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RESEARCH ARTICLE

Ammi Analysis and its Application to Sugarcane Regional Trials in Venezuela

**Ramón Rea · Orlando De Sousa-Vieira ·
Miguel Ramón · Gleenys Alejos · Alida Díaz ·
Rosaura Briceño**

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Abstract The problem of genotype by environment interaction (G × E) is that often complicates the interpretation of trials in multiple locations, making it difficult to select genotypes adapted to different environments. AMMI model was adopted to analyze ten sugarcane genotypes in ten Venezuelan environments evaluated through two years of cultivation. The objectives of this study were to identify stable and adaptable genotypes in different locations and determine the magnitude of G × E interaction. The analysis of variance showed that 72% of the total sum of squares was attributed to environmental effect, indicating that the sites were diverse. The first two principal component axes were significant, and both sums contributed to 61.09% to the total of G × E interaction. The V77-12 genotype exhibited high yield and wide adaptability to different environments. However, the CP74-2005, CP72-2086, PR61-632, PR980, and V78-2 genotypes showed high yield but with specific adaptations through locations. The application of AMMI model facilitated the visual comparison and identification of superior genotypes for each set of environments.

Keywords AMMI model · G × E interaction · Principal component · *Saccharum* spp. *hybrid*

Introduction

Sugarcane is grown in a wide range of environments and hence, yields of several genotypes tested across locations and over years, differed due to high genotype by environment interaction (G × E). This makes difficult for breeders to develop widely adapted, stable and high yielding genotypes in Venezuela (Rea and De Sousa-Vieira 2002). The ideal situation for plant breeders is that the rank orders of genotypes should be constant across environments, so that; the best genotype in one environment is also the best in all others. However, this is not the case in real applications; because, any deviation from the ideal situation represented by identical rank orders, is the result of genotype by environment interactions (Hühn 1990). Several statistical methods have been developed to analyze G × E interaction and predict the phenotypic response to environmental changes (Hill 1975; Lin et al. 1986; Wescott 1986; Crossa 1990; Van Eeuwijk 1995; Flores et al. 1998; Kang 1998). A strong regional basis to G × E interactions in sugarcane has been identified in Queensland (Australia). Its magnitude varies from negligible in Central Queensland to highly significant in North Queensland, where; it is difficult to broadly identify adapted varieties (Hogarth and Bull 1990; Jackson et al. 1991; Bull et al. 1992; Jackson and Hogarth 1992). Tai et al. (1982) evaluated phenotypic stability of sugarcane cultivars by measuring regression coefficients (b values) and mean square deviations from regression (s_d) for several traits in Florida, USA. Kang and Miller (1984) evaluated three methods of partitioning G × E interaction into stability-variance components assigned to each cultivar in sugarcane. However, in these models, the parameters account for only a small proportion of the interaction sum of squares; while, the remaining variance is unexplained. In recent years, quantification of

R. Rea (✉) · O. De Sousa-Vieira · G. Alejos · A. Díaz ·
R. Briceño
Instituto Nacional de Investigaciones Agrícolas - Yaracuy, Km 3
via aeropuerto sector La Ermita, mcpio. Cocorote edo,
San Felipe 3201, Yaracuy, Venezuela
e-mail: rrea@inia.gov.ve; ramonrea@hotmail.com

M. Ramón
Instituto Nacional de Investigaciones Agrícolas-Portuguesa,
Km 5 Carretera Nacional Acarigua-Barquisimeto, Araure edo,
Guanare 3301, Portuguesa, Venezuela

G × E interaction and yield stability, based on multivariate procedures such as principal component analysis (PCA) (Jackson and Hogarth 1992; Quemè et al. 2005; Guerra et al. 2009) and principal coordinate analysis (PCO) (Wescott 1986), have become an important method in G × E interaction studies.

