

# Sugarcane Family Selection and Genetic Parameter Prediction via the REML/BLUP Methodology

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## Abstract

Most sugarcane breeding programs tend to evaluate low heritability characteristics during the initial stages of genotype selection. Thus, family selection has been recently preferred. In this context, the aim of the present study was to select the best family among 78 sugarcane families, as well as estimate genetic values through the mixed models of restricted-maximum likelihood and best non-bias predictor (REML/BLUP) methodology, originating from the República Brasil 2005 (RB05) series. This strategy was deemed efficient, and 34 to 38 families were chosen from four evaluated characteristics underexplored by genetic researchers such as total plot mass (MTT), mean mass of one tiller in the plot (M1C), stature (EST), and mean number of canes per square meter (NCM). The family increments ranging from 6.02 to 82.11%, in the next genetic culture improvement program selection phases.

**Keywords:** likelihood, mixed model, *Saccharum* spp., sugarcane breeding

## 1. Introduction

Due to Brazil's privileged position regarding sugarcane (*Saccharum* spp.) cultivation, crop breeding programs have focused on developing new cultivars with high productive sugarcane and sugar potential. In this context, it is crucial to select materials during the early stages of the breeding program. Usually, low heritability characteristics are evaluated during these initial stages. However, a high number of individuals is generally selected, as these characteristics present high coefficients of variation. To avoid this, the family selection procedure is adopted, which aims to select the best sugarcane families and reject the worst (Silva, Barbosa, Resende, Peternelli, & Pedrozo, 2015), since the best families tend to be more effective in generate promising clones for the next breeding program phase.

Family selection has been previously reported in other studies, due to its crucial importance in increasing genetic gain in breeding programs, not only by measuring an individual's potential to be a future genitor, but also in predicting potential values. This allows for strategy alterations in the next selection steps, if necessary, increasing experiment efficiencies and estimating the additive variance of the plants (Brasileiro, Paula Mendes, Peternelli, Silveira, Resende, & Barbosa, 2016; Almeida, Viana, Amaral Júnior, & Júnior, 2014; Atkin, Dieters, & Stringer, 2009).

Among family selection methodologies, REML/BLUP is the most noteworthy (Meyer, 1991; Resende, 2002). BLUP has been routinely applied in animal breeding and, recently, in plant breeding programs (Almeida Filho, Tardin, Guimarães, & Resende, 2016; Oakey, Verbyla, Pitchford, Cullis, & Kuchel, 2006; Oakey, Verbyla, Cullis, Wei, & Pitchford, 2007), as it is more precise than other methodologies, such as AMMI, for example, as it applies genotype correlation information from individuals. REML exhibits certain advantages compared to the least squares (ordinary or generalized) method (Kennedy & Sorensen, 1988), as it applies information regarding the individuals themselves (or from the genitors, if necessary), making it unbiased. In addition, it also takes into account the genetic covariance among treatments, weighing genotype imbalances within the adopted statistical design.

Variable responses regarding heritability in the narrow sense, from low to medium magnitude, are available in the literature, including clump mass, °Brix, tons of cane per hectare and average mass of the tiller, among others, which fit mixed models and family selection methodologies (Castro, Peternelli, Resende, Marinho, Costa, Barbosa, & Moreira, 2016; Oliveira et al., 2008; Pedroso et al., 2009).

In this context, the aim of the present study is to select genetic materials by applying the RELM/BLUP methodology for the RB05 series from the Sugarcane Genetic Improvement Program (PMGCA), from the Inter-University Network for the Development of the Sugaralcohol sector (RIDESA), in its first improvement phase (T1). Genetic parameters for four underexplored sugarcane characteristics, namely total plot mass (MTT), mean mass of one tiller in the plot (M1C), stature (EST), and mean number of canes per square meter (NCM) were also evaluated.

## **2. Material and Methods**

The field experiment comprised a total of biparental cross 78 families (Table 1) (a cross where the male and female parents are known), in a Federer block arrangement (Federer, 1956) with five replicates, where each experimental plot was considered as being one clump of sugarcane, planted in two 5 m rows, with a 1.40 m space between rows and 0.50 m between individuals, in the municipality of Paranaíba (22°58' S, 52°28' W, 503 m a.s.l.), in the state of Paraná (PR), Brazil.

