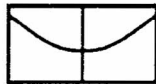


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Nagib Nassar (Convener)*

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Selection of Cassava Parents by morPHological and Agronomic TRAITS, and Genetic Divergence Analysis

Alejandra S. Albuquerque
EMBRAPA-Amazônia Oriental,
Belém-Pará, CEP 66.095-100, Brazil

Introduction

Brazil has been suggested as the center of origin and domestication of cassava (Allem 1987, Olsen and Schaal 1999, 2001). In the Amazon region, cassava is mainly grown as a subsistence crop by small farmers, thanks to its ease of cultivation, cheap production and its ability to tolerate poor soils. Moreover it suffers from few serious pests and diseases and it is available throughout the year. Although cassava suffers from fewer diseases than other major food plants, in northeast Pará State, Brazil, *Phytophthora drechsleri* root rot (Fig. 1) can cause significant damage in crop and loss can reach 80 to 100% when susceptible cultivars are grown.



Fig. 1 – *Phytophthora drechsleri* root rot

Significant cassava genetic improvement only can be achieved for resistance to biotic factors, root quality and good productivity through the intensive selection of complementary parents, and transfer of improved gene pools to breeding programs. The aim of this research was to group elite genotypes by genetic divergence analysis on agronomic traits to indicate what accessions can be used more intensively as parents in crossing blocks.

Materials and Methods

The preliminary trial held at the EMBRAPA – Amazônia Oriental, included 10 flour purpose cassava genotypes showing more than 25% starch storage root content and fresh root yield above 5 kg per plant. The accessions were 01-Pacajá, 34-Pretinha, 51-Caravela 1, BGM 911-59, BGM 019, BGM 844-2, Maranhense 2, Milagrosa 20, Taxi-Mo and Vermelhão. Therefore, these elite genotypes were evaluated, at 12 months after planting, for other seven morphological and agronomic features (Fukuda and Guevara 1998) such as plant height (m), first ramification height (m), total number of roots (per plant), number of rot roots (per plant), root length (cm), root diameter (cm) and shoot mass (kg plant⁻¹). Ten plants for each elite genotype were measured for these features and genetic diversity was evaluated by Tocher's method. Standardized average Euclidean distance was used as dissimilarity measure.

Results and Discussion

Morphological and agronomic averages for elite genotypes held at the EMBRAPA – Amazônia Oriental are given in Table 1.

Table 1. Morphological and agronomic averages for elite genotypes

Elite genotypes	Plant height (m)	First ramification height (m)	Total number of roots (per plant)	Number of rot roots (per plant)	Root length (cm)	Root diameter (cm)	Shoot mass (kg plant ⁻¹)	Root mass (kg plant ⁻¹)	Starch storage (root %)
01-Pacajá	2.45	0.95	10.00	0.60	25.60	3.58	3.40	4.84	26.71
34-Pretinha	2.50	1.45	7.20	0.20	23.60	5.18	2.40	5.50	26.00
51-Caravela 1	2.10	0.80	8.00	0.20	25.10	5.75	1.70	5.23	27.00
BGM 911-59	2.42	0.71	6.20	0.20	29.20	5.46	3.04	5.72	16.58
BGM 019	2.67	1.21	9.40	1.40	23.50	5.20	2.88	5.20	27.46
BGM 844-2	1.98	0.85	7.24	0.25	23.90	5.00	4.50	5.50	29.99
Maranhense 2	2.47	0.33	4.40	0.80	31.50	6.52	5.00	7.50	26.02
Milagrosa 20	3.32	0.43	13.80	0.80	22.20	5.24	3.64	7.30	25.00
Taxi-Mo	2.11	0.29	10.80	1.80	25.70	5.40	2.90	5.25	25.32
Vermelhão	2.91	0.65	7.40	0.40	28.30	4.51	5.24	8.04	25.48

The flour purpose elite cassava genotypes 01-Pacajá, 34-Pretinha, 51-Caravela 1, BGM 911-59, BGM 019, BGM 844-2, Maranhense 2, Milagrosa 20, Taxi-Mo and Vermelhão were grouped into three similar clusters according to Tocher's method (Table 2).

Table 2. Elite cassava genotypeclusters according to Tocher's method

Cluster	Elite genotypes
Group 1	34-Pretinha, BGM 911-59, 51-Caravela 1, BGM 844-2, BGM 019, 01-Pacajá, Taxi-M
Group 2	Maranhense 2, Vermelhão
Group 3	Milagrosa 20

The best accession in each Tocher's cluster for their starch storage root content 34-Pretinha in Group 1 and Maranhense 2 in Group, whereas Milagrosa 20 was the only accession in Group 3. Since accessions in a Tocher's cluster are similar to each other, the best in each cluster for starch storage root content will be further used as parents in crossing blocks receiving pollen from root rot tolerant genotypes. This breeding approach should therefore exploit the great genetic variability in the segregant population derived from high yielding, disease tolerant parents.

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