A Study on Genetic Diversity of Sweet and Bitter Cassava Ethnovarieties from Different Agroecosystems in Brazil

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Introduction

In this work, the objective was to extend the description of the genetic diversity of cassava present in Brazil nowadays, using DNA markers (microsatellites).

As Brazil have one or more putative centers of domestication of cassava, the results of studies on Brazilian genetic material can be useful in clarifying questions relative to the evolutionary dynamic of the domestication process of the species.

The understanding of the *in situ* (on farm) organization of cassava germplasm in Brazil can help in delimitating heterotic groups and the in using them in breeding programs as well as directing conservation programs of the genetic diversity.

Material and Methods

The analysis includes 623 bitter (=brava) and sweet (=macaxeira) cassava varieties, collected originally in three great agroecologycal regions, divided in 10 sub-regions. (Figure1):

1. Amazon Region (Sub-Regions: High Negro River, Medium and Low Negro River, Medium Amazon River, Tapajós River, High Juruá River and High Xingu River).

2. Sub-Tropical Continental Region (Sub-Regions: Cerrado (=Savana), Pantanal, Sub-Tropical Continental)

3. Sub-Tropical Littoral Region

A feel varieties from Brazilian Northeast Region (Sub-Regions Semiarid and Tropical Northeast) were also included.

For these analysis 10 microsatellite DNA markers were used: GA021, GA126, GA131, GA134, GA136, SSRY009, SSRY013, SSRY089, SSRY164.

The statistical analysis was made with the computer programs: NTSYS, Genetix and STATISTICA.

The genetic similarity index used were: DICE, PSA (individual) and Nei 1972 (populations)

The dendrograms were constructed from UPGMA analysis.

Agroecosystems	
Amazonia	318
Sub-tropical (littoral)	31
Sub-tropical (continental)	102
Pantanal	24
Savana	113
Semi-arid	8
TOTAL	596

Results

A resumed view of the data obtained until now is presented in the graphics below.

There is a general distribution in that cassava varieties are organized in three big groups: Group I (were bitter varieties predominate), Groups II and III (were *macaxeiras* predominate) (Figures 2 to 5).

These are not well delimitated groups, as we can see in PCoA graphics and dendrograms.

The distinction between the three groups is made more by differences in allelic frequencies than by the presence of unique alleles in each group.

Almost the totality of the Amazonian varieties is grouped in Groups I and II, with most bitter varieties included in Group I and the *macaxeiras* in Group II (Figure 6). The dispersion of varieties from Amazon Sub-Regions follow similar pattern, except the Sub-Region High Juruá River, in that bitter varieties are not included in Group I but in Group II together with the *macaxeiras*. (Figure 7)

The varieties from Region Sub-Tropical Littoral are dispersed in Groups I and II as the Amazonian ones. *Macaxeiras* are mostly in Group II. Bitter varieties are divided between Group I and Group II (Figure 8).

Macaxeiras from the Sub-Tropical Continental Region (including all Sub-Regions) are localized more frequently in Group III followed by Group II. The bitter varieties are preferentially found in Group I and some of them are in Group II (Figures 9 to 11).
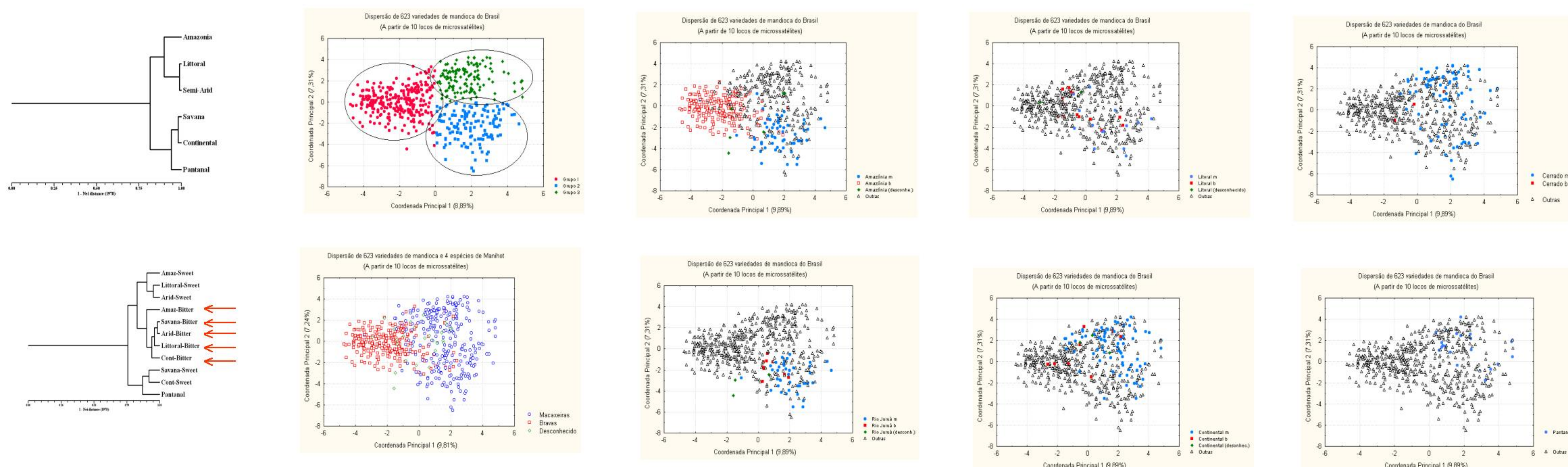
Discussion

At present we are working in an extensive and comprehensive analysis and discussion on the data. We consider that in this discussion some questions should be considered:

The genetic structure of cassava populations in Brazil, today, results directly from *phenomena* of social and natural environmental type, which occurred in a scale of time that could be estimated in some *milenia*.

Important factor would be: one or more domestication events happened involving one or more natural population of *Manihot esculenta* ssp. *flabellifolia* in the transitional region between Amazon and *cerrado* (savana). Perhaps also other domestication events in other places in Brazil or out of Brazil, involving other Manihot species.

The management of the culture based on vegetative propagation associated to the incorporation of spontaneous plants originated from spontaneous sexual reproduction.

Human migrations of cassava breeders before and after the European colonization, in the American Continent.

Exchange of cassava varieties between different human populations.

Introduction of cassava populations into different agroecossistems as a result of migration and exchange of genetic material between human populations.

Genetic introgression involving different cultivar populations and different wild populations of correlated species.

Crossing between cultivars from different origins, possibly even between varieties originated from different domestication events.

Erosion of indigenous cultures and of the agricultural culture of other rural populations and environment erosion, causing genetic erosion in cassava populations and changes in the management of the culture.

Suggestions and comments are wellcome to the discussion of our data. Complete raw data and PCoA and dendrograms with partial data are available to anyone who could possibly be interest in more details.

Future perspectives

An extensive and detailed analysis of all data is being prepared and a complete and comprehensive report will be soon available.

Papers with the most important observations are being prepared to be submited in 1994.

The continuity of the studies of the genetic organization of *in situ* (on farm) cassava germplasm and the genetic structure of the wild related species is being done with collection of samples and monitoring of wild populations of *Manihot esculenta* spp. *flabellifolia* in Rondonia.

We also plan to complete the picture of distribution of genetic diversity of the cultivar with a good sampling of the varieties from the semiarid region.