

ARTICLE

Evaluation of sugarcane genotypes and production environments in Paraná by GGE biplot and AMMI analysis

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Received 29 November 2012

Accepted 18 February 2013

Abstract – The purpose of this study was to evaluate sugarcane genotypes for the trait tons of sugar per hectare (TSH), stratifying five production environments in the state of Paraná. The performance of 20 genotypes and 2 standard cultivars was analyzed in three consecutive growing seasons by the statistical methods AMMI and GGE Biplot. The GGE Biplot grouped the locations into two mega-environments and indicated the best-performing genotypes for each one, facilitating the selection of superior genotypes. Another advantage of GGE Biplot is the definition of an ideal genotype (G) and environment (E), serving as reference for the evaluation of genotypes and choice of environments with greater GE interaction. Both models indicated RB006970, RB855156 and RB855453 as the genotypes with highest TSH and São Pedro do Ivai as the environment with the greatest GE interaction. Both approaches explained a high percentage of the sum of squares, with a slight advantage of AMMI over GGE Biplot analysis.

Key words: *Saccharum spp.*, adaptability, stability, environment stratification.

INTRODUCTION

The development of sugarcane and other crops is affected by effects of the environment (E), genotype (G) and their interaction (GE), of which the latter causes significant variations in cultivar performance between different locations (Mohammadi et al. 2007).

The evaluation of genotypes, aside from the stratification of production environments, is fundamental for the study of relations between genotypes and environments (GE), especially to identify similar response patterns of genotypes in the environments of the experimental network (Cruz et al. 2001).

One of the most recent evaluation methods is the AMMI (Additive Main Effects and Multiplicative Interaction) analysis. In this model, statistical techniques such as analysis of variance and principal component analysis, respectively, are combined to adjust the main effects and GE interaction effects (Duarte and Vencovsky 1999).

Yan et al. (2000) proposed the GGE Biplot method and pointed out that although the yield data are the combined

effect of genotype (G), environment (E) and the interaction of both (GE), only G and GE are relevant and should be considered simultaneously in the evaluation of genotypes. Furthermore, the biplot technique is also used to approach and evidence the G and GE effect in a multi-environmental trial, which coined the term “GGE Biplot”.

Recently, several methods were used simultaneously to evaluate genotypes and production environments of different crops (Silva and Duarte 2006, Cargnelluti Filho et al. 2007, Melo et al. 2007, Silva Filho et al. 2008, Pereira et al. 2009, Guerra et al. 2010, Nunes et al. 2011, Gouvêa et al. 2011). However, the AMMI has seldom been used together with the GGE Biplot in studies on sugarcane. Other crops, for example, wheat (Kaya et al. 2006, Yan et al. 2007), soybean (Asfaw et al. 2009), sorghum (Rao et al. 2011), and carrot (Silva et al. 2012) were evaluated.

The objective of this study was to evaluate 22 sugarcane genotypes in 5 production environments, based on the adaptability and stability of genotypes using 2 statistical methods, GGE Biplot and AMMI.

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MATERIALS AND METHODS

We evaluated 20 sugarcane genotypes, plus 2 cultivars as controls: RB855156 and RB855453 in the growing seasons of 2009/10, 2010/11 and 2011/12.

The tests were conducted in five environments: Astorga (23°05'S, 51°36'W, 634 m asl), Bandeirantes (lat 23°06'S, long 50°22'W, and alt 492 m asl), Colorado (lat 22°50'S, long 51°54'W, and alt 400 m asl), Goioerê (lat 24°10'S, long 53°01'W, and alt 550 m asl) and São Pedro do Ivaí (lat 23°52'S, long 51°41'W, and alt 40 m asl), in the state of Paraná. The climate in all environments was Cfa, according to Köppen.

