

## GENETIC DIVERSITY AMONG ACCESSIONS OF SPECIES FROM THE *MANIHOT* GENUS WITH FORAGE POTENTIAL

Antonio RP<sup>1</sup>, Da Silva Neto JL<sup>1,2</sup>, Da S. Santos JD<sup>1</sup>, Lira ICdeSA<sup>1</sup>.

<sup>1</sup>Embrapa Tropical Semi-Arid, Zip Code: 56302-970, Petrolina, PE, Brazil, <sup>2</sup>State University of Pernambuco, Zip Code: 56328-903, Petrolina-PE, Brazil. <sup>2</sup>Agronomy Department, Federal Rural University of Pernambuco, Zip Code: 52171-900, Recife, PE, Brazil.

*Manihot* species such as cassava (*M. esculenta*) and maniçoba (*M. pseudoglaziovii*), are already being used by small farmers for animal feeding, but this practice is still incipient. The use of wild relatives of cassava species in breeding programs is limited because they are not readily available to breeders or many of them cannot be grown outside their natural environment. Wild species of *Manihot* are important sources of genes of interest to be transferred to cultivated species for the development of improved varieties of cassava that are more resistant to biotic and abiotic factors and more productive. The knowledge of the genetic diversity among accessions in Germplasm Banks is important for genetic resources conservation purposes and use in breeding programs. The aim of this work was to study the genetic diversity among cassava accessions and their wild relatives with potential for animal feeding and adapted to semi-arid climate through morphological and agronomic descriptors. They were characterized based on fifteen morphological and agronomic descriptors, 58 accessions of the genus *Manihot* with 13 cassava cultivars used for human consumption, 30 accessions of the Embrapa Tropical Semi-Arid Cassava Regional Germplasm Bank and 15 accessions of wild *Manihot* species from the Embrapa Tropical Semi-Arid collection with potential to animal feeding. The descriptors were subjected to variance analysis, performed with the aid of Multivariate techniques, where the hits were grouped using the Tocher method, from generalized Mahalanobis distance (D2). The Tocher grouping method detected the formation of 12 groups. Especially the groups one, two and four comprised only cassava accessions totaling 48 genotypes and three groups. Groups five and six were composed of wild *Manihot* species. The other groups were formed only by an accession each, differing from each other with respect to species, demonstrating great variability among the accessions. This promising result therefore indicates the possibility of using these groups to obtain interspecific hybrids between wild species and varieties of cassava in breeding programs.

Corresponding author: Rafaela Priscila Antonio, [rafaela.antonio@embrapa.br](mailto:rafaela.antonio@embrapa.br)