

CORRELATION AMONG PREDICTED GENOTYPIC VALUES AND ADAPTABILITY AND STABILITY ESTIMATES OF SUGARCANE CLONES IN A MIXED MODELS CONTEXT

CORRELAÇÃO ENTRE VALORES GENOTÍPICOS PREDITOS E ESTIMATIVAS DE ADAPTABILIDADE E ESTABILIDADE DE CLONES DE CANA-DE-AÇÚCAR NO CONTEXTO DE MODELOS MISTOS

Irlane Todelo BASTOS¹
Márcio Henrique Pereira BARBOSA²
Marcos Deon Vilela de RESENDE³
Cássia Ângela PEDROZO⁴
Cristiane Gamarano MELO⁵
Luiz Alexandre PETERNELLI⁶
Paulo Mafra de Almeida COSTA⁷
Clariana Valadares XAVIER⁷
David Carlos Ferreira BAFFA⁸

ABSTRACT

The objective of the present study was to apply the mixed model theory to predict the genotypic values and to estimate the adaptability and stability parameters of sugarcane clones evaluated in augmented blocks designs in several environments and to assess the correlation among these predicted and estimated values. Methodologies by Wricke (Wricke & Webber, 1986), Eberhart & Russell (1966) and Carneiro (1998) were used. The predicted genotypic values free from genotype x environment interaction were strongly correlated with the parameters estimated by the Carneiro's methodology, moderately correlated with adaptability parameter (β_{ii}) of Eberhart and Russell and weakly correlated with the Wricke ω_i (%) parameter and with R^2_i (%) parameter of Eberhart and Russell. The Wricke ω_i (%) parameter only presented significant correlation with the R^2_i (%) parameter of Eberhart and Russell, indicating the similarity of both in assessing the stability of genotypes. These results show that the predicted genotypic values free from genotype x environment interaction effects correlate better with adaptability than with stability.

Key-words: sugarcane trials; augmented blocks; genotype by environment interaction.

RESUMO

O presente trabalho teve por objetivo aplicar a teoria de modelos mistos para prever os valores genotípicos e estimar os parâmetros de adaptabilidade e estabilidade de clones de cana-de-açúcar avaliados no delineamento de blocos aumentados em vários ambientes e, também, avaliar a correlação existente entre estes valores preditos e, ou estimados. Foram utilizadas as metodologias de Wricke (Wricke & Webber, 1986), Eberhart & Russell (1966) e Carneiro (1998). Os valores genotípicos preditos livres dos efeitos da interação genótipos x ambientes mostraram-se fortemente correlacionados com os parâmetros estimados pela metodologia de Carneiro, moderadamente correlacionados com os parâmetros de adaptabilidade (β_{ii}) do método de Eberhart and Russell e fracamente correlacionados com o parâmetro ω_i (%) de Wricke e com o parâmetro R^2_i (%) de Eberhart and Russell. O parâmetro ω_i (%) apresentou correlação significativa apenas com o parâmetro R^2_i (%) de Eberhart e Russell, indicando a semelhança de ambos em avaliar a estabilidade dos genótipos. Esses resultados revelam que os valores genotípicos preditos livres dos efeitos da interação genótipos x ambientes correlacionam-se mais com a adaptabilidade do que com a estabilidade.

Palavras-chave: ensaios de cana-de-açúcar; blocos aumentados; interação genótipo x ambiente.

1 Engenheira Agrônoma, Professora da Faculdade Vértice, Matipó, MG – Brasil. E-mail: irlanecosta@ig.com.br.

2 Engenheiro Agrônomo, Professor do Departamento de Fitotecnia da Universidade Federal de Viçosa (UFV). Campus da UFV, Departamento de Fitotecnia, 36570-000, Viçosa, MG – Brasil. E-mail: barbosa@ufv.br. Autor para correspondência.

3 Engenheiro Agrônomo, Pesquisador da Embrapa Florestas, Viçosa, MG – Brasil. E-mail: marcos.deon@gmail.com.

4 Engenheira Agrônoma, Doutoranda em Genética e Melhoramento, Universidade Federal de Viçosa, Viçosa, MG – Brasil. E-mail: cassiapedrozo@yahoo.com.br.