The experiments were arranged in a randomized complete block design with three replications in plots of four 8m-rows spaced 1.40 m apart. In March 2009, 18 buds were planted per meter. The harvest of each growing seasons occurred in April 2010, 2011 and 2012. At harvest, three samples of 15 stalks without tips per plot were collected without burning the sugarcane from the two central rows, while in front and at the end of the plot, 1 meter was not evaluated (border). The samples were used to estimate the average weight per stalk (MIC) and the trait pol % cane (PC). The number of stalks per plot was also counted, to determine the number of stalks per meter (NSM). These values were used to define the traits of tons of stalks per hectare (TSH) and tons of sugar per hectare (TSH), by the following expressions: $TSH = NCM \times MIC \times 7.142$, where the fixed value 7.142 indicates the area estimated for planting, according to the spacing and $TSH = (TSH \times PC)/100$.

Based on the TSH data, analyses of variance were conducted for each production environment and for plant cane, first ratoon and second ratoon. Once the differences between the treatments were detected, combined analysis of variance was performed (Ramalho et al. 2000), providing complementary information to the analysis.

After detecting the GE interaction (P test significant) by combined analysis of variance, the phenotypic adaptability and stability was analyzed by the GGEBiplot (Yan et al. 2000) and AMMI methods (Zobel et al. 1988).

The first evaluation was performed using the GGEBiplot, based on the following model: $y_{ij} - y_j = y_1 \epsilon_i 1 p j 1 + y_2 \epsilon_i 2 p j 2$, where: y_{ij} represents the average yield of the i-th population in the j-th environment; y_i is the overall mean of population j in environment j; $y_1 \epsilon_i 1 p j 1$ is the first principal component (PCI1); $y_2 \epsilon_i 2 p j 2$ is the second major component (PCI2); y_1, y_2 are the eigenvalues associated to PCI1 and PCI2, respectively; ϵ_1 and ϵ_2 are the scores of the first and second main component, respectively, of the i-th population;

$p j 1$ and $p j 2$ are the scores of the first and second principal component, respectively, for the j-th environment; and ϵ_{ij} is the error associated with the model of the i-th population and j-th environment (Yan and Kang 2003).

The second analysis applied AMMI, based on the model described by Duarte and Vencovsky (1999):

$$y_{ij} = \mu + g_i + a_j + \sum_{k=1}^n \lambda_k \gamma_{ik} \alpha_{jk} + \rho_{ij} + \epsilon_{ij};$$

where: y_{ij} is the mean response of genotype i (i = 1, 2, ..., G genotypes) in environment j (j = 1, 2, ..., A environments), μ is the overall mean of the tests; g_i is the fixed effect of genotype i (i = 1, 2, ..., g); and α_j is the random effect of environment j (j = 1, 2, ..., a). The GE interaction is influenced by the factors: λ_k , which is the singular value for the k-th principal component of interaction (PCI), (k = 1, 2, ..., p, where p is the maximum number of estimable principal components); γ_{ik} is the singular value of the j-th environment in the k-th PCI; α_{jk} is the singular value of the i-th genotype in the k-th PCI; k are nonzero characteristic roots, $k = [1, 2, \dots, \min(g-1, e-1)]$. Item ρ is the residue of the GE interaction or AMMI residue (noise in the data) and ϵ is the average experimental error, assumed as independent.

RESULTS AND DISCUSSION

The combined analysis showed that the yield of sugarcane genotypes was significantly influenced by the environment (E), which explained 70.5% of the total phenotypic variation while the genotypic traits (G) and the interaction between genotype and environment (GE) explained 10.43 and 10%, respectively, of the total variation (Table 1). Gauch and Zobel (1996) reported that in multi-environment trials, the environment (E) normally explains up to 80% of the variation while genotype (G) and the genotype - environment (GE) interaction both usually represent around 10 - 15% of each variation.

The analysis of variance also showed that the effects of sources of variation, genotype, environment, and GE interaction were significant for the variable analyzed (Table 1). This result indicated that the genotypes were characterized as environmentally-induced changes.

For the percentage of explanation of the interaction axes of AMMI and GGE Biplot, it was observed that the first two principal components explained 78.2 and 74.5% of the variation, respectively (Table 1). This value was higher than that reported by Guerra et al. (2009) and by Verissimo et al. (2012), who applied AMMI analysis to sugarcane, and similar to results of Chavanne et al. (2007) and Silva et al. (2012), who used GGE Biplot analysis for sugarcane and carrots, respectively.

