

## Breeding new sugarcane clones by mixed models under genotype by environmental interaction

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**ABSTRACT:** Sugarcane (*Saccharum* spp.) is one of the most important crops cultivated in the tropics and subtropics and plays a significant economic and environmental role in Brazil. Twenty-four new clones were evaluated in different locations as potential models for recommendation as new varieties. The mixed model methodology, using the harmonic mean of the relative performance of genetic values (MHPRVG), facilitated the analysis of genotypic stability and adaptability, culminating in the recommendation of clones for each location. MHPRVG ranked clones RB92579, RB867515, SP81-3250, RB947520 and RB931530 as the best five, and, additionally, clones with greater genotypic potential were identified for each test in the six localities.

Edited by: Natalia de-Leon

Received April 17, 2013

Accepted September 03, 2013

### Introduction

Sugarcane (*Saccharum* spp.) is one of the most important species cultivated in the tropics and subtropics and plays a significant economic and environmental role in Brazil, occupying a total area of 8.527 million hectares in the agricultural years 2011/2012, according to data from the Companhia Nacional de Abastecimento (Conab, 2012) (National Supply Company).

A large number of clones are evaluated every year in sugar cane breeding programs, in experiments conducted in different harvests, seasons and regions. It is becoming increasingly difficult to select the best genotypes phenotypically. One of the most important aspects in genetic breeding is the prediction of the genetic values of genotypes, which requires estimating variance components that are either known or accurately estimated. Thus, the optimal procedure for predicting the best linear unbiased prediction (BLUP) of genetic values and the optimal procedure for estimating the residual or restricted maximum likelihood (REML) variance components are both associated with a mixed linear model.

In studies on genetic breeding, consideration of treatment effects as random effects leads to greater predictive accuracy. This is relevant in genetic breeding programs and allows for genetic selection. Otherwise, the selection is phenotypic rather than genetic (Viana et al., 2011; Viana et al., 2012).

The simultaneous consideration of all environments commands the use of a univariate model for selection, taking into account average productivity in the various environments. However, a more complete methodology may allow additional inferences, such as selection of the following: specific genotypes for each

location, stable genotypes across locations, genotypes responsive to environmental improvement and selection on three attributes (productivity, stability and adaptability) simultaneously, Mendes et al. (2012).

The present study aimed to select the most productive clones of sugar cane for a region in the southeast of Brazil, through experimentation on clones in the final stage of evaluation, by investigating adaptability and stability parameters through mixed modeling.

### Materials and Methods

In March and April of 2005, six experiments were carried out in Campos dos Goytacazes, in the state of Rio de Janeiro (21°45'15" S, 41°19'28" W - sites 1 and 2); Conceição da Barra, in the state of Espírito Santo (ES) (18°35'36" S, 39°43'56" W - site 3); Linhares-ES (19°23'28" S, 40°04'20" W - site 4); Itapemirim-ES (21°00'40" S, 40°50'02" W - site 5); and Serra dos Aimorés, in the state of Minas Gerais (17°46'57" S, 40°14'51" W - site 6).

Twenty-four clones were assessed at each site, five of which were considered as standard, while the other 19 were genotypes with potential for recommendation in the regions under evaluation, some of which have already been launched as varieties in other regions of the country. The relationship between the clones is set out in Table 2. The clones were grown under rainfed cultivation and received management treatments, including fertilization and weed control, in accordance with the standard practices in force at each sugar mill field.

The experiments were conducted in a randomized block design with four replications, and each plot formed consisted of four 5-m cane furrows. The experiments were evaluated over three agricultural years, and the last harvest was carried out in 2008. The plots were

harvested and evaluated prior to detrash with fire in commercial plantations in the chosen localities. The trait tons of Pol per hectare were evaluated by the product of the variable ton of cane per hectare and the percentage of sucrose in the cane.

