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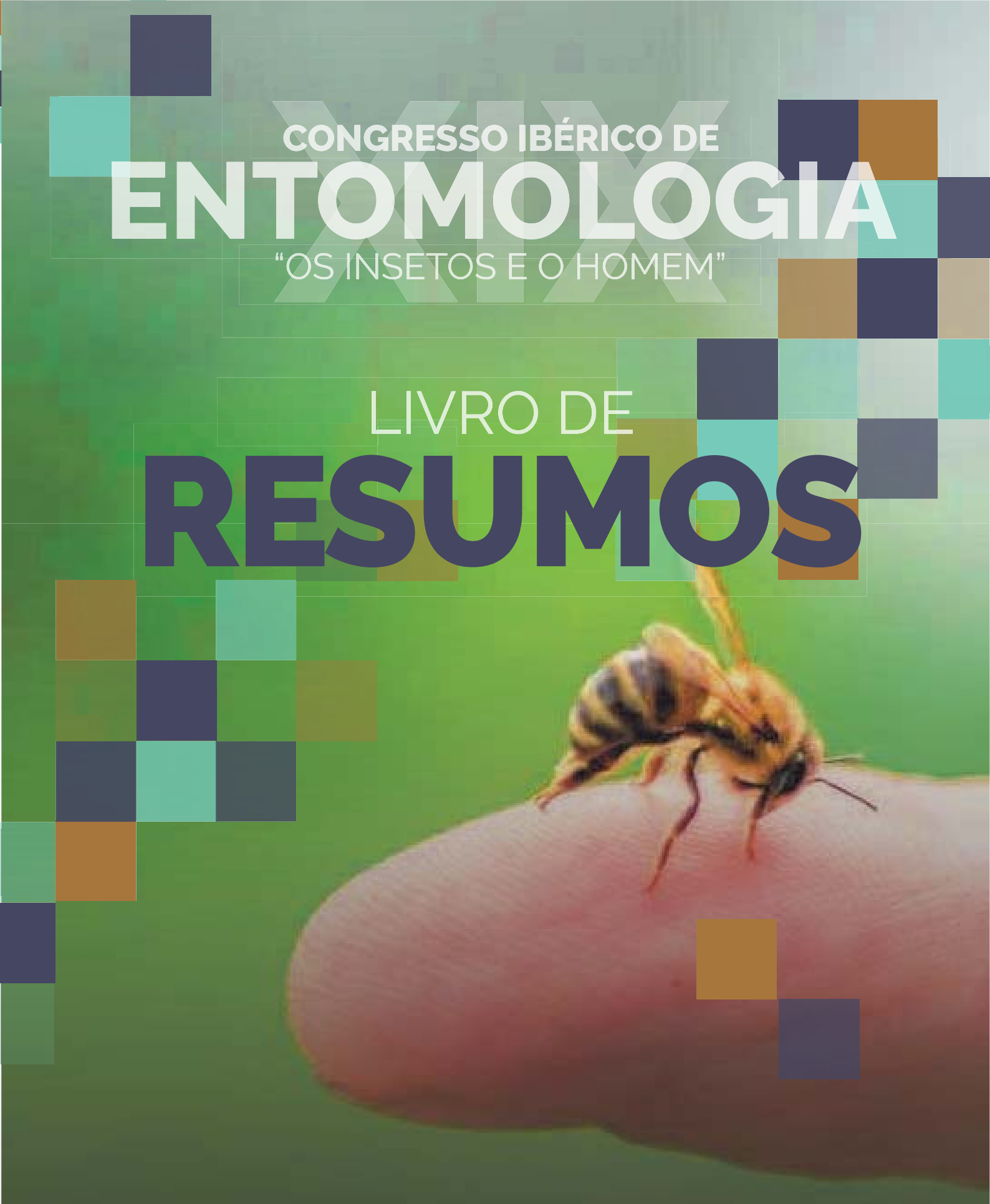
LIVRO DE RESUMOS



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Comparing two in-house developed SNP assays for inferring population structure in the honey bee (*Apis mellifera* L.)

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The honey bee, *Apis mellifera* L., is under pressure globally due to several factors, one of them is the large-scale introduction of foreign queens and/or colonies which act as vectors of pathogens, and also threaten the genetic integrity of native populations. Different molecular tools have been developed to monitor the genetic integrity of the populations. SNPs (Single Nucleotide Polymorphism) have been preferred because are easily transferred between laboratories, have a low genotyping error, provide high-quality data, and are suitable for automation. Here, we compared the genotyping results obtained with two medium-density-SNP assays previously developed. One of assays was designed from 88 whole genomes of *Apis mellifera iberiensis* and 44 C-lineage individuals (the main ancestry of commercial bees) using fixed SNPs (F_{ST}=1) distributed in the 16 honey bee chromosomes. The other assay was designed from variation in immune genes using a discovery panel of 123 whole genomes, representing seven subspecies (*A. m. iberiensis, A. m. mellifera, A. m. intermissa, A. m. sahariensis, A. m. ligustica, A. m. carnica, A. m. siciliana* and three lineages (A, M and C). All the samples are from the native range of each subspecies and they were taken from inside the hives, placed in absolute ethanol and stored at -20ºC until DNA extraction. The tools were compared using 473 samples from the Azores, which harbour a genetically complex honey bee population. The samples were genotyped using the iPLEX MassARRAY® MALDI-TOF system. The membership proportions of each individual (Q-value) were calculated using ADMIXTURE considering two genetic groups (K=2), with 10,000 iterations in 20 independent runs. Our results show that both assays provide similar Q-values, with a Pearson's correlation of 0.89. Only 9.5% of the samples have an absolute Q-value difference > 0.10. The choice of the best SNP assay depends on the subspecies and the aim of the project. While the immune assays can be applied in different subspecies the other assay was specifically designed for *A. m. iberiensis*. Furthermore, if there is disease data available, the immune assay can not only be used to infer genetic structure but also in case-control association studies.

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Palavras chave: *Apis mellifera*; Conservation; Molecular tools; SNPs