

Genetic variability in *Melipona quinquefasciata* (Hymenoptera, Apidae, Meliponini) from northeastern Brazil determined using the first internal transcribed spacer (ITS1)

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Genet. Mol. Res. 8 (2): 641-648 (2009)

Received December 12, 2008

Accepted January 26, 2009

Published June 2, 2009

ABSTRACT. *Melipona quinquefasciata* is a ground-nesting South American stingless bee whose geographic distribution was believed to comprise only the central and southern states of Brazil. We obtained partial sequences (about 500-570 bp) of first internal transcribed spacer (ITS1) nuclear ribosomal DNA from *Melipona* specimens putatively identified as *M. quinquefasciata* collected from different localities in northeastern Brazil. To confirm the taxonomic identity of the northeastern samples, specimens from the State of Goiás (Central region of Brazil) were included for comparison. All sequences were deposited in GenBank (accession numbers EU073751-EU073759). The mean nucleotide divergence (excluding sites with insertions/deletions) in the ITS1 sequences was only 1.4%, ranging from 0 to 4.1%. When the sites with insertions/deletions were also taken into account, sequence divergences varied from

0 to 5.3%. In all pairwise comparisons, the ITS1 sequence from the specimens collected in Goiás was most divergent compared to the ITS1 sequences of the bees from the other locations. However, neighbor-joining phylogenetic analysis showed that all ITS1 sequences from northeastern specimens along with the sample of Goiás were resolved in a single clade with a bootstrap support of 100%. The ITS1 sequencing data thus support the occurrence of *M. quinquefasciata* in northeast Brazil.

Key words: *Melipona quinquefasciata*; Stingless bee; Nuclear ribosomal DNA; Internal transcribed spacer; Genetic variability