



European Society for Evolutionary Biology

**ORAL PRESENTATION ABSTRACTS AND LIST  
OF POSTERS**

14<sup>th</sup> Congress, Lisbon, Portugal, 19 - 24 August 2013

**D21SY27PS1323**

**INTROGRESSION LEVELS OF THE ITALIAN AND CARNIOLAN HONEY BEE SUBSPECIES INTO THE BLACK HONEY BEE: A COMPARISON BETWEEN MICROSATELLITE AND SINGLE NUCLEOTIDE POLYMORPHISM (SNP) MARKERS**

Dora Sofia M Henriques<sup>1</sup>, Laura Jara<sup>2</sup>, Julio Chávez-Galarza<sup>1</sup>, José Rufino Amaro<sup>1</sup>, Pilar De la Rúa<sup>2</sup>, Maria Alice Pinto<sup>1</sup>

<sup>1</sup>*Escola Agrária, Insituto Politécnico de Bragança, Portugal*

<sup>2</sup>*Departamento de Zoología y Antropología Física, Universidad de Murcia, Spain*

dorasmh@gmail.com

Human activities have been shaping the distribution of honey bee subspecies in Europe. In fact, during the last decades there has been an extensive introduction of the beekeepers' favorite eastern European (lineage C) subspecies *A. m. ligustica* (Italian) and *A. m. carnica* (carniolan) into western Europe. Because of these introductions, there has been gene flow, and even replacement, of the native western European subspecies *A. m. mellifera* (black honey bee), which belongs to lineage M. Assessing levels of introgression is an important activity in breeding programs, especially when conservation of native subspecies is a major concern. Previous surveys of the *A. m. mellifera* populations estimated the introgression of lineage C into lineage M honey bees by using mtDNA and microsatellite markers. Others markers, such as SNPs, have some advantages as they provide a genome wide coverage, higher quality data, and at the same time they are suitable for automatic and standardization in high throughput technologies. Previous studies indicate that the discriminatory power of SNPs to detect population structure is lower than that of microsatellites; about 100 SNPs are needed to provide the same power of 10-20 microsatellites. In this study we will compare introgression levels between microsatellites and SNPs as estimated by the software STRUCTURE using the admixture model and correlated allele frequencies in a black honey bee collection originating from several countries across western Europe. This collection was genotyped for 12 microsatellites and 1183 SNPs. The introgression levels were first estimated using both full datasets. Then, to have similar discriminatory power between the 12 microsatellite and SNPs, we used between 60 and 120 SNP loci from the initial 1183 SNP dataset by selecting SNPs located nearby the microsatellite loci. With this work we want to verify which is the best strategy for assessing the levels of introgression in honey bee breeding programs.