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CROP BREEDING AND
APPLIED BIOTECHNOLOGY

Genotypic evaluation and selection of sugarcane clones in three environments in the State of Paraná

Ricardo Augusto de Oliveira, Marcos Deon Vilela de Resende, Edelclaiton Daros, João Carlos Bespalhok Filho, José Luis Camargo Zambon, Oswaldo Teruyo Ido, Heroldo Weber, and Henrique Soares Koehler

ABSTRACT - *The objective of this study was to estimate genetic parameters and predict genotypic values in sugarcane clones (series RB96) by the Reml/Blup methodology. The trial was installed in an unbalanced block design to evaluate the yield at three locations in the state of Paraná. The ranking of the clones regarding yield differed from one location to the other, due to the genotypic correlation of intermediate magnitude (0.62) across the locations. Heritabilities of the clone mean? were moderate to high, allowing a selection accuracy of 53 to 74%. The two best clones presented a mean superiority of 28% (RB955466) and 19% (RB965518) over the general mean of the three locations. A comparison of the methods Mhprvg (harmonic mean of the relative performance of genetic values, according to Resende 2004) and Lin and Binns (1988) showed that both selected practically the same clones but the Mhprvg method presented the advantage of providing results in the measurement scale of the evaluated trait.*

Key words: Saccharum spp., clone selection, Reml/Blup, Mhprvg method.

INTRODUCTION

Sugarcane is one of the main foreign exchange sources of Brazil and covers an area of over five million hectares. The selection of more productive clones by different genetic improvement programs is one of the various factors that have made this crop a success in Brazil. Technical details regarding sugarcane improvement programs in Brazil are given by Barbosa (2000), Cesnik and Miocque (2005) and Matsuoka et al. (2005).

The improvement program of RIDESA/UFPR evaluates new clones in various environments, allowing the identification and recommendation of region-specific superior clones as well as clones with broad adaptability and yield stability across several environments. A univariate model that considers all locations simultaneously is usually appropriate for selection targeting the mean yield across all environments. Still, a more complete model can allow additional conclusions on: selection of location-specific genotypes, selection of stable genotypes across locations, selection of responsive genotypes (highly adaptable) to improved environments, and simultaneous selection for the three attributes (yield, stability and adaptability). The simultaneous selection for these three attributes can be realized by the methods of Lin and Binns (1988) and Resende (2004).

Our study had the objectives of genotypic evaluation of sugarcane clones of the series RB96 in the State of Paraná, the estimation of genetic parameters using the Reml procedure, prediction of genotypic values of clones for each location and for the mean environment of all locations as well as an evaluation of the adaptability and stability of the genotypic values predicted by the Blup procedure.

MATERIAL AND METHODS

The clones for the present study were obtained from crossings realized in the Flowering and Crossing Station/ UFAL/RIDESA in Serra do Ouro, county of Murici, state of Alagoas, in 1996. The progenies derived from the crossings were planted at the station of the Centro de Ciências Agrárias of UFSCar, county of Araras, state of São Paulo. A total of 150.000 T1 or T1? plantlets were planted out on the field at the experimental stations of Araras, Valparaíso (UFSCar) and Paranavaí (UFPR). For phase T2, 1490 clones were selected and finally 180 clones passed on to phase T3 (see Matsuoka et al. (2005) for in-depth information on the different stages of sugarcane improvement).

In 2002, the best T3 clones were tested in three production environments: one in the county of Colorado, on an experimental area of the mill Alto Alegre; another in the county of Paranavaí, at the experimental station of Paranavaí/SCA/UFPR; and the third in the county of Mandaguaçú, on an experimental area of the mill Santa Terezinha/Iguatemi. All these counties lie in the northwestern region of the State of Paraná. The trials were planted in April 2002 (Colorado 12/04, Paranavaí 02/04 and Mandaguaçú 04/04), plant cane harvested in June 2003 (15/06, 18/06 and 20/06, respectively) and the first ratoon harvested in July 2004 (09/07, 13/07 and 20/07, respectively).

