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CROP BREEDING AND
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Evaluation of phenotypic stability of cassava clones by AMMI analysis in northwestern Paraná state

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ABSTRACT: *High yield stability and adaptability of storage root are highly desirable attributes of cassava clones. The objective of this study was therefore to evaluate the effect of the genotype x environment interaction (G x E) and the stability of cassava clones developed at IAC. A subset of eight cassava genotypes was chosen in trials of storage root yield, arranged in a randomized complete block design with four replications, in two counties (Araruna and Maringá), in the northwestern region of Paraná State, over five growing seasons (1997-2001). The G x E interaction was evaluated by joint variance analysis and stability and adaptability by AMMI analysis. The G x E interaction was significant (P<0.05) for storage root yield. Results indicated AMMI analysis as an efficient tool for the evaluation of phenotypic adaptability and stability of cassava clones and IAC 190 as the most promising clone.*

Key words: *Manihot esculenta*, genetic variability, G x E interaction, stability, AMMI.

INTRODUCTION

Cassava is one of the major crops in tropical regions and is, along with rice, wheat and corn, the fourth most important staple product for approximately one billion people (FAO/FIDA 2000). In general, it is cultivated on small and medium-sized farms in marginal agriculture areas. Cassava roots are used for both human and animal consumption and transformed into a broad range of products by industrial processes (CIAT 2004).

The current world production of cassava roots is about 184 million tons (FAO 2004); Brazil is one of the major producers, with a volume of 23 million tons grown on an area of 1,663,000 ha (IBGE 2004). The state of Paraná has contributed there to with 2.4 million tons

produced on an area of 112,000 ha and is considered the second largest national producer with an average productivity of about 21.42 t ha^{-1} (Groxko 2004).

Even though the cassava production in Paraná is considered high, it could be boosted even further by some techniques, as for example by more productive and disease-resistant cultivars. Cassava diseases such as bacterial blight and superelongation can cause yield drops of up to 50% or even more, depending on the weather conditions and the resistance level and quality of cultivars (Fukuda et al. 1984, Fukuda et al. 1986). One way to avoid such yield losses is to introduce resistant and/or tolerant cassava genotypes with high yield potential under constant evaluation. Moreover, such introductions represent a simple, easy-to-use and,

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regarding yield, promising improvement method (Farias et al. 1997, Fukuda 1999).

In some situations, the genotype x environment interaction is high (Fukuda 1996), and the significant effect of this interaction hampers work with cassava genotype evaluation and during the selection stages for release. In such cases, the significance and magnitude of this interaction is verified by specific methodologies. One of the options is to apply analysis methodologies of the phenotypic stability and adaptability of genotypes (Alliprandini et al. 1994). In the present study the AMMI analysis was applied to evaluate the G x E interaction effect and the phenotypic adaptability and stability for the trait storage root yield using cassava clones developed at IAC cultivated in the northwestern region of Paraná state.

MATERIAL AND METHODS

Experiments were carried out in different environments in the counties Maringá (Iguatemi Experimental Farm – UEM) and Araruna, both in the northwestern region of Paraná State. The soil was classified as a dystrophic Red Latosol (Embrapa 1999) in all locations. Eight experiments were carried out in eight environments: Maringá: E1 (1996/1997), E2 (1997/98), E3 (1998/99), E5 (1999/00) and E7 (2000/01), and in Araruna: E4 (1998/99), E6 (1999/00) and E8 (2000/01). The climate type in Maringá is Cw'h (Köppen classification), with an annual mean temperature of 22.4 °C and precipitation of about 1,638.9 mm. In Araruna, the weather was classified as Cfb with an annual mean temperature of 21.5 °C and precipitation of about 1,617 mm.

Five cassava clones were used as treatments: IAC 48 (*G4*), IAC 55 (*G5*), IAC 153 (*G6*), IAC 184 (*G7*), and IAC 190 (*G8*), which participated in the Cassava Breeding Program of the Agronomic Research Institute of Campinas (IAC), in Campinas, São Paulo State, Brazil, and were selected in 1989. The clones IAC 48, IAC 55 and IAC 153 were obtained by artificial crosses between SRT 59 – Branca de Santa Catarina and SRT 1174 – Rainha cultivars, whereas the clones IAC 184 and IAC 190 were obtained by self-pollination of the cultivar SRT 1287 – Fibra (Lorenzi et al. 1996). Cultivars IAC 12 (*G1*), Fibra (*G2*) and Branca de Santa Catarina (*G3*) were used as controls.