Table 1. Combined analysis of variance for tons of sugar per hectare (TSH) and proportion of the sum of squares of genotype - environment interaction for each axis of the main components of the GGE Biplot and AMMI analyses for 22 sugarcane genotypes in five environments in the State of Paraná.

Source of variation	df	SS	AMMI		GGE Biplot	
			% Expl.	% Acc.	% Expl.	% Acc.
Block/Env.	10	190.19				
Genotype	21	996.22**	10.43		10.43	
Environment	4	6731.36**	70.5		70.5	
Gen x Env.	84	1820.95**	10.		10.	
	PC 1	44	957.82**	52.6	52.6	
	PC 2	21	466.16**	25.6	78.2	
	PC 3	13	262.22**	14.4	92.6	
	PC 4	6	134.75**	7.4	100	
	PC1	42	895.91**			49.2
	PC2	21	460.70**			25.3
	PC3	11	234.90**			12.9
	PC4	6	142.03**			7.8
	PC5	4	87.41**			4.8
Residue	870	13125.07				

P - P test significant at 1% probability; % Expl. - Explained percentage of sum of squares % Acc. - Accumulated Percentage.

For the methodologies that use principal component analysis, the first interaction axes contain a greater standard percentage, with a decrease in the subsequent axes. Thus, as the number of selected axes is increased, the noise percentage increases, reducing the predictive power of the analysis (Oliveira et al. 2003). Based on this definition and the high accumulated value of explanation of percentages of the sum of the squares on the two first axes of interaction by both approaches (Table 1), the adaptability and stability of sugarcane genotypes can be graphically interpreted, considering only biplots with the first two axes of GE interaction.

The values of TSH were highest for the genotypes RB006991 (G19), RB006970 (G10), RB005916 (G1), RB005935 (G4) and RB855156 (G21), respectively, in Astorga, Bandeirantes, Colorado, Goioerê, and São Pedro do Ivaí (Table 7).

Figure 1A of the GGE Biplot analysis is important to study the possible existence of mega-environments within a growing region (Yan and Rajcan 2002). A polygon was drawn connecting the genotypes that are further away from the biplot origin, (RB855156 (G21), RB006970 (G10), RB006973 (G13), RB006988 (G18), RB005991 (G9), RB006991 (G19)) (Figure 1A). These genotypes have the largest vectors in their respective directions; the vector length and direction represent the extent of the response of the genotypes to the tested environments. All other genotypes are contained within the polygon and have smaller vectors, i.e., they are less responsive in relation to the interaction with the environments within that sector. The vectors originating from the center of the biplot (0; 0), perpendicular to the sides of the polygon, divided the graph into six sectors (Figure 1).

The polygon of the GGE biplot (Figure 1A) grouped the test locations in mega-environments. Mega-environments are those sectors which comprise one or more environments. In this case, there were two mega-environments: I - Astorga, Colorado and São Pedro do Ivaí and II - Bandeirantes and Goioerê.

In Figure 1A, the genotype of the vertex of the polygon, contained in a mega-environment, had the highest yield in at least one environment and was one of the best-performing genotypes in the other environments (Yan and Rajcan 2002). Thus, genotype RB855156 (G21) was the best in São Pedro do Ivaí and performed well in Colorado and Astorga and genotype RB006970 (G10) obtained highest yields in Bandeirante and was among the best in Goioerê (Figure 1A and Table 2).

The genotype yield and stability were evaluated from the average environment coordination (AEC) (Yan and Rajcan 2002). The greater the projection of the genotype on the axis of the AEC ordinate, the greater the instability of the genotype, representing a greater interaction with the environments. In this sense, the genotypes G22 (RB85545), G15 (RB006976), G3 (RB005924), G4 (RB005935), and G1 (RB005916) were identified as the most stable. Although the yield variation of genotypes G21 (RB855156) and G10 (RB006970) was great, they were always among the best genotypes in all tested environments (Figure 1B and Table 2). Based on the average TSH yield in the three seasons and at the five locations, the genotypes with above-average yields were ranked in decreasing order: G21 (RB855156), G10 (RB006970), G22, G15, G3, G14, G4, G1, G2, G19, and G17.