An experiment was installed in each environment in a complete random block design with two replications. The experimental plots consisted of two five meter long rows spaced 1.4 meters apart. Six stalk segments meter-1 with three buds each were used for planting. Fertilization consisted of 600 kg ha-1 of the formula 05:25:25 and 600 kg ha-1 of the formula 20:00:20 onto ratoon (in a proportion of 80 kg ha-1 of N, 140 kg ha-1 of P2O5 and 140 kg ha-1 of K20) and a topdressing of 120 kg ha-1 of N.

One hundred and eighty clones of the series RB96 were evaluated together with promising clones of the series RB89, RB94, and RB95 plus two commercial standard cultivars RB72454 and RB835486.

The experiment was harvested and sampled by biometry; three samples of 20 stalks were weighed and the number of stalks in one meter along rows of each experimental plot counted. The yield was calculated as follows: TCH = (W1S x NSM) x 1000/SPF, where TCH expresses tons of cane hectare-1, W1S the weight of one stalk in kg, NSM the number of stalks in a meter, and SPF the spacing between planting rows.

The following statistical model was adopted for the evaluation of clones in the randomized block design with one observation per plot and in various environments or locations:

$y = Xb + Zg + Wc + e$, where:

y, b, g, c, e = data vectors of fixed effects (block means), of (random) genotypic effects of clones, of (random) effects of the genotype x environment interaction, and of random errors, respectively.

X, Z and W = matrixes of incidence of b, g and c, respectively.

Distributions and structures of means and variances:

$$E \begin{bmatrix} y \\ g \\ c \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix}; \quad Var \begin{bmatrix} g \\ c \\ e \end{bmatrix} = \begin{bmatrix} I\sigma_g^2 & 0 & 0 \\ 0 & I\sigma_c^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

Mixed model equations:

$$\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z+I\lambda_1 & Z'W \\ W'X & W'Z & W'W+I\lambda_2 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{g} \\ \hat{c} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}, \text{ where:}$$

$$\lambda_1 = \frac{\sigma_e^2}{\sigma_g^2} = \frac{1-h_g^2-c^2}{h_g^2}; \quad \lambda_2 = \frac{\sigma_e^2}{\sigma_c^2} = \frac{1-h_g^2-c^2}{c^2}.$$

$h_g^2 = \dfrac{\sigma_g^2}{\sigma_g^2 + \sigma_c^2 + \sigma_e^2}$: individual broad-sense heritability within a block;

$c^2 = \dfrac{\sigma_c^2}{\sigma_g^2 + \sigma_c^2 + \sigma_e^2}$: coefficient of determination of the effects of genotype x environment interaction;

σ_g^2 : genotypic variance among clones;

σ_c^2 : variance of the genotype x environment interaction;

σ_e^2 : residual variance among plots;

$r_{gloc} = \dfrac{\sigma_c^2}{\sigma_g^2 + \sigma_c^2} = \dfrac{h_g^2}{h_g^2 + c^2}$: genotypic correlation across the environments.

Estimators of components of variance by Reml via algorithm EM:

$$\hat{\sigma}_e^2 = [y'y - \hat{b}'\ X'y - \hat{g}'\ Z'y - \hat{c}'\ W'y]/[N - r(x)]$$

$$\hat{\sigma}_g^2 = [\hat{g}'\hat{g} + \hat{\sigma}_e^2\ tr\ C^{22})]/q$$

$$\hat{\sigma}_c^2 = [\hat{c}'c + \hat{\sigma}_e^2\ tr\ C^{33}]/s$$

where:
C^{22} and C^{33} were derived from:

$$C^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} \\ C_{21} & C_{22} & C_{23} \\ C_{31} & C_{32} & C_{33} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} & C^{13} \\ C^{21} & C^{22} & C^{23} \\ C^{31} & C^{32} & C^{33} \end{bmatrix}$$

C = matrix of the coefficients of the mixed model equations;
tr = trace of a matrix operator;
r(x) = rank of matrix X;
N,q,s = total number of data, number of clones and number of genotype x environment combinations, respectively.

In this model, the interaction-free predicted genotypic values considering all locations are given by u + g, where u is the mean of all locations. For each location j, the genotypic values are predicted by $u_j + g + ge$, where u_j is the mean of location j.

