



## Selection of sugarcane families and parents by Reml/Blup

Márcio Henrique Pereira Barbosa<sup>1\*</sup>, Marcos Deon Vilela de Resende<sup>2</sup>, José Antônio Bressiani<sup>3</sup>, Luís Cláudio Inácio da Silveira<sup>1</sup>, and Luiz Alexandre Peternelli<sup>4</sup>

Received 17 November 2004

Accepted 6 October 2005

**ABSTRACT** - Were evaluated 113 full-sib families obtained by unbalanced diallel matings in three experiments in an augmented block design (ABD) planted side by side in the same area. The individual and joint analyses of the experiments were performed by the Reml/Blup method. The use of the ABD without replication did not prove adequate in experiments of family selection owing to the low heritability estimate at the level of family means in comparison to the joint analysis of the three experiments. The results presented predominance of the additive effects for all evaluated traits: number of stalks, tons of stalks per hectare and mean stalk weight. The components of estimated means via Blup allowed the selection of families and superior parents.

**Key words:** Incomplete blocks, mixed models, prediction of crossings, augmented blocks, genetic improvement.

### INTRODUCTION

The augmented block design (ABD) had originally been proposed by Federer (1956) for the use in a sugarcane genetic improvement program of the Hawaiian Sugar Planter's Association - HSPA in Hawaii. The objective was to develop an experimental design that could make the evaluation of a large number of sugarcane clones without replication viable, since in the first clone generation the number of stalks available for the experiment is limited.

This design has been used for the evaluation of first and second generation of sugarcane clones in the genetic improvement program of the Rede Interuniversitária para Desenvolvimento do Setor Sucroalcooleiro - RIDESA ([www.ridesa.org.br](http://www.ridesa.org.br)) (Inter-university network for the development of the sugar/alcohol sector). The advantages

of ABD are: a) operational easiness for the implantation of sugarcane experiments, b) possibility of evaluating large numbers of treatments without replication, in view of the restricted number of stalks of the first and second generation clones, c) flexibility to adjust different block sizes in the same experiment and d) no need of estimating lost plots or such with any kind of problem during the data collection.

The possibility of using this design in experiments of family evaluation has recently been evaluated (Barbosa et al. 2004). The authors underlined the importance of raising the number of replications to increase the heritability at the level of family means. In this case, instead of using one ABD experiment one would use three or more experiments in ABD, which would represent the replications. Such experiments usually comprise over 100 families and would best be

<sup>1</sup> Departamento de Fitotecnia, Universidade Federal de Viçosa (UFV), 36.570-000, Viçosa, MG, Brasil. \*E-mail: [barbosa@ufv.br](mailto:barbosa@ufv.br)

<sup>2</sup> Embrapa Gado de Corte, BR 262, km 4, C. P. 154, 79.002-970, Campo Grande, MS, Brasil

<sup>3</sup> Centro de Tecnologia Canavieira, Fazenda Santo Antônio, S/N, Bairro Santo Antônio, C. P. 162, 13.400-970, Piracicaba, SP, Brasil

<sup>4</sup> Departamento de Informática (UFV)

evaluated by the mixed model methodology with estimation of components of variance by Reml and prediction of additive genetic and genotypic values by the Blup method, as proposed by Barbosa et al. (2004).

The objective of the present study was the estimation of genetic parameters and the prediction of genetic additive and genotypic values for the selection of parents and families, respectively, based on augmented block experiments analyzed by the Reml/Blup procedure.

**MATERIAL AND METHODS**

**Experimental details**

Three experiments in an augmented block design (each experiment with 8 blocks of 16 regular treatments and three controls, or checks) were installed side by side on an experimental area of the Centro de Pesquisa e Melhoramento da Cana-de-Açúcar (CECA) of the Universidade Federal de Viçosa (UFV). CECA lies in the county of Oratórios, state of Minas Gerais (MG) (lat 20° 25' S, long 42° 48' W, alt 494 m asl, soil type LVE).

From the altogether 128 regular treatments (families of full and half-sibs), 113 full-sib families obtained by unbalanced diallel matings were used for the statistical analyses. The common treatments consisted of three cultivars: RB72454, RB835486 and RB739359. Variety RB72454 was planted along the border of the experiment. Fertilization consisted of 500 kg ha<sup>-1</sup> of a formula with 5% N, 25% P<sub>2</sub>O<sub>5</sub> and 25% K<sub>2</sub>O.

