

Introduction

Cassava breeding is difficult and, compared with other crops, inefficient. Each cycle of selection takes about six years for completion. Initially a large number of genotypes are evaluated and visual selection is performed on *Clonal Evaluation Trials* (CETs) based on single row plots with 8 plants per plot. Selection is usually based on a visual inspection of the plots with few or no data taken. Because no data is taken, a good opportunity for determining the general combining ability (GCA) of the parental lines whose progenies are evaluated is missed.

Objectives

- A procedure for an approximation to estimations of GCA of progenitors involved in the production of segregating progenies.
- A reduction in the environmental effect of field variations in the large experimental plots usually required in cassava breeding.

Materials and Methods

All the clones from a given family to be evaluated in the CET were separated in three groups with an approximate number of clones per group. The experimental plot for the CET at each environment was divided in three blocks of about the same area, where the three groups of each family were respectively planted.

This new approach for planting the CETs implied that each clone was still planted in one row with eight plants. However, all the clones from a given family were distributed in the three blocks. Therefore, three replications were available for each family of crosses. The blocking of the experimental field follows the same criteria for stratified massal selection suggested by Gardner (1).

Results

Table 1 presents the results from three CETs targeting different agro-ecological zones. Average performances across the whole experiment and the respective means for each block in which they were stratified are included. The clones from each family are randomly assigned to each of the three blocks therefore reducing the environmental effect (measured here as differences in the mean performance of each block) on the mean performance of each family of clones.

The blocking of each CET allowed for a more precise estimation of the mean performance of each family. Selections were performed individually for each block. In Table 2 the results of the best and worst five families from each CET are summarized. Since each family was divided into three groups assigned randomly to the three blocks in each CET, the results presented are across the three blocks. It is obvious that large differences in the mean performance of each family (here illustrated by the number of selected clones) could be observed.

Table 1. Results of the Clonal Evaluation Trials for three different target environments (within parenthesis # of clones).

Parameter (# clones)	Yield (t/ha)		Harvest Index (0 to 1)	Plant type (1 to 5)	Dry matter content (%)
	Fresh roots	Dry matter			
SUB-HUMID TROPICS					
Block 1 (749)	14.19	3.70	0.50	2.87	26.09
Block 2 (746)	14.37	3.91	0.46	2.88	27.21
Block 3 (705)	12.89	3.38	0.44	2.87	26.26
Across	13.85	3.72	0.47	2.87	26.50
ACID-SOIL SAVANNAS					
Block 1 (412)	20.88	6.66	0.50	3.33	31.59
Block 2 (412)	21.73	6.88	0.49	3.35	31.24
Block 3 (411)	22.30	7.28	0.50	3.48	32.44
Across	21.64	6.94	0.50	3.39	31.76
MID-ALTITUDE VALLEYS					
Block 1 (605)	24.05	8.86	0.63	2.68	36.61
Block 2 (588)	28.08	10.21	0.57	2.63	36.02
Block 3 (568)	27.51	9.76	0.54	2.97	35.09
Across	26.51	9.50	0.58	2.75	35.92

Table 2. Results of the best and worst five families within each Clonal Evaluation Trial for three target environments. For each family the % of selected and total number of clones (within parenthesis) is presented. Large differences in the number of selected clones within each family can be observed. These differences are related to known agronomic traits.

Sub-humid tropics		Acid soil savannas		Mid-altitude valley	
Family	Selected	Family	Selected	Family	Selected
Best five families for each target environment					
CT 59	61.6 (73)	SM 2642	37.5 (24)	GM 295	48.9 (45)
CT 57	53.1 (32)	SM 2658	33.3 (15)	SM 2858	47.5 (59)
CT 54	40.6 (32)	CM 9903	32.6 (46)	SM 2652	47.1 (17)
GM 288	36.4 (22)	GM 240	28.6 (14)	GM 297	46.9(49)
SM 2547	29.4 (68)	GM 276	27.8 (36)	CM 9903	46.5(43)
Worst five families for each target environment					
SM 2829	2.4 (42)	SM 2850	0.0 (9)	SM 2867	9.5 (42)
CM 9775	0.0 (56)	SM 2844	0.0 (15)	SM 2663	7.9 (38)
SM 2667	0.0 (53)	SM 2649	0.0 (16)	GM 270	5.0 (20)
SM 2835	0.0 (33)	SM 2842	0.0 (22)	SM 2665	4.8 (21)
SM 2949	0.0 (35)	GM 115	0.0 (30)	SM 2999	2.7 (37)

Conclusions

It can be concluded that stratification in the CETs lead to a more precise selection of the best performing clones. The disagreement of selected clones between stratified and non-stratified selection ranged from 10 to 15%. Family averages are used to derive information about the breeding values of the parental clones used to generate the progenies evaluated in the CETs. This is a first approach for selecting parents in a cassava breeding program based on their genetic rather than phenotypic characteristics.

(1) Gardner, C.O. 1961. An evaluation of effects of mass selection and seed irradiation with thermal neutrons on yields of corn. Crop Sci 1: 241-245.