Table 1. Number of biparental crosses, relationship between female and male parents and codes used to identify the crosses used herein regarding the study of *Saccharum* spp. sibling species families from the RB05, Paranavai municipality, Paraná, Brazil

Nº	Female	Male	Family Code	Nº	Female	Male	Family Code
1	Co434	RB946915	F23M76	40	RB855511	RB961530	F01M39
2	Co775	RB855035	F27M56	41	RB931604	RB957751	F19M29
3	Laica98-208	RB855035	F32M56	42	RB945961	RB956911	F10M51
4	RB945956	RB855035	F70M56	43	RB945961	RB957751	F10M29
5	RB855035	RB945956	F56M70	44	RB92606	RB971537	F04M40
6	RB945956	IAC87-3396	F70M30	45	RB92606	RB971551	F04M79
7	RB945956	RB945065	F70M75	46	RB971537	RB943339	F40M74
8	RB945956	RB947501	F70M48	47	RB943339	RB971537	F74M40
9	RB945065	RB945956	F75M70	48	IAC93-7009	H83-9998	F11M69
10	RB947501	RB945956	F48M70	49	RB71114	SP91-1049	F44M02
11	RB941531	IAC87-3396	F66M30	50	RB855563	SP91-1049	F34M02
12	IAC87-3396	RB855063	F30M36	51	RB896342	RB961527	F26M55
13	RB912695	RB945065	F49M75	52	RB896342	RB92508	F26M65
14	RB947501	SP80-3280	F48M41	53	RB915141	RB855322	F57M12
15	RB739735	SP80-3280	F63M41	54	RB91537	SP91-1049	F81M02
16	SP80-3280	RB947501	F41M48	55	RB925211	SP70-1143	F67M37
17	SP80-3280	L60-14	F41M22	56	RB925211	SP91-1049	F67M02
18	SP80-3280	RB72454	F41M82	57	RB925345	RB915124	F54M07
19	SP80-3280	RB835486	F41M60	58	RB93522	RB957689	F35M06
20	SP80-3280	RB867515	F41M64	59	RB936001	RB965586	F45M78
21	SP80-3280	RB872552	F41M21	60	RB945962	RB947532	F59M18
22	SP80-3280	RB965911	F41M20	61	RB945962	RB9620	F59M50
23	SP80-3280	SP70-1284	F41M53	62	RB945964	SP91-1049	F42M02
24	SP80-3280	SP71-6949	F41M47	63	RB946022	RB925211	F09M67
25	SP83-2847	L60-14	F14M22	64	RB951015	RB957712	F13M17
26	RB72454	RB855511	F82M01	65	RB915141	SP89-1115	F57M46
27	RB9557	RB72454	F80M82	66	RB957610	RB93522	F62M35
28	SP83-2847	RB72454	F14M82	67	RB957712	RB93522	F17M35
29	RB835486	IAC86-2210	F60M16	68	RB957712	RB945954	F17M25
30	RB835486	RB835089	F60M52	69	RB962002	RB965921	F03M33
31	RB835486	RB855127	F60M43	70	RB965586	RB936001	F78M45
32	RB835486	RB931604	F60M19	71	RB966920	SP89-1115	F58M46
33	RB835486	RB945961	F60M10	72	SP80-1842	RB83102	F61M38
34	RB835486	RB961539	F60M71	73	SP85-3877	RB961005	F05M68
35	SP71-6949	CB45-155	F47M31	74	SP89-1115	RB735200	F46M72
36	SP83-2847	RB855206	F14M08	75	SP89-1115	RB855536	F46M73
37	RB863129	SP83-2847	F15M14	76	SP89-1115	RB915124	F46M07
38	RB92606	SP83-2847	F04M14	77	SP89-1115	RB935860	F46M28
39	RB855511	RB855156	F01M24	78	SP91-1049	RB9364	F02M77

The MTT was obtained with the aid of a scale in the field. The sugarcane stem was cut close to the ground and green leaves were discarded and weighed. The MIC was obtained by counting the number of tillers from the experimental plot and the MTT ratio was calculated by counting tillers. EST was measured with a 5-by-5 cm graduated ruler, totaling 4 m, placed in the center of the clump, and height was measured to the first visible dewlap, thus characterizing leaf +1 (Dillewijn, 1952). The ratio for the area was calculated at the planting line intersections (1.4 m × 5 m), totaling 7 m<sup>2</sup>, in order to calculate NCM.