The crossings were realized by COPERSUCAR (www.ctc.com.br) in Camamu, state of Bahia (BA). To prevent self-pollination, all inflorescences used as female were emasculated with hot water (Machado Júnior et al. 1996).

The seeds were germinated in August 1999 and the seedlings planted out on the field in November 1999. Plots were represented by two furrows with ten plants each, for the families as much as for the cultivars. The furrows were spaced 1.40 meters and plants 0.5 meter apart. In July 2000, all plants were cut manually with a machete, subjecting the seedlings to natural selection for their capacity of ratooning under unfavorable environmental conditions, that is, during the dry and cold season. In May 2001, data of ratoon cane were collected.

The studied traits at the plot level were: a) total number of industrially useful stalks - NS and b) weight of 20 randomly sampled stalks, with posterior transformation

to mean stalk weight - MSW. The yield expressed in tons of stalks per hectare (TSH) was obtained by the product of NS and MSW.

**Data analyses**

Individual and joint analyses of the three experiments were carried out next. For the joint analysis each experiment was considered as one replication.

The statistical analyses were realized by software Selegen-Reml/Blup (Resende 2002a) for genetics and statistics.

The mixed model equations (Resende 2002b) were used to calculate the Blups of the genetic values and specific combining ability (SCA) of each family for NS, MSW and TSH, considering the relationship matrix as described below

$$y = Xl + Za + Wc + Ub + e, \text{ where}$$

**Mixed linear model**

$y, l, a, c,$  and  $e$ : vectors of data, of the fixed effects of experiment, of the random additive genetic effects, of the random SCA effects, of the random block effects and of the random errors, respectively.  
 $X, Z, W$  and  $U$ : incidence matrices of  $l, a, c$  and  $b$ , respectively.

**Distributions and structures of means and variances**

$$\begin{aligned} y & \mid l, V \sim N(Xl, V) \\ a & \mid A, \sigma_a^2 \sim N(0, A\sigma_a^2) \\ c & \mid \sigma_c^2 \sim N(0, I\sigma_c^2) \\ b & \mid \sigma_b^2 \sim N(0, I\sigma_b^2) \\ e & \mid \sigma_e^2 \sim N(0, I\sigma_e^2) \\ \text{Cov}(a, c') &= 0; \quad \text{Cov}(a, b') = 0; \quad \text{Cov}(a, e') = 0 \\ \text{Cov}(c, b') &= 0; \quad \text{Cov}(c, e') = 0; \quad \text{Cov}(b, e') = 0, \text{ or else:} \end{aligned}$$

$$E \begin{bmatrix} y \\ a \\ c \\ b \\ e \end{bmatrix} = \begin{bmatrix} Xl \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{ and } \text{Var} \begin{bmatrix} y \\ a \\ c \\ b \\ e \end{bmatrix} = \begin{bmatrix} V & ZA\sigma_a^2 & Wl\sigma_c^2 & Ul\sigma_b^2 & l\sigma_e^2 \\ A\sigma_a^2 Z' & A\sigma_a^2 & 0 & 0 & 0 \\ l\sigma_c^2 W' & 0 & l\sigma_c^2 & 0 & 0 \\ l\sigma_b^2 U' & 0 & 0 & l\sigma_b^2 & 0 \\ l\sigma_e^2 & 0 & 0 & 0 & l\sigma_e^2 \end{bmatrix}$$

$$V = \text{Var}(y) = ZA\sigma_a^2Z' + W\sigma_c^2W' + U\sigma_b^2U' + I\sigma_e^2,$$

where  $A$  is the genetic additive relationship matrix between the parents used in a cross.