5 Engenheira Agrônoma, Mestre em Genética e Melhoramento, Universidade Federal de Viçosa, Viçosa, MG – Brasil. E-mail: cristianegamarano@yahoo.com.br.

6 Engenheiro Agrônomo, Professor do Departamento de Informática da Universidade Federal de Viçosa, Viçosa, MG – Brasil. E-mail: petermelli@ufv.br.

7 Estudante de Agronomia, Universidade Federal de Viçosa, Viçosa, MG – Brasil. E-mail: paulomafra@gmail.com, clarianavaladares@yahoo.com.br.

8 Engenheiro Agrônomo, Mestrando em Genética e Melhoramento, Universidade Federal de Viçosa, Viçosa, MG – Brasil. E-mail: davidbaffa@yahoo.com.br.

INTRODUCTION

In sugarcane breeding programs, breeders carry out experiments with promising clones from local and regional improvement programs. These experiments are carried out in various sugar mills and distilleries and they are harvested three times on average (Ferreira et al., 2005) and the performance of the new clones is compared with the performance of widely commercially grown cultivars. These studies permit assessment of the magnitude of the genotype x location and genotype x harvests or years interactions, that are generally significant and influential on clone selection, and they also permit adaptability and stability studies.

Different methodologies to assess adaptability and stability have been developed and, or, improved. These are generally based on analysis of variance, linear regression, nonlinear regression, multivariate analysis and nonparametric statistics. Studies comparing these methodologies are common in the literature (Yadav et al., 2007; Silva Filho et al., 2008; Rosse et al., 2002). These comparisons are usually carried out by performing correlation among the estimates of parameters or, when possible, as in the case of regression or multivariate analyses, the efficiency of each method is assessed in terms of the ability of explaining the performance of the genotypes. This efficiency is evaluated by the fit of the regression equation to the observed data or by the fraction of interaction that is explained by model.

An alternative way of carrying out adaptability and stability analysis would be to use the predicted genotypic values (Resende, 2002; Oliveira et al., 2005; Bastos et al., 2007) obtained under models with genotype x environment effects, instead of the phenotypic means. The advantage of this approach is the fact that genotypic stability rather than phenotypic stability can be evaluated, which is a more precise and appealing approach.

A similar analysis in sugarcane would be important because currently the field data obtained from augmented blocks designs are analyzed using the mixed model methodology. According to Aguiar et al. (2000), there are few results concerning the efficiency of these designs in ordering the best treatments and, above all, in estimating the genetic and phenotypic parameters. Souza (1997) reported low precision in estimates of parameters using augmented blocks. However, this author concluded that the use of this design is only viable when the selection intensity is moderate.

Simulation studies varying the nature of the effects of blocks and treatments, to consider all the possible combinations among fixed and random combinations, suggested mixed models can improve the inference and, therefore, the success of breeding programs (Santos, 2000; Duarte & Venkovsky, 2001). Nowadays, advances in computation technology and the development of specialized computing programs have allowed the use the mixed model approach with greater ease.

Taking the genetic values as random

effects, they can be predicted using a mixed model methodology that combines the best linear unbiased estimation (BLUE) of fixed effects such environmental ones and best linear unbiased prediction (BLUP) of the random effects, such as genotypes and blocks effects.

Thus the objectives of this study were: i) to apply the mixed model theory to predict the genotypic values of sugarcane clones conducted in augmented blocks in several environments and ii) to assess the genotypic adaptability and stability of these clones and the correlation among these parameters, using the methodologies by Wricke (Wricke & Weber, 1986), Eberhart & Russel (1966) and Carneiro (1998) and also the correlation of these parameters with the predicted genotypic values free from genotype x environment interaction effects.

MATERIAL AND METHODS

The experimental areas selected for this study are representative of the main sugarcane producing regions in Minas Gerais State (Koffler et al., 1988). The clone and cultivar competition experiments were carried out in the following units at Minas Gerais State: Agropéu Distillery (AGR), Atenas Distillery (ATE), Alvorada do Bebedouro Distillery (DAB), WD Distillery (DWD), Passos Mill (UAP), Jatiboca Mill (UJA) and Triálcool Mill (UTR), located in the Pompéu, São Pedro dos Ferros, Guaranésia, João Pinheiro, Passos, Uracânia, Canápolis districts, respectively.

