

# Sixth European Conference of Apidology



Murcia (Spain) 9 -11 September 2014



### **What do whole genome sequences tell us about the population history of honeybees?**

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We performed whole genome sequencing of 140 samples of *Apis mellifera* collected from across the globe to comprehensively characterize patterns of variation across the genome, resulting in the identification of 8.3M SNPs. We applied coalescent approaches to illuminate the population history of honeybees and the processes underlying the patterns of diversity. A major finding of this study is that a substantial proportion of variation is shared between all continental groups. Levels of variation were surprisingly high in all populations we sampled. These values correspond to population sizes of several orders of magnitude larger than previously estimated from local variation at drone congregation areas. Domestic and Africanized lineages appear as diverse as their ancestral populations, indicating a lack of domestication or founder bottlenecks. In general, loss of genetic variation does currently not appear to be a major threat to honeybees. However, we uncover evidence that honeybee population sizes have varied greatly over evolutionary time. We demonstrate that linkage disequilibrium decays extremely rapidly in bees and we infer extremely high recombination rates across the genome, consistent with rates measured in experimental crosses. We used patterns of variation to investigate population history using a genealogical concordance method. We estimate that major continental groups diverged from each other ~200,000 years ago, but that current subspecies with similar ancestry are much younger, only 20,000-30,000 years old.

### **The gene geographic analysis of Burzyan population of *Apis mellifera mellifera* L.**

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High honeybee colony losses in North America and Europe again recalled the importance of preservation of one's gene pool (Johnson, 2010). The 43 Apimondia Congress (2013) have noted the research of local aborigine populations as a key direction of modern conservation beekeeping. Aborigine honeybee populations are being restored in Sicily (Costa, 2013), Greece, Cyprus (Bouga, Hatjina, 2013) and other parts of Europe. Since 2008 the gene geographic analysis of Burzyan population of *A.m. mellifera* in the South Urals was performed by mitochondrial (tRNA-Leu - COII) and 9 microsatellite (Ap243, 4A110, A24, A8, A43, A113, A88, Ap049 и A28) markers. The population area, genetic structure and molecular diversity have been analyzed in this study. In total samples from 1102 colonies, 206 apiaries and 10 districts in a mountain-wood zone were analyzed. The sequence of the locus COI-COII mtDNA helped identify new M line mitotypes, which can be used as genetic markers for Ural honeybee. The population border was mapped, one

is occupying an area two times greater than previously thought. The total number of genetically pure colonies reaches nearly 10 thousand. The genetic differentiation of Burzhan population from other *A.m. mellifera* in the Urals was shown with the optimal conservation strategy for the honeybee in Russian conditions being proposed.

**Reintroduction of the endangered *A. m. siciliana* in Sicily: genetic and morphometric tools to support management of mating stations and conservation islands.**

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Efforts for *A. m. siciliana* conservation began in the late '80s, when colonies were isolated on the small Ustica island to avoid introgression with the Italian yellow bee *A. m. ligustica*. A single queen breeder and CRA-API (*Apiculture and Sericulture Unit* of the Agricultural Research Council) cooperated until the present days to preserve a pure population on small conservation islands.

The three year reintroduction project APESLOW: "Reintroduction and conservation of endangered subspecies *Apis mellifera siciliana*, Dalla Torre 1896: a tribute to Prof. Genduso", has come to its final year: here we present a brief overview of the project and the results of the first two years of monitoring on *A. m. siciliana* populations. About 400 honeybee colonies have been investigated at mitochondrial and nuclear level, results on about 150 samples were confirmed with morphometrical methods, in order to maximize the reintroduction effort on Sicily main island, to achieve an efficient management of main island mating stations and to implement original conservation islands' population with additional genetic variability.

**Preserving local bee population and beekeeping heritage in a French national park**

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The Cevennes National Park is a protected area that has been recently recognised for its exceptional biological and cultural heritage by UNESCO. Cevennes region is known for centuries as a 'land of honey' where beekeeping used to be characterized by a traditional beehive made out of hollow chestnut-trunks. Log-hive apiaries constitute an extremely old beekeeping practice, and were originally populated by local black bees (*Apis mellifera mellifera*). Nowadays, global change, influences practices and most beekeepers have adopted framehives. Changes have also led to decrement of the local bee subspecies and to its genetic homogenization. In order to preserve its natural and cultural heritage,