**Mixed model equations**

$$\begin{bmatrix} X'X & X'Z & X'W & X'U \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'W & Z'U \\ W'X & W'Z & W'W + I\lambda_2 & W'U \\ U'X & U'Z & U'W & U'U + I\lambda_3 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{c} \\ \hat{b} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ U'y \end{bmatrix}$$

where:

$$\lambda_1 = \frac{\sigma_e^2}{\sigma_a^2} = \frac{1 - h^2 - c^2 - b^2}{h^2};$$

$$\lambda_2 = \frac{\sigma_e^2}{\sigma_c^2} = \frac{1 - h^2 - c^2 - b^2}{c^2};$$

$$\lambda_3 = \frac{\sigma_e^2}{\sigma_b^2} = \frac{1 - h^2 - c^2 - b^2}{b^2}.$$

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_c^2 + \sigma_b^2 + \sigma_e^2}$$

individual heritability in the narrow sense

$$c^2 = \frac{\sigma_c^2}{\sigma_a^2 + \sigma_c^2 + \sigma_b^2 + \sigma_e^2}$$

coefficient of determination of the dominance effects among families

$$b^2 = \frac{\sigma_b^2}{\sigma_a^2 + \sigma_c^2 + \sigma_b^2 + \sigma_e^2}$$

coefficient of determination of the block effects

The components of variance were obtained by the Restricted Maximum Likelihood (Reml) method and used to compute the estimates of individual heritability at the level of full-sib family means according to Resende (2002b).

**Iterative estimators of the components of variance by Reml via EM algorithm**

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

$$\hat{\sigma}_a^2 = [\hat{a}'A^{-1}\hat{a} + \hat{\sigma}_e^2 \text{tr}(A^{-1}C^{22})] / q$$

$$\hat{\sigma}_c^2 = [\hat{c}'\hat{c} + \hat{\sigma}_e^2 \text{tr}(C^{33})] / s_1$$

$$\hat{\sigma}_b^2 = [\hat{b}'\hat{b} + \hat{\sigma}_e^2 \text{tr}(C^{44})] / s_2, \text{ where}$$

$C^{22}$ ,  $C^{33}$  and  $C^{44}$  are derived from  $C$ .

$C$ : matrix of the coefficients of the mixed model equations.

$\text{tr}$ : matrix trace operator.

$r(x)$ : rank of the  $X$  matrix.

$N$ ,  $q$ ,  $s_1$  and  $s_2$ : total number of data, of parents, of crossings, and of blocks, respectively.

The estimator of the component of variance of dominance among families is given by  $\hat{\sigma}_d^2 = \hat{\sigma}_c^2$ , that is, it is equal to the component of variance associated with the specific combining ability. In this case,  $\hat{\sigma}_d^2$  is 1/4 of the genetic variance of total dominance present in the population.

**Selection procedures**

Two selection procedures, of families and of parents, were considered. The families were selected by their genotypic values, predicted by  $(1/2)(\hat{a}_i + \hat{a}_j) + \hat{c}_{ij}$ , where  $\hat{a}_i$  and  $\hat{a}_j$  are the predicted additive genetic values of parent  $i$  and  $j$ , respectively, and  $\hat{c}_{ij}$  is the specific combining ability of the cross of parents  $i$  and  $j$ .

**RESULTS AND DISCUSSION**

**Estimates of genetic parameters**

The analysis of the design in augmented blocks (ABD) traditionally considers the effects of treatments and blocks as fixed, by means of the so-called intrablock analysis. In genetic plant improvement it is common to consider mixed models, i.e., models that contemplate the fixed as much as the random effects in a particular analysis. According to Resende et al. (1996) and Smith et al. (2001) the purely environmental effects are considered fixed and the genetic effects random in the analysis of mixed models. So, all effects of the model were considered random in the present study, with exception of the common treatment and the experiment or replication effects, considered as fixed in the joint and individual analysis for the three cited experiments. The effects for blocks are not purely environmental,

since the same are incomplete and therefore contain genetic information that should be recovered.

Table 1 presents the estimates of the genetic parameters for the individual and joint analyses of experiments in the augmented block design. The joint analysis was realized using and not using common treatments. There were practically no alterations in the magnitudes of the estimated genetic parameters due to the fact of using or not using common treatments. These results are in agreement with the ones obtained by Barbosa et al. (2004). This can be explained by the fact that several progenies were related, so that even without checks the blocks are linked by means of the parents that have progenies in the different blocks. Note that the effects of controls were considered fixed. This is essential in the analysis procedure when the controls have a different genetic structure from the rest of the treatments, as in the case of our study.

