



Relationships between methods of variety adaptability and stability in sugarcane

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ABSTRACT. The identification and recommendation of superior genotypes is crucial for the growth of industrial crops, and sugarcane breeding performs a vital role by developing more productive cultivars. The study of genotype x environment interaction has been an essential tool in this process. Thereby, the purpose of this study was to investigate the relationship between methods of adaptability and stability in sugarcane. Data were collected from trials using a randomized block design with three repetitions and 15 clones of sugarcane in nine environments in the State of Minas Gerais, Brazil. Methodologies based on analysis of variance, linear regression, multivariate analysis, nonparametric statistics, and mixed model were used. The methods of Lin and Binns, Annicchiarico, and harmonic mean of relative performance of genotypic values (MHPRVG) were similar in their classification of genotypes. The additive main effect and multiplicative interactions (AMMI) and Wricke methods tended to select the most stable genotypes; however,

genotypes were less productive, coinciding with the stability parameter of Eberhart and Russell. The MHPRVG method is preferred over the methods of Lin and Binns and Annicchiarico because it includes the concepts of productivity, adaptability, and stability, and it provides direct genetic values of individuals. The use of the MHPRVG and Eberhart and Russell methods is recommended because the combination of these methods is complementary and leads to greater accuracy in the identification of genotypes of sugarcane for different environments.

Key words: Genotype x environment interaction; Sugarcane breeding; Mixed model; Multi-environment trials; *Saccharum* spp

INTRODUCTION

The production of sugarcane plays a crucial role in Brazil's economy, and its importance has been growing, especially with the interest in obtaining renewable energy sources. In the 2011/2012 harvest, sugarcane was cultivated on about 9 million hectares, from which about 560 million tons of sugarcane was produced, which corresponds to an average yield of 63 tons per hectare (CONAB, 2012). To meet the growing global demand for sugar and ethanol, it is necessary not only to incorporate new areas of production but also increase productivity.

Sugarcane breeding performs a vital role by developing more productive cultivars. The breeding program of sugarcane, Rede Interuniversitária para o Desenvolvimento do Setor Sucroalcooleiro (RIDESA), developed varieties with the letters RB (Republic of Brazil) for the different environments of Brazil, thus contributing to the growth of the sugarcane agribusiness nationally. Among the varieties released by RIDESA, cultivar RB867515 is currently the most widely grown in various regions of Brazil, covering 22% of the national area (Barbosa et al., 2012; dos Santos et al., 2012).

The economic return provided by this crop depends heavily on the cultivar productivity. Cultivars help maintain production over several years. Thus, the steps that are used to assess, identify, and recommend superior genotypes are crucial for the growth of industrial crops. The study of genotype x environment (GE) interaction has been an essential tool in this process because it analyzes the existence of differential behavior of genotypes in different environments (Verissimo et al., 2012). If there is a complex GE interaction, one seeks to find the performance of genotypes for adaptability and stability. Adaptability refers to the ability of the genotypes to advantageously harness the environmental stimulus, and stability refers to a highly predictable behavior of the genotypes to environmental changes (Cruz et al., 2012).

Therefore, different procedures have been used to evaluate the stability and adaptability in breeding programs. Deciding which method is more efficient to design genotypes that are adaptive and stable is not always an easy task. Different methods have been compared using different crops such as soybean (Rocha et al., 2006), bean (Pereira et al., 2009), wheat (Mohammadi and Amri, 2008), popcorn (Scapim et al., 2010), and rubber tree (Gouvêa et al., 2012). According to Cargnelutti Filho et al. (2007) methods can be arranged in classes: those based on analysis of variance, linear regression, multivariate analysis, and nonparametric statistics. The methods of Wricke (1965), Eberhart and Russell (1966), additive main effect and multiplicative interactions (AMMI) (Zobel et al., 1988), and Lin and Binns (1988) are exam-

ples of each class, respectively. In addition, there are also mixed model methodologies, such as the method of harmonic mean of the relative performance of genotypic values (MHPRVG), which is recommended by Resende (2007a).

Because several methods have been used to study the adaptability and stability in sugarcane and few articles have reported comparisons between methods that belong to different classes, such a study is required. Thus, the objective of this study was to investigate the relationship between different methods of adaptability and stability in sugarcane.

