congenomics . 2016

Conference on Conservation Genomics

3 – 6 May 2016 | Campus de Vairão, Portugal | CIBIO-InBIO

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Searching for signatures of selection in the Iberian honey bee (*Apis mellifera iberiensis*) using allele-environment association approaches

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In the current context of a global human-mediated environmental crisis, understanding which genes and mechanisms are responsible for adaptation to different climates will enable predictions on how organisms will respond to a rapidly changing world. This is particularly important for the honey bee, a key-stone species for ecosystem functioning and economy, which is facing increasing pressures from the effects of intensified land use, climate change, and the spread of pests and pathogens. In this study we used Illumina technology to sequence the whole genomes of 86 Iberian honey bees, collected across three longitudinal transects in the Iberian Peninsula. Then, we searched for signatures of selection using two different methods (LFMM and Samβada), which combine genetic and non-genetic (environmental) data. The LFMM approach identified 2193, 449 and 275 SNPs for FDR values of 0.05, 0.02, and 0.01, respectively. The environmental variables associated with the highest number of SNP outliers were precipitation, latitude and longitude. The LFMM findings were concordant with those obtained with Samβada. Gene ontology analyses show that clusters with higher score are related with immune system development and sensory organ development for the outlier genes associated with longitude. Precipitation is associated with genes related with biological regulation and sequence-specific DNA binding. This represents the most comprehensive study of positive selection that integrates genetic information, and environmental variables performed so far in Iberian honeybees.