The results also suggest that it would be possible to use many ABDs, each one representing a replication for the evaluation of families. This would be particularly important for the traits TSH, NS and MSW, given that the heritabilities estimated in the analyses of the individual ABDs were practically zero. As observed earlier by Barbosa et al. (2004), the traditional ABDs without replication thus proved inadequate for sugarcane improvement.

The estimate of the narrow-sense heritability obtained for number of stalks (0.18) is similar to that (0.21) reported by Bressiani et al. (2003) in ratoon cane as well as to that (0.23) observed by Hogarth (1971). For mean stalk weight (0.16) it is also similar to the one (0.19) reported by Bressiani et al. (2003) in ratoon and that (0.21) reported by Hogarth (1971). The heritability obtained for TSH (0.13) is identical to that observed by Barbosa et al. (2004).

**Table 1.** Estimates of genetic parameters in the Reml/Blup analysis of full-sib sugarcane families and in the individual and joint analyses for three concomitantly planted experiments in augmented block design

	Genetic parameters							Acc.	Gen. mean	CV <sub>e</sub> %	CV <sub>f</sub> %
	$\hat{\sigma}_a^2$	$\hat{\sigma}_d^2$	$\hat{\sigma}_e^2$	$\hat{h}_r^2$	$\hat{h}_a^2$	$\hat{h}_{\beta}^2$	$\hat{h}_{fm}^2$				
<b>Tons of stalks hectare</b>											
Joint analysis											
With com. treat.	52.8	0.07	234	0.13	0.13	0.06	0.25	0.50	53.5	28.5	9.60
Without c. treat.	57.8	0.07	217	0.15	0.15	0.07	0.28	0.53	53.8	27.4	9.98
Individual analysis											
Experiment 1	1.98	0.79	286	.006	.008	.003	-	-	62.4	27.1	1.74
Experiment 2	2.00	1.28	290	.005	.008	.003	-	-	55.4	30.7	2.07
Experiment 3	2.04	0.46	250	.006	.007	.003	-	-	45.7	34.6	2.32
<b>Number of stalks</b>											
Joint analysis											
With com. treat.	102	0.10	342	0.18	0.18	0.09	0.31	0.55	99.1	18.6	7.23
Without c. treat.	98	0.11	350	0.17	0.17	0.08	0.29	0.54	100.2	18.6	7.00
Individual analysis											
Experiment 1	3.34	0.23	365	.008	.008	.004	-	-	103.2	18.4	1.27
Experiment 2	4.16	1.04	519	.005	.007	.003	-	-	105.7	21.5	1.44
Experiment 3	3.34	1.10	464	.005	.007	.003	-	-	93.8	22.9	1.48
<b>Mean stalk weight</b>											
Joint analysis											
With com. treat.	.004	.0000	.015	0.15	0.15	0.07	0.30	0.55	0.74	16.8	6.44
Without c. treat.	.005	.0000	.011	0.22	0.22	0.11	0.42	0.65	0.73	14.5	7.23
Individual analysis											
Experiment 1	.0003	.0000	.022	.012	.012	.006	-	-	0.84	17.7	1.45
Experiment 2	.0001	.0000	.014	.006	.006	.003	-	-	0.72	16.3	0.97
Experiment 3	.0006	.0000	.015	.030	.030	.015	-	-	0.66	18.5	2.59

With com. treat: With common treatment; Without c. treat: Without common treatment; Acc: Accuracy; Gen. mean: General mean;  $\hat{\sigma}_a^2$ : additive genetic variance;  $\hat{\sigma}_d^2$ : genetic variance of dominance between families;  $\hat{\sigma}_e^2$ : residual variance;  $\hat{h}_r^2$ : individual heritability in the narrow sense;  $\hat{h}_a^2$ : individual heritability in the broad sense;  $\hat{h}_{\beta}^2$ : heritability in the broad sense at the mean family level;  $\hat{h}_{fm}^2$ : heritability of family in the broad sense at the individual level; CV<sub>e</sub> %: coefficient of environmental variation; CV<sub>f</sub> %: coefficient of genetic variation between full-sib families

The coefficients of genetic variation between families oscillated from 7 to 10%. These values are coherent with those (11 to 13.5%) obtained by Bressiani et al. (2005) as well as the ones obtained in Australia (7 to 14.5%) by the same authors.