The joint selection for yield, stability and adaptability of the plant material was based on statistics denominated harmonic mean of the relative performance of the predicted genetic values (Mhprvg), as described by Resende (2004). Results of the Mhprvg are similar to those obtained by the methods described by Lin and Binns (1988) and Annicchiarico (1992). All analyses were performed on software Selegen-Reml/Blup, model 54 (Resende 2002).

RESULTS AND DISCUSSION

Components of variance and genetic parameters

The results obtained for components of variance and genetic parameters at the three locations Colorado, Paranavaí and Mandaguaçú in the State of Paraná and for the joint analysis are presented in Table 1, for trait TCH (t ha^{-1}).

The presence of significant genetic variability among the clones under study was verified, as demonstrated by the estimates of heritability and their standard errors (Table 1). In comparison with the heritability magnitudes the

standard errors were of small magnitude, warranting that the latter would not reach value zero via the lower limits of the confidence interval (provided by approximately -2 times the standard errors), a fact that would indicate an absence of genetic variability. The coefficients of genotypic variation presented values of over 10% in all locations, confirming the presence of considerable genetic variability. The presence of this genetic variability shows the possibility of effective selection among clones.

The heritability estimates at the mean level of clones attained moderate to high values (0.28 to 0.55), resulting in a good accuracy (0.53 to 0.74) in the clone selection (Table 1). The genotypic correlation of the clone performance across environments was 0.62, presenting a moderate level of genotype x environment interaction of the complex type, showing that the best clones in one environment are not necessarily the best in another. This justifies that the clones' stabilities and adaptabilities are taken into consideration for selection. Bressiani (2001) also verified the presence of interaction genotype x environment of the complex type in his studies of cane improvement.

The estimates of broad-sense heritabilities at the individual level for TCH presented values between 0.13 and 0.38 (Table 1), presenting the lowest value in the joint analysis, due to the effects of the genotype x environment interaction. These values are in line with the ones presented by Barbosa et al. (2004) and Matsuoka et al. (2005), which ranged from 0.10 to 0.14 and 0.10 to 0.48, respectively. The coefficients of experimental variation for trait TCH presented moderate magnitudes, expressing good experimental precision.

Genotypic selection by location and the set of environments

Table 2 presents the ranking and predicted genotypic values of the best 22 clones (20 of which are new and 2 check clones) and genetic gains estimated for the selection of the five best, for trait TCH (t ha^{-1}), in each one of the three locations and also for the joint analysis of the three locations. For a mean environment represented by the three locations, the five best clones were RB945273, RB955466, RB965602, RB965731, and RB965718. Among these five superior genotypes, three are new clones. Genotypes RB945273 and RB965731 were evaluated in only one environment; nevertheless, the Blup methodology allowed their inclusion in the ranking for the mean environment represented by the three locations. Their predicted genotypic values for location 3 were penalized by a

Table 1. Estimates of coefficients of individual heritability in the broad sense ( ), heritability of the clone mean ( ), genotypic variance ( ), variance of genotype x environment interaction ( ), residual variance among plots ( ), individual phenotypic variance ( ), genotypic correlation across locations ( ), accuracy in clone selection ( ), general mean, coefficient of genetic variation (CVg%), and coefficient of experimental variation (CVe%) for trait TCH (tons of cane per hectare) in sugarcane clones (series RB96) in three environments in the State of Paraná.

Estimates	Environment 1 (Colorado)	Environment 2 (Paranavaí)	Environment 3 (Mandaguaçú)	Joint analysis
($\hat{h}^2_g$)	0.38 ± 0.09	0.33 ± 0.08	0.16 ± 0.06	0.13 ± 0.03
($\hat{h}^2_{mc}$)	0.55	0.50	0.28	0.45
($\hat{\sigma}^2_g$)	182.80	246.84	378.15	149.75
($\hat{\sigma}^2_c$)				
-------	-------	-------	92.86	
($\hat{\sigma}^2_e$)	297.99	492.30	1959.76	891.47
($\hat{\sigma}^2_f$)	480.79	739.14	2337.92	1134.09
$\hat{r}_{gloc}$	-------	-------	-------	0.62
$\hat{r}_{g\hat{g}}$	0.74	0.71	0.53	0.67
General mean	72.77	93.39	152.78	106.45
(CVg%)	18.58	16.82	12.73	11.49
(CVe%)	23.72	23.76	28.97	28.05

fraction given by the magnitude of the interaction genotype x environment. Genetic gains at a level of 21.27% can be obtained with the selection of these five clones.