The data were analyzed using the software SELEGEN-REML/BLUP (Resende, 2007), under model 35 (Incomplete Blocks and One Plant per Plot, Non-Similar Genitors):

$$y = Xr + Za + Wf + Sb + e \quad (1)$$

Where,  $y$  is the data vector,  $r$  is the vector of repetition effects (assumed to be fixed) added to the general means,  $a$  is the vector of individual additive genetic effects (assumed to be random),  $f$  is the vector of family dominance effects of sibling species (assumed to be random),  $b$  is the vector of block effects (assumed to be random) and  $e$  is the vector of errors or residues (assumed to be random).  $X$ ,  $Z$ ,  $W$  and  $S$  represent the incidence matrices for the effects.

The means and variances of this model present the following distributions and structures:

$$\begin{aligned} y|r, V &\sim N(Xr, V) \\ a|A1\hat{\sigma}_a^2 &\sim N(0, A1\hat{\sigma}_a^2) \\ f|I\hat{\sigma}_f^2 &\sim N(0, I\hat{\sigma}_f^2) \\ b|I\hat{\sigma}_b^2 &\sim N(0, I\hat{\sigma}_b^2) \\ e|I\hat{\sigma}_e^2 &\sim N(0, I\hat{\sigma}_e^2) \end{aligned} \quad (2)$$

How,

$$E = \begin{bmatrix} y \\ a \\ f \\ b \\ e \end{bmatrix} = \begin{bmatrix} Xr \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{ and } \text{Var} \begin{bmatrix} y \\ a \\ f \\ b \\ e \end{bmatrix} = \begin{bmatrix} V & ZA\sigma_a^2 & WI\sigma_f^2 & SI\sigma_b^2 & I\sigma_e^2 \\ A\sigma_a^2 Z' & A\sigma_a^2 & 0 & 0 & 0 \\ I\sigma_f^2 W' & 0 & WI\sigma_f^2 & 0 & 0 \\ I\sigma_b^2 S' & 0 & 0 & SI\sigma_b^2 & 0 \\ I\sigma_e^2 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix} \quad (3)$$

So,

$$V = \text{Var}(y) = ZA\hat{\sigma}_a^2 Z' + WI\hat{\sigma}_f^2 W' + SI\hat{\sigma}_b^2 S' + I\hat{\sigma}_e^2 \quad (4)$$

with  $A$  being the additive genetic correlation matrix among the individuals evaluated in this study. Therefore,  $\text{Cov}(a, b') = 0$ ;  $\text{Cov}(a, e') = 0$ ;  $\text{Cov}(f, b') = 0$ ;  $\text{Cov}(f, e') = 0$  and  $\text{Cov}(b, e') = 0$ .

The equations of the model were,

$$\begin{bmatrix} X'X & X'V & X'W & X'S \\ Z'X & Z'Z+A^{-1}\lambda_1 & Z'W & Z'S \\ W'X & W'Z & W'W+I\lambda_2 & W'S \\ S'X & S'Z & S'W & S'S+I\lambda_3 \end{bmatrix} \begin{bmatrix} \hat{r} \\ \hat{a} \\ \hat{f} \\ \hat{b} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ S'y \end{bmatrix} \quad (5)$$

On what,

$$\lambda_1 = \frac{\hat{\sigma}_e^2}{\hat{\sigma}_a^2} = \frac{1 - \hat{h}_a^2 - \hat{c}_{fam}^2 - \hat{c}_{bloc}^2}{\hat{h}_a^2}, \quad \lambda_2 = \frac{\hat{\sigma}_e^2}{\hat{\sigma}_f^2} = \frac{1 - \hat{h}_a^2 - \hat{c}_{fam}^2 - \hat{c}_{bloc}^2}{\hat{c}_{fam}^2}, \quad \lambda_3 = \frac{\hat{\sigma}_e^2}{\hat{\sigma}_b^2} = \frac{1 - \hat{h}_a^2 - \hat{c}_{fam}^2 - \hat{c}_{bloc}^2}{\hat{c}_{bloc}^2} \quad (6)$$