The genotypes for propagation were obtained from experimental fields (IAC) in Assis, São Paulo State

and then multiplied in Maringá. The stem of each selected clone was cut into 0.15-0.20 m long segments by a machete or circular saw (stem cuttings). Each stem cutting was placed in an approximately 0.10 m deep hole and covered with soil. The commonly used cropping practices for cassava were applied as described by Normanha and Pereira (1950) and Conceição (1987).

In Maringá the experimental plot size was 4.0 x 8.0 m and consisted of four rows spaced 1.0 m with plants spaced 0.80 m apart. The sampling unit consisted of the two central rows of which 0.80 m were eliminated from either end, resulting in a total area of 12.80 m^2, with 16 plants per sampling unit. The experimental plots in Araruna consisted of 5.0 x 6.4 m plots with five plant rows spaced as described. The sampling unit consisted of three central rows of which 0.80 m were eliminated from either end, amounting to a total area of 14.4 m^2, with 18 plants per sampling unit. Each trial was laid out in a randomized complete block design with four replications (Pimentel Gomes 1990).

Data were analyzed using joint analysis of variance to verify the significance of the effect of the genotype and environment interaction (Cruz and Regazzi 2001). Genotypes and environments were considered as fixed and randomized effects, respectively. The phenotypic adaptability and stability of cassava clones were therefore evaluated by AMMI analysis (Zobel et al. 1988).

AMMI analysis is a methodology that mixes additive components for the study of the main effects with multiplicative components for the study of G x E interaction effects. It combines variance analysis and the decomposition of singular value analysis for a clearer understanding of the G x E effects. According to Duarte and Vencovsky (1999), one part of $SS_{(GxE)}$ is due to the genotype and environment effects, respectively, whereas the other part represents the residue. The isolated effect caused by genotypes and environments in $SS_{(GxE)}$ is therefore denominated standard, whereas the residue present in $SS_{(GxE)}$ is designated noise. The appropriate model to look into the G x E interaction is the one which recovers only $SS_{(GxE)}$ standard and eliminates all residues or noises (Gauch Jr 1988). The AMMI analysis is therefore focused on restoring the part related to the effect of the genotypes and environments (standard), instead of restoring the entire $SS_{(GxE)}$ (Duarte and Vencovsky 1999). Besides the advantage of the high evaluation power of the

significance of the G x E interaction, AMMI analysis could also be used to select superior genotypes even in the presence of a significant G x E interaction. Based on the predicted means of the chosen AMMI model, it is safe to say each genotype contributes to the square sum of the respective selected AMMI model. This contribution can be calculated by:

$$A_i = \sum_{j=1}^{n} (GxE_{AMMI_n})^2_{ij} \quad \text{and} \quad A_i\% = (A_i / \sum_i A_i)x100 \; .$$

AMMI analysis allows the presentation of the interaction effects for each genotype and environment in a biplot graph, which makes the exploration of specific genotypes x environments interactions possible (Gabriel 1971). The software Genes (Cruz 2001) and SAS (SAS Institute 1997) were used for the statistical analyses.

RESULTS AND DISCUSSION

The rationale for using these methodologies to analyze stability and adaptability was the significant G x E interaction effect for storage root yields, i.e., the genotypes tended to different performances in contrasting environmental conditions. The highest means of storage root yields were attained by the genotypes IAC 153 (26.77 t ha^{-1}), Fibra (26.46 t ha^{-1}), IAC 190 (25.33 t ha^{-1}) and IAC 184 (24.24 t ha^{-1}), respectively.

