Analysis of genotype by environment interactions in cassava using the AMMI model

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Introductions

Cassava is a major source of energy for more 500 million people in tropical countries of Africa, Asia and Latin America. Cassava is grown in a wide range of environments between latitudes 30° N and 30°S from sea level up to 1800 meters above sea level. Although its most common product is the starch root, the foliage has an excellent nutritional quality for animal and human consumption and offer s great potential. Cassava is recognized by its capacity to grow and produce competitively under environmental constraints where few other crops can compete. However, the crop is also distinctive for its remarkable magnitude of genotype by environment interactions, perhaps due to contrasting environments where it is grown.

Objectives

To analyze the stability yield performance of thirty-eight cassava elites clones in thirteen environments and to determine the magnitude of genotype by environment interaction.

Materials and methods

Thirty-eight cassava clones were evaluated in uniform trials across thirteen environments with three replications in each trial. All locations were in the northern coast of Colombia from Pitalito in the Atlántico Department to Mutatá in the Urabá region (Antioquia Department). Trials at two locations (Carepa and Necoclí), both in the Urabá region were repeated for two consecutive years in 2001 and 2002. The additive main effects and multiplicative interaction effects (AMMI) model [1] was used to examine the patterns of interaction of the clones evaluated over different environments in the northern coast of Colombia.

Department	Environment	Fresh root (t/ha)			Dry matter (t/ha)		
		Maximum	Minimum	Average	Maximum	Minimum	Average
Atlántico	Pital	33.4	14.2	23.3	10.9	5.0	7.8
	Santo Tomas	30.4	9.5	18.9	9.3	2.8	6.3
	Caracolí	29.7	13.7	18.3	9.1	4.5	6.3
	Baranoa	39.9	16.2	25.8	13.2	5.8	9.1
Sucre	La Unión	37.3	14.8	26.4	12.3	4.1	9.2
	Corozal	37.6	5.8	22.1	10.5	1.3	6.8
Córdoba	C. de Oro	34.8	12.3	23.9	12.2	3.3	8.1
	Sahagun	29.3	7.1	14.8	8.0	1.6	4.3
Urabá	Necoclí-1	42.2	16.7	31.4	15.8	5.3	10.5
	Carepa-1	58.5	24.1	35.3	20.4	8.0	13.0
	Necoclí-2	46.9	22.0	32.8	17.3	7.9	11.4
	Carepa-2	70.0	31.2	53.0	25.1	11.0	18.9
	Mutatá	37.6	16.2	26.6	15.0	6.0	10.1

Figura 1. Biplot of the Principal components (PC) scores for fresh root yield of thirty cassava clones evluated in thirteen environmentes in the northern coast of Colombia.
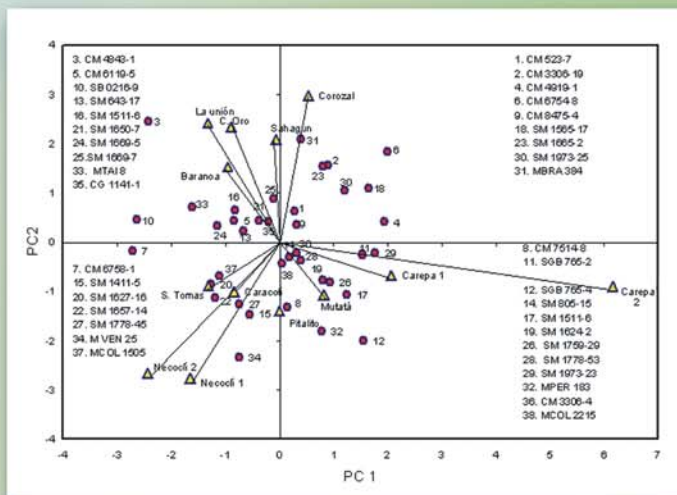

Table 1. Maximum, minimum and average for Fresh root yield and dry matter of 38 cassava clones evaluated in 13 environments in the Northern Coast of Colombia.

Results

Large variation of mean productivity was observed among the clones cassava ranging from 36.2 (SM 1565-17) to 20.9 (SM 1657-14) t/ha of fresh roots. The mean yield fresh roots across all environments was 27.1 t/ha ranging from 52.9 (Carepa cycle 2002-2003) to 14.8 (Sahagun) t/ha.

Yields obtained in the Urabá region were outstanding. Carepa had an average dry matter yield of 18.9 t/ha The worst environment was Mutatá with 10.1 t/ha the dry matter, which is still and excellent average yield and highlights the potential the cassava as source of raw material for the industry.

Carepa environment showed much variability from year to year in main and interactions effects, whereas Necocli environment differed only in interactions, effects but not in mean yields.

Clones 9, 14, 28, 35, 36, 38 showed the smallest PC scores, and are therefore the most stable genotypes. Some clones were favored by specific environmental conditions. This was the case of clones 11 (SGB 765-2) and 29 (SM 1973-23) that have positive interaction with the Carepa 2 environment.

Three groups of environments were evident as showed figure 1: group 1 included Carepa and Mutata; group 2 Necoclí, Caracolí and Santo Tomas; and Corozal, Sahagun, Cienaga de Oro, La Unión and Baranoa. Conformed Group 3. Environments within each group were positively correlated.

Conclusions

The AMMI analysis was useful in distinguishing different locations and separating those genotypes that did not significantly interact with the environment from those that contributed significantly to the genotype by environment interaction sum of squares. AMMI facilitated identifying preferential adaptation of clones to particular group of environments and was useful in identifying clones with high productivity and wide adaptation (low genotype by environment interaction).

[1] Vargas M., Crossa J., Van Eeuwijk F. A., Ramirez M. and Sayre K. 1999. Using Partial Least Squares Regression, Factorial Regression, and AMMI Models for Interpreting Genotype x Environment Interaction. Crop Science. v. 39, p. 955-967.