Such that,

$$\hat{h}_a^2 = \frac{\hat{\sigma}_a^2}{\hat{\sigma}_a^2 + \hat{\sigma}_{fam}^2 + \hat{\sigma}_{bloc}^2 + \hat{\sigma}_e^2}: \text{individual heritability, in the narrow sense;}$$

$$\hat{c}_{fam}^2 = \frac{\hat{\sigma}_{fam}^2}{\hat{\sigma}_a^2 + \hat{\sigma}_{fam}^2 + \hat{\sigma}_{bloc}^2 + \hat{\sigma}_e^2}: \text{coefficient of determination of the effects of specific combining ability (SCC) or the familial dominance effects of sibling species;}$$

$$\hat{c}_{bloc}^2 = \frac{\hat{\sigma}_{bloc}^2}{\hat{\sigma}_a^2 + \hat{\sigma}_{fam}^2 + \hat{\sigma}_{bloc}^2 + \hat{\sigma}_e^2}: \text{coefficient of determination of the block effects;}$$

$\hat{\sigma}_a^2$ : additive genetic variance estimator;

$\hat{\sigma}_{fam}^2$ : SCC variance or genetic variance estimator among families of sibling species;

$\hat{\sigma}_{bloc}^2$ : variance estimator between blocks;

$\hat{\sigma}_e^2$ : error or residual variance estimator.

The iterative estimators were obtained to calculate the estimates of the variance components by the REML methodology, by using the EM algorithm (Expectation-Maximization), where,

$$\hat{\sigma}_e^2 = \frac{(y'y - \hat{t}'X'y - \hat{a}'Z'y - \hat{t}'W'y - \hat{b}'S'y)}{N - r(x)} \quad (7)$$

$$\hat{\sigma}_a^2 = \frac{[\hat{a}'A^{-1}\hat{a} + \hat{\sigma}_e^2 \text{tr}(A^{-1}C^{22})]}{q} \quad (8)$$

$$\hat{\sigma}_{fam}^2 = \frac{[\hat{t}'\hat{t} + \hat{\sigma}_e^2 \text{tr}(C^{33})]}{s_1}, \quad \hat{\sigma}_{bloc}^2 = \frac{[\hat{b}'\hat{b} + \hat{\sigma}_e^2 \text{tr}(C^{44})]}{s_2} \quad (9)$$

$C^{22}$ ,  $C^{33}$  and  $C^{44}$  derive from  $C^{-1}$ :

$$C^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} & C_{14} \\ C_{21} & C_{22} & C_{23} & C_{24} \\ C_{31} & C_{32} & C_{33} & C_{34} \\ C_{41} & C_{42} & C_{43} & C_{44} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} & C^{13} & C^{14} \\ C^{21} & C^{22} & C^{23} & C^{24} \\ C^{31} & C^{32} & C^{33} & C^{34} \\ C^{41} & C^{42} & C^{43} & C^{44} \end{bmatrix} \quad (10)$$

where, C: is the coefficient matrix of the model equations; tr: trace matrix; r(x): rank of matrix X; N: total number of data; q: total number of genitors; S1 and S2: total number of crosses and total blocks, respectively.

Mean family heritability was estimated by:

$$\hat{h}_{fam}^2 = \frac{\hat{\sigma}_p^2}{\left\{ \left[ \hat{\sigma}_e^2 \left( \frac{\hat{\sigma}_a^2}{2} \right) \right] n^{rep} + \hat{\sigma}_p^2 \right\}} \quad (11)$$

The genotypic variance among families is given by the formula:

$$\hat{\sigma}_p^2 = \left( \frac{\hat{\sigma}_a^2}{2} \right) + \hat{\sigma}_{bloc}^2 \quad (12)$$

Variance of prediction error of genotypic values (PEV):

$$(PEV) = (1 - \hat{h}_{mf}^2) \hat{\sigma}_p^2 \quad (13)$$

Predicted genotypic standard deviation (SEP):

$$(SEP) = \sqrt{PEV} \quad (14)$$

Selective accuracy among families:

$$A_{c_{fam}} = \sqrt{\hat{h}_{fam}^2} \quad (15)$$

Coefficient of genetic variation (CV<sub>gi</sub>%):

$$CV_{gi}\% = \left( \frac{\hat{\sigma}_p^2}{\mu_g} \right) \times 100 \quad (16)$$

where,  $\mu_g$ : general mean.