In the AMMI analysis of stability and adaptability (Table 1), seven PCA axes were necessary to explain the whole G x E. However, only the first axis was significant, which means a great proportion of the standard, although the noise plots were not significant. Nevertheless, the first PCA axis was able to explain only 55% of $SS_{(GxE)}$, with only 13 degrees of freedom, representing 26.53% of the 49 total degrees of freedom that composed the $SS_{(GxE)}$, which seems interesting according to Duarte and Vencovsky (1999). On the other hand, the second PCA axis explained over 17%, amounting to a total of 72% of this G x E. But this PCA axis was not significant, indicating a high noise proportion of the interaction explanation. This case is not interesting, since the main objective of the analysis is to separate noise and standard to explain the G x E effect better, making plant breeders' work with genotype selection easier. For common bean, Borges et al. (2000) obtained 43% of interaction explanation in the first PCA axis, in stability analyses by AMMI methodology and inferred that this methodology was not effective

enough. Annicchiarico and Mariani (1996) obtained two significant axes studying the G x E interaction in wheat genotypes, which explained 63% of the interaction in the first, and 27% in the second axis. For corn cultivars Crossa et al. (1990) obtained an explanation of 54.6% of the original $SS_{(GxE)}$ with the first PCA axis, with only 8.9% degrees of freedom. Zobel et al. (1988) observed no significant interaction by the usual ANOVA methodology when comparing variance analysis with AMMI proceedings for the G x E interaction study in soybean. Unlike the interaction observed by ANOVA analysis, which was not significant, the AMMI analysis was significant and also explained approximately 76% of the total G x E interaction ($SS_{(GxE)}$), which accounted for only 41 of the total 244 degrees of freedom.

Zobel et al. (1988) pointed out the superior capacity of AMMI over ANOVA analysis to identify the G x E significance and to separate errors from main effects. Still, the information in Table 1 does not allow a detailed interpretation of the performance of each genotype as affected by environmental variations, but only of the significance of each PCA axis in the G x E explanation. Complementary to previous results, the scores of each genotype were graphically plotted in an AMMI1 biplot (Duarte and Vencovsky 1999).

Each genotype presented a refined contribution to the G x E interaction matrix of storage root yields of the cassava genotypes. Moreover, genotypes and environment averages with their respective estimated scores of the PCA1 axis are graphically plotted in an AMMI1 biplot (Figure 1). The genotypes Fibra and IAC 153 showed a high mean of storage root yields, as well as a high G x E reflected in the high PCA1 scores. For instance, IAC 184 and IAC 190 also presented high storage root yields and PCA1 scores closer to zero, and were therefore considered to be more stable than genotypes Fibra and IAC 153. The genotypes IAC 12, Branca de Santa Catarina and IAC 48 showed a higher response capacity to specific environments because their PCA1 scores were positive and high. These genotypes did not present satisfactory means of storage root yields and adaptability to unfavorable environments, as seen in environments 1 and 2. In relation to the environments, the graph showed that environments 3 and 4 influenced the G x E interaction in a lower proportion, reflected in the lower magnitude of PCA1 scores. According to the estimated $A_i\%$ values (data not shown), IAC 190 and IAC 184 were the most

Table 1. AMMI analysis of variance for storage root yield of cassava genotypes

Source of Variation	df	SS	MS	F	% (G x E) accumulated
Genotypes	7	471.34	67.33		-
Environments	7	780.22	111.46		-
Genotype x Environment	49	374.87	7.650		-
PCA 1	13	205.78	15.829*	4.06	54.89
PCA 2	11	65.96	5.996	1.54	72.49
PCA 3	9	58.36	6.484	1.66	88.05
PCA 4	7	31.42	4.489	1.15	96.44
PCA 5	5	8.55	1.710	0.44	98.72
PCA 6	3	3.38	1.126	0.29	99.62
PCA 7	1	1.43	1.431	0.37	100.00
Error	168		3.8964		-