Estimates of the variance components and predictions of the genetic values were made using the REML/BLUP procedure. The simultaneous selection for yield, stability and adaptability of clones was based on the harmonic mean of the relative performance of the predicted genetic values (MHPRVG). All these analyses were done using the model below (Mendes et al., 2012).

$$y = Xf + Zg + Qge + Tgm + Wgml + Sp + e \quad (1)$$

where "y" is the vector of data; "f" the vector of the effects of replication-environment-year combinations (assumed to be fixed) added to the overall average; "g" the vector of the genotypic effects (assumed to be random); "ge" the vector of the effects of the interaction between genotypes and environments (random); "gm" the vector of the effects of genotype × year interaction; "gml" the vector of the effects of the genotype × environment × year triple interaction (assumed to be random); "p" the vector of the permanent effects of the plot within environments (assumed to be random), and "e" the vector of errors or residues (random). The capital letters refer to the matrices of incidence for these effects, and the adjustment of the model was derived from the following mixed model equations:

$$\begin{bmatrix} X'X & X'Z & X'Q & X'T & X'W & X'S \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'Q & Z'T & Z'W & Z'S \\ Q'X & Q'Z & Q'Q + A^{-1}\lambda_2 & Q'T & Q'W & Q'S \\ T'X & T'Z & T'Q & T'T + A^{-1}\lambda_3 & T'W & T'S \\ W'X & W'Z & W'Q & W'T & W'W + A^{-1}\lambda_4 & W'S \\ S'X & S'Z & S'Q & S'T & S'W & S'S + A^{-1}\lambda_5 \end{bmatrix} \begin{bmatrix} \hat{f} \\ \hat{g} \\ \hat{g}e \\ \hat{g}m \\ \hat{g}ml \\ \hat{p} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ Q'y \\ T'y \\ W'y \\ S'y \end{bmatrix} \quad (2)$$

$$\text{where: } \lambda_1 = \frac{\sigma_g^2}{\sigma_g^2}, \lambda_2 = \frac{\sigma_g^2}{\sigma_g^2}, \lambda_3 = \frac{\sigma_g^2}{\sigma_{ge}^2}, \lambda_4 = \frac{\sigma_g^2}{\sigma_{gm}^2}, \lambda_5 = \frac{\sigma_g^2}{\sigma_{gml}^2} \quad (3)$$

where:  $h_e^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_{ge}^2 + \sigma_{gm}^2 + \sigma_{gml}^2 + \sigma_e^2}$ , the genotypic correlation over the years was estimated by  $rg_{years} = \frac{\sigma_{ge}}{\sigma_g + \sigma_{ge}}$ , the genotypic correlation of the environments  $rg_{location} = \frac{\sigma_{gm}}{\sigma_g + \sigma_{gm}}$ , the genotypic correlation of the environment × year interaction was estimated by  $rg_{years} = \frac{\sigma_{gml}}{\sigma_g + \sigma_{gml} + \sigma_e^2}$ .

The BLUP prediction of genotypic averages in each environment was estimated based on the sum of the average values and effects of genotypes and their interaction. The genotypic values predicted for clone i in each environment j used, simultaneously, the data from all the environments and were estimated by  $VG_{ij} = \mu_i + g_i + ge_{ij} + gm_{ik} + p_i$ , where  $\mu_i$  is the average of environment j. The joint selection considering, simultaneously, ton of Pol per hectare, stability and adaptability, was given by the statistical harmonic mean of relative performance for the predicted genotypic values,  $MHPRVG = \frac{n}{\sum_{i=1}^n \frac{1}{VG_{ij}}}$ , where n = number of environments in which clone i was evaluated, and  $VG_{ij}$  is the genotypic value of clone i in the environment j, expressed as the ratio of

the average for this environment. For the analyses SELE-GEN software was used.

## Results and Discussion

Estimates of average heritability of clones ( $h^2m$ ) were made where averages were used as the unit of evaluation. This calculation of heritability is of great interest, since its prediction is based on the averages of several replications. The estimate of the index found for this study was 0.65, which is considered moderate to high, and encourages expectations of superior clone selection.

The genotypic correlation of the response of clones in the environments ('gl) provides a degree of reliability with regard to how constant the ranking of clones will be in these various environments. For such, a value of 0.38 was found, suggesting a high level of genotype × environment interaction and indicates that the best clone in one environment may not be the best in another. Silva et al. (2012) found this value to be 0.635, which indicates the existence of a wide genotype × environment interaction.

The genotypic correlation estimate of the performance of clones over the years has provided a value only marginally superior to  $r_{ge}$ . However, this value ( $r_{ge} = 0.68$ ) is still rated as low, which indicates interaction between genotypes and harvests. Therefore, clones should be evaluated in more than one cropping season in breeding programs.

When the estimation of the genotypic correlation of the behavior of clones in environments and years (environments) is considered, the importance of studies on adaptability and stability becomes evident, since its value is extremely low, namely, 0.22, which indicates a complex genotype × environment interaction. In other words, the classification of clones will not be the same in different environments.