### Family selection

The evaluation of families in experimental designs allows a quantification of their genotypic values for selection of superior ones. Table 2 presents the genotypic values for TSH, NS and MSW of the 40 families selected based on TSH, that is, a selected proportion of 35.39%. The means of the selected families for TSH, NS and MSW were 58.37, 104.47 and 0.78, respectively. This represents expected gains with selection among families of 1.29, 0.78 and 1.22% for TSH, NS and MSW, respectively.

Based on the results of this study it was possible to indicate superior families that could be reproduced in the next round of crossings aiming at the production of a greater quantity of seeds for posterior selection and establishment of clones. In the case of our experiment there were only 60 plants of each cross. Despite 60 plants represent a sufficient sample size for inferences on the mean of TSH of a particular cross according to Barbosa et al. (2001), it is also a number that does not allow the exploitation of all possible desirable combinations for the appearance of a superior plant. The individual selection that aims at the establishment of clones within each family is based on visual criteria that involve a series of morphological traits. It is therefore highly desirable to have an expressive number of genotypes which increase the probability that a certain plant would associate various traits of agronomical interest once the genotype will be fixed (clone) by selection.

The hybrid combinations that exceed the expected mean yield based on the general combining ability of the parents are said to have a higher specific combining ability – SCA. In the present study the SCA values were negligible for the three traits. These results evidence that the additive effects for this population were predominant, in agreement with Mariotti et al. (1999), Bressiani et al. (2002) and Barbosa et al. (2004) who showed in their studies that the general combining ability (GCA) was superior to SCA for TSH, corroborating the results presented in Table 1. Similarly, Hogarth (1977) also found predominance of the additive effects for MSW. On the other hand, Bastos et al. (2003) reported predominance of the additive as much as of the non additive effects for MSW.

Some studies on quantitative genetics (Hogarth 1977 and Hogarth et al. 1981) realized with sugarcane showed that the additive and non-additive genetics effects are equally important in the expression of TSH. On the other hand, Bastos et al. (2003) observed predominance of SCA for TSH. The predominance of GCA or SCA depends on the genetic proprieties (allelic frequencies, complementarity, divergence) of the evaluated populations and crossings. Closer related populations (with a higher mean coefficient of relatedness among plants) tend to have a higher additive variation and lower variation of dominance.

### Parent selection

The experiments of family evaluation also bring forth information on the additive genetic effects of the parents involved in the crossings, as shown in Table 3. The table shows the number of times that a particular parent participated in the crossings. Clone SP81-5450 was the genotype that participated most in the crossings, ten times as female and once as male. There are several clones that participated in only one cross, used as male or female. This imbalance evidences the potential of the Blup to proceed with the genetic analyses realized here. According to Panter and Allen (1995), in the case of unbalanced data the fixed model effects can lead to imprecise estimates of the family effects and there is a tendency to select poorly tested parents.

Knowledge on the estimates of additive genetic effects allows the selection of parents with a greater combining ability. These parents could in turn be crossed with others and among each other (in combinations that were not yet evaluated) in order to exploit the SCA in the next rounds of crossings.

A strategy that should be used by these sugarcane improvement programs is the construction of a database with the parents' genetic information. This could be very useful to apply the interpopulational recurrent selection strategy proposed by Barbosa (2000) for sugarcane improvement.

These additive genetic effects would be better estimated by topcross experiments, in other words, a group of clones of a certain population receives pollen from a clone of another population and vice-versa, resulting in predictions of the interpopulation additive effects, that is, information on the interpopulational GCA. The clones of best combining ability would be used in crossings aiming at the SCA exploitation. The topcross strategy is a very important step given the high number of promising clones that enter the Estação de Floração e Cruzamentos da Serra do Ouro in Murici, state of Alagoas

(www.ridesa.org.br). This station produces the seed used by the net of federal universities that join their efforts to develop cultivars labeled RB (Ridesa Brazil).

## CONCLUSIONS

- 1) The magnitudes of the genetic parameters estimated by the Reml procedure were independent of the fact whether common treatments were used or not used in the analysis of the augmented blocks design of a large number of families.
- 2) There was predominance of the additive genetics effects for tons of stalks hectare<sup>-1</sup>, number of stalks

and mean stalk weight.