The additive main effect and multiplicative interaction (AMMI) method integrates analysis of variance and principal component analysis into a unified approach that, also, can be used to analyze multilocation trials (Zobel et al. 1988; Crossa et al. 1990; Gauch and Zobel 1996). AMMI uses the analysis of variance (ANOVA) approach to study the main effects of genotypes and environments and a principal component for the residual multiplicative interaction between genotypes and environments. AMMI is theoretically the most effective model to catch G × E interaction sum of squares (SS) with a minimum number of degrees of freedom. In addition to its effectiveness in accounting for G × E interaction, the AMMI model has several important features: First, it quantifies both the contribution to G × E interaction SS for each genotype and each environment simultaneously; second, these hypothesized variables can be easily related to the real environment and genotypic variables; thus, facilitating biological interpretation of G × E interaction; third, AMMI quantified environmental and genotypic scores can be conveniently displayed in the form of a "biplot" graph (Gauch and Zobel 1988; Gauch and Zobel 1996; Yan and Hunt 2003). Using the biplot technique, the genotypes and the environments can be mutually classified at the same time (Kempton 1984).

Although, the regional variety trials have been part of the Sugarcane Breeding Program in Venezuela for many years, the relative magnitudes of genotype by environment interaction have not been well documented. This paper reports and discusses the importance of G × E interaction and the utilization of AMMI analysis in selecting sugarcane genotypes in Venezuela. The experiments were conducted to (i) evaluate cane yield, (ii) determine the nature of G × E interactions, and (iii) study the adaptation of different sugarcane genotypes using the biplot technique.

Materials and Methods

Ten cultivars of sugarcane were grown in replicated trials in the Central-Western Region of Venezuela. The cultivars were: V77-9, V77-11, V77-12, V78-2, V64-10 PR980, PR61-632, Mex64-1486, CP72-2086 and CP74-2005. All materials were evaluated at ten environments [Los Caobos I, Los Caobos II, La Pastora-Turbio and Central La Pastora in Lara State, Yaritagua I, Yaritagua II, and Central Matilde in Yaracuy State, Canaima I, Canaima II and Morita in Portuguesa State] each having two years of cultivation (plant cane and first ratoon). These sites represented the major sugarcane ecological areas of production in the country. The trait studied was cane yield in tons of cane per hectare (TCH). The trials were laid out in a randomized block design with three replications at each location. Plots were three rows wide, with 1.5 m between rows, and 10 m long. The cane was burned and then cut by hand at 12 months. All three rows were harvested to measure cane yield.

Yield and stability analysis of genotypes in different environments was then subject to a multivariate analysis by the AMMI method. For AMMI, the following model was used:

$$Y_{ij} = \mu + G_i + E_j + \sum \lambda_n \gamma_{in} \delta_{jn} + \varepsilon_{ij;}$$

where μ is the overall mean, G_i and E_j are genotypic and environmental main effect, N is the number of PCA axes considered, λ_n is the singular value of the nth PCA axis, γ_{in} and δ_{jn} are scores for the ith genotype and jth environment on the nth PCA axis and ε_{ij} is the residual term which includes the experimental error.

AMMI generates a family of models with different values of N. The simplest model by AMMI0 with N equal to zero considers only the additive effects, namely genotypes and environments mean to explain the data matrix. The second model AMMI1 considers main effects and one interaction principal component axis interpreting the residual matrix. Similarly, AMMI2 involves main effects and two interaction principal component axes for no additive (interaction) variation, and so on. The resulting PCA interaction scores for genotypes and environments were used to construct the biplot charts (Kempton 1984; Yan et al. 2000). Genotype and environment are plotted on the same diagram, facilitating inference about specific interaction of individual genotypes and environments by using the sign and magnitude of PCA1 values. Any genotype with a PCA1 value close to zero shows general adaptation to the tested environments. A large genotypic PCA1 scores having the same sign reflects more specific adaptation to environments (Kempton 1984; Romagosa et al. 1993). In AMMI analyses of variance, the *F* tests applied to each variation source of interest, and the biplot graphs corresponding to the AMMI1 and AMMI2 models were calculated using Vargas and Crossa (2000) programs, which run on SAS statistical package (SAS 2001).

