



Genetic diversity in natural populations of mangaba in Sergipe, the largest producer State in Brazil

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ABSTRACT. Mangaba (*Hancornia speciosa* Gomes) is found in areas of coastal tablelands in the Brazilian Northeast and Cerrado regions. This species has been subjected to habitat fragmentation that is mainly due to human activity, and requires conservation strategies. The aim of this study was to analyze the structure and inter- and intrapopulation genetic diversity of natural populations of *H. speciosa* Gomes using inter-simple sequence repeat (ISSR) molecular markers. A total of 155 individuals were sampled in 10 natural populations (ITA, PAC, IND, EST, BC, PIR, JAP, BG, NEO, and SANT) in the State of Sergipe, Brazil. Fifteen primers were used to generate 162 fragments with 100% polymorphism. Genetic analysis showed that the variability between populations (77%) was higher than within populations (23%). It was

possible to identify five different groups by the unweighted pair group method with arithmetic mean and principal coordinate analysis, and only one individual (E10) remained isolated. Using ISSR markers it was possible to obtain a molecular profile of the populations evaluated, showing that these markers were effective and exhibited sufficient polymorphism to estimate the genetic variability of natural populations of *H. speciosa* Gomes.

Key words: Genetic variability; *Hancornia speciosa* Gomes; ISSR marker; Species preservation