



# **EurBee 8** **8th Congress of Apidology**

**18-20 SEPTEMBER 2018**  
**Ghent, Belgium**  
**Program & Abstract Book**



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### Genome-wide analysis of structural and single nucleotide variation at candidate loci for behavioural traits in Carniolan honeybee (*Apis mellifera carnica*)

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The honeybee (*Apis mellifera*) is regarded as a valuable model organism for genetic studies of social behavior. Among behavioral traits, aggressiveness plays an important role and significant variability of this trait was found among races but also among individual colonies. Carniolan bee is known for its calm and non-aggressive behavior, making it suitable for honey production in densely as well as sparsely populated areas. Our preliminary bioinformatics analysis showed that many genes involved in shaping of behavioral traits in bees are highly conserved among different species of social insects, however, the most prominent differences could be expected in the regulatory regions of these genes. Since subspecies of bees were subjected to different selection pressures, it is possible that binding sites for transcription factors, which were shaped by cis-regulatory evolution were modified and so they represent molecular basis for certain adaptive traits. Among most prominent candidate genes for behavioral traits are genes involved in biosynthesis of juvenile hormone genes coding enzymes for its degradation. Juvenile hormone esterase is the enzyme that degrades juvenile hormone and contributes to the regulation of hormone amount in hemolymph. In the current study, publicly available whole genome sequences of *Apis mellifera carnica* were compared with reference genome of *A.m. ligustica* and analyzed for structural and SNP variation within the candidate gene regions, related to behavioral traits. Several SNPs were found in genes coding juvenile hormone modifying enzymes: juvenile hormone esterase (406066), juvenile hormone epoxidase (406152), juvenile hormone methyl transferase (724216). In addition, SNPs were also found in the coding region of the dopamine receptor gene (406133) in exons and introns of farnesyl diphosphate synthase gene (107964026) and in introns of alpha glucosidase gene (406131). In the majority of candidate gene regions for behavioral traits structural variants could not be found. However, in the coding region of the odorant receptor gene (OR37), which is involved in organoleptic perception, extensive structural variation has been observed.

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### Applying reduce SNP assays for inferring C-lineage introgression patterns in Iberian honeybee populations of the Azores archipelago

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The genetic composition of the honeybee populations of the Macaronesian archipelago of the Azores is poorly known. Until now, only honeybee populations of the island of São Miguel have been surveyed for genetic variation through the use of the tRNA<sup>leu</sup>-cox2 intergenic mitochondrial DNA region and microsatellites. Here, we combine data from the mtDNA obtained with the Dral test (intergenic region) and from the nuclear DNA obtained with newly developed reduced SNP assays to provide a complete picture of introgression patterns in the Azorean honeybee populations at both mitochondrial and nuclear compartments. The sampling was carried out in 2014 and 2015 and comprised 474 colonies widely distributed across the 8 islands populated by honeybees. Our cyto-nuclear results show that C-derived introgression varies across the archipelago ranging from virtually pure populations of the Iberian honeybee in the island of Santa Maria (Q-values <5%) to highly introgressed populations in the island of Graciosa (Q-values >30%). The introgression levels are alarming and contrast with those of the Iberian honeybee populations of the mainland in Iberia, which are still virtually free of C-derived introgression, despite frequent importation of commercial queens.

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