Coefficient of environmental variation (CV<sub>e</sub>%):

$$CV_e\% = \left[ \frac{\sqrt{\hat{\sigma}_e^2 + (\hat{\sigma}_a^2/2)}}{\mu_g} \right] \times 100 \quad (17)$$

Relative variation coefficient (CV<sub>r</sub>):

$$CV_r = \frac{CV_{gi}\%}{CV_e\%} \quad (18)$$

### 3. Results and Discussion

The genetic parameters estimated by model 35 for the evaluation of 78 sugarcane families in the present study are presented in Table 2.

Table 2. Estimated variance components and genetic parameters for the following variables: total plot mass (MTT), mean mass of 1 tiller in the plot (M1C), height (EST) and mean number of canes per square meter (NCM) of the 78 series RB05 sibling species *Saccharum* spp. families, Paranavaí municipality, Paraná, Brazil

Estimators	MTT (kg)	M1C (kg)	EST (m)	NCM
$\hat{\sigma}_a^2$	2.1328	0.2470	0.0015	0.0116
$\hat{\sigma}_{bloc}^2$	0.0067	0.0160	0.0051	0.0134
$\hat{\sigma}_{fam}^2$	11.7617	0.0001	0.0186	0.0369
$\hat{\sigma}_e^2$	15.1174	0.1250	0.0850	0.0786
$\hat{h}_a^2$	0.0735±0.0058	0.6364±0.0701	0.0136±0.0108	0.0824±0.0108
$\hat{c}_{bloc}^2$	0.0002	0.0411	0.0463	0.0952
$\hat{c}_{fam}^2$	0.4053	0.0003	0.1688	0.2626
$\hat{h}_{fam}^2$	0.7985	0.7133	0.5307	0.7166
$\mu_g$	6.7493	0.7672	2.1624	1.3927
$\hat{\sigma}_p^2$	12.8281	0.1236	0.0194	0.0427
PEV	1.8857	0.0354	0.0091	0.0121
SEP	1.3732	0.1883	0.0954	0.1100
$A_{c_{fam}}$	0.9236	0.8445	0.7281	0.8465
$CV_{gi}\%$	53.0667	45.8248	6.4329	14.8350
$CV_e\%$	57.6082	46.2308	13.5028	20.2205
$CV_r$	0.9212	0.9912	0.4764	0.7337

Note. ( $\hat{\sigma}_a^2$ : additive genetic variance), ( $\hat{\sigma}_b^2$ : variance between blocks), ( $\hat{\sigma}_{fam}^2$ : SCC variance or genetic variance of dominance between families), ( $\hat{\sigma}_e^2$ : residual variance), ( $\hat{\sigma}_f^2$ : individual phenotypic variance),  $\hat{h}_a^2$ : heritability in the narrow sense in the block, i.e., of the additive effects), ( $\hat{h}_g^2$ : heritability in the broad sense, i.e., of the total genotypic effects), ( $\hat{c}_{bloc}^2$ : coefficient of determination of the effects of blocks), ( $\hat{c}_{fam}^2$ : coefficient of determination of SCC effects).

According to the classification proposed by Resende (2002), heritability can be considered as low magnitude when  $\hat{h}_a^2 < 0.15$ , medium magnitude when  $0.15 < \hat{h}_a^2 < 0.50$  and high magnitude when  $\hat{h}_a^2 > 0.50$ . Thus, MTT and M1C responses evaluated herein presented high heritability, while EST and NCM presented very low heritability, demonstrating that the latter two are highly influenced by the environment. EST presented average heritability among high-magnitude sugarcane families, suggesting an inter-family genetic difference regarding this characteristic, with no difference observed between individuals from the same family.