MATERIAL AND METHODS

The experiments were conducted in a randomized complete-block design with three replications and 15 genotypes. The trials were established between February and March 2004. The experimental unit consisted of four rows that were 10 m long with a spacing of 1.40 m between rows and a distribution of 18 buds per linear meter that were planted manually. The locations (Minas Gerais State, Brazil) are described in Figure 1.

The sugarcane stalks were harvested in August 2005 (plant cane) and in the same

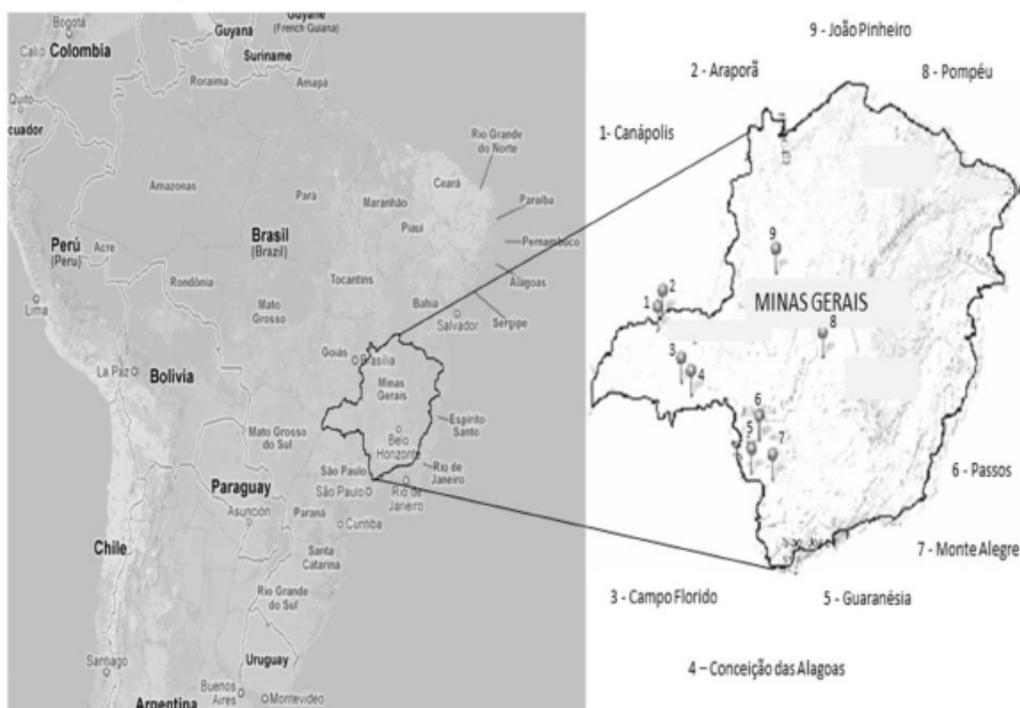


Figure 1. Locations (Minas Gerais State, Brazil) where the experiments were conducted with 15 genotypes of sugarcane in the crop seasons 2004/2005 and 2005/2006.

month in 2006 (first ratoon). Weighing was done in the field using a dynamometer. From the values of the weight of stalks (kg) per plot, tons of stalks per hectare (TSH) were estimated.

The pol content (PC) was obtained from juice analysis of 10 stalks from each plot. Therefore, the variable ton of pol per hectare (TPH) was obtained as follows: $TPH = (TSH \times PC)/100$.

The analyses were performed using the mean values of TPH that were obtained from the plant cane and first ratoon. The analysis of variance was performed considering the effect of genotype as fixed and that of environment as random, according to the following statistical model: $Y_{ijk} = m + B/E_{jk} + G_i + E_j + GE_{ij} + \varepsilon_{ijk}$, where Y_{ijk} represents the i th genotype in the j th environment and the k th block, m is the overall mean, B/E_{jk} corresponds to the block within the j th environment in the k th block, G_i is the effect of the i th genotype, E_j is the effect of the j th environment, GE_{ij} is the effect of interaction of the i th genotype with the j th environment, and ε_{ijk} is the effect of experimental error. The combined analysis of variance was performed after determining the homogeneity of the residual mean squares, where the ratio between the highest and lowest residual mean square was not more than seven (Cruz et al., 2012).