At the first location, the five best clones were RB955466, RB955560, RB965602, RB965699, and RB965674. At the second location, the five best clones were RB955466, RB965674, RB965648, RB965718, and RB965518. At the third, the five best clones were RB965602, RB945273, RB965689, RB965564, and RB965518 (Table 2). Among the five best, at least two clones in each location are coincident with the best in the mean of the three locations. This selection by location uses the information of all locations together and is therefore a superior and more precise procedure than selection based on the data of each detached location.
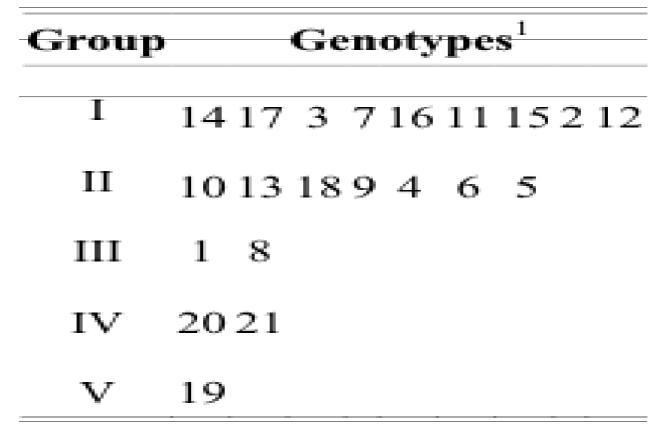
Joint selection for yield, stability and adaptability

Among the various methodologies used to estimate the stability and adaptability, the most commonly used are those based on linear regression, as for example that of Eberhart and Russell (1966). In this methodology, the stability and the adaptability are estimated by distinct parameters (coefficient of regression (b_i) and regression deviations (S^2d_i), respectively), making the simultaneous interpretation of results and selection for productivity, stability and adaptability difficult.

Currently, more simple interpretation procedures are preferred for the analysis of stability (constancy of genotypic performance across environments) and adaptability (ability of response to environment improvement). In this sense, measures that incorporate both (stability and adaptability, together with yield) in a single statistical analysis have been acclaimed, such as the methods of Annicchiarico (1992), Lin and Binns (1988) and modified procedures (Cruz and Carneiro 2003). In the context of the mixed models, one method of ranking genotypes simultaneously for its genetic values (yield) and stability is the Blup procedure under harmonic means

Table 2. Genotypic values of the 22 sugarcane genotypes under study and predicted genetic gains of the five best ones for trait TCH (tons of cane per hectare) in three environments (Colorado, Paranavaí and Mandaguaçú in the State of Paraná) and in the joint analysis. 2004. The sum of ui + g + gei is equal to the mean of location i (u_i) plus the effects of genotypes (g) and the genotypes x location interaction i (ge_i).

Group	Genotypes[1]
I	14 17 3 7 16 11 15 2 12
II	10 13 18 9 4 6 5
III	1 8
IV	20 21
V	19

* Standards in use in the State of Paraná.

(Resende 2002). The lower the standard error of the genotypic performance across locations, the higher the harmonic mean of the genotypic values across locations. This means that the selection for Mhgv implies a simultaneous selection for yield and stability.

In terms of adaptability, a simple and effective measure in the context of the mixed models is the relative performance of genotypic values (Prvg) across the environments. In this case, the predicted genotypic values (or original data) are expressed as a proportion of the general mean of each location and later the mean value of this proportion across locations is obtained. The relative performance of phenotypic data has commonly been used for a long time (Wright et al. 1966) and represents the basis of the method of Annicchiarico (1992).