One likely explanation for this behavior is due to the low number of replicates in the experiment, as, even though each family had been distributed five times in the field, some plants throughout the cropping cycle did not sprout after the first cut or simply did not develop to the point to be able to generate any nonzero data. Another explanation for the event is precisely due to the nature of the Federer blocks design, (Federer, 1956), where most of the treatment and block effects are assumed to be fixed when adopting the vector  $r$  as random (due to the unbalance of family repetitions), leading to a random model. Consequently the effects of repetitions would be distributed confusingly within the block effects, which, in turn, could erroneously inflate the non-additive genetic variance portion.

The high genetic variability observed for MTT, is, in part, due to the high magnitude of additive variance, making this variable promising when performing family selection, since this characteristic can probably be passed on to the next generation.

In sugarcane populations, both dominance (non-additive) and additive effects depend, mainly, on allele frequency, complementarity and genetic divergence (Barbosa, Resende, Bressiani, Silveira, & Peternelli, 2005).

With the exception of EST, all the evaluated variables were explained by the additive genetic variance portion, corroborating with other studies (Bastos, 2003; Barbosa et al., 2005; Silva et al., 2015).

The high genetic variation coefficients for MTT and M1C (319% and 24%, respectively) suggest that sugarcane families can be selected for these characteristics, as a significant genetic variability among the evaluated families exist. This was not observed at the same intensity for EST and NCM, explained, probably, by the fact that crosses were carried out between parents with a very narrow genetic base between both EST and NCM, that is, very close, corroborating previous studies (Daniels & Roach, 1987; Jackson, 2005; Silva, Vidigal, Vidigal Filho, Scapim, Daros, & Silvério, 2005).

Since values for all study variables allowed for family selection, MTT, presented a high genotypic value for the first five families (F75M70, F60M19, F41M82, F78M45 and F66M30), if selecting only these five families. On average, MTT would be increased by 82.11% in the next stages of the breeding program. The criterion for judging a family as “better” is observed when the relative means (%) generated by their selection adds up to values other than zero. The opposite is also true; families with relative genotypic values ( $V_{gc} \leq 0$ ) were disregarded. Thus Table 3 lists only the best families. According to this data, the first 34 families could be used regarding MTT, since a relative gain in family selection of 31.76% (means of the 34 best families) would be observed in relation to the experimental means (5.9044 kg).

Table 3. Genotypic values ( $V_{gc}$ ) and general means of the 78 *Saccharum* spp. sibling species series RB05 families for total mass of the plot (MTT), average mass of 1 tiller in plot (M1C), height (EST) and mean number of stems per square meter (NCM), Paranavaí municipality, Paraná, Brazil