Each company where the experiments were set up was assumed as environment, totalizing seven environments for genotype adaptability and stability studies.

As regular treatments, 70 clones in stage III developed by the Sugarcane Genetic Breeding Program at the Federal University of Viçosa, in the Sugarcane Research and Breeding Center – CECA, located in Oratórios, MG were used.

The conventional planting procedure was performed with stalks with three or four buds, obtaining a density of 18 shoots per linear meter of drill. The experiments were set up in February and March 2001. Augmented blocks designs with five blocks were used. Two experiments in augmented blocks were established side by side in each location with the same clones and check varieties. The plots consisted of two 5.00 m long drills, without borders. Borders were only used around the experiments. The common treatments were the commercial varieties RB72454 and RB835486. The between row spacing was 1.40 m. The treatments were placed randomly in the blocks, and each block consisted of two controls and 14 new clones, totaling 16 treatments per block.

The assessments were carried out on the plant cane and first ratoon in 2002 and 2003, respectively. Manual harvesting was carried out at 17 months in the first cuts and at 12 months in the second. The procedures were: 1) three Brix readings in different stems, with the sample taken

at the fifth internode, counted from the base to the tip using a manual refractometer; 2) counting of the total number of stems per drill; 3) random sampling and weighing of 10 stalks per drill, using a dinamometer, discarding the tips. The Brix tons per hectare was calculated from this data and used for the statistical analyses.

The data standardization is recommended in group of experiments. This procedure excludes the scale effect of the studied characters and reduces the heterogeneity of the variances among environments. All the sampled data were standardized at the level of replication per environment using the formula (Resende, 2002):

$$Z_{ijk} = \hat{\mu}_e + (Y_{ijk} - \hat{\mu}_e) \times \frac{\hat{\sigma}_{\hat{f}}}{\hat{\sigma}_{fe}}$$

where: $\hat{\mu}_e$ is the mean of the experiment, $\hat{\sigma}_{\hat{f}}$ is the mean phenotypic standard deviation of all experiments and $\hat{\sigma}_{fe}$ is the phenotypic standard deviation of the experiment e.

After standardizing the data as a mean to remove the heterogeneity of variance across blocks and sites, the analyses to obtain the genotypic values were obtained by joint analysis across environments, using Selegen-REML/BLUP software (Resende et al., 1994; Resende, 2002). In these analyses the components of variance were estimated by the restricted maximum likelihood (REML) and the genotypic values were predicted by the best linear unbiased prediction (BLUP). The regular treatments (new clones) were taken as random effects and the checks were assumed as fixed effects, as they belong to different populations.

The standardized data of the clones evaluated in the augmented blocks design in several environments were analyzed according to following statistical model (Bastos et al., 2007):

$$y = Xr + Zg + Wb + H\theta + e,$$

where: y is the vector of data, r is the vector of environment and experiments fixed effects, g is the vector of clone random effects (predicted genotypic values) with $g \sim N(0, I\sigma_g^2)$, b is the vector of block random effects with $b \sim N(0, I\sigma_b^2)$, θ is the vector of clone x environment interaction random effects with $\theta \sim N(0, I\sigma_{\theta}^2)$ and e is the vector of errors with $e \sim N(0, I\sigma_e^2)$. X, Z, W and H are incidence matrices for r, g, b and θ , respectively (Resende, 2002).

The mixed model equations corresponding to mentioned model for estimation of random and fixed effects is given by:

$$\begin{bmatrix} XX & XZ & XW & XH \\ ZX & ZZ+A^{-1}\lambda_1 & ZW & ZH \\ WX & WZ & WW+D_2 & WH \\ HX & HZ & HW & HH+D_3 \end{bmatrix} \begin{bmatrix} \hat{r} \\ \hat{g} \\ \hat{b} \\ \hat{\theta} \end{bmatrix} = \begin{bmatrix} Xy \\ Zy \\ Wy \\ Hy \end{bmatrix}$$

where,

$$\lambda_1 = \frac{\sigma_g^2}{\sigma_g^2} = \frac{1-h^2-b^2-\theta^2}{h^2}; \quad \lambda_2 = \frac{\sigma_g^2}{\sigma_b^2} = \frac{1-h^2-b^2-\theta^2}{b^2}; \quad \lambda_3 = \frac{\sigma_g^2}{\sigma_{\theta}^2} = \frac{1-h^2-b^2-\theta^2}{\theta^2}$$