The basic supposition of the analysis of variance and regression analysis, in studies on adaptability and stability, is the independence of errors, which is a procedure that in practice, in more complex situations is imprecise; while the REML method (restricted maximum likelihood) may not take this assumption into consideration and can be more flexible in its application. Furthermore, the analysis of variance shows limitations in joint analyses in the case of heterogeneity of residual variances between environments, which does not occur in REML (Viana et al., 2011; Viana et al., 2012).

In the case of mixed models with random treatment effects, the main properties of BLUP are: (i) maximization of selective accuracy, (ii) minimization of prediction error in non-biased prediction of genetic values, and (iii) maximization of genetic gain per cycle of selection and maximization of likelihood of selecting the best among several genotypes. BLUP is the most efficient selection index for the use of information from relatives. The BLUP of the effects of genotype × environment

interaction ( $g \times e$ ) takes into account the heritability of the effects of the  $g \times e$  interaction, thereby eliminating noise or the residual effects of the interaction during the process of the  $g \times e$  prediction.

Table 1 presents the classification of the genotypic values of the 24 clones evaluated for the trait tons of pol per hectare (TPH) for the 18 environments (six localities  $\times$  three harvests). The clones RB92579, RB867515, SP81-3250, RB947520 and RB758540 present the highest BLUP values for genotypic values for the environment without capitalizing the genotype  $\times$  environment interaction ( $\mu + g$ ). When genotypic values ( $\mu + g$ ) are used for genotype classification, they can be applied in environments different from those where they were evaluated, since this estimate is not capitalized with the effect of the genotype  $\times$  environment interaction (Bastos et al., 2007; Maia et al., 2009). Therefore, the same response is expected for the average in different environments.

When the genotype  $\times$  environment interaction ( $\mu + g + ge$ ) is capitalized, recommendations should be put into practice in areas of the same experimental network or in areas with the same pattern of genotype  $\times$  environment interaction. By applying  $\mu + g + ge_m$ , the same five clones sorted for  $\mu + g$  are selected from those with the

highest genotypic values. Although these two selections are identical as regards the clones selected, the predictions of genotypic values are higher for  $\mu + g + ge_m$ . However, this superiority will only be capitalized if the clones are planted in areas with the same standards of interaction between genotypes and environments as the experimental network evaluated. Thus, the genotypic averages based on  $\mu + g$  are more reliable.

The predicted genetic gains with the cultivation of the five best clones in each location (underlined values), in relation to the average, are 11, 8, 9, 11, 12 and 12 % for sites 1, 2, 3, 4, 5 and 6, respectively. BLUP values obtained for each sugar mill take into account the information from the entire experimental network. Therefore, these estimates are more accurate than the calculation of BLUP values obtained through analyses per environment.

The inferences previously found were applied to clone selection through genotypic values, whether the genotype  $\times$  environment interaction were capitalized or not. However, when analysing adaptability and stability, it was necessary to apply other methodologies. Nowadays, there are numerous methodologies that can be used to evaluate phenotypic adaptability and stabil-

Table 1 – Estimates of the genotypic values without capitalizing the genotype  $\times$  environment ( $\mu + g$ ) interaction and capitalizing the average genotype  $\times$  environment interaction ( $\mu + g + ge_m$ ) and capitalizing the genotype  $\times$  environment interaction for each location ( $\mu + g + ge$ ) for the trait tons of pol per hectare evaluated in six Localities<sup>1</sup>, during three years in 24 clones of sugarcane.  $\mu+g$ .

