



Genetic diversity in natural populations of *Theobroma subincanum* Mart. in the Brazilian Amazon

L.H. Rivas¹, L.D. Giustina¹, L.N. Luz², I.V. Karsburg¹, T.N.S. Pereira² and A.A.B. Rossi¹

¹Laboratório de Genética Vegetal e Biologia Molecular, Centro de Tecnologia da Amazônia Meridional, Faculdade de Ciências Biológicas e Agrárias, Campus Universitário de Alta Floresta, Universidade do Estado de Mato Grosso, Alta Floresta, MT, Brasil

²Laboratório de Melhoramento Genético Vegetal, Centro de Ciências e Tecnologias Agropecuárias, Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brasil

Corresponding author: A.A.B. Rossi
E-mail: anabanrossi@gmail.com

Genet. Mol. Res. 12 (4): 4998-5006 (2013)

Received March 14, 2013

Accepted August 17, 2013

Published October 24, 2013

DOI <http://dx.doi.org/10.4238/2013.October.24.12>

ABSTRACT. The genus *Theobroma*, recently reclassified in the family Malvaceae, comprises some species with high economic potential, including the cupuí, *Theobroma subincanum* Mart., which has not yet been domesticated, and whose genetics and population structure are mostly unknown. This study aimed to assess the population structure and genetic diversity in natural populations of *T. subincanum* Mart., using inter-simple sequence repeat (ISSR) markers. A total of 59 individuals were sampled in three geographically separate populations, CFA, CMN, and CPT. Nei's genetic distance was estimated to characterize populations with the use of 13 polymorphic primers. The analysis of

molecular variance revealed that the variability between populations (51.71%) was higher than that within populations (48.29%). Among the three populations, CPT showed the highest diversity index and percentage of polymorphism. The ISSR molecular markers were efficient and presented sufficient polymorphism to estimate genetic diversity in populations of *T. subincanum* Mart.

Key words: Cupuí; ISSR; Genetic diversity