience to climate change and biotic stressors, which is the main goal of the MEDIBEES project. This goal will be addressed by the following objectives: a) elucidate the genetic background of the Mediterranean subspecies, b) uncover the genetic basis of their adaptation to the local conditions, c) evaluate the respective conservation status, and d) assess their resilience to climate change. To that end, over 1300 geo-referenced colonies representing 9 subspecies (*A. m. ligustica, A. m. siciliana, A. m. ruttneri, A. m. sahariensis, A. m. intermissa, A. m. syriaca, A. m. anatoliaca, A. m. caucasia* and *A. m. meda*) are being sampled in 6 Mediterranean countries (Algeria, Italia, Jordan, Lebanon, Malta and Turkey). The samples will be whole-genome sequenced using Illumina technology. These newly generated genome datasets will be combined with those previously obtained for *A. m. iberiensis* from Spain and Portugal, and the data will be subjected to a battery of analytical tools. Here, we describe how the massive whole-genome dataset will be scrutinized to fully address the MEDIBEES objectives. This project promises to generate unprecedented knowledge on the differential vulnerability and resilience of the Mediterranean honey bee subspecies to the main environmental stressors typical of this region.

Keywords: honey bee genomics, whole-genome sequencing, genetic basis of adaptation, genotype x environment associations