;

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_b^2 + \sigma_e^2 + \sigma_{\theta}^2}$$

: broad sense individual heritability in an experiment;

$b^2 = \sigma_b^2 / (\sigma_g^2 + \sigma_b^2 + \sigma_e^2 + \sigma_{\theta}^2)$: correlation due to common environment in the block;

$\theta^2 = \sigma_{\theta}^2 / (\sigma_g^2 + \sigma_b^2 + \sigma_e^2 + \sigma_{\theta}^2)$: proportion of the total phenotypic variance explained by the genotype x environment interaction;

σ_g^2 : genotypic variance among clones;

σ_b^2 : environmental variance among blocks;

σ_{θ}^2 : variance of the genotype x environment interaction;

σ_e^2 : residual variance.

After obtaining the predictions of genotypic values of the clones and clone x environment interaction effects by the joint analyses, a data file was set up for genotypic adaptability and stability studies based on the genotypic values in each environment given by: $\hat{y} = u + \hat{g} + \hat{\theta}$, where u is the general mean over all trials. The following methodologies were used for these analyses: Wricke (Wricke & Weber, 1986), Eberhart & Russell (1966) and differences regarding the weighted bi-segmented linear regression by coefficient of residual variation (Carneiro, 1998). The last methodology consisted of an adaptation of the methodology by Lin & Binns (1988) making it more efficient to analyze the genotype performance. The equation used in this methodology was:

$$P_{ig} = \frac{\sum_{j=1}^{f+d} (Y_{ij} - Y_{gj})^2 \times \frac{CV_j}{CVT}}{2f}$$

; general P_i statistics of the modified Lin & Binns (1988) method, considering all the environments;

$$P_{if} = \left[\frac{\sum_{j=1}^f (Y_{ij} - Y_{gj})^2}{2f} \right] \times \frac{CV_j}{CVT}$$

; P_i statistics of the modified Lin & Binns (1988) method, concerning to favorable environments and;

$$P_{id} = \left[\frac{\sum_{j=1}^d (Y_{ij} - Y_{gj})^2}{2d} \right] \times \frac{CV_j}{CVT}$$

; P_i statistics of the modified Lin & Binns (1988) method, concerning to unfavorable environments.

where: f is the number of favorable environments (positive environmental index including the value zero); d is the unfavorable environments (negative environmental index); Y_{gj} is the predicted genotypic value of genotype i in environment j; Y_{gj} is the response of hypothetical ideal genotype in environment j estimated by the bi-segmented model by Cruz et al. (1989): $E(Y_{gj}) = \beta_{0g} + \beta_{1g}I_j + \beta_{2g}T(I_j)$, where: b_{0g} is the value given so that the ideal

response is the maximum for all the environments, that is, the maximum genotypic value predicted in all the experiments; b_{1g} and b_{2g} are values set at 0.5 and 1.0, respectively, to reflect low response to the unfavorable environments ($b_{1g} = 0.5$), and response to favorable conditions ($b_{1g} + b_{2g} = 1.5$); I_j is the codified environmental index; $T(I_j) = 0$ if $I_j \leq 0$, and $T(I_j) = I_j - I_+$ if $I_j > 0$, and I_+ is the mean of the positive indexes. CV_j is the residual coefficient of variation of environment j and CVT is the summation of the coefficients of variation of all the environments.

The correlations among estimates of adaptability and stability parameters by mentioned methodologies and predicted genotypic values of clones were calculated by the Ordinal Spearman Correlation (STEEL et al., 1997).

All the biometric analyses referring to stability were carried out with the help of the computer program in genetics and statistics GENES (Cruz, 2001).

RESULTS AND DISCUSSION

The methodology by Wricke classified the clone RB937568 as the most stable (Table 1). However, considering a 20% selection rate, this clone would not be selected for the next breeding stage because it was not among the first 14 clones (excluding the controls) with greater genotypic values predicted by the joint analysis across all environments. This fact has been reported as a disadvantage of this methodology that tends to classify the genotypes with lower predicted genotypic values as being more stable. Thus, considering stability and high genotypic value, clones RB957697, RB967603, RB967623 and SP86-42 were selected from the 14 most stable. Regarding the stability presented by the controls, it was detected that RB72454 was much more stable ($\omega_i = 0.65\%$) than RB835486 ($\omega_i = 3.53\%$).

