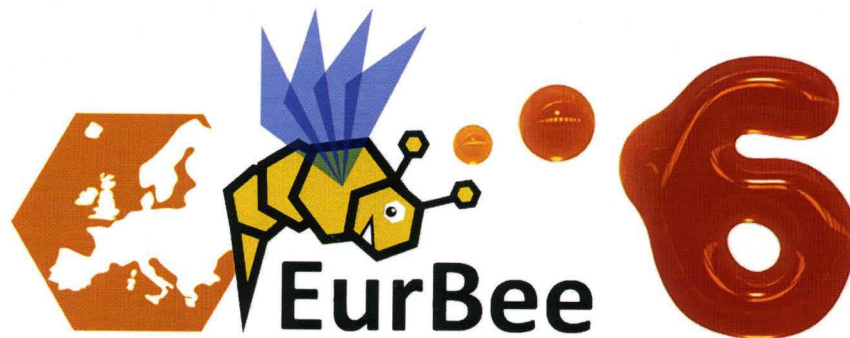


# Sixth European Conference of Apidology



Murcia (Spain) 9 -11 September 2014



**Sixth European Conference of Apidology**  
**9-11 September 2014**

Edited by Pilar De la Rúa

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Antifreeze proteins (AFPs) were isolated from many organisms living in cold polar regions. These proteins have unique ice-binding affinity and can effectively inhibit ice crystals growth, so depress the freezing point of body liquids in polar organisms. AFPs can inhibit ice recrystallization, thus preventing thawed cells from mechanical damage caused by ice regrowth. As reported by others, AFPs can stabilize cell membrane organization during freezing. However, to our knowledge, there are no reports on the use of AFPs for honey bee spermatozoa cryopreservation despite studies in the fish, bull, ram and chimpanzee. These studies have reported improved sperm quality after cryopreservation with AFPs. In our research we are aiming on possible improvement of honey bee spermatozoa cryopreservation protocol with the use of AFPs.

#### **Morphometric analysis of *Apis mellifera sahariensis* populations from Algeria**

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The study of morphometric characters of honeybees is one of the steps of conservation program diversity. The objective of this study is to determine the morphometric characteristics of *Apis mellifera sahariensis* of south regions in Algeria to determine the purity of bee colonies. Honeybees are sampled from 92 colonies in 2008-2009, 42 colonies Tellian race divided between the coastal zone and the Tell Atlas and 50 colonies of the Saharan race from the steppe and Saharan zones. Reference samples are considered to be 14 colonies Tellian bee colonies and 9 of the Saharan race from Morocco and 9 colonies of *Apis mellifera iberiensis*. The study of 38 morphometric characters of bees sampled in Algeria has set standards for the average 38 of them measured. The principal component analysis (PCA) has separate populations of the bee Saharan studied in 5 distinct groups. These populations are compared with other populations of Algerian, Moroccan and Spanish. The PCA has revealed the existence of three distinct groups. The first group includes the Iberian bee colonies. In the second group there are still two subgroups, one set consisting of samples of the bee subspecies *A. m. intermissa*, regardless of Algerian or Moroccan origin, and *A. m. sahariensis* of Algerian origin, except for bees locality Skhouna (Ain Sefra), the other formed by *A. m. sahariensis* Morocco.

#### **Maternal structure of Iberian honey bees inferred from whole mitochondrial genomes**

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The maternally inherited mitochondrial DNA has been the marker of choice for as-

sessing Iberian honeybee variation, particularly the intergenic tRNA<sup>leu</sup>-cox2 region. The data generated by massive sampling of this region confirmed early findings of coexistence of African (A) and western European (M) lineages, forming a south–north cline, and revealed unparalleled levels of haplotype diversity and complexity.

Accordingly, it has been suggested that Iberia served as a glacial refuge, and as a place of secondary contact between European and African lineages. While we have learned a great deal with this region, due to its high levels of variation and repetitive structure, there are evolutionary questions that can only be properly addressed using other mitochondrial regions. In this study, we used NGS technology to sequence the whole mitogenomes of 70 *A.m. iberiensis*, 7 *A.m. intermissa*, 7 *A.m. sahariensis*, and 8 *A.m. mellifera*. The data was analyzed using a phylogeographical framework to address the following questions: When did M and A lineages split? How divergent are African-derived Iberian honey bees from both African subspecies? Is there evidence of multiple range expansions of northern African honey bees? Which African subspecies is the most probable source of African genes in Iberian honey bees? The powerful data set generated in this study is providing the opportunity to decipher the Iberian honey bee history at an unprecedented resolution. At the same time, it will supply a strong scientific basis for conservation decisions, which is increasingly important in face of the escalating threats to honey bee diversity.

#### **Fine-scale analysis of Iberian honeybee populations reveals a strong maternal structure and the presence of novel mitochondrial haplotypes**

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*Apis mellifera* is naturally located in Europe, Africa, and Middle East. Adaptation to different environmental conditions has enabled the evolution of 30 subspecies, which are grouped into four lineages (A–African, M–western European, C–eastern European, and O–Middle Eastern). In Western Europe, Iberia naturally harbors the Iberian honeybee subspecies, *A.m. iberiensis*. Previous mitochondrial DNA surveys of Iberian populations have revealed a complex haplotype pattern due to the coexistence of two highly divergent lineages (A and M) forming a well-defined southwestern-northeastern cline. However, these surveys did not cover the whole territory of Iberia, missing an important part such as the Atlantic. To fill this spatial gap, over 711 colonies were sampled across three north-south transects. The samples were sequenced for the highly polymorphic tRNA<sup>leu</sup>-cox2 mitochondrial region and the sequences were analyzed using MEGA and NETWORK. In addition to confirming the previously reported cline, our results show (i) the presence of 25 novel haplotypes (16 African and 9 European); (ii) a higher proportion of colonies belonging to the A than to the M-lineage; (iii) a low level of introgression from C lineage; and possibly a novel African sub-lineage. While providing a more complete picture of the Iberian honeybee maternal variation, this study suggests that in spite of intensive