



Investigating genetic diversity in sapucaia using inter simple sequence repeat markers

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ABSTRACT. Sapucaia is a tree species originating from the Brazilian Amazon and is widely distributed in Brazil, especially in the mid-north region (Piauí and Maranhão states). Its seeds are rich in calories and proteins, and possess great potential for commercialization. Little is known about the genetic variability in the germplasm of most *Lecythis* species. Here, 11 inter-simple sequence repeat primers were used to estimate the genetic variability among 17 accessions, and to determine the levels of genetic variation and the standards of population structure in sapucaia. The accessions were obtained from the active germplasm bank (AGB) of Embrapa Meio-Norte, Teresina, PI, Brazil, and corresponded to four occurrence areas. Ninety-six loci were analyzed

among the studied individuals. High variation was found at the species level, where the percentage of polymorphic bands was 94.79%, Nei's genetic diversity (h) was 0.3110, and Shannon's index (I) was 0.4732. In the analyzed populations, the percentage polymorphism ranged from 20.83 to 94.79%, Nei's genetic diversity ranged from 0.0863 to 0.2969, and Shannon's index ranged from 0.1260 to 0.4457. Significant genetic differentiation was detected among the populations ($\Phi_{ST} = 10.66\%$); however, the greatest genetic differentiation was found within the populations (89.34%), between which there was an intermediate level of gene flow ($N_m = 1.10$). Accessions BGS 2 and BGS 4 were the most divergent, whereas accessions BGS 14 and BGS 15 were the most similar. Therefore, sapucaia analyzed from the AGB present an elevated level of genetic diversity and may have potential use in genetic breeding programs.

Key words: Chestnut tree; Genetic variability; Germplasm bank; *Lecythis pisonis*