Simultaneous selection for yield, stability and adaptability in the context of mixed models can be realized by the method Mhprvg. The method allows the simultaneous selection for the three cited attributes and has the following advantages: (i) it considers the genotypic effects as random and therefore provides stability and adaptability at the genotypic and not the phenotypic level; (ii) it is able to deal with unbalanced data; (iii) able to deal with a nonorthogonal design; (iv) able to deal with heterogeneity of variances; (v) and able to consider correlated errors within locations; (vi) it provides genetic values which already include the discounting (penalization) of the instability ; (vii) it can be used with any number of environments; (viii) it is able to consider the stability and adaptability in the plant selection within a progeny; (iv) it does not depend on the estimation of other parameters such as coefficients of regression; (x) it brings forth results in the same dimension or scale of the evaluated trait; (xi) it allows to compute the genetic gain with selection by the

three attributes simultaneously. These last two factors are quite important. Other methods such as that of Lin and Binns (1988) provide results that are not directly interpreted as genetic values and do therefore not allow the calculation of the genetic gain in the trait composed of yield, stability and adaptability. The method of Annicchiarico (1992) additionally depends on suppositions of Z values.

Table 3 presents results of stability and productivity (Mhgv - harmonic mean of the genotypic values across locations), adaptability and productivity (Prvg - relative performance of the genotypic values in relation to the mean of each location), and stability, adaptability and productivity simultaneously (Mhprvg - harmonic mean of the relative performance of the genotypic values) for trait TCH (t ha^{-1}) in the 20 best clones among those evaluated in all locations.

Table 3 shows that the ten best clones based on the criteria Prvg, Mhgv and Mhprvg are not exactly the same best ten by the criterion of mean productivity (Table 4). The accordance was 80% among the best ten and the order among the matches was inverted. This evidences that the use of these new attributes or criteria of selection can enhance selection. The two best clones by the criterion Mhprvg presented a mean superiority of 28% (RB955466) and 19% (RB965518) over the general mean of the three locations. To compute these values the instability of clones across the locations was discounted and simultaneously the ability of response (adaptability) to environment improvement added. These proprieties are intrinsic to method Mhprvg. The values of Prvg and Mhprvg indicate exactly the mean superiority of the genotype in relation to the mean of the environment where it was cultivated (Table 3), so genotype RB955466 responds in the mean 1.28 times to the mean of the environment where it was planted. The Mhprvg *MG value provides the genotypic mean value of the clones in the evaluated locations, a value which already includes the penalization by the instability and capitalization on adaptability.

The five best clones for the Mhprvg method-based selection were RB955466, RB965518, RB965648, RB965718, and RB965743. This selection provides a gain of 19.80% over the general mean of the three environments, simultaneously considering yield, stability and adaptability across locations.

Table 4 presents (only the 20 best of the clones evaluated in all locations) results of the simultaneous selection for yield, adaptability and stability using the method of Lin and Binns (1988) for the predicted genotypic values. The genotypic values capitalizing on the interaction mean effects (gem) in the various locations are presented in the same table.

Among the 10 best clones selected by Mhprvg, nine coincide with the 10 clones selected by the method of Lin and Binns (1988). By this method, the plants with lowest Pi statistics values represent the best material. According to the method of Lin and Binns (1988), the only genotype that was not coincident was RB966200 ranked tenth by this method and thirteenth by the Mhprvg method, i.e., in very close positions. The estimated correlation between the parameters of the two methods was of high magnitude (-0.9487). The method of Annicchiarico (1992) was also computed and presented an absolute correlation of the same magnitude (though positive) with the Mhprvg method. This confirms that the three methods use basically the same principles and concepts. Method Mhprvg has the advantage of providing results in the same measurement scale of the trait, which can be interpreted directly as genetic values for the evaluated trait. This also makes the calculation of the genetic gain with simultaneous selection for yield, adaptability and stability possible, whereas it is not possible with the method of Lin and Binns (1988). So the Mhprvg statistics can be used advantageously in the context of mixed models with random genetic effects. The consideration of the genetic effects and the interaction g x e as random also offers an advantage over the method Ammi (Gauch 1988), which deals with these effects as fixed and therefore acts at the phenotypic and not the genotypic level. It is important to point out that the Blup of the interaction effects already eliminates the noises of these effects, similar to the Ammi method, as described by Resende (2004).

