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P6.3

Introgression of lineage C honeybees into black honeybees: a genome-wide estimation using SNP.

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The black honeybee, *Apis mellifera mellifera* L., is probably the honeybee subspecies more threatened by introgression from foreign subspecies, specially lineage C *A. m. carnica* and *A. m. ligustica*. In fact, in some areas of its distributional range, intensive beekeeping with foreign subspecies has driven *A. m. mellifera* populations to nearly replacement. While massive and repeated introductions may lead to loss of native genetic patrimony, a low level of gene flow can also be detrimental because it may compromise honeybee survival and local adaptation by disrupting co-evolved gene complexes. Assessing levels of introgression is an important activity in breeding programmes, especially when conservation of native races is a major concern. Previous surveys of *A. m. mellifera* populations estimated the introgression of lineage C honeybees by using mtDNA and microsatellites markers. In this presentation we used both mtDNA (sequence data of the tRNAleu-cox2 intergenic region) and over 1245 SNPs to ascertain introgression levels of *A. m. carnica* and *A. m. ligustica* in *A. m. mellifera* populations (some included in conservation programmes) sampled in France, Switzerland, Denmark, Holland, Norway, England, and Scotland. We used different model-based approaches, implemented by different software applications (Structure, Admixture, NewHybrids). We found varying levels of introgression ranging from less than 3% (in Norway) to over 65% (in France).

P6.4

16s rDNA diversity of *Apis mellifera* subspecies in Turkey.

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Mitochondrial DNA variation can be used to infer honeybee evolutionary relationships. In this study, the diversity of mitochondrial 16s rDNA region was investigated in 95 honeybees from ten different populations in Turkey which mainly consist *A. m. anatoliaca*, *A. m. caucasica* and *A. m. meda*. Samples were amplified by PCR and then subjected to RFLP pattern analysis using 18 restriction enzymes. A total of 10 restriction enzymes were found to have at least one recognition site in 16s rDNA region. Nucleotide polymorphisms were revealed using restriction enzymes Bsp143I, DraI and SspI in 16s rDNA. The polymorphisms were subsequently confirmed by direct DNA sequencing with sequences thereafter deposited in NCBI Genbank Database. Molecular phylogenetic analysis revealed that Konya/Sızma and Antalya/Elmalı populations were the most distant from all the other Turkish honeybee populations surveyed.