Table 2. Average production of tons of sugar per hectare (TSH) of the 22 sugarcane genotypes, in each of five tested environments and overall average

Label	Genotype	Astorga	Bandeirantes	Colorado	Goioerê	São Pedro do Ivai	Mean
G1	RB005916	11.67	14.83	12.19	11.82	18.13	13.73
G2	RB005918	10.25	16.66	10.06	11.84	16.71	13.11
G3	RB005924	11.45	16.00	9.82	12.89	18.32	13.70
G4	RB005935	9.21	15.87	10.54	15.73	17.77	13.83
G5	RB005968	9.01	12.70	7.65	10.93	18.70	11.80
G6	RB005971	12.32	16.20	9.08	12.42	14.19	12.85
G7	RB005982	9.51	14.80	8.54	12.14	15.27	12.06
G8	RB005987	8.68	14.49	9.20	12.30	17.30	12.40
G9	RB005991	8.35	12.14	7.38	12.20	13.82	10.78
G10	RB006970	11.86	18.96	9.47	12.32	18.46	14.22
G11	RB006971	12.30	13.83	8.90	11.50	17.08	12.73
G12	RB006972	9.60	12.79	9.79	11.57	12.71	11.30
G13	RB006973	8.62	16.74	8.23	11.53	13.29	11.69
G14	RB006974	12.85	13.57	9.10	14.53	19.38	13.89
G15	RB006976	10.51	16.22	9.19	12.61	19.27	13.56
G16	RB006981	11.39	12.47	9.71	11.92	17.82	12.67
G17	RB006984	12.96	12.05	9.76	11.77	18.38	12.99
G18	RB006988	10.98	16.14	8.98	12.48	11.82	12.08
G19	RB006991	13.74	12.23	9.79	11.24	18.70	13.14
G20	RB006992	11.12	12.38	10.56	12.51	14.28	12.18
G21	RB855156	12.73	14.94	10.48	14.44	20.29	14.58
G22	RB855453	12.10	15.44	11.30	12.97	19.54	14.27
	Mean	10.97	14.61	9.53	12.44	16.87	12.889
	S	1.60	1.90	1.11	1.14	2.48	

Values in bold indicate the genotype with highest TSH production in the corresponding environment; G - genotype, S - standard deviation.

An ideal genotype should have an invariably high average yield in all environments concerned. This ideal genotype is graphically defined by the longest vector in PC1 and without projections in PC2, represented by the arrow in the center of the concentric circles (Figure 1C). Although this genotype is but an estimate, it is used as a reference for the evaluation of genotypes. The standard cultivars RB855156 (G21) and RB855453 (G22), and genotype RB006970 (G10), RB006976 (G15), RB005924 (G3), RB005935 (G4) and RB005916 (G1) were contained in the second concentric circle (Figure 1C); these genotypes are closest to the ideal and can be considered desirable in terms of yield and stability of the trait TSH.

Figure 1D shows the relationship between yield and stability from the vectorial standpoint of the environments, and they are connected by vectors with the origin of the biplot. In environments with small vectors, the yield stability is high. The difference between the average yield of genotypes was lowest in Colorado and Goioerê (Figure 1D and Table 2), i.e., they contributed less to the GE interaction.

For environments that contributed most to the GE interaction, the environments Bandeirantes and São Pedro do Ivai were the most unstable, in other words, the interaction between genotypes and environments was greater (Figure

1D). In this figure, the values of the cosines of the angles between the vectors of each environment corresponded to the correlation coefficient between them. Most environments are positively correlated, because the cosine of the angle between them is positive. The only exception was the correlation between Astorga and Bandeirantes, which is negative, i.e., the angle between their vectors is $> 90^\circ$. Positive and negative correlations between test environments were also detected by Kaya et al. (2006), who used the GGE biplot approach to assess wheat and its production environments.

An ideal environment should have a high PC1 score (greatest power of genotype discrimination in terms of main genotype effects) and zero score for PC2 (greatest representativeness of all other environments). In Figure 1E, this environment is represented on the axis of abscissa AEC by an arrow in the center of the concentric circles. Similarly to the ideal genotype, the ideal environment is only an estimate and serves as a reference for site selection for multi-environment trials. The most desirable is the one closest in the graph of the ideal environment (Yan and Rajcan 2002).