The analysis of adaptability and stability were performed using the methods by Wricke (1965), Annicchiarico (1992), Eberhart and Russell (1966), Lin and Binns (1988), AMMI (Zobel et al., 1988), and MHPRVG (Resende, 2007a). The first three methods used the statistical GENES software (Cruz, 2006) of the Universidade Federal de Viçosa (UFV). The SAS software (SAS Institute, 2002) was used for AMMI analysis, and the Selegen-REML/BLUP software (Resende, 2007b) of the Brazilian Agricultural Corporation EMBRAPA was used for the other two methods.

The mean of stability of genotypes by the Wricke (1965) method was estimated by $w_i = \sum_{j=1}^n (g_e)_{ij}^2$, using $(g_e)_{ij} = Y_{ij} - \bar{Y}_i - \bar{Y}_j - \bar{Y}$, where Y_{ij} is the mean of genotype i in environment j , \bar{Y}_i is the mean of genotype i in all environments, \bar{Y}_j is the mean of environment j for all the genotypes, \bar{Y} is the general mean, g is the number of genotypes accessed, and e is the number of environments.

Annicchiarico (1992) proposed the calculation of a risk index for each genotype (I_i) as a measure of stability, which is given by $I_i = Y_i - Z(1 - \alpha)S_i$, where I_i is the confidence index (%), Y_i is the average of the genotype i expressed as a percentage, Z is the percentile $(1 - \alpha)$ of the cumulative normal distribution function, and S_i is the standard deviation of earnings. The confidence interval was 75%, or $\alpha = 0.25$.

The model used for Eberhart and Russell (1966) analysis was: $Y_{ij} = \beta_0 + \beta_1 I_j + \sigma_{ij}^2 + e_{ij}$, where Y_{ij} is the observed mean of genotype i in environment j , β_0 is the general mean of genotype i , β_1 is the coefficient of regression of genotype i , I_j is the environmental index j , σ_{ij}^2 is the deviation of the regression of genotype i in environment j , and e_{ij} is the mean error associated with the average. The environmental index was calculated by $I_j = \bar{Y}_j - \bar{Y}$, with $\sum_{j=1}^n I_j = 0$, where n is the number of environments.

Lin and Binns (1988) used the following estimator of phenotypic stability: $P_i = \sum_{j=1}^n (X_{ij} - M_j)^2 / 2n$, where P_i is the index of superiority of the i th cultivar, X_{ij} is the yield of the i th cultivar at environment j , M_j expresses the maximum response obtained among all cultivars at environment j , and n represents the number of environments. This expression was partitioned in $P_i = \left[n(X_i - \bar{M})^2 + \sum_{j=1}^n (X_{ij} - \bar{X}_i - M_j + \bar{M})^2 \right] / 2n$, where \bar{X}_i is the mean yield of cultivar i obtained in n environments, and \bar{M} is the mean of the maximum responses of all cultivars in all environ-

ments. The first term of the equation represents the sum of squares related to the genetic effect, and the second term represents the sum of squares of the GE interaction.

The AMMI method, as described in Zobel et al. (1988) used the following statistical model: $Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \alpha_{ik} y_{jk} + r_{ij} + \varepsilon_{ij}$, where Y_{ij} is the mean response of genotype i in the environment j , μ is the overall mean, g_i is the fixed effect of genotype i ($i = 1, 2, \dots, g$), e_j is the random effect of environment j ($j = 1, 2, \dots, e$), ε_{ij} is the average experimental error, the GE interaction is represented by the factors, λ_k is a unique value of the k th interaction principal component analysis (IPCA) ($k = 1, 2, \dots, p$, where p is the maximum number of estimable main components), α_{ik} is a singular value for the i th genotype in the k th IPCA, y_{jk} is a unique value of the j th environment in the k th IPCA, r_{ij} is the error for the GE interaction or AMMI residue (noise present in the data), and k is the characteristic non-zero roots where $k = [1, 2, \dots, \min(G - 1, E - 1)]$.

The method described by Resende (2007a) refers to a simultaneous measurement of the yield, stability, and adaptability to use the MHPRVG, which is given by $MHPRVG = n / \sum_{j=1}^n \frac{1}{V_{gij}}$, where n is the number of environments where the clone i was evaluated, and V_{gij} is the genotype value of the clone i in environment j ; it is expressed as a ratio of the local mean. Model 54 from Selegen-RELM/BLUP software (Resende, 2007b) was used. The statistical model was given by $Y = Xr + Zg + Wi + e$, where Y is the data vector, r is the vector of repetition effects (assumed to be fixed) added to the overall mean, g is the vector of genotypic effects (assumed to be random), and i is the vector or errors (random). The capital letters represent the incidence matrices for these purposes.