TABLE 1 – Estimates of the predicted genotypic values ($u + \hat{g}$) free from genotype x environment interaction, genotypic adaptability and stability parameters according to the methodologies by Wricke (Wricke and Weber, 1986), Eberhart and Russel (1996) and Carneiro (1998) for the characteristic Brix tons per hectare (TBH) and the ranking of 20 sugarcane genotypes for these parameters, assessed in seven environments in augmented blocks experimental designs. Genotypic values were predicted by the mixed model methodology, using the REML/BLUP procedure of the Selegen-Reml/Blup software.

Genotype	BLUP		Wricke and Weber		Carneiro						Eberhart and Russell			
	$u + \hat{g}$	RK**	ω_i (%)	Rk	P_{ig}	Rk	P_{if}	Rk	P_{id}	Rk	$\hat{\beta}_{1i}$	Rk	R^2_i	Rk
RB72454	24.90	20	0.65	10	27.40	14	18.80	26	33.90	12	1.01	36	96.90	24
RB835486	22.10	60	3.53	70	34.50	63	28.60	67	38.90	45	0.68*	72	85.90	69
RB845210	24.10	31	0.65	11	30.90	43	20.40	39	38.80	44	1.06	23	97.40	19
RB855595	24.40	25	0.74	13	29.20	24	19.60	32	36.40	25	1.03	29	96.70	26
RB867515	26.60	4	1.04	28	24.70	4	13.80	2	32.90	9	1.16	13	98.00	12
RB896391	25.00	18	2.01	61	28.50	20	16.90	13	37.10	30	1.22	2	96.70	25
RB896406	25.60	13	1.23	36	28.40	19	15.70	8	38.00	39	1.17	12	97.60	17
RB928064	26.60	5	1.05	30	25.90	8	14.30	3	34.60	16	1.17	10	98.40	8
RB928168	23.50	47	2.68	65	30.10	33	25.80	60	33.30	10	0.76	68	88.20	68
RB937553	22.50	55	0.88	21	32.90	54	22.70	53	40.60	55	0.97	43	95.60	40
RB937568	23.80	39	0.17	1	30.80	41	21.90	45	37.50	35	0.97	45	99.20	1
RB937570	26.00	10	1.26	39	26.60	11	15.20	6	35.20	19	1.18	9	98.00	14
RB937638	21.10	66	1.09	31	37.40	66	24.80	57	46.80	70	1.00	37	94.90	49
RB947501	24.10	32	1.55	52	31.20	44	17.70	21	41.30	58	1.15	16	96.00	34
RB947506	23.00	50	1.23	37	33.20	56	17.80	22	44.70	65	1.19	8	98.10	11
RB947519	23.60	43	1.55	53	30.70	39	25.20	58	34.80	17	0.74	70	98.50	6
RB947520	28.00	1	1.53	51	22.70	1	12.50	1	30.40	4	1.11	19	94.90	46
RB947532	24.50	23	2.19	63	28.90	22	17.30	18	37.60	37	1.17	11	94.50	50
RB947547	19.70	69	1.00	26	39.10	70	29.50	69	46.30	69	0.84	64	96.60	28
RB947565	18.80	70	1.84	60	42.60	71	29.40	68	52.60	71	1.02	32	91.90	61
RB947568	20.90	67	0.83	18	37.50	67	27.10	64	45.30	66	0.89	58	96.50	29
RB947575	24.50	24	1.75	59	29.30	27	19.60	33	36.50	26	1.07	22	93.20	59