[*] Significant at 1% probability by the F test, respectively
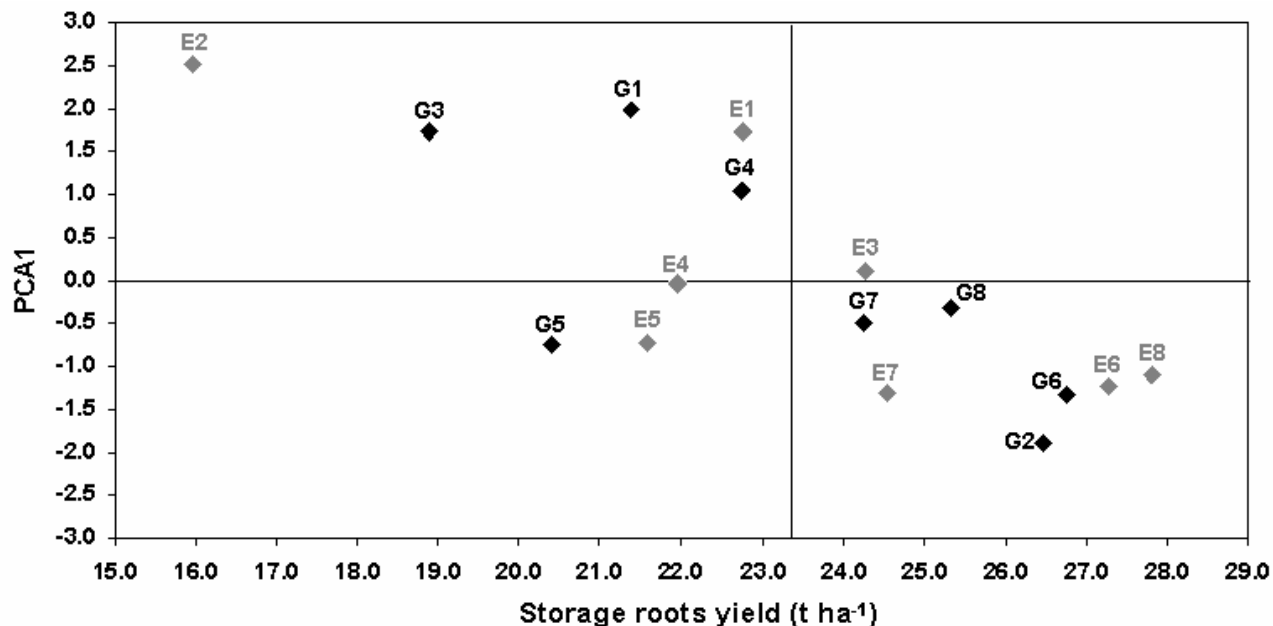
Figure 1. Biplot of AMMI 1 model for cassava root yield of eight clones grown in eight environments. *Environments*: E1: Maringá (1996/1997), E2: Maringá (1997/98), E3: Maringá (1998/99), E4: Araruna (1998/99), E5: Maringá (1999/00), E6: Araruna (1999/00), E7: Maringá (2000/01) and E8: Araruna (2000/01). *Genotypes*: G1: IAC 12, G2: Fibra, G3: Branca de Santa Catarina, G4: IAC 48, G5: IAC 55, G6: IAC 153, G7: IAC 184, and G8: IAC 190

stable genotypes in view of the lowest values for this parameter, which were in accordance to the results of the biplot graphs. The $A_i\%$ values of IAC 190 and IAC 184 clones were 0.70% and 1.73%, respectively.

Considering some factors such as the dry matter content, cassava bacterial blight, superelongation and root rot incidence, morphologic traits (data not shown), storage root yield, and phenotypic stability IAC 190 was found to be a very promising clone for recommendation for the northwestern region of Paraná. On the other hands, the genotypes IAC 12, Fibra and Branca de Santa Catarina were the least stable, which

showed Ai(%) values of 27.78%, 24.87% and 20.85%, respectively.

Estabilidade fenotípica de clones de mandioca no noroeste do Paraná por meio de análise AMMI

RESUMO - *Alta estabilidade e adaptabilidade para produção de raízes tuberosas são atributos muito desejáveis para clones de mandioca. Dessa forma, o objetivo deste trabalho foi avaliar os efeitos da interação G x A e a estabilidade de clones de mandioca desenvolvidos pelo IAC. Foi avaliada a produção de raízes tuberosas de oito genótipos. Os experimentos foram instalados em delineamento de blocos completos casualizados com 4 repetições, em dois municípios da região noroeste do estado do Paraná (Maringá e Araruna) durante 5 anos agrícolas (1997-2001). A presença de G x A foi avaliada usando análise de variância conjunta e a estabilidade e a adaptabilidade foram avaliadas por meio da análise AMMI. Foi verificado efeito significativo para G x A (P<0,05) para produção de raízes tuberosas. De forma geral, a análise AMMI se mostrou eficiente na avaliação da estabilidade e da adaptabilidade, indicando o clone IAC 190 como o mais promissor.*

Palavras-chave: *Manihot esculenta*, variabilidade genética, interação G x A, estabilidade, AMMI.

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