The statistics of stability and adaptability were compared using the Spearman correlation. The parameters analyzed were: (i) ecovalence (ω_j) from the Wricke method, (ii) confidence index (I_j) from Annicchiarico, (iii) variance of absolute values of regression deviations (σ_{di}^2) and coefficient of regression of genotype (β_i), (iv) the index of superiority (p_i) by Lin and Binns (1988), (v) the weighted average of the absolute scores (AMMI) of the two first principal components for each genotype weighted by the percentage of variation explained by each component, and (vi) MHPRVG. The SAS CORR procedure (SAS Institute, 2002) was used in the Spearman analysis of correlation.

RESULTS AND DISCUSSION

Significant differences for the source of genotypic variation were observed at 1%. The environment was significant at the 1% probability, indicating the existence of variability among locations. These significant differences between the locations can be explained by discrepancies in soil and climate conditions in the environments that were evaluated. Significant differences were observed at 1% probability by the F-test for GE interaction. This indicates that specifically adapted genotypes in more specific environments can be identified, which therefore justifies a detailed study of the adaptability and stability of genotypes (Table 1).

The experimental coefficient of variation was 10.1%, and the ratio between the largest and smallest mean square residual was 2.9 (Table 1). According to Cruz et al. (2012), the approximate ratio of 7:1 between the highest and lowest mean square residual can be used as a threshold to assume homogeneity of error variances, allowing the combined analysis of variance from data of different environments.

The classifications of genotypes by different methods for adaptability and stability, as well as the order of TPH, are shown in Table 2. The adaptability parameter (β_i) from Eberhart

and Russell (1966) was verified, and only two clones (RB937570 and RB957689) showed specific adaptability to favorable environments because their β_1 were significantly different ($P < 0.05$) from one. Using the stability parameter (σ_{di}^2), seven clones (RB987935, RB935641, RB935686, RB987934, RB945065, RB957689, and RB977625) showed low stability, i.e., statistically different from zero using the F-test ($P < 0.05$). Genotype RB957689 was the only clone with simultaneous specific adaptability and low stability.

Table 1. Analysis of variance, mean, coefficients of variation (CV), and the coefficient of the relationship between the larger and lower mean square error (MSE) for the variable tons of pol per hectare (TPH) of 15 genotypes in nine environments in Minas Gerais State, Brazil, in the crop seasons of 2005 and 2006.

Source of variation	Degree of freedom	Mean square
Blocks/environments	18	5.8
Environments (E)	8	534.7**
Genotypes (G)	14	50.0**
GE	112	7.6**
Error	252	3.4
Means (tons/ha)		18.2
CV (%)		10.1
Larger MSE/lower MSE		2.9

**P < 0.01 by the F-test.

Table 2. Stability and adaptability statistics from sugarcane TPH in nine environments.

Genotypes	Statistics ¹															
	TPH mean	Class ²	β_1	Class	σ_{di}^2	Class	p_i	Class	AMMI	Class	ω_i	Class	I_i	Class	MHPRVG	Class
RB987935	20.71	1st	1.01	W	2.21*	L	1.74	2nd	6.36	13	8.25	10	111.76	1st	20.57	1st
RB867515	20.44	2nd	1.2	W	0.46	H	1.64	1st	4.13	8	5.32	6	110.26	2nd	20.27	2nd
RB935641	19.81	3rd	0.95	W	3.49*	L	4.53	3rd	7.36	14	11.46	15	106.22	3rd	19.71	3rd
RB925211	19.16	4	1.14	W	0.89	H	5.27	4	5.47	11	5.61	7	102.93	4	19.05	4
RB935686	18.87	5	0.97	W	2.25*	L	5.68	5	5.41	10	8.38	11	101.58	5	18.82	5
RB937570	18.65	6	1.24*	S	0.52	H	7.17	6	2.44	3rd	6.05	8	99.92	6	18.54	6
RB987934	18.24	7	0.8	W	2.12*	L	9.67	7	6.27	12	9.36	13	98	7	18.26	7
RB956911	17.87	8	0.89	W	0.7	H	9.72	8	4.03	7	4.95	5	96.5	8	17.9	8
RB945065	17.62	9	0.88	W	2.27*	L	11	9	3.12	6	8.85	12	94.85	9	17.65	9
RB72454	17.22	10	0.89	W	0.14	H	12.57	10	2.61	4	3.55	4	93.25	10	17.27	10
RB957689	17.08	11	1.22*	S	1.24*	L	13.51	11	4.26	9	7.52	9	90.07	14	16.97	11
RB977625	16.88	12	0.84	W	3.06*	L	15.89	15	8.78	15	11.25	14	90.07	15	16.93	12
RB977619	16.85	13	1.08	W	-0.16	H	14.02	12	2.9	5	2.65	1st	90.47	12	16.85	13
RB977508	16.75	14	0.89	W	0.1	H	15.17	14	2.38	2nd	3.43	3rd	90.75	11	16.76	15
RB987905	16.75	15	1	W	0.23	H	14.99	13	1.84	1st	3.36	2nd	90.24	13	16.79	14