Class <sup>1</sup>	MTT (Kg)		M1C (Kg)		EST (m)		NCM	
	Family	$V_{gc}$	Family	$V_{gc}$	Familia	$V_{gc}$	Family	$V_{gc}$
1	F57M46	9.1064	F04M14	0.9636	F57M46	3.0511	F75M70	1.7559
2	F75M70	9.0272	F05M68	0.9594	F60M16	3.0358	F47M31	1.6977
3	F47M31	8.9789	F62M35	0.9477	F34M02	3.0245	F41M64	1.6801
4	F60M19	8.8532	F10M29	0.9462	F60M19	2.9833	F57M46	1.6414
5	F66M30	8.6201	F13M17	0.9458	F60M43	2.8512	F66M30	1.6185
6	F78M45	8.3717	F60M19	0.9421	F47M31	2.8425	F35M06	1.6094
7	F04M14	8.2547	F27M56	0.9398	F41M64	2.8277	F60M19	1.6067
8	F41M64	8.2482	F70M30	0.9390	F78M45	2.8125	F03M33	1.5984
9	F13M17	8.1555	F41M82	0.9366	F14M08	2.8021	F70M75	1.5980
10	F41M21	8.0775	F14M08	0.9336	F60M10	2.7706	F23M76	1.5828
11	F35M06	7.8854	F19M29	0.9281	F66M30	2.7462	F41M21	1.5798
12	F03M33	7.7339	F60M10	0.9277	F75M70	2.7453	F67M37	1.5779
13	F41M82	7.7289	F15M14	0.9274	F44M02	2.7225	F60M71	1.5754
14	F34M02	7.6205	F26M65	0.9216	F04M14	2.7215	F17M35	1.5468
15	F41M48	7.5850	F34M02	0.9208	F41M48	2.6796	F78M45	1.5453
16	F70M30	7.5586	F66M30	0.9044	F41M47	2.6197	F01M39	1.5379
17	F30M36	7.5067	F82M01	0.9042	F62M35	2.5993	F56M70	1.5271
18	F46M07	7.4973	F57M46	0.8903	F41M22	2.5906	F44M02	1.5270
19	F60M43	7.4963	F30M36	0.8874	F61M38	2.5115	F70M30	1.5256
20	F60M71	7.4892	F70M48	0.8873	F82M01	2.4569	F60M43	1.5190
21	F82M01	7.2387	F17M25	0.8830	F41M21	2.4346	F41M48	1.5137
22	F57M12	7.1862	F60M16	0.8767	F41M60	2.4286	F46M07	1.5089
23	F11M69	7.1567	F75M70	0.8670	F41M53	2.4243	F57M12	1.4972
24	F17M35	7.1389	F78M45	0.8655	F56M70	2.4170	F04M14	1.4686
25	F27M56	7.1022	F47M31	0.8643	F01M24	2.4120	F17M25	1.4684
26	F44M02	7.0406	F10M51	0.8614	F70M48	2.4071	F48M41	1.4652
27	F56M70	7.0324	F41M48	0.8537	F70M30	2.4005	F41M20	1.4610
28	F67M37	7.0196	F26M55	0.8433	F15M14	2.3767	F41M82	1.4454
29	F01M39	6.9768	F41M21	0.8329	F57M12	2.3557	F82M01	1.4452
30	F23M76	6.9564	F54M07	0.8258	F54M07	2.3409	F11M69	1.4245
31	F60M16	6.9543	F57M12	0.8114	F26M65	2.3092	F41M60	1.4234
32	F15M14	6.9477	F14M82	0.8076	F70M56	2.2832	F04M40	1.4174
33	F05M68	6.8980	F41M60	0.7997	F14M22	2.2669	F48M70	1.4166
34	F26M65	6.8394	F41M22	0.7937	F67M37	2.2364	F59M50	1.4030
35	F62M35	6.8262	F01M24	0.7924	F60M52	2.2128	F60M52	1.3998
36	F17M25	6.7787	F41M64	0.7783	F02M77	2.1969	F41M53	1.3992
37	F70M75	6.7738	F46M07	0.7754	F40M74	†	F45M78	1.3986
38	F04M40	†	F81M02	†	F30M36	†	F70M56	1.3979
Mean		6.7493		0.7672		2.1624		1.3927

Note. <sup>1</sup> Classification; †: Disregarded values, since they were below the respective experimental means.

The MIC for the first five families (F04M14, F05M68, F62M35, F27M56 and F70M30) would increase in 42.58% in the next stages of the breeding program, and the relative means of the 37 best families would increase in 15.17% compared to the experimental means (0.5916 kg). For EST, an increase of approximately 14.87% for the the five best families (F57M46, F60M16, F34M02, F60M19 and F60M43) would be observed in the next stages of the program, with a relative means increase of 6.02 %, for the 38 best families compared to the experimental average (0.5916 m). Finally, an approximate gain of 21.96% would be observed by using the first five families (F75M70, F47M31, F41M64, F57M46 and F35M06), with a relative means increase of 9.77% for the 36 best families compared to the experimental average (1.3938).

All four evaluated characteristics led to the selection of 34, 37, 38 and 36 families, respectively, representing 43.59%, 47.44%, 48.72% and 46.15% of the evaluated family means, within the means of the four evaluated variables, of 46.48%, of the RB05 series families, corroborating previous studies (Cox, Hogarth, & Smith, 2000; Silva et al., 2015).

#### 4. Conclusions

The evaluated variables (MTT, MIC, EST and NCM) were susceptible between medium and high magnitude concerning family selection accuracy, with values ranging between 0.4675 and 0.8446.

Families were selected allowing for increases in the four evaluated variables for the next phases of the breeding program.

