



Intraspecific differentiation of *Hancornia speciosa* revealed by simple sequence repeat and random amplified polymorphic DNA markers

C.A. Nogueira¹, N.B. Stafuzza², T.P. Ribeiro³, A.D.L. Prado³, I.P.P. Menezes⁴, N. Peixoto³, P.J. Gonçalves⁵ and L.M. Almeida¹

¹Universidade Estadual de Goiás, Campus Anápolis de Ciências Exatas e Tecnológicas, Anápolis, GO, Brasil

²Departamento de Ciências Exatas, Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual de São Paulo "Júlio de Mesquita Filho", Jaboticabal, SP, Brasil

³Universidade Estadual de Goiás, Campus Ipameri, Ipameri, GO, Brasil

⁴Laboratório de Genética e Biologia Molecular, Instituto Federal Goiano, Urutaí, GO, Brasil

⁵Instituto de Física, Universidade Federal de Goiás, Goiânia, GO, Brasil

Corresponding author: L.M. de Almeida

E-mail: almeidalm@hotmail.com

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ABSTRACT. *Hancornia speciosa*, popularly known as mangabeira, is a fruit tree native to the Brazilian Cerrado that shows great economic potential, due to its multiple uses. Intraspecific classification of this species is difficult because it shows high morphological diversity. An early study of the species reported that there are six botanic varieties that differ morphologically mainly in the shapes of their leaves and flowers. Except to note the wide morphological variation and economic potential of this species, few studies have been published about the genetic diversity of

mangabeira. Knowledge of the genetic variability of this species among populations would be useful for genetic conservation and breeding programs. Therefore, we tested the transferability of 12 simple sequence repeats from expressed sequence tags (EST-SSRs) from *Catharanthus roseus* to *H. speciosa* and used 10 random amplified polymorphic DNA markers to evaluate the genetic variability among botanical varieties of *H. speciosa*. We obtained a high transferability frequency of EST-SSR markers from *C. roseus* to *H. speciosa* (75%). However, EST-SSR markers showed low heterozygosity and locus variability (two or three alleles by locus), which suggest low genetic diversity in the mangabeira samples. The Jaccard dissimilarity index and an examination of geographic distances indicated a non-spatial structuring of the genetic variability. Our markers were unable to distinguish *H. speciosa* botanical varieties.

Key words: Cerrado; Genetic variability; *Hancornia speciosa*; Mangabeira; Molecular markers; Transferability frequency