Clone	Site 1	Site 2	Site 3	Site 4	Site 5	Site 6	Average Environment	
	$\mu + g + ge$	$\mu + g + ge$	$\mu + g + ge$	$\mu + g + ge$	$\mu + g + ge$	$\mu + g + ge$	$\mu + g + ge_m$	$\mu + g$
RB92579	12.61	12.14	15.54	17.80	14.23	18.11	15.07	14.75
RB867515	12.80	12.90	17.53	16.76	12.24	<u>15.92</u>	<u>14.69</u>	<u>14.45</u>
SP81-3250	11.92	12.04	<u>16.33</u>	<u>18.10</u>	12.00	<u>17.74</u>	<u>14.69</u>	<u>14.45</u>
RB947520	12.28	12.45	<u>15.52</u>	<u>17.97</u>	<u>12.96</u>	15.30	<u>14.42</u>	<u>14.24</u>
RB758540	<u>13.10</u>	<u>12.47</u>	<u>15.75</u>	16.43	12.68	15.48	<u>14.32</u>	<u>14.16</u>
RB931530	<u>13.62</u>	<u>12.63</u>	14.31	15.70	<u>14.35</u>	15.18	14.30	14.14
RB92606	12.60	<u>13.11</u>	14.69	16.20	12.08	15.91	14.10	13.99
RB955971	11.05	11.91	15.25	<u>17.50</u>	<u>14.08</u>	14.36	14.02	13.93
RB882698	12.46	11.80	14.12	14.82	13.20	<u>16.85</u>	13.88	13.81
RB956916	12.21	11.42	15.41	<u>17.20</u>	12.51	14.40	13.86	13.80
RB92596	12.32	11.43	15.28	16.50	11.88	15.64	13.84	13.79
RB72454	11.42	11.76	14.77	15.42	12.22	<u>16.16</u>	13.62	13.61
RB855511	11.40	<u>12.57</u>	15.25	16.19	12.04	13.32	13.47	13.49
RB937568	11.76	10.93	15.30	15.49	11.44	15.37	13.38	13.42
RB918639	11.33	11.51	14.03	15.82	12.21	15.12	13.34	13.39
RB956911	10.37	11.84	14.12	16.20	12.82	13.94	13.21	13.29
RB918625	<u>12.76</u>	11.07	13.31	15.38	11.78	14.39	13.12	13.22
RB955970	11.71	11.98	14.02	14.80	12.02	13.94	13.08	13.19
RB935903	10.73	11.48	14.73	15.59	11.40	13.76	12.95	13.09
RB947603	11.64	11.05	13.84	15.14	10.72	15.10	12.92	13.06
RB956918	10.75	10.86	13.84	15.21	11.77	14.19	12.77	12.95
RB858927	10.22	11.29	13.13	14.13	11.72	14.79	12.55	12.77
RB9362	10.49	10.54	14.30	14.18	11.09	14.17	12.46	12.70
RB9344	10.26	10.51	13.29	13.15	10.87	13.67	11.96	12.31
Average	11.74	11.74	14.74	15.91	12.26	15.12	13.58	13.58
Genetic Gain (%)	11	8	9	11	12	12	8	6

<sup>1</sup>Localities: Sites 1 and 2: Campos dos Goytacazes-RJ; Site 3: Conceição da Barra-ES; Site 4: Linhares-ES; Site 5: Itapemirim-ES; Site 6: Serra dos Aimorés-MG. Genetic gain were estimated by selection for best five genotypes each location.

ity, but the simplest interpretation procedures have been more appreciated. Thus, measures that incorporate both stability and adaptability in a single statistical figure are the prevailing ones.

Most procedures for the analysis of adaptability and stability use phenotypic averages after performing the analysis of variance, including the methodologies of Eberhart and Russell (1966) and Lin and Binns (1988), which estimate adaptability and phenotypic stability. In turn, the MHPRVG method, proposed by Mendes et al. (2012), is based on genotypic values predicted via mixed models, where the term adaptability and genotypic stability can be used, which aggregates productivity, stability and adaptability into a single statistical datum.

As for the inferences for expected productivity, genotypic values should be used as follows (Pedrozo et al., 2011): i) for planting in the field of each sugar mill: considering genotypic values by using the genotype  $\times$  environment interaction for each environment ( $\mu + g + ge$ ); ii) for planting in other places with the same standard of genotype  $\times$  environment interaction as the experimental network: considering genotypic values by using the genotype  $\times$  average environment interaction ( $\mu + g + ge_m$ ) or the adaptability of genotypic values (PRVG); iii) for planting in other unknown environments or when using a standard of genotype  $\times$  environment interaction different from the experimental network or

with high environmental heterogeneity within the environment that takes into account genotypic values without capitalizing genotype  $\times$  environment interaction ( $\mu + g$ ) or the stability of genotypic values (MHVG); iv) and for planting in several other environments with different standards of genotype  $\times$  environment interaction: considering stability and adaptability of genotypic values (MHPRVG).

The MHPRVG method was adopted for this study. Table 2 presents the results for the stability of genotypic values (MHVG), adaptability of genotypic values (PRVG and PRVG  $\times$   $\mu$ ) and the stability and adaptability of genotypic values (MHPRVG and MHPRVG  $\times$   $\mu$ ) for the trait TPH, as predicted by BLUP analysis for 24 clones of sugar cane.