- 3) The Blup method allowed the selection of families and of superior parents based on a structure of unbalanced diallel crossings, generating essential information for cane improvement programs.

## ACKNOWLEDGEMENTS

The genetic sugarcane improvement program of the UFV was supported financially by CNPq, FAPEMIG, RIDESA and sugar and alcohol mills in Minas Gerais. COPERSUCAR provided the seeds.

**Table 2.** Genotypic values for tons of stalks per hectare (TSH), number of stalks (NS) and mean stalk weight (MSW) for the 40 sugarcane progenies selected based on TSH

Female	Male	TSH	NS	MSW	Female	Male	TCH	NC	MSH
SP84-7017	SP80-185	64.39	103.27	0.88	SP86-91	SP85-162	57.72	103.49	0.78
SP80-180	SP84-7017	63.76	107.79	0.84	SP88-721	SP84-7017	57.54	95.48	0.84
SP80-3280	SP80-185	62.15	106.51	0.81	IAC86-2210	SP84-2029	57.52	104.36	0.78
SP84-7017	SP81-306	61.81	104.77	0.82	SP80-1230	SP80-3280	57.34	106.41	0.74
SP81-5450	SP80-180	61.57	113.55	0.76	SP80-180	SP82-3530	57.25	105.52	0.76
RB855036	SP80-185	61.42	101.54	0.83	RB825336	SP84-2268	57.14	101.04	0.80
SP81-306	SP85-162	60.57	105.51	0.80	SP81-5450	SP86-155	56.95	107.23	0.73
SP80-185	SP84-5019	60.52	104.69	0.80	RB825336	SP80-1836	56.81	105.10	0.75
SP80-185	SP81-231	60.40	105.2	0.81	SP84-2029	SP81-1763	56.72	107.73	0.73
SP80-180	SP80-1842	60.31	107.87	0.79	SP80-1230	SP84-1192	56.72	106.01	0.74
SP79-2233	SP80-180	60.17	108.64	0.77	SP84-7017	SP86-45	56.46	97.01	0.81
SP84-1192	SP84-7017	59.36	102.96	0.80	SP81-5450	SP79-2233	56.44	106.71	0.73
SP80-180	SP88-797	59.27	108.61	0.76	RB865526	RB855584	56.28	98.53	0.79
SP80-1816	SP80-180	58.90	108.87	0.75	SP81-5450	SP83-2847	56.07	104.26	0.75
SP84-7017	SP84-5019	58.34	101.53	0.80	SP84-2029	SP88-819	56.05	110.86	0.70
RB825336	SP81-5450	58.06	109.08	0.74	SP79-2233	SP80-1230	55.99	104.01	0.74
SP84-7017	SP84-2025	57.94	98.77	0.83	SP84-2029	SP82-6108	55.92	104.61	0.74
SP82-3530	SP80-185	57.88	101.00	0.80	RB855036	TUC77-42	55.87	100.12	0.76
SP84-2268	SP85-162	57.88	98.57	0.83	SP81-5450	SP84-2025	55.75	104.53	0.74
SP84-2029	SP88-754	57.85	109.14	0.74	SP82-3530	SP84-7017	55.71	97.83	0.79

**Table 3.** Additive genetics effects (a) predicted by BLUP for tons of stalks per hectare (TSH), number of stalks (NS) and mean stalk weight (MSW) of the parents of 113 full-sib sugarcane families evaluated in three concomitantly planted experiments in augmented block design