Comparison among the various predictions of genotypic values

Six modalities of genotypic values were predicted for each clone: (a) per location (u + g + ge, Table 2); (b) for various locations, free of the g x e interaction (u + g, Table 2); (c) for the location mean, capitalizing on the mean effect of the interaction (u + g + gem, Table 4); (d) for various locations, penalizing by the instability of each genotype (Mhgv, Table 3); (e) for the mean of locations, capitalizing on the genotype-specific ability of response to environment improvement (Prvg, Table 3); (f) for the location means, penalizing by the instability and capitalizing on the adaptability (Mhprvg, Table 3).

In terms of inferences on the expected yield, the genotypic values must be used as follows:

Table 3. Stability of genotypic values (MHGV), adaptability of genotypic values (PRVG), stability and adaptability of genotypic values (MHPRVG) to TCH (tons of cane per hectare) of the 20 best clones plus two controls.

Genotype	MHGV	Genotype	PRVG	PRVG*MG	Genotype	MHPRVG	MHPRVG*MG
RB955466	**126.79**	**RB955466**	**1.29**	**137.39**	**RB955466**	**1.28**	**136.21**
RB965560	**116.71**	**RB965648**	**1.19**	**126.43**	**RB965518**	**1.19**	**126.23**
RB965648	**116.37**	**RB965518**	**1.19**	**126.36**	**RB965648**	**1.18**	**126.14**
RB965518	**116.13**	**RB965560**	**1.18**	**125.62**	**RB965718**	**1.17**	**124.58**
RB965718	**115.13**	**RB965718**	**1.17**	**124.95**	**RB965743**	**1.17**	**124.50**
RB965743	**114.55**	**RB965743**	**1.17**	**124.63**	**RB965560**	**1.17**	**124.34**
RB965657	**113.63**	**RB965689**	**1.17**	**124.14**	**RB965689**	**1.17**	**124.12**
RB965689	**113.01**	**RB965657**	**1.16**	**123.50**	**RB965657**	**1.16**	**123.33**
RB965699	**112.87**	**RB882698**	**1.15**	**122.82**	**RB882698**	**1.15**	**122.70**
RB882698	**112.61**	**RB965741**	**1.15**	**122.53**	**RB965741**	**1.15**	**122.36**
RB965741	112.60	RB965699	1.15	121.95	RB965699	1.14	121.29
RB965688	112.08	RB965688	1.14	121.58	RB965688	1.14	121.28
RB966200	111.23	RB966200	1.14	121.32	**RB966200**	1.14	121.26
RB966256	109.31	RB966256	1.13	119.86	RB966256	1.13	119.81
RB965658	108.92	RB965574	1.12	119.31	RB965574	1.12	119.29
RB965591	108.39	RB965564	1.12	118.91	RB965564	1.12	118.76
RB965564	108.33	RB965658	1.11	118.70	RB965658	1.11	118.63
RB966215	107.61	RB965591	1.11	118.59	RB965591	1.11	118.57
RB893161	107.14	RB965625	1.10	116.99	RB965625	1.10	116.91
RB965625	107.13	RB965614	1.10	116.92	RB966215	1.10	116.70
RB72454*	103.70	RB72454*	1.07	113.62	RB72454*	1.07	113.61
RB835486*	91.61	RB835486*	0.95	100.89	RB835486*	0.95	100.87

* Standards in use in the State of Paraná.

(i) For planting in each location of the experimental network: consider genotypic values (genetic means) as described in (a);

(ii) For planting in various other locations with the same pattern of interaction g x e of the experimental network: consider genotypic values (genetic means) described in (c) or (e);

(iii) For planting in other unknown locations or with a different pattern of g x e interaction from the one of the experimental net or with high environmental heterogeneity within locations: consider genotypic values (genetic means) described in (b) or (d);

(iv) for planting in various other locations with a varied pattern of interaction g x e: consider genotypic values (genetic means) described in (f).