Results and Discussion

AMMI analysis of variance of TCH over two cuttings and ten environments showed that 72.03% of the total SS was

Table 1 AMMI analysis of variance for cane yield of genotypes across environments

Source	DF	SSAMMI	MS-AMMI	% SS
TRT	99	333978.95	35252.45	
GEN	9	46301.71	5144.97**	13.84
ENV	9	240859.81	26762.20**	72.03
G × E	81	46814.43	3345.28*	14.00
PCA 1	17	20285	1193.28**	43.33
PCA 2	15	8312.29	554.15*	17.76
Residual	49	18154.74	1874.98	

**,* Significant at the 5 and 1% level of probability, respectively

attributable to environmental effects, 13.84% to genotypic effects and 14.00% to G x E interaction effects (Table 1). A large SS for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in TCH. Results from AMMI analysis also showed that the PCA1 and PCA2 axes explained 43.33 and 17.76% of the total G × E interaction. The mean square for PCA1 and PCA2 were significant at $P < 0.01$ and $P < 0.05$ respectively; and, cumulatively contributed to 61.09% of the total G × E interaction. The F-test at $P < 0.01$ and $P > 0.05$ suggested that the two principal component axes from the interaction were significant to the model with 32 degrees of freedom. Hence, the AMMI model with only two PCA interactions was the best predictive model, which is in agreement with Zobel et al. (1988) and Annicchiarico (1997).

Yield Performance of the Genotypes

The mean cane yield of sugarcane genotypes varied among environments ranging from 52.16 TCH for Canaima II environment to 146.73 TCH for Morita environment. The mean cane yield for the 15 genotypes extended from 82.07 to 123.94 TCH. The G × E interaction was a crossover type as revealed by differential ranking of genotypes across environments (Table 2). CP74-2005 cultivar was the top ranking genotype at three environments and recorded the top yield of 198.03 TCH at the highest yielding environment (Yaritagua I). Meanwhile, CP72-2086 genotype was the highest yielder (68.16 TCH) at the lowest yielding environment (Canaima II).

AMMI Biplot: Interpreting Specific Pattern

The results of AMMI analysis can also be easily comprehended by using AMMI1 biplot as presented in Fig. 1. The mean performance and IPCA1 scores, for both genotypes and environments used to construct the biplot, are presented in Table 2. The biplot from AMMI analysis is a useful tool in explaining the specific patterns of main effects and G x E interactions of genotypes and environments simultaneously (Crossa et al. 1990; Kempton 1984). Regarding the biplot, the points for generally adapted genotypes would be at right hand side of the grand mean level (this suggests high mean yield); also, close to the line showing PCA1 = 0 (this suggests negligible or no G × E interaction). However, the points for the specifically adapted genotypes would be away from the line with PCA1 = 0 and next to the grand mean level. Thus, it was clear from Fig. 1 that V77-12 genotype, scattered at the right-hand side of the grand mean level and close to PCA1 = 0 line, was declared by the AMMI model as having general adaptability to all locations. However, five genotypes: CP74-2005, CP72-2086, PR61-632, V78-2 and PR980 resulted in high mean and large PCA1 scores; hence, these materials specifically suited to the favorable locations. For example, Morita was the most advantageous location for CP74-2005 and CP72-2086 genotypes; Central Matilde location was mainly associated with genotypes PR61-632 and PR 980, and Central La Pastora location was most suited for V78-2 genotype. The genotypes adapted to lower yielding environments were Mex 64-1487 and V77-9.

