



Does beekeeping reduce genetic variability in *Melipona scutellaris* (Apidae, Meliponini)?

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Genet. Mol. Res. 8 (2): 758-765 (2009)
Received December 12, 2008
Accepted January 26, 2009
Published June 30, 2009

ABSTRACT. Many factors have contributed to reductions in wild populations of stingless bees, such as: deforestation, displacement and destruction of nests by honey gatherers, as well as use of insecticides and other agrochemicals. All of these can potentially affect the populational structure of native species. We analyzed genetic variability and populational structure of *Melipona scutellaris*, based on five microsatellite loci, using heterologous primers of *M. bicolor*. Samples were taken from 43 meliponaries distributed among 30 sites of four northeastern States of Brazil (Pernambuco, Alagoas, Sergipe, and Bahia). Thirty-one alleles were found to be well distributed among the populations, with sizes ranging from 85 to 146 bp. In general, there was a variable distribution and frequency of alleles among populations, with either exclusive and/or fixed alleles at some sites.

The population of Pernambuco was the most polymorphic, followed by Bahia, Alagoas and Sergipe. The heterozygosity was $H_o = 0.36$ on average, much lower than what has been reported for *M. bicolor* ($H_o = 0.65$). Most populations were not under Hardy-Weinberg equilibrium. We found a higher variation within rather than among populations, indicating no genetic structuring in those bees maintained in meliponaries. This apparent homogenization may be due to intense beekeeping activity, including exchange of genetic material among beekeepers. Based on our findings, we recommend more studies of meliponaries and of wild populations in order to help orient management and conservation of these native pollinators.

Key words: Stingless bees; Molecular markers; Single sequence repeats