RB947577	25.00	19	1.57	54	27.70	15	15.90	9	36.60	28	1.13	17	95.30	43
RB947583	23.00	51	0.99	25	32.40	48	23.40	55	39.10	47	0.87	60	96.00	35
RB947596	24.00	34	1.18	33	30.70	40	19.80	35	38.90	46	0.97	42	94.20	53
RB947603	24.20	29	0.40	4	29.40	28	21.10	43	35.60	20	0.93	51	98.30	9
RB947609	22.40	56	1.52	50	33.40	58	28.00	66	37.40	33	0.77	67	96.10	32
RB947624	23.90	37	0.47	6	30.70	38	20.60	41	38.20	41	1.03	27	98.00	13
RB947625	21.60	64	2.30	64	35.70	65	30.30	70	39.90	50	0.75	69	91.60	64
RB947639	21.30	65	2.17	62	37.80	68	26.80	63	46.10	68	0.99	40	90.10	66
RB947643	24.80	22	3.33	68	30.00	32	16.20	10	40.30	51	1.19	7	91.50	65
RB947645	22.40	57	1.02	27	33.60	59	22.40	49	41.90	59	0.93	50	94.90	47
RB947648	22.20	59	0.80	16	33.10	55	25.70	59	38.60	42	0.85	61	97.60	18
RB947649	24.40	26	1.14	32	29.50	30	20.30	37	36.40	24	1.02	33	94.90	48
RB947653	20.50	68	3.54	71	38.90	69	31.70	71	44.30	64	0.69*	71	85.00	70
RB947656	22.40	58	1.21	35	32.40	49	23.00	54	39.50	48	0.90	55	94.10	54
RB947663	23.70	41	1.48	49	30.90	42	22.50	50	37.30	32	0.90	56	92.70	60
RB947677	23.60	44	0.38	3	30.40	37	19.20	29	38.70	43	1.05	24	98.60	5
RB947679	23.90	38	1.62	55	31.40	46	18.40	25	41.10	57	1.15	15	95.80	37
RB957508	22.60	53	1.47	48	33.90	60	22.10	46	42.70	61	1.07	21	94.40	51
RB957509	23.00	52	0.68	12	32.80	53	22.40	48	40.50	54	1.05	25	97.20	23
RB957544	23.80	40	1.45	46	31.40	45	20.50	40	39.50	49	1.11	18	95.30	42
RB957546	17.20	71	3.30	67	46.50	72	37.10	72	53.50	72	0.79	66	83.80	72
RB957554	22.10	61	0.79	15	34.10	61	23.50	56	42.10	60	1.00	39	96.20	31
RB957569	24.00	35	1.34	41	30.10	34	19.70	34	37.90	38	0.96	46	93.40	58
RB957575	23.10	48	3.61	72	33.40	57	17.20	15	45.50	67	1.32*	1	95.70	39
RB957576	23.10	49	0.55	7	32.70	52	22.50	51	40.40	52	1.00	38	97.30	20
RB957610	26.40	6	1.63	57	25.20	6	14.40	4	33.40	11	1.22	3	97.70	16
RB957612	25.70	12	1.38	45	27.00	13	17.60	19	34.10	13	1.03	30	93.90	55
RB957615	24.90	21	0.97	24	28.50	21	16.30	12	37.60	36	1.16	14	98.20	10
RB957638	23.70	42	0.56	8	30.30	36	21.10	44	37.30	31	0.94	48	97.30	21
RB957649	26.20	8	0.92	22	25.00	5	18.20	24	30.10	2	0.92	52	95.60	41
RB957689	24.10	33	1.04	29	29.20	25	22.50	52	34.30	14	0.88	59	95.30	44
RB957695	22.00	63	1.37	44	34.20	62	26.00	61	40.40	53	0.80	65	95.80	38
RB957697	25.80	11	0.59	9	26.40	10	18.10	23	32.60	8	1.02	31	97.30	22
RB957712	27.30	2	3.35	69	24.30	2	17.30	17	29.50	1	0.95	47	84.50	71
RB957743	23.60	45	1.19	34	32.40	50	17.60	20	43.50	63	1.20	6	98.60	3
RB957751	23.60	46	1.27	40	30.20	35	22.20	47	36.20	21	0.90	57	93.90	56
RB967505	24.20	30	0.95	23	29.90	31	20.40	38	37.10	29	0.97	44	95.30	45
RB967510	22.60	54	1.72	58	32.40	51	27.40	65	36.30	22	0.85	62	91.90	62
RB967561	25.60	14	3.24	66	28.40	18	15.60	7	38.00	40	1.10	20	88.70	67
RB967585	24.40	27	0.82	17	29.20	26	19.50	31	36.50	27	1.02	34	96.20	30
RB967589	24.30	28	0.85	19	28.90	23	21.00	42	34.90	18	0.90	54	96.10	33
RB967590	25.60	15	1.34	43	27.80	16	14.90	5	37.50	34	1.21	5	98.50	7
RB967603	26.20	9	0.29	2	26.00	9	17.30	16	32.60	7	1.03	28	98.80	2
RB967623	25.20	17	0.78	14	27.90	17	19.20	28	34.50	15	1.04	26	96.70	27
RB967672	22.10	62	1.46	47	34.70	64	26.50	62	40.90	56	0.84	63	93.60	57
RB977509	26.30	7	1.25	38	25.40	7	18.80	27	30.40	3	1.01	35	94.20	52
SP853877	25.30	16	1.63	56	26.70	12	19.20	30	32.40	6	0.94	49	91.90	63
SP86-42	27.10	3	0.42	5	24.60	3	16.20	11	30.80	5	0.98	41	97.90	15
SP87-365	24.00	36	1.34	42	31.90	47	17.00	14	43.10	62	1.21	4	98.60	4