¹ β_1 and σ_{di}^2 = Eberhart and Russel (1966); p_i = Lin and Binns (1988); AMMI = Zobel et al. (1988); ω_i = Wricke (1965); I_i = Annicchiarico (1992); MHPRVG = Resende (2007); ²Class = classification or order; W = wide adaptability; S = specific adaptability to favorable environment; H = high stability; L = low stability; *, P < 0.05 by the t-test for the hypothesis $\beta_1 = 1$ and by the F-test $\sigma_{di}^2 = 0$.

The methods of Lin and Binns (1988), Annicchiarico (1992), and MHPRVG (Resende, 2007a) were similar in their classification of genotypes, with 100% similarity for the first 10 positions. Furthermore, the same clones were in the first 10 positions relative to TPH (Table 2). The AMMI method (Zobel et al., 1988) classified the genotypes RB987905, RB977508, and RB937570 in first, second, and third place, respectively. These clones were the 15th, 14th, and 6th position relative to TPH (Table 2). A similar trend was observed by the method proposed by Wricke (1965), where the last three genotypes allocated positions in relation to TPH

that were classified as the most stable for the three parameters (Table 2).

The similarities between the methods were further evaluated using Spearman correlation (Table 3). All of the pairwise correlations between the methods of Lin and Binns (1988), Annicchiarico (1992), and MHPRVG were positive and of high magnitude ($P > 0.93$). Additionally, these methods were also highly positively correlated with TPH ($P = 0.9714$, $P = 0.9429$, and $P = 0.9964$, respectively). The AMMI method obtained significant negative correlation ($P = -0.5535$) with the MHPRVG method and the TPH ($P = -0.5571$). Significant positive correlation was shown with the stability parameter (σ_{di}^2) of Eberhart and Russell (1966) and the Wricke's method (1965), with magnitudes equal to 0.8218 and 0.7929, respectively. The latter method, in turn, also demonstrated high correlation ($\rho = 0.9513$) with parameter σ_{di}^2 . Therefore, the AMMI and Wricke (1965) methods tended to select the most stable genotypes, coinciding with the stability parameter (σ_{di}^2) of Eberhart and Russell (1966) (Table 3).

Table 3. Correlation (ρ) between stability and adaptability statistics from TPH in sugarcane.

	β_1	σ_{di}^2	p_i	AMMI	ω_i	I_i	TPH
MHPRVG	-0.2722	-0.4010	0.9750**	-0.5535*	-0.4643	0.9357**	0.9964**
β_1		-0.3841	-0.3430	-0.1748	-0.2677	-0.2124	-0.2600
σ_{di}^2			-0.2540	0.8218**	0.9513**	-0.2312	-0.3992
p_i				-0.4036	-0.3214	0.9643**	0.9714**
AMMI					0.7929**	-0.3464	-0.5571*
ω_i						-0.2714	-0.4678
I_i							0.9429**

*, **Significant at 5 and 1% probability, respectively. β_1 and σ_{di}^2 = Eberhart and Russel (1966); p_i = Lin and Binns (1988); AMMI = Zobel et al. (1988); ω_i = Wricke (1965); I_i = Annicchiarico (1992); MHPRVG = Resende (2007).