The genotypes were also represented on the biplots by the points derived from their scores as a result of the first two components; and the environments as the vectors from the biplot origin to their respective points (Fig. 2). The cosine of angle involving a pair of environment or genotype vectors approximates correlation between them (Yan and Kang 2003). An acute angle (<90°) indicates a strong positive correlation; an angle close to 90° indicates the environments are not correlated; whereas, an obtuse angle close to 180° represents a strong negative relationship. Vectors having <90° angle corresponded to the following environments: La Pastora-Turbio (E7) and Morita (E5); Yaritagua I (E6), Canaima I (E3), Yaritagua II (E10), Los Caobos II (E8) and Canaima II (E9), suggesting that these environments tend to discriminate among genotypes in a similar manner. For instance, locations as Yaritagua I (E6) and Yaritagua II (E10); and also, Canaima I (E3) and Canaima II (E9) would be desirable to leave only one between them. The environmental vectors related to Morita (E5) and La Pastora-Turbio (E7) drew an angle nearly 180° with Yaritagua I (E6) and Central La Pastora (E4) environments. The genotypic discrimination was therefore expected to be almost opposite in direction among them.

The PR61-632 and CP74-2005 genotypes had specific adaptation to Central Matilde (E2) and La Pastora-Turbio (E7) environments because their angle was less than 90° and their G × E interaction was positive; CP74-2005 was

Table 2 Mean yield (TCH) of ten sugarcane genotypes at ten environments in Venezuela

Genotype	Environments										Mean	PC1	PC2
	Yaracuy state			Lara state				Portuguesa state					
	Central Matilde	Yaritagua I	Yaritagua II	La Pastora Turbio	Los Caobos I	Los Caobos II	Central La Pastora	Canaima I	Canaima II	Morita			
V78-2	117.79	159.24	138.80	77.49	96.96	107.41	104.26	108.00	64.43	135.46	111.03	−2.741	0.283
CP72-2086	122.20	*163.41*	133.68	116.37	*118.14*	109.03	109.96	107.23	*68.16*	191.26	123.94	3.059	2.876
PR61-632	119.87	152.22	136.25	114.79	96.00	95.33	*124.98*	86.61	55.32	170.79	115.22	1.769	2.649
Mex 641487	95.96	119.43	132.37	74.36	89.44	74.23	96.75	90.91	31.35	124.87	92.97	−1.167	2.696
V77-11	80.80	138.61	121.80	61.91	39.80	65.79	87.38	89.28	34.51	100.84	82.07	−3.248	−2.732
PR980	101.97	134.89	135.18	90.21	63.28	*122.82*	101.05	79.03	55.19	151.82	103.54	0.369	−2.521
CP74-2005	126.69	133.53	*155.78*	*119.01*	72.84	82.16	92.99	109.18	58.06	*198.03*	114.83	5.975	−1.678
V77-9	78.82	127.69	129.00	77.65	53.66	83.10	82.30	79.67	59.37	137.40	90.87	0.454	−3.290
V64-10	102.61	142.45	146.84	88.94	79.42	88.11	116.45	74.56	36.11	109.42	98.49	−3.699	1.591
V77-12	*128.06*	154.31	130.80	87.23	88.52	105.98	99.37	*109.74*	58.56	147.39	111.03	−0.771	0.127
Mean	107.48	142.58	136.05	90.83	79.81	93.40	101.56	93.42	52.16	146.73	104.40		
LSD	21.55	40.67	33.08	14.19	19.26	24.43	23.00	18.22	10.06	23.22			
PC1	0.261	−2.632	−1.272	2.701	−0.809	−1.768	−2.691	−0.885	−0.284	7.378			
PC2	1.010	−0.267	−1.999	0.465	5.616	−1.671	1.470	−1.520	−2.915	−0.190			

Values in italics indicate LSD ($\alpha = 0.05$)

Fig. 1 AMMI1 biplot showing the first principal axis of interaction (PCA1) versus mean yield of tons of cane per hectare (TCH) from ten genotypes at ten environments in Venezuela