The environment São Pedro do Ivai contained in the fifth concentric circle is the location with greatest ability to discriminate genotypes, favoring the selection of superior

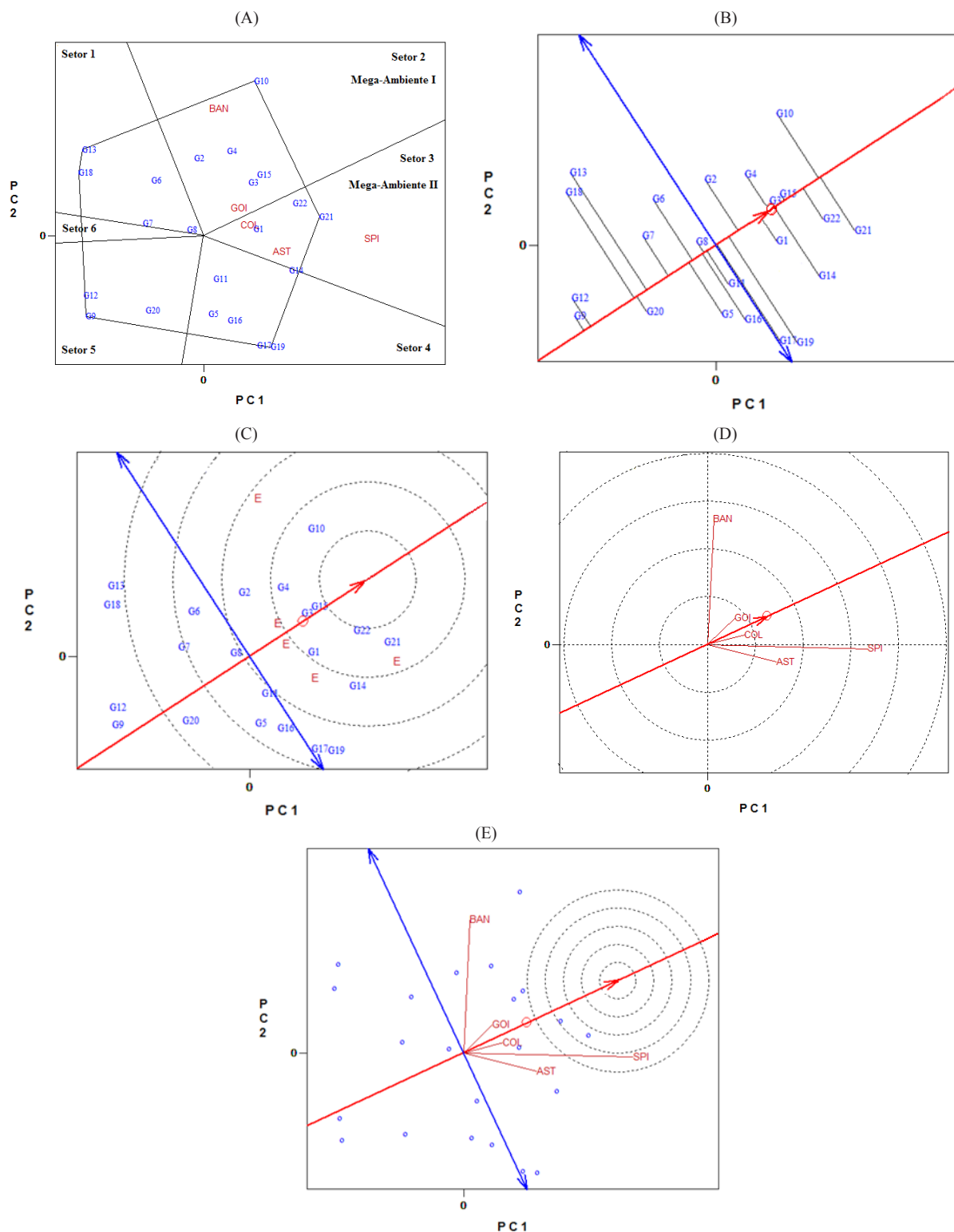


Figure 1. GGE Biplot methodology, with the first two principal axes of the interaction (PC1 and PC2) for the average yield per ton of sugar per hectare (TSH) of 22 genotypes in 5 production environments in the state of Paraná. AST – Astorga, BAN – Bandeirantes, COL – Colorado, GOI – Goioerê and SPI – São Pedro do Ivaí.

