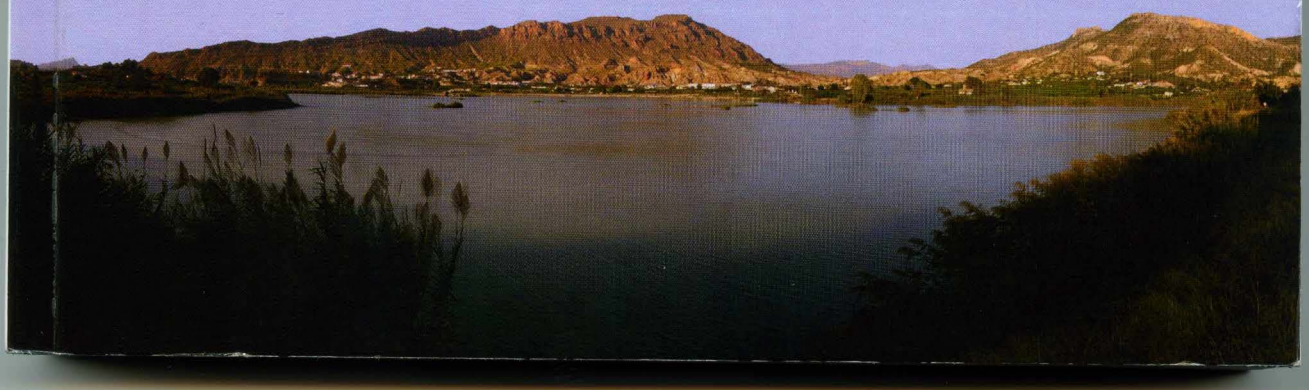
Sixth European Conference of Apidology

EurBee 6

Murcia (Spain) 9 -11 September 2014



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no transfers are currently occurring between mites coming from the two hosts in Northern Vietnam. Furthermore, the genetic diversity of the mite within its new host is very limited as host switch has only occurred in rare cases and the mite reproduces quasi-clonally. To further identify traces of selection within *V. destructor* genome involved in host switching, we sequenced the whole genome of mites coming from both hosts and compared it.

Evaluating the performance of a variable number of SNPs for genetic identification and introgression analysis in the dark honey bee

Irene Muñoz, Dora Henriques, Julio Chávez-Galarza, José Rufino, John S. Johnston, Maria Alice Pinto

Mountain Research Centre (CIMO), Polytechnic Institute of Bragança, Campus de Sta. Apolónia, Apartado 1172, 5301-855 Bragança, Portugal

E-mail: irenemg@um.es

Genetic identification and introgression analysis using molecular markers is an important tool for management and conservation of honey bee subspecies. High density assays featuring Single Nucleotide Polymorphism (SNP) markers can be exploited to create a reduced panel containing the most informative markers for these purposes. The objective of this study was to determine the minimum number of SNP loci required to verify the origin of dark honey bee individuals and to provide accurate estimates of the level of C-lineage introgression into their genome. We estimated allele frequencies of 1183 SNPs from 113 drone honey bee individuals sampled in the natural ranges of *A. m. mellifera*, *A. m. carnica* and *A. m. ligustica*, and evaluated the discriminant power of the SNPs using a variety of metrics and approaches including the Weir & Cockerham's FST, Delta, informativeness (In), PCA and an FST-based outlier test. Taking into account the less expensive multiplex assays made available by Illumina®, we created 5 panels of 48-, 96-, 144-, 192- and 384-SNPs with the average top-ranked loci and tested them to obtain the probability of assigning individuals to the correct origin and to calculate the admixture level using each panel. The analyses showed no significant differences in the introgression proportions produced by the different SNP panels, suggesting that a low number of loci is sufficient to produce accurate estimates.

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Distribution of *Apis florea* in different geographic locations of Pakistan

Naheed Rajper, R. Farooqi Shakeel

Department of Genetics, University of Karachi, Pakistan

E-mail: rajpernaheed28@gmail.com

Southeast Asia has been reported to be the primary distribution center for *Apis florea*. Oman, Iran and Pakistan with warmer climates have been reported as the habitats for