The harmonic mean of genetic values (MHVG) classifies genotypes for genotypic values (productivity) and stability, the lower the standard deviation of the genotypic performance between environments, the higher the MHVG value. Thus, selection based on this value implies simultaneous selection for yield and stability, (Mendes et al., 2012). Bastos et al. (2007) evaluated 70 clones and two controls of sugarcane in seven environments and found high correlation between the genotypic values by capitalizing the genotype  $\times$  environment interaction with the values predicted by MHPRVG, which were effective for genotype selection.

Table 2 – Stability of genotypic values (MHVG); adaptability of genotypic values (PRVG and PRVG  $\times$   $\mu$ ); stability and adaptability of genotypic values (MHPRVG and MHPRVG  $\times$   $\mu$ ) for the trait tons of pol per hectare predicted by BLUP analysis for 24 clones of sugarcane.

Clone	MHVG	Clone	PRVG	PRVG $\times\mu$	Clone	MHPRVG	MHPRVG $\times\mu$
RB92579	14.72	RB92579	1.11	15.03	RB92579	1.10	14.99
RB867515	14.39	RB867515	1.08	14.68	RB867515	1.08	14.64
RB931530	14.23	SP81-3250	1.07	14.58	SP81-3250	1.07	14.51
SP81-3250	14.18	RB931530	1.06	14.42	RB947520	1.06	14.38
RB947520	14.14	RB947520	1.06	14.40	RB931530	1.06	14.34
RB758540	14.14	RB758540	1.06	14.35	RB758540	1.06	14.34
RB92606	13.92	RB92606	1.04	14.13	RB92606	1.04	14.11
RB955971	13.70	RB955971	1.03	14.01	RB955971	1.03	13.94
RB882698	13.69	RB882698	1.02	13.92	RB882698	1.02	13.86
RB956916	13.58	RB956916	1.02	13.84	RB956916	1.02	13.81
RB92596	13.55	RB92596	1.02	13.81	RB92596	1.02	13.80
RB72454	13.36	RB72454	1.00	13.61	RB72454	1.00	13.59
RB855511	13.26	RB855511	0.99	13.49	RB855511	0.99	13.44
RB918639	13.11	RB937568	0.98	13.34	RB918639	0.98	13.33
RB937568	13.07	RB918639	0.98	13.33	RB937568	0.98	13.32
RB955970	12.97	RB956911	0.97	13.21	RB956911	0.97	13.16
RB918625	12.95	RB918625	0.97	13.16	RB955970	0.97	13.12
RB956911	12.95	RB955970	0.97	13.13	RB918625	0.97	13.12
RB935903	12.69	RB935903	0.95	12.93	RB935903	0.95	12.91
RB947603	12.65	RB947603	0.95	12.90	RB947603	0.95	12.87
RB956918	12.54	RB956918	0.94	12.76	RB956918	0.94	12.76
RB858927	12.34	RB858927	0.92	12.55	RB858927	0.92	12.53
RB9362	12.21	RB9362	0.92	12.44	RB9362	0.91	12.42
RB9344	11.79	RB9344	0.88	11.97	RB9344	0.88	11.96

MHVG: harmonic mean of genotypic values; PRVG: relative performance of genotypic values; MHPRVG: harmonic mean of the relative performance of genotypic values;  $\mu$ : overall average.

Out of the five best clones for MHVG (RB92579, RB867515, RB931530, SP81-3250 and RB947520), four are among the five best clones classified by joint analysis of genotypic values (excluding clone RB931530).

In relation to type of studies, Bastos et al. (2007) concluded that the MHVG method is a selection that is sufficiently reliable where the aim is stability and productivity. However, Mendes et al. (2012) reported that this methodology cannot be considered reliable for analyzing information from unbalanced experiments where not all clones are present in all environments.

The method of relative performance of genotypic values (PRVG) estimates the adaptability of genetic values in different environments. In this methodology, the predicted genotypic values are expressed as a ratio of the overall average of each location. Then, the average value of this ratio is obtained through the environments (Mendes et al., 2012). It is possible to observe that the five best clones rated by MHVG were also the best using PRVG.

