



Molecular identification of Amazonian stingless bees using polymerase chain reaction single-strand conformation polymorphism

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ABSTRACT. In countries containing a mega diversity of wildlife, such as Brazil, identifying and characterizing biological diversity is a continuous process for the scientific community, even in face of technological and scientific advances. This activity demands initiatives for the taxonomic identification of highly diverse groups, such as stingless bees, including molecular analysis strategies. This type of bee is distributed in all of the Brazilian states, with the highest species diversity being found in the State of Amazônia. However, the estimated number of species diverges among taxonomists. These bees are considered the main pollinators in the Amazon rainforest, in which they obtain food and shelter; however, their persistence is constantly threatened by deforestation pressure. Hence, it is important to classify the number and abundance of bee specie, to measure their decline and implement meaningful, priority conservation strategies. This study

aims to maximize the implementation of more direct, economic and successful techniques for the taxonomic identification of stingless bees. Specifically, the genes 16S rRNA and COI from mitochondrial DNA were used as molecular markers to differentiate 9 species of Amazonian stingless bees based on DNA polymorphism, using the polymerase chain reaction-single-strand conformation polymorphism technique. We registered different, exclusive SSCP haplotypes for both genes in all species analyzed. These results demonstrate that SSCP is a simple and cost-effective technique that is applicable to the molecular identification of stingless bee species.

Key words: Stingless bee; Amazônia; mtDNA; SSCP