Genotype	a			n		Genotype	a			n	
	TSH	NS	MSW	♀	♂		TSH	NS	MSW	♀	♂
SP80-185	12.73	6.21	0.14	2	4	SP80-4439	-0.23	2.76	-0.03	1	3
SP80-180	11.46	15.25	0.07	4	3	RB845239	-0.27	-5.86	0.03	0	1
SP84-7017	8.38	-0.12	0.13	6	4	SP88-797	-0.59	1.51	-0.02	0	1
SP81-306	7.54	9.19	0.02	1	2	SP88-721	-0.97	-9.36	0.07	4	2
SP85-162	5.91	1.37	0.09	1	4	SP88-819	-1.09	8.50	-0.07	1	2
SP84-2029	5.52	12.77	0.00	6	1	SP80-1816	-1.34	2.03	-0.04	6	2
RB865526	4.61	2.08	0.07	1	0	SP82-6108	-1.36	-3.98	0.02	0	1
RB825336	4.42	6.31	0.03	4	0	SP84-5124	-1.89	8.79	-0.10	0	5
SP81-5450	4.01	11.39	-0.03	10	1	RB835205	-2.05	0.79	-0.04	2	1
SP80-3280	3.89	6.36	0.00	2	1	RB815521	-2.10	0.00	-0.04	0	1
L60-14	3.86	3.53	0.03	2	0	SP87-365	-2.88	-1.39	-0.05	0	3
SP80-1230	3.10	6.00	0.01	3	1	RB855113	-2.97	-6.15	-0.02	0	1
SP84-1192	2.66	5.58	0.00	3	1	RB835089	-3.05	-3.83	-0.03	1	0
SP88-754	2.49	5.06	0.01	1	0	RB855598	-3.07	-7.22	0.00	1	0
SP77-5181	2.49	1.89	0.05	0	2	SP70-1143	-3.11	-4.53	-0.03	0	1
RB855036	2.43	-3.58	0.05	2	0	SP86-45	-3.14	-6.29	0.00	0	3
SP86-155	2.21	2.62	0.01	0	2	RB815627	-3.27	-2.28	-0.04	1	1
SP84-2268	2.16	-4.68	0.09	2	2	RB855156	-3.30	-6.25	-0.01	1	0
SP88-607	2.11	-0.29	0.05	1	1	RB855002	-3.40	-8.65	0.01	1	0
RB825548	1.89	2.33	0.01	0	1	SP80-144	-3.63	-6.23	-0.02	1	0
IAC86-2210	1.85	-4.49	0.09	7	0	RB845210	-4.03	-7.78	-0.02	1	1
SP86-91	1.84	5.16	-0.01	3	3	SP82-3530	-4.65	-4.66	-0.02	6	3
RB835486	1.73	-0.77	0.04	1	2	SP79-1011	-5.41	-6.85	-0.03	1	1
TUC77-42	1.63	3.37	0.00	0	1	RB855536	-5.47	-9.95	-0.03	1	1
SP80-1836	1.51	3.43	0.00	2	1	RB72454	-5.52	-8.87	-0.03	1	0
SP80-1842	1.48	0.03	0.04	1	2	NA56-79	-5.80	-5.63	-0.08	0	1
SP79-2233	1.20	1.58	0.00	3	1	SP83-1483	-6.11	-9.53	-0.01	1	1
RB75126	1.10	-2.12	0.04	0	1	RB855046	-6.42	-11.99	-0.02	1	1
SP84-5019	0.63	2.73	-0.01	0	4	SP81-3251	-6.54	-5.49	-0.06	2	2
SP83-2847	0.46	-3.32	0.04	0	2	RB855181	-6.77	-12.82	-0.02	0	1
SP81-231	0.39	3.74	-0.01	4	1	SP80-3480	-6.94	-7.73	-0.06	0	2
RB855584	0.26	-5.46	0.04	0	1	SP85-7227	-7.16	-3.83	-0.07	2	4
SP81-1763	0.23	2.24	-0.01	1	1	SP87-425	-8.07	-13.31	-0.04	0	4
RB855035	0.20	-3.17	0.05	1	1	SP81-3250	-9.03	-12.14	-0.05	2	2
SP84-2025	-0.18	-2.79	0.04	0	7	SP86-96	-10.24	-6.02	-0.15	1	3

n: Number of times a particular genotype participated in the crossings as female (♀) or male (♂)

## Seleção de famílias e de genitores de cana-de-açúcar via Reml/Blup

**RESUMO** - Foram avaliadas 113 famílias de irmãos-completos obtidas sob cruzamentos dialélicos desbalanceados em três experimentos no delineamento em blocos aumentados (DBA) plantados de forma adjacente na mesma área.

*A análise individual e conjunta dos experimentos foi feita pelo método Reml/Blup. O emprego do DBA sem repetição em experimentos de seleção de famílias não se mostrou adequado em virtude das baixas estimativas da herdabilidade ao nível de médias de famílias em comparação à análise conjunta dos três experimentos. Os resultados revelaram predominância dos efeitos aditivos para todos os caracteres avaliados: número de colmos, toneladas de colmos por hectare e peso médio de colmos. Os componentes de médias estimados via Blup possibilitaram a seleção de famílias e de genitores superiores.*

**Palavras-chave:** Blocos incompletos, modelos mistos, predição de cruzamentos, blocos aumentados, melhoramento genético.