Similar conclusions were reported by Silva and Duarte (2006) in soybean, where the AMMI analysis showed stronger correlation with the Wricke (1965) and Eberhart and Russell (1966) methods. According to these authors, the correlation between these methods was due to the statistical principle similarity between the AMMI and Wricke (1965) methods, which are based on the genotypic contribution to the GE interaction, which also coincides with the agronomic stability parameter (σ_{di}^2) and Eberhart and Russell (1966) method. Furthermore, correlations between these same methods were reported by Gouvêa et al. (2012) and Mohammadi and Amri (2008) in evaluations with rubber tree and wheat, respectively. Scapim et al. (2010) also reported highly positive correlations between the method of Wricke (1965) and the parameter (σ_{di}^2) of Eberhart and Russell (1966) in popcorn.

Bajpai and Kumar (2005) stated that better results can be achieved using the AMMI method than models based on regression because the component of variability due to the GE interaction tends to be quite high in sugarcane. Regression models describe the suitable behavior of genotypes throughout the different environments and is only valid when the genotype response is linear. Therefore, the adaptability parameter of Eberhart and Russell (1966) did not correlate with any of the other methods (Table 3) because of the assumption of linearity.

Figure 2 shows the trend of the AMMI and Wricke (1965) methods, and it indicates that genotypes that are less productive as more stable. The classification indicates that as productivity increased, the parameters of the clones decreased. However, the opposite is observed in relation to the methods of Lin and Binns (1988), Annicchiarico (1992), and MHPRVG because these methods tend to select the most productive genotypes.

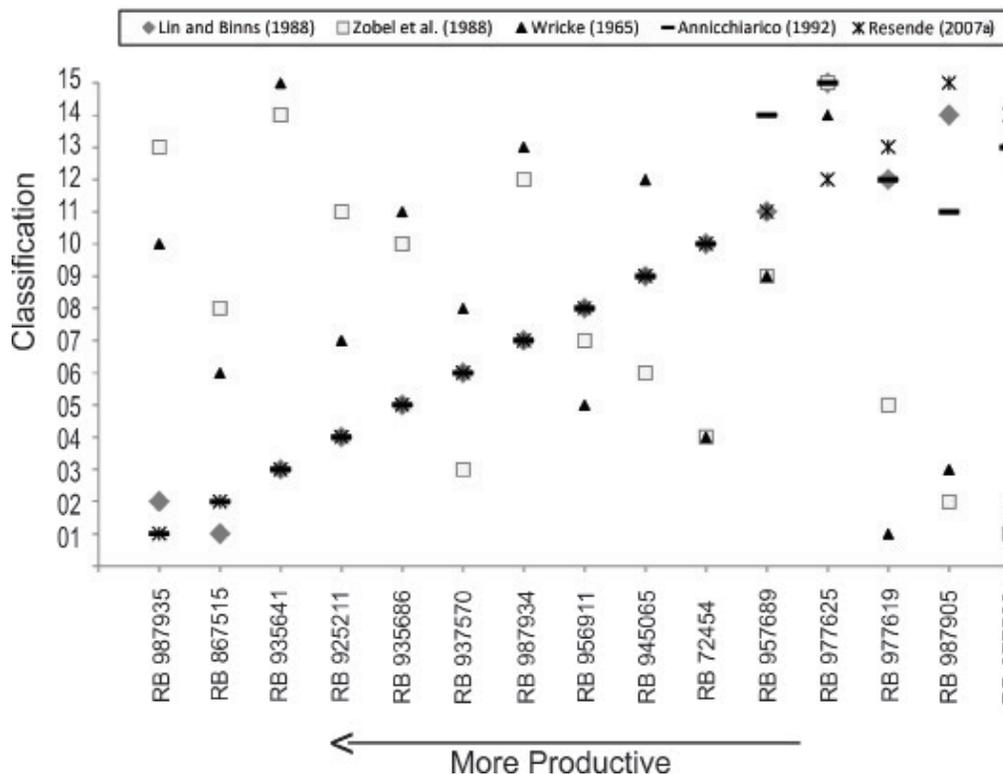


Figure 2. Classification plot of genotypes according to the methods of Lin and Binns (1988), Zobel et al. (1988), Wricke (1965), Annicchiarico (1992), and Resende (2007a).