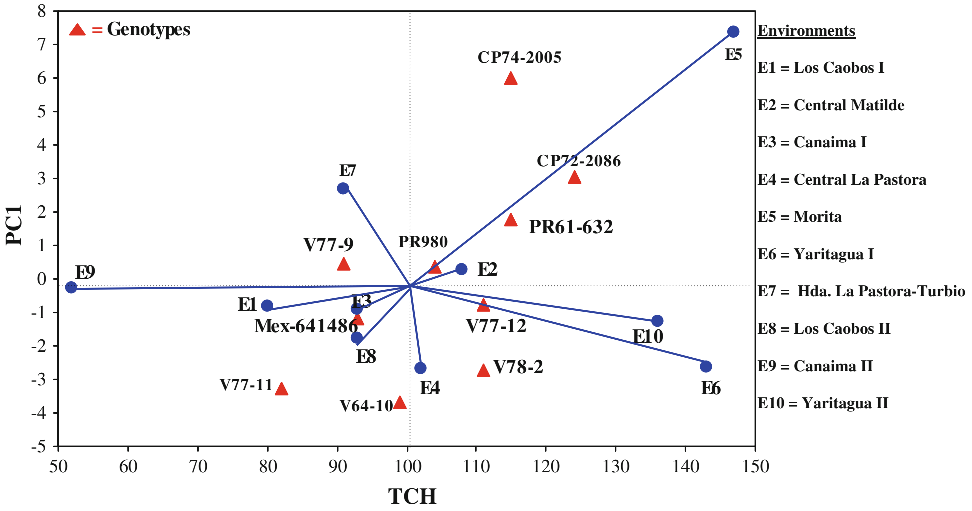
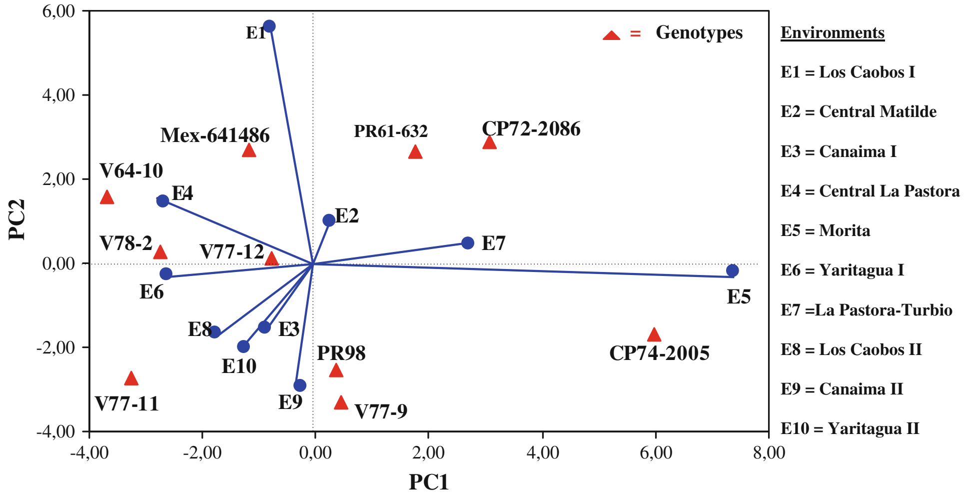


Fig. 2 AMMI2 biplot showing the first two principal axes of interaction (PCA1 and PCA2) corresponding to tons of cane per hectare from ten genotypes at ten environments in Venezuela



associated with Morita (E5) environment. V77-12 genotype was located around the center of the biplot, having mean yield over the grand mean; then, this genotype can be considered as stable with high performance.

Conclusions

The magnitude of G × E interaction for cane yield of the ten genotypes evaluated at ten environments in Central-Western Region of Venezuela was slightly higher than the effect of genotype, but much smaller than the effect of the environment.

The use of graph in AMMI model facilitates the selection of stable and high yield genotypes in sugarcane.

Indirect selection among environments could be used to reduce the number of regional trials by eliminating those that are correlated with each other, allowing to save and to optimize resources.

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