The methods that penalize the predicted genotypic values most are, in order, (d) and (b); (f), (e) and (c); (a). Among these, (d) and (b) are similar, although (d) tends to be superior, in consideration of the concept of stability, by specifying the interaction for each genotype better. Methods (c), (e) and (f) also generate more similar results to each other. Generally speaking, one can say that the methods Mhgv and Mhprvg are safe options and Mhgv is a little more conservative.

In the present study, clone RB955466 ranked first for all criteria (yield, stability, adaptability) and the three jointly among the genotypes evaluated in all locations. In the other positions there was a certain criterion-dependent variation of genotypes (Tables 3 and 4).

Table 4. Genotypic values capitalizing the mean interaction (gem) in the different locations, as well as stability and adaptability of genotypic values for TCH (tons of cane per hectare) by means of the method (Pi) of Lin and Binns (1988) where $Pi = \sum_{i}(VG_{ij} - M_{j})^2/(2L)$, VG_{ij} is the genotypic value of genotype i in location j, M_{j} is the maximum genotypic value in location j and L is the number of locations.

Genotype	u + g + gem	Genotype	Pi
RB955466	**134.87**	**RB955466**	**63.34**
RB965718	**129.76**	**RB965518**	**136.92**
RB965648	**126.91**	**RB965689**	**140.29**
RB965518	**126.34**	**RB965648**	**146.00**
RB965743	**126.07**	**RB965743**	**167.58**
RB965699	**124.49**	**RB965718**	**181.94**
RB965689	**124.22**	**RB965657**	**194.15**
RB965560	**123.22**	**RB882698**	**199.46**
RB882698	**122.03**	**RB965741**	**207.35**
RB965591	**121.29**	**RB966200**	**218.54**
RB966256	121.04	RB966256	238.00
RB965657	120.96	RB965574	247.05
RB965625	120.56	RB965688	255.73
RB965741	120.34	RB965564	266.88
RB966200	120.19	RB965591	268.14
RB965688	119.83	RB965560	277.93
RB965574	119.66	RB965658	282.70
RB965564	119.53	RB965699	293.65
RB955452	118.74	RB965698	320.17
RB965658	118.07	RB965625	320.81
RB72454*	113.43	RB72454*	385.63
RB835486*	101.26	RB835486*	798.76

* Standards: commonly used cultivars in the State of Paraná.

CONCLUSIONS

The heritabilities of the clone mean? presented moderate to high magnitudes, allowing selection accuracy in a range of 53% to 74%.

Among the clones evaluated in all locations, the two best presented a mean superiority of 28% (RB955466) and 19% (RB965518) over the general mean of the three locations.

The values of genetic gain were calculated including the penalizing of clones by the instability across locations and simultaneously capitalizing on the adaptability, using intrinsic proprieties of the Mhprvg method.

The methods Mhprvg, Lin and Binns (1988) and Annicchiarico (1992) selected practically the same clones for TCH. The Mhprvg method however presented the advantage of providing results in the same scale of measurement of the evaluated trait and further allows the calculation of the genetic gain with selection of these three attributes jointly.

Avaliação genotípica e seleção de clones de cana-de-açúcar em três ambientes no Estado do Paraná

RESUMO - *O objetivo deste trabalho foi estimar parâmetros genéticos e realizar a predição de valores genotípicos em clones de cana-de-açúcar, série RB96, utilizando a metodologia Reml/Blup. O experimento foi instalado em blocos, desbalanceados, sendo avaliada a produtividade em três locais de produção no Paraná. Observou-se alteração no ordenamento dos clones para a produção ao longo dos locais, devido à correlação genotípica de média magnitude (0,62) através dos locais. As herdabilidades da média de clones apresentaram magnitudes moderadas a altas, permitindo acurácias seletivas de 53 a 74%. Os dois melhores clones apresentaram superioridade média de 28% (RB955466) e 19% (RB965518) sobre a média geral dos três locais. Ao comparar os métodos Mhprvg (média harmônica da performance relativa, conforme Resende 2004) e Lin e Binns (1988), observou-se que ambos selecionaram, praticamente, os mesmos clones. Entretanto, o método Mhprvg apresenta vantagem de fornecer resultados na escala de medição do caráter avaliado.*

Palavras-chave: Saccharum spp., Seleção clonal, REML/BLUP, Método MHPRVG.

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