* Significantly different from zero at 5% of probability of Type I error; ω_i (%) stability parameter according to Wricke (Wricke & Weber, 1986); P_{ig} , P_{if} and P_{id} : MAEC parameters considering all the environments, only the favorable environments and only the unfavorable environments, according to the differences in relation to the weighted bi-segmented regression line by the coefficient of residual variation adapted by Carneiro (1998) respectively; β_{ii} and R^2_i (%) Regression coefficient and determination coefficient estimated by the methodology by Eberhart & Russell (1966) respectively; ** Rk; genotype ranking

The methodology by Carneiro classified the DAB, DWD and UAP environments as being favorable and the AGR, ATE, UJA and UTR environments as unfavorable (Table 1). The clone RB947520 was that had the best performance when all the environments ($P_{ig} = 22.7$) or only the favorable environments ($P_{if} = 12.5$) were considered. In the unfavorable environments this method classified clone RB957712 as having the best performance ($P_{id} = 29.5$). The controls did not perform well in any environmental classification, but RB72454 was better (27.4, 18.8 and 33.9 to P_{ig} , P_{if} and P_{id} , respectively) than RB835486 (34.5, 28.6 and 38.9 to P_{ig} , P_{if} and P_{id} , respectively) in all situations.

According to the methodology by Eberhart and Russel clones RB947653 and RB957575 presented specific adaptability to unfavorable ($\hat{\beta}_i = 0.69$) and favorable environments ($\hat{\beta}_i = 1.32$), respectively (Table 1). However, the clone RB947653 is recommended only for the unfavorable environment, where it was more productive, because it was inferior to the controls in the other unfavorable environments (AGR, UJA and UTR). For all the other clones, the significance tests of the regression coefficients did not reject the nullity hypothesis indicating their general adaptability. The control RB72454 presented general adaptability ($\hat{\beta}_i = 1.01$), while RB835486 presented specific adaptability ($\hat{\beta}_i = 0.68$) to unfavorable environments.

The stability or adaptability predictability was high for most of the clones and controls, showing that the linear regression was efficient in explaining the performance of the genotype under environmental variations.

All the correlation values between the stability and adaptability parameters can be observed in the Table 2. The genotypic values ($u + \hat{g}$) predicted by BLUP from the joint analysis were significantly correlated with the MAEC (measure of behavioral adaptability and stability) parameters (-0.9731 , -0.8708 and -0.7875 to P_{ig} , P_{if} and P_{id} , respectively) estimated by Carneiro's methodology. P_{ig} , P_{if} and P_{id} are referring to the modified statistic P_i of Lin & Binns (1988), associated to general (all environments), favorable and unfavorable environments, respectively. These correlations high and negative were expected, indicating that the genotypes with greater predicted genotypic values presented lower estimates for the P_i parameter. This relationship is important, because it permits the breeder to select highly productive clones with good performance in the environments of interest. The predicted genotypic values also correlated significantly with the $\hat{\beta}_{1i}$ (0.5247) and R^2_{1i} (0.2627) parameters, but these correlations were classified as moderate and weak, respectively. This shows that the predicted genotypic values free from genotype x environment interaction effects correlate better with adaptability than with stability.

