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Abstracts



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A SNP assay for assessing diversity in immune genes in the honey bee (*Apis mellifera* L.)

Dora Henriques¹, Ana R. Lopes¹, Nor Chejanovsky², Anne Dalmon³, Mariano Higes⁴, Clara Jabal-Uriel⁴, Yves Le Conte³, Maritza Reyes-Carreno³, Victoria Soroker², Raquel Martin-Hernandez^{4,5}, M. Alice Pinto¹

(1) Centro de Investigacao de Montanha, Instituto Politecnico de Braganca, Campus de Santa Apolonia, 5300-253 Braganca, Portugal;

(2) Agricultural Research Organization, The Volcani Center, Israel;

(3) INRAE, Unite Abeilles et Environnement, Avignon, France;

(4) IRIAF. Instituto Regional de Investigacion y Desarrollo Agroalimentario y Forestal, Laboratorio de Patologia Apicola, Centro de Investigacion Apicola y Agroambiental (CIAPA), Consejerla de Agricultura de la Junta de Comunidades de Castilla-La Mancha, Marchamalo, Spain;

(5) Instituto de Recursos Humanos para la Ciencia y la Tecnologia (INCRECYT-FEDER), Fundacion Parque Cientifico y Tecnol6gico de Castilla-La Mancha, 02006 Albacete, Spain.

With a growing number of parasites and pathogens experiencing large-scale range expansions, monitoring diversity in immune genes of host populations has never been so important because it can inform on the adaptive potential to resist the invaders. Population surveys of immune genes are becoming common in many organisms, yet they are missing in the honey bee (*Apis mellifera* L.), a key-stone species that has been severely affected by biological invasions. To fill the gap, here we identified single nucleotide polymorphisms (SNPs) in honey bee immune genes and then developed an assay to be genotyped using the high-sample-throughput iPLEX MassARRAY system that can be readily used for population surveys. The assay was constructed using SNPs detected in whole-genome scans of 123 individuals originating from a wide geographical area, representing seven *A. mellifera* subspecies and three evolutionary lineages (M-Western European, C- Eastern European, A- African). In this dataset, a total of 35,782 SNPs distributed through 180 genes were found. Only polymorphic SNPs (MAF>0.05) SNPs located in putatively functional regions were retained. Other filtering criteria inked to the MassARRAY® MALDI-TOF genotyping system were used and an assay with 107 SNPs was obtained. A total of 16 SNPs were discarded either due to inconsistent calls and/or misidentification of heterozygous positions. The final assay contains 91 quality-proved functional SNPs covering 89 innate immune genes. The 89 genes belong to several families and pathways, such as IMD, JAK-STAT, Toll and RNAi. This gene set also includes genes that have been found to be expressed in honey bees infected with the viruses SINV, IAPV, DWV and *Nosema* spp. This medium-density-SNP assay was applied to 156 samples from four countries (Portugal, Spain, France and Israel) and the admixture analysis clustered the samples according to their lineage and subspecies, suggesting that the immune SNPs can be also used to reconstruct population structure. This newly-developed SNP assay can be applied to monitoring diversity in immune genes, identifying the genetic basis of disease susceptibility, and even inferring genetic structure.