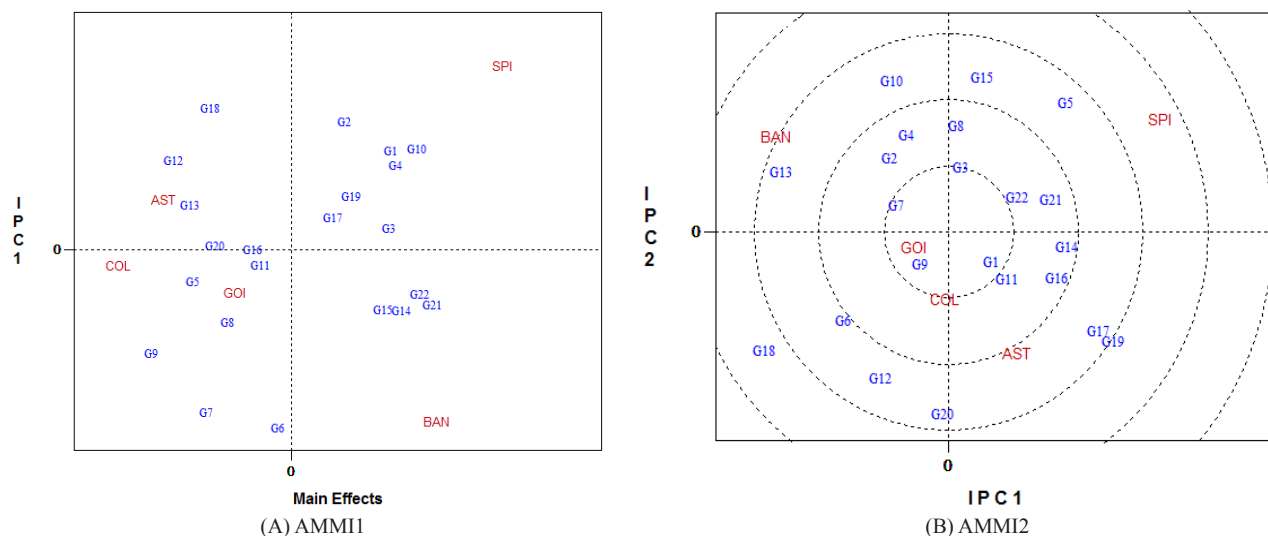


Figure 2. Biplot AMMI1 (A) with the first principal axis of interaction (PCI1) x average yield of tons of sugar per hectare (TSH), and AMMI2 (B), with the first and second principal axis of interaction (PCI1 and PCI2) of 22 sugarcane genotypes at 5 locations in Paraná. AST – Astorga, BAN – Bandeirantes, COL – Colorado, GOI – Goioerê and SPI – São Pedro do Ivai.

genotypes (Fig. 1E). In the same graph, Bandeirantes represented a high yield potential, but no capacity of genotype discrimination, since the standard deviation between the mean TSH of the genotypes was lower than of São Pedro do Ivai (Table 6).

According to AMMI analysis, seven genotypes (RB006970 (G10), RB005916 (G1), RB005924 (G3), RB005935 (G4), RB006974 (G14), RB006976 (G15), and RB006961 (G19)), had an average yield similar to the controls (Figure 2A and Table 2), but only genotype RB005916 (G1) had above-average yield and low instability (Figure 2A, B). The stability of genotype RB005991 (G9) was high, compared with the standards, for being close to the origin of AMMI2, but its average yield was much lower than that of the other genotypes (Figure 1B and Table 2). In general, the most stable genotypes were RB005987 (G8), RB005916 (G1), RB855453 (G22), RB855156 (G21), RB006971 (G11), RB005935 (G4), and RB005982 (G7), because the GE interaction scores were lowest and positions closest to the center of the AMMI2 biplot. In this same biplot, the most unstable genotypes were RB006970 (G10), RB006961 (G19) and RB006992 (G20), all distant from the center of AMMI2 biplot (Figure 1B).