TABLE 2 – Estimates of the Spearman's ordinal correlation among the predicted genotypic values ($u + \hat{g}$), genotypic adaptability and stability parameters estimated by methodologies by Wricke (Wricke & Weber, 1986), Eberhart & Russel (1996) and Carneiro (1998), obtained by the analysis of 72 sugarcane genotypes, assessed in seven environments in the augmented blocks experimental design by mixed model approach.

	ω_i (%)	P_{ig}	P_{if}	P_{id}	$\hat{\beta}_{1i}$	R^2_{1i} (%)
$u + \hat{g}$	-0.1228	-0.9731**	-0.8708**	-0.7875**	0.5247**	0.2627*
ω_i (%)		0.1630	0.0304	0.1746	0.0173	-0.6656**
P_{ig}			0.7936**	0.8778**	-0.4003**	-0.2404*
P_{if}				0.4492**	-0.8141**	-0.3767**
P_{id}					0.0038	-0.1168
$\hat{\beta}_{1i}$						0.4035**

*, ** Significantly different from zero at 5% and 1% probability of Type I error, respectively; ω_i (%) stability parameter according to Wricke (Wricke & Weber, 1986); P_{ig} , P_{if} and P_{id} : MAEC parameters considering all the environments, only the favorable environments and only the unfavorable environments, respectively, according to the differences in relation to the weighted bi-segmented regression line by the coefficient of residual variation adapted by Carneiro (1998); $\hat{\beta}_{1i}$ and R^2_{1i} (%) regression coefficient and determination coefficient estimated by the methodology by Eberhart & Russell (1966).

The P_{ig} , P_{if} and P_{id} parameters were highly correlated among each other (varying from 0.4492 to 0.8778), showing that a genotype that presents better performance considering all the environments also tends to perform better when the environments are separated.

The ω_i (%) parameter by Wricke was consistently related to the R^2_i (%) determination coefficient by Eberhart and Russell (-0.6656), indicating both parameters were equivalent in assessing the stability of the genotypes in the different environments. This negative correlation showed that the genotypes considered stable by the Wricke's methodology presented high estimate of the determination coefficient (Table 2). All the other studied parameters presented non-significant correlations with ω_i (%).

The $\hat{\beta}_{ii}$ parameter presented significant correlations with $u + \hat{g}$ (0.5247), P_{ig} (-0.4003) and P_{if} (-0.8141) parameters. The $\hat{\beta}_{ii}$ correlations with the ω_i (%) and P_{id} parameters were nil.

Farias et al. (1997) employed the Spearman's correlation and obtained correlations in the order of -0.55 and -0.96 between the Lin & Binns (1988) P_i parameter and the Eberhart and Russell regression coefficient. As those methodologies tended to same result, the authors recommended the use of P_i , because it does not present the inconvenience of regression analysis, which is the dependency among the variables and also indicates materials whose performance is close to the maximum value in the different environments.

Studies by Arias (1996) also showed that results obtained by regression analysis and the Lin & Binns (1988) non-parametric analysis were coincident in assessing genotypes.

Other studies concerning to stability and adaptability parameters in a mixed model methodology context has been published (Oliveira et al., 2005; Bastos et al., 2007). Such papers employed another approach using a new methodology. This differs from the present paper which uses traditional methods applied on predicted genotypic values. A comparison between these two approaches is needed in a future paper.

CONCLUSIONS

1) The genotypic values free from genotype x environment interaction ($u + \hat{g}$) were strongly correlated with the Carneiro P_{ig} , P_{if} and P_{id} parameters and weakly correlated with the Wricke ω_i (%) parameter.

2) The genotypic values correlated significantly with the Eberhart and Russell parameters, but the correlation with R^2_i (%) was low.

3) As expected, the ω_i (%) parameter by Wricke was shown to be consistently related to the R^2_i (%) parameter by Eberhart and Russell.

4) The $\hat{\beta}_{ii}$ and R^2_i (%) parameters by Eberhart and Russell correlated significantly with the P_{ig} and P_{if} parameters, but neither presented significant correlation with the P_{id} parameter.

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