In Figure 2, all clones were ranked at least once below the fifth place for the methods that were used, with the exception of genotypes RB977625 and RB957689. The display of the absolute values of the parameters of Eberhart and Russell (1966) in Figure 3 shows that the genotype RB977625 presented low stability, and genotype RB957689 presented low stability and adaptability specifically. Considering the statistical significance of the parameters, clones RB867515, RB925211, RB956911, RB72454, RB977619, RB977508, and RB987905 were the genotypes that simultaneously have wide adaptability and high stability (Figure 3). Among these, we highlight the merits of RB867515 and RB925211, which were assigned second and fourth place in TPH, respectively.

In this study, we noticed that the methods of Lin and Binns (1988), Annicchiarico (1992), and MHPRVG were highly correlated, indicating roughly similar results. Carbonell et al. (2007) reached the same conclusion when comparing these methods in evaluations of common bean lines. Bastos et al. (2007) and Oliveira et al. (2005) also showed similar results with sugarcane when they compared the MHPRVG, Lin and Binns (1988), and Silva and Duarte (2006) methods, and when they used soybeans to compare the Annicchiarico (1992) and Lin and Binns (1988) methods.

Yet, according to Bastos et al. (2007), Carbonell et al. (2007), and Oliveira et al.

(2005), the MHPRVG method has the advantage of providing results on the same measurement scale as the character evaluation, which can be directly interpreted as genetic values. Another advantage is that the method penalizes the instability of genotypes through environments and simultaneously capitalizes responsiveness (adaptability) when the environment improves. This method is based on predicted genotypic values via mixed models and aggregates productivity, stability, and adaptability in a single statistic.

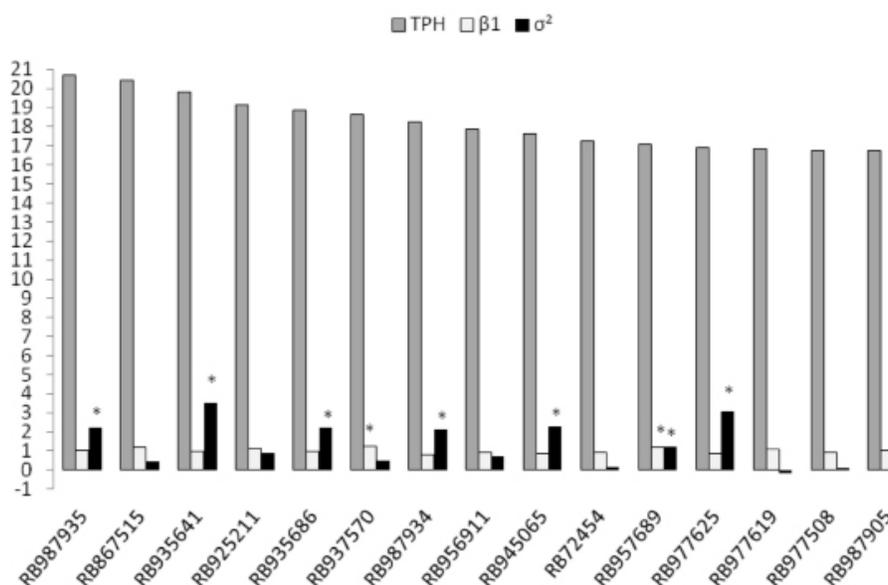


Figure 3. Comparison between ton of pol per hectare (TPH) and absolute values of the adaptability parameter (β_1) and the stability parameter (σ^2) (Eberhart and Russel, 1966) in 15 genotypes of sugarcane in nine environments. *, $P < 0.05$ by the t -test for the hypothesis $\beta_1 = 1$ and by the F-test $\sigma^2 = 0$.

Thus, it is clear that to improve the efficiency of sugarcane genotype adaptability and stability to different environments, it is important to use different methods in a complementary analysis. Therefore, we concluded that the MHPRVG method is preferable over the methods of Lin and Binns (1988) and Annicchiarico (1992) because it has the advantage of encompassing the concepts of productivity, adaptability, and stability, and it provides direct genetic values of individual genotypes. Compared to other methods, the Eberhart and Russell (1966) method is recommended because its parameter stability was similar to that of the AMMI and Wricke (1965) methods; however, its adaptability parameter produced parameters that were different from those of other methods, which is indicated by their low correlations. Thus, the MHPRVG (Resende, 2007a) and Eberhart and Russell (1966) methods are recommended.

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