

GENETIC DIFFERENTIATION AMONG ACCESSIONS OF ‘SUGARY’ CASSAVA SAMPLED IN THE STATES OF PARÁ AND AMAZONAS, BRAZIL

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Sugary cassava (*Manihot esculenta*) represents a type of cassava that accumulates sugar in its root due to a deficiency in one of the enzymes that convert sugar into starch. This type of cassava is usually found in the Brazilian Amazon. The genetic variability of a group of 39 accessions of sugary cassavas sampled in the States of Amazonas and Pará in Brazil and conserved in two germplasm banks was investigated with eleven microsatellite loci. All eleven loci were polymorphic, with 65 alleles and 5.91 alleles per locus. Twenty private alleles (the ones that appear in only one genotype) were identified. Analyses indicated that 14 of the 39 accessions had the same multiloci profile and represented four genotypes, with 4.03×10^{-7} of probability of identity. All of these putative duplicated accessions were sampled in the Northeast of Pará. Duplicates were discarded and 29 genotypes were used in the genetic analyses for groups. Structure analysis, a model-based Bayesian procedure, divided the 29 genotypes into two groups ($K = 2$), where group 1 contained only genotypes sampled in the Northeast of the State of Pará and group 2 contained genotypes sampled in the Amazonas, West of Pará and one genotype from the Northeast of Pará. The analysis of molecular variance (AMOVA) indicated high differentiation among the two States ($\Phi_{ST} = 0.374^{**}$) and among the two groups detected by Structure ($\Phi_{ST} = 0.45^{**}$). Genetic parameters indicated higher genetic diversity among genotypes of group 2 detected by Structure. Results indicated that there are two genetic groups of sugary cassavas conserved in the germplasm banks of Brazil. It reflects a higher chance to identify different sources of mutations in genes and promoters associated with starch conversion rate that can be used in genetic breeding and genetic engineering of cassava.

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