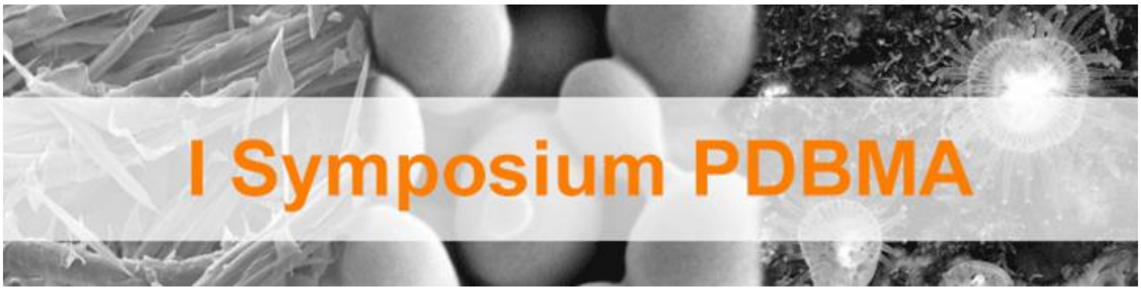

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Book of Abstracts

CENTRO DE BIOLOGIA MOLECULAR E AMBIENTAL
CENTRE OF MOLECULAR AND ENVIRONMENTAL BIOLOGY

Name	Julio César Chávez-Galarza
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PhD / Master and Edition	PDBMA 2011/2015
Title of the Work	Unraveling the local adaptation and population structure of Iberian honey bee (*Apis mellifera iberiensis*)
Supervisors	Filipe Costa Oliveira, Maria Alice Pinto
Abstract	Unraveling the complex evolutionary history of *Apis mellifera iberiensis* is a challenging task. Several studies have been carried out in the Iberian honey bee to explain its origin, suggesting two possible hypotheses: a primary intergradation process (morphology and allozymes), or a secondary contact process (mtDNA) supported by an abrupt southwestern-northeastern cline formed by two divergent lineages. Surveys with microsatellites support neither hypothesis. The goal of this work is to unravel the evolutionary history of the Iberian honey bee using SNPs. To that end, 711 individuals of *A. m. iberiensis* were collected in 23 sites across three north-south transepts in the Iberian Peninsula. This collection was genotyped for 1536 SNPs using the GoldenGate assay of Illumina. The SNP dataset was examined in search for signatures of selection by coalescence, Bayesian and spatial analysis. Then, the population structure was inferred by using Bayesian methods and multivariate and spatial analysis. Analysis of selection detected 10 *loci* exhibiting strong selection signal. Their putative functions were determined using the honey bee genomic resources and mapped to putative genes with diverse biological functions, which included vision, detoxification metabolism, and immunity. On the other hand, the population structure recovers the cline southwestern-northeastern found using mtDNA markers.
Authors of the work	Chávez-Galarza, J. C.; Costa, F.; Pinto, M. A.