## REFERENCES

- Barbosa MHP (2000) Perspectivas para o melhoramento da cana-de-açúcar. In: Raposo FV, Lambert ES, Alves GF, Mendonça HA, Faria MV and Gomes MS (eds.) **Anais do IV Simpósio de Atualização e Melhoramento de Plantas**. Editora UFLA, Lavras, p. 1-17.
- Barbosa MHP, Peternelli LA and Silveira LCI (2001) Plot size in sugarcane family selection experiments. **Crop Breeding and Applied Biotechnology 1**: 271-276.
- Barbosa MHP, Resende MDV, Peternelli LA, Bressiani JA, Silveira LCI, Silva FL and Figueiredo ICR (2004) Use of REML/BLUP for the selection of sugarcane families specialized in biomass production. **Crop Breeding and Applied Biotechnology 4**: 218-226.
- Bastos IT, Barbosa MHP, Cruz CD, Burnquist WL, Bressiani JA and Silva FL (2003) Análise dialélica em clones de cana-de-açúcar. **Bragantia 62**: 199-206.
- Bressiani JA, Burnquist WL, Fuzatto SR, Bonato AL and Geraldi IO (2002) Combining ability in eight selected clones of sugarcane (*Saccharum* spp). **Crop Breeding and Applied Biotechnology 2**: 411-416.
- Bressiani JA, Vencovsky R, Silva JAG (2003) Repeatability within and between selection stages in a sugarcane breeding program. **American Society of Sugarcane Technologists 23**: 40-47.
- Bressiani JA, Vencovsky R and Burnquist WL (2005) Modified Sequential Selection in Sugarcane. In: **Proceedings of International Society of Sugarcane Technologists**. ISSCT, Guatemala, p. 459-467.
- Federer WT (1956) Augmented (or Hoonuiaku) designs. **The Hawaiian Planters' Record 55**: 191-208.
- Hogarth DM (1971) Quantitative inheritance studies in sugarcane. I. Estimation of variance components. **Australian Journal of Agricultural Research 22**: 93-102.
- Hogarth DM (1977) Quantitative inheritance studies in sugar cane. III The effect of competition and violation of assumptions on estimation of genetic variance components. **Australian Journal Research 28**: 257-268.
- Hogarth DM, Wu KK and Heinz DJ (1981) Estimating genetic variance in sugar cane using a factorial cross design. **Crop Science 21**: 21-25.
- Machado Junior GR, Walker DI, Bressiani JA and Silva JAG (1996) Emasculation of sugarcane tassels using hot water. In: Cock JH and Brekelbaum T (eds.) **Proceedings of the XXII Congress of the International Society of Sugarcane Technologists in the 1995**. ISSCT, Cali, p. 346-352.
- Mariotti, JA, Cuenya, MI and Salas and MBG (1999) Análisis de componentes familiares e intra-familiares em progenies de combinaciones biparentales de canã de azucar (*Saccharum* spp.). **Revista Industrial y Agrícola de Tucumán 76**: 52-57.
- Panter DM and Allen FL (1995) Using Best Linear Unbiased Predictions to Enhance Breeding for yield in soybean: I Choosing parents. **Crop Science 35**: 397-405.
- Resende MDV (2002a). **Software Selegen-REML/BLUP**. Embrapa Floresta, Curitiba, 67p (Documentos 77).
- Resende MDV (2002b) **Genética biométrica e estatística no melhoramento de plantas perenes**. Embrapa Informação Tecnológica, Brasília, 975p.
- Resende MDV, Prates DF, Jesus A and Yamada CK (1996) Estimación de componentes de variância e predição de valores genéticos pelo método da máxima verossimilhança restrita (REML) e melhor predição linear não viciada (BLUP) em *Pinus*. **Boletim de Pesquisa Florestal 32/33**: 18-45.
- Smith A, Cullis B and Gilmour A (2001) The analysis of crop variety evaluation data in Australia. **Australian New Zealand Journal of Statistics 43**: 129-145.