Estimates of MHVG, and PRVG and MHPRVG in cashew plants made by Maia et al. (2009) allowed for selection of more productive genotypes. They concluded that these methodologies can be used in breeding programs for this crop. The MHPRVG method (harmonic mean of the relative performance of genetic values) proposed by Mendes et al. (2012) is among the mixed models and allows simultaneous selection for productivity, stability and adaptability.

Clones RB92579, RB867515, SP81-3250, RB947520 and RB931530 stood out in simultaneous selection for productivity, stability and adaptability and were rated in the five first positions. It is possible to observe certain maintenance of the order of materials in these three methodologies, which indicates that the methods MHVG, PRVG and MHPRVG have a certain degree of agreement in the positioning of genotypes.

For different strategies, a comparison between the methodologies of Lin and Binns (1988) and MHPRVG, with the selection of the ten best clones, as sorted by MHPRVG, showed that eight clones selected by MHPRVG coincide with the ten clones selected using the methodology of Lin and Binns (1988). However, there was also some reverse order among some overlapping clones. Nevertheless, high correlation is observed between the two methods, also reported by Bastos et al. (2007). Mendes et al. (2012) showed that the MHPRVG

methodology has the advantage of providing results in the very scale used for measuring the trait, which allows for calculating genetic gain with simultaneous selection for yield, adaptability and stability.

Several clones were ranked among the five best for more than one of the six localities tested (Table 3), which demonstrates great productive potential. Clones RB92579 (five localities), RB867515 (four localities) and clones RB758540, RB931530, SP81-3250 and RB947520 stood out and were among the most productive in three out of the six localities evaluated.

As the effects of treatments (clones) were accepted as random, tests for multiple comparisons of treatment means are inappropriate (Viana et al., 2012; Piepho, 1998). REML/BLUP (treatments as random effects) should be used, instead of a comparison of means (treatments as fixed effects).

RB92579, RB867515, SP81-3250, RB947520, RB758540 and RB931530 were the best suited clones for planting in other environments with the same pattern of interaction between genotypes and the environment of the experimental network (Table 4). These clones were recommended for planting in other unknown environments, or where there is a pattern of the interaction between genotypes and different environments of the experimental network or high environmental heterogeneity within the environment. Clones RB92579, RB867515,

Table 4 – Clones included among the best five genotypic values for items ii, iii and iv for the six localities evaluated for the trait tons of pol per hectare for 24 clones of sugarcane.

Management Suggested				
ii		iii		iv
$\mu + g + ge_m$	PRVG	$\mu + g$	MHVG	MHPRVG
RB92579	RB92579	RB92579	RB92579	RB92579
RB867515	RB867515	RB867515	RB867515	RB867515
SP81-3250	SP81-3250	SP81-3250	RB931530	SP81-3250
RB947520	RB931530	RB947520	SP81-3250	RB947520
RB758540	RB947520	RB758540	RB947520	RB758540

ii: planting in other environments with the same pattern of interaction between genotype and environment of experimental network, iii: planting in other unknown environments or with pattern of genotype  $\times$  environment interaction different from that of the experimental network or with high environmental heterogeneity within the environment; iv: planting in many other environments with different patterns of genotype  $\times$  environment interaction. PRVG: relative performance of genotypic values, MHVG: harmonic mean of genotypic values, MHPRVG: harmonic mean of the relative performance of genotypic values.

Table 3 – Clones included in the five highest genotypic values for sugarcane, capitalizing the genotype  $\times$  environment interaction ( $\mu + g + ge$ ), for the six localities evaluated for the trait tons of pol per hectare.

Site 1	Site 2	Site 3	Site 4	Site 5	Site 6
RB92579	RB867515	RB92579	RB92579	RB92579	RB92579
RB867515	RB758540	RB867515	SP81-3250	RB947520	RB867515
RB758540	RB931530	SP81-3250	RB947520	RB931530	SP81-3250
RB931530	RB92606	RB947520	RB955971	RB955971	RB882698
RB918625	RB85511	RB758540	RB956916	RB882698	RB72454

<sup>1</sup>Localities: Sites 1 and 2: Campos dos Goytacazes-RJ; Site 3: Conceição da Barra-ES; Site 4: Linhares-ES; Site 5: Itapemirim-ES; Site 6: Serra dos Aimorés-MG.



SP81-3250, RB947520 and RB758540 were selected for planting in several other environments with different patterns of genotype  $\times$  environment interaction.

In conclusion, the mixed model methodology proved adequate for evaluating adaptability and stability, as well as for selecting genotypes with responsive superiority in assessments of various plantation environments.

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