

Book of Abstract



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SESSION XII

SOCIAL INSECTS AND APIDOLOGY

Characterization of the *Apis mellifera* population on the island of Pantelleria (Sicily, Italy).

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Apis mellifera Linnaeus, 1758 has some peculiarities that make it a key organism for the conservation of biodiversity and, therefore, the global ecological balance. Unmanaged western honey bee colonies were present in the recent past everywhere and for several millenniums they have coexisted with managed colonies. In the last 35 years, unmanaged colonies have almost completely disappeared in most of Europe due to the spillover of the parasitic mite *Varroa destructor* (Anderson & Trueman, 2000) to western honey bee colonies. However, in recent years, unmanaged colonies have been apparently sharply increasing. These colonies are at the attention of the world of bee research and European beekeepers for the occurrence, in such conditions, of possible situations of resilience to changing climatic aspects and health problems, as well as for the protection of the indigenous subspecies of *Apis mellifera*. On the island of Pantelleria, where there have always been some beekeepers, managed colonies and unmanaged colonies of honey bees coexist. Many unmanaged colonies were recently recorded using the smartphone app BeeWild. Therefore, in this study, carried out mainly within the National Park of Pantelleria island, we described the morphometry and haplotype distribution of the honey bee colonies living in this isolated and very particular context, trying to point out the possible differences between managed and unmanaged colonies.

Honey bee individuals (workers) were collected from 32 colonies in the summer of 2021 and subjected to morphometric and molecular analyses. For morphometric analyses, 16 wing characters were used. A discriminant analysis, including Pantelleria honey bees, *A. m. siciliana* Dalla Torre 1896, *A. m. ligustica* Spinola 1806, *A. m. carnica* Pollmann 1879, *A. m. intermissa* Buttel-Reepen 1906, *A. m. caucasica* Pollman 1889 and *A. m. mellifera* Linnaeus 1758, was carried out. For molecular analyses different molecular markers were used (COI-COII intergenic region of mitochondrial DNA and SNIPs). As a reference *Apis mellifera mellifera* Linnaeus 1758, *A. m. ligustica* Spinola 1806, *A. m. carnica*, *A. m. jemenitica* Ruttner 1976, *A. m. siciliana* Dalla Torre 1896, *A. m. iberiensis* Engel 1999, *A. m. intermissa* Buttel-Reepen 1906, and *A. m. ruttneri* Sheppard, Arias, Grech et Meixner 1997 were used. Evolutionary lineages and haplotypes for each individual were analyzed by sequence blast on GenBank. Based on the results of morphometric analysis 68% of the colonies were similar to *A. m. siciliana*, 4% to *A. m. ligustica* and 28% were apparently hybrids (i. e. *A. m. siciliana* x *A. m. intermissa*). Furthermore, Pantelleria honey bees cluster separately from *A. m. siciliana* as well other subspecies. With the genetic analyses we found that the A evolutionary lineage is dominant on the island (71% of the samples overall), and even more so in the unmanaged colonies (93%). The most frequent A haplotype was A1, which was found in *A. m. siciliana* in the course of the reintroduction project APESLOW, followed by A4 and A2, also previously reported in *A. m. siciliana*. Furthermore, as the proportion of A lineage haplotypes was higher in the unmanaged colonies, we can hypothesise that the local population has an adaptive advantage over imported genotypes. Further analysis should be carried out to better understand the identity of Pantelleria honey bees.

KEY WORDS: Honey bee, local populations, morphometry, genetics.

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