Genotype RB006970 (G10) was one of the most productive and specifically adaptable to less restrictive environments. The yield of this genotype was higher in environments with more clayey soils (Bandeirantes and São Pedro do Ivai), and reduced in sandy- soil environments (Colorado, Goioerê and Astorga) (Table 2). For genotype RB005916

(G1), high stability but low yield was found (Figure 2A and B and Table 2).

The environments Bandeirantes and São Pedro do Ivai contributed most to the GE interaction, that is, the instability was greatest, since the scores were the highest on the axes of interaction (Figure 2B). In turn, the more stable environments Astorga, Colorado and Goioerê had lower PCI1 scores (Figure 2B). Guerra et al. (2009) reported that environmental stability indicates the reliability of genotype ranking in a given test environment, in relation to the average ranking of the tested environments. Based on this definition, the greater stability of the locations Colorado, Goioerê and Astorga than of Bandeirantes and São Pedro do Ivai suggests that the genotype classification of the former group should have lower standard deviation of genotype performances than the classification in other production environments.

Genotypes and environments with the same sign in the AMMI2 biplot (Figure 2B) must interact positively and if the signs are opposite, negatively (Duarte and Venkovsky 1999). Guerra et al. (2009) and Verissimo et al. (2012) identified genotypes and environments with same-sign PCI scores, with positive specific interactions for sugarcane. The classification of genotypes and environments established by Oliveira et al. (2003) and Silva et al. (2012) for soybean and carrot, respectively, was the same.

The environments Goioerê and Colorado lie very close to each other (Figure 2B) within the same quadrant and with the same sign, indicating similar genotype yields. The

proximity of genotype RB005991 (G9) to environments Goioerê and Colorado indicates a specific genotype adaptability to these environments.

The results of production environments with low GE interaction, as in Colorado and Goioerê, can be extrapolated to other environments. These can be used, for example, in the early stages of a sugarcane breeding program, using a large number of genotypes (seedlings) planted without replications and at only one location.

Conversely, highly instable production environments, i.e., with high GE interaction, as for example São Pedro do

Ivaí and Bandeirantes, should be used in genotype competition trials, for facilitating the selection of superior plants.

CONCLUSIONS

The stability and adaptability of GGE biplot and AMMI indicated the same genotypes RB006970, RB855156 and RB855453 as the most productive in tons of sugar per hectare (TSH) and also indicated São Pedro do Ivaí as the environment with the greatest effect of GE interaction. The percentage of explanation of the sum of squares was high by both methods, with a small advantage of the AMMI over the GGE Biplot analysis.

Avaliação de genótipos de cana-de-açúcar e ambientes de produção no Paraná via GGE Biplot e AMMI

Resumo – O objetivo deste trabalho foi avaliar genótipos de cana-de-açúcar, considerando toneladas de pol por hectare (TPH), estratificando cinco ambientes de produção no Paraná. Foram analisados 20 genótipos e dois padrões, em três safras consecutivas. Os métodos estatísticos utilizados foram AMMI e GGE Biplot. O GGE Biplot agrupou os locais em dois mega-ambientes e apresentou quais genótipos estiveram entre os melhores para cada mega-ambiente, facilitando a seleção dos genótipos superiores. Outra vantagem do GGE Biplot foi a representação do genótipo e do ambiente ideal, que serviram de referência para a avaliação dos genótipos e para escolha de ambientes com maior interação GxE. Ambos os modelos, mostraram que os genótipos mais produtivos em TPH, foram: RB006970, RB855156 e RB855453 e que o ambiente São Pedro do Ivaí apresentou maior interação GxE. Ambas metodologias apresentaram elevada porcentagem de explicação das soma dos quadrados, tendo a metodologia AMMI uma pequena vantagem sobre o GGE Biplot.

Palavras-chave: Saccharum spp., adaptabilidade, estabilidade, estratificação ambiental.

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