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P6.1

Genetic-morphological variability of *Melipona subnitida* (Apidae, Meliponini) in northeast Brazil.

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The *Melipona subnitida* bee is an endemic stingless bee to northeastern Brazil. In spite of its importance to local people, these bees are currently largely threatened due to the destruction of their habitat and their natural nests for honey collection. Nevertheless, population studies of stingless bee species are still very scarce, as well as the urgency in understanding the structure and dynamics of their populations for monitoring and species conservation. Under this scenario, we aimed to evaluate the variability of *M. subnitida* in different localities in northeastern Brazil through geometric morphometrics of the forewing and sequencing of COI mitochondrial gene fragment. To analyse the pattern of wing venation, we used approximately ten workers per colony, and eleven landmarks were plotted on each wing.

The results showed groups structures with separation statistically significant ($\alpha < 0,0001$). The cross-validation test correctly identified 88,89% of individuals within their respective areas. Molecular analysis identified eleven haplotypes and presence of high number of exclusive haplotypes among the populations. The nucleotide diversity (π) of 0,00543 and haplotype diversity (H_d) of 0,79. Both morphological and molecular results indicated that variability among the sampled populations is related both to the environment in which samples were collected as to the geographical distance between these locations, indicating the existence of locally adapted ecotypes.

P6.2

Effect of linkage disequilibrium on inferences of population structure and introgression of Iberian and black honeybees.



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Identification of population structure, a primary goal in population genetics, is easily performed because there is a number of methods available, implemented by user-friendly software packages. However, the user must be cautious when inferring population structure because spurious results may be obtained when there is strong linkage disequilibrium. With recent development of high-density SNPs we have now more power to interrogate the honeybee genome. However, the greater the number of loci genotyped the greater the chance of scoring loci that are linked. In addition, events such as population bottleneck, small effective population size, genetic drift, and admixture may also generate strong linkage disequilibrium. According to Kaeuffer et al. (2007), correlation r_{LD} is the best way to deal with linkage disequilibrium. These authors recommend removing loci with r_{LD} higher than 0.5 when inferring structure. In this study we used the GoldenGate Assay of Illumina to genotype over 1221 loci in individuals sampled from populations of *A. m. iberiensis* and *A. m. mellifera*. In this dataset we used the genetic distance between SNPs and r_{LD} to test the effect of linkage in the number of clusters and the introgression level inferred by the clustering method implemented in the software STRUCTURE.