



Genetic diversity among homonymy accessions maintained in the Cassava Regional Brazilian Genebank

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ABSTRACT

In the Amazon region, the cassava cultivation has great social and economic importance because its production is source of food for traditional population and income for small farmers. The cassava farmer fields are results of the tradition and the preference of consumption and represent the genetic variability of many characters related to the mode of use and the quality of cassava root. The identification of genotypes to generate improved clones has been supported by germplasm conservation, evaluation and molecular characterization. SSR (Simple Sequence Repeat) markers has proved to be a consistent method for the the characterization of cassava germplasm. In this work, twelve groups of manioc accessions with same common name from the Active Germplasm Bank (AGB) of Embrapa Western Amazon were evaluated using ten SSR loci. The genetic diversity parameters estimated for the groups defined by accessions common names were high. The results obtained in the AMOVA showed that more genetic variation was found within groups defined by common names (94%) than among them (6%). The analyzes indicated that there is high genetic diversity within the groups of cassava varieties with the sames names, suggesting that the nomenclature used by farmers to discriminate local cassava varieties is complex.

Keywords: Germplasm; Genetic diversity; Microsatellites; Amazon.

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a kind of food security in various tropical regions of the world. In the Amazon region, the cassava cultivation has great social and economic importance because its production is source of food for traditional population and income for small farmers. The cassava farmer fields are results of the tradition and the preference of consumption and represent the genetic variability of many characters related to the mode of use and the quality of cassava root.

Local varieties of cassava grown by traditional farmers in the Amazon region are very important for plant breeding programs, because of the amount genotypes with different characteristics and names planted together in a single field (Siqueira *et al.*, 2010; Alves-Pereira *et al.*, 2011), The traditional exchange of planting material between farmers expands genetic diversity, which continuously originates an infinite number of new clones (McKey *et al.*, 2010).

The traditional agriculture practiced by family farmers maintains or increases genetic diversity through cultivation of different varieties (Ferguson *et al.* 2011). These practices may contribute to the creation of population genetic structure due to different preferences in different regions, and seedling incorporation and exchange can reduce structure (Sousa *et al.*, 2017). The identification of genotypes to generate improved clones has been supported by conservation, evaluation and germplasm molecular characterization. SSR (Simple Sequence Repeat) markers has proved to be a consistent method for the characterization of cassava from germplasm banks in Brazil (Siqueira *et al.* (2010) and Sousa *et al.* (2017).



In this work SSR markers was applied to analyze the genetic relationship among cassava accessions with the identical names and different geographical origins from Manioc Active Germplasm Bank (AGB) at Embrapa Western Amazonia.

MATERIAL AND METHODS

Twelve groups of manioc accessions with same common name from the Active Germplasm Bank (AGB) of Embrapa Western Amazonia were evaluated using SSR markers. Passport data were also used to categorize the accessions in five river basins, Solimões, Purus, Madeira, Negro and Amazonas rivers. Genomic DNA was extracted using the cationic detergent CTAB protocol in the Molecular Biology Laboratory at Embrapa Western Amazonia. Ten microsatellite loci were used: GAGG5, GA12, GA126, GA131, GA134, GA136, GA140 were designed and described by Chavarriaga-Aguirre *et al.* (1998), and SSRY13, SSRY89, SSRY164 by Mba *et al.* (2001) (Table 1). The genetic diversity parameters and Analysis of Molecular Variance (AMOVA) were performed in the software package GenAlex 6.5.

RESULTS AND DISCUSSION

The genetic diversity parameters estimated for the groups defined by accessions common names were high (Table 1). The lowest mean observed heterozygosity for the Preta/Pretinha group (0.46) and the highest mean expected heterozygosity for the Roxa/Roxinha group (0.66), The Shannon diversity index ranged from 0.10 (Jabuti group) to 1.49 (Amarela/Amarelinha group). High genetic diversity has been detected in the cassava germplasm from different geographical origins. This wide genetic variability is due to the ease of cross-pollination, fruit dehiscence, high heterozygosity of the species, and to the occasional use of seeds in propagation (McKey *et al.*, 2010).

The results obtained in the AMOVA showed that more genetic variation was found within groups defined by common names (94%) than among them (6%) (Table 2). This result revealed the extent of plant material exchange between and within river basins despite the critical problem of the local names attributed by cassava farmers. Exchange is more common within communities than between, but occasionally may be long distance (Emperaire and Peroni 2007; Kawa *et al.* 2013). The result reported here confirms that identification based only in passport and morphological data can lead to errors of genetic discrimination in cassava accessions.

CONCLUSION

The analyzes indicated that there is high genetic diversity within the groups of cassava varieties with the same names, suggesting that the nomenclature used by the farmers to discriminate local cassava varieties is complex.

ACKNOWLEDGMENTS

Research supported by Embrapa (Brazilian Agricultural Research Corporation - grant number 106010071400), the National Counsel for Scientific and Technological Development (CNPq - Conselho Nacional de Desenvolvimento Científico e Tecnológico - grant number 407991/2013-1).

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Table 1: Genetic parameters of cassava accessions maintained in the Active Germplasm Bank of Embrapa Western Amazonia grouped by identical names.

Identical names	River Basin Origin	N	H _o	H _e	I
Manteiga	Solimões (2) Purus (1) Madeira (7)	10	0.56	0.66	1.31
Seis Meses	Solimões (1) Amazon (3) Madeira (2)	6	0.53	0.62	1.12
Pão	Solimões (2) Purus (1) Madeira (7)	11	0.53	0.61	0.21
Preta/Pretinha	Solimões (2) Amazon (6) Purus (1) Madeira (2)	12	0.46	0.65	0.35
Jabuti	Solimões (1) Madeira (5)	6	0.58	0.57	0.10
Roxa/Roxinha	Solimões (2) Madeira (4) Negro (3)	7	0.66	0.65	1.31
Branca/Branquinha	Amazon (2) Madeira (3) Negro (1)	9	0.62	0.67	1.31
Manicoera	Solimões (1) Amazon (4)	5	0.54	0.47	0.80
Amarela/Amarelinha	Solimões (4) Amazon (7) Purus (1) Madeira (6) Negro (1)	19	0.53	0.70	1.49
Açaí	Solimões (4) Madeira (4)	8	0.50	0.61	1.17
Tartaruga	Amazon (2) Madeira (4)	6	0.60	0.56	1.00
Coraci	Amazon (5)	5	0.52	0.57	1.10
Overall		104	0.55	0.61	1.18

N - number of accessions. H_o - mean observed heterozygosity. H_e - mean expected heterozygosity and I - mean Shannon index.

Table 2: Molecular analyses of variance of cassava accessions in the Active Germplasm Bank at Embrapa Western Amazon based on groups used in Table 1.

Identical Names	Source of variance	df	SS	MS	s ²	%
Varieties	Between groups	11	121.120	11.011	0.348	6
	Within groups	92	740.755	8.052	8.052	94

DF - degrees of freedom; SS - sum of squares; MS - mean squares; s² - variance estimation.