The genetic variations for MTT and MIC were explained by the additive genetic portion, while much of this explanation was due to the non-additive portion for EST and NCM.

The REML/BLUP methodology is important in the selection of sugarcane families in unbalanced experiments, revealing information from genetic parameters estimates to the breeder, to more accurately guide the next stages of the crop breeding program.

#### References

- Almeida, L. M., Viana, A. P., Amaral Júnior, A. T., & Júnior, J. B. C. (2014). Breeding full-sib families of sugar cane using selection index. *Cienc. Rural*, 44(4), 605-611. <https://doi.org/10.1590/S0103-84782014000400005>
- Almeida Filho, J. E., Tardin, F. D., Guimarães, J. F., & Resende, M. D. (2016). Multi-trait BLUP model indicates sorghum hybrids with genetic potential for agronomic and nutritional traits. *Genet. Mol. Res.*, 15(1), 1-9. <https://doi.org/10.4238/gmr.15017071>
- Atkin, F. C.; Dieters, M. J., & Stringer, J. K. (2009). Impact of depth of pedigree and inclusion of historical data on the estimation of additive variance and breeding values in a sugarcane breeding program. *Theor. Appl. Genet.*, 119(3), 555-565. <https://doi.org/10.1007/s00122-009-1065-7>
- Barbosa, M. H. P., Resende, M. D. V., Bressiani, J. A., Silveira, L. C. I., & Peternelli, L. A. (2005). Selection of sugarcane families and parents by Reml/Blup. *Crop Breeding and Applied Biotechnology*, 5, 443-450. <https://doi.org/10.12702/1984-7033.v05n04a10>
- Bastos, I. T., Barbosa, M. H. P., Cruz, C. D., Burnquist, W. L., Bressiani, J. A., & Silva, F. L. (2003). Análise dialélica em clones de cana-de-açúcar. *Bragantia*, 62, 199-206. <https://doi.org/10.1590/S0006-87052003000200004>
- Brasileiro, B. P., Paula Mendes, T. O., Peternelli, L. A., Silveira, L. C. I. da, Resende, M. D. V. de, & Barbosa, M. H. P. (2016). Simulated Individual Best Linear Unbiased Prediction versus Mass Selection in Sugarcane Families. *Crop Sci.*, 56, 570-575. <https://doi.org/10.2135/cropsci2015.03.0199>
- Castro, R. D., Peternelli, L. A., Resende, M. D. V., Marinho, C. D., Costa, P. M. A., Barbosa, M. H. P., & Moreira, E. F. A. (2016). Selection between and within full-sib sugarcane families using the modified BLUPIS method (BLUPISM). *Genet. Mol. Res.*, 15(1), 1-10. <https://doi.org/10.4238/gmr.15017334>
- Cox, M.; Hogarth, M., & Smith, G. (2000). Cane breeding and improvement. In M. Hogarth, & P. Allsopp (Eds.), *Manual of cane growing* (pp. 91-108). Brisbane, Australian.
- Daniels, J., & Roach, B. T. (1987). Taxonomy and evolution. In D. J. Heinz (Ed.), *Sugarcane Improvement Trought Breeding* (pp. 7-84). Amsterdam, Holland. <https://doi.org/10.1016/B978-0-444-42769-4.50007-2>
- Dillewijn, C. V. (1952). *Botany of sugarcane*. The Chronica Botanica: Waltham.
- Federer, W. T. (1956). Augmented (or Hoonuiaku) designs. *Hawaiian Planters Record*, 55(2), 191-208.



- Jackson, P. A. (2005). Breeding for improved sugar content in sugarcane. *Field Crops Research*, 92, 277-290. <https://doi.org/10.1016/j.fcr.2005.01.024>
- Kennedy, B. W., & Sorensen, D. A. (1988). Properties of mixed-model methods for prediction of genetic merit. In B. S. Weir, E. J. Eisen, M. M. Goodman, & G. Namkoog (Eds.), *Second international conference on quantitative genetics* (pp. 91-103). Sunderland, England.
- Meyer, K. (1991). Estimating variances and covariances for multivariate animal models by restricted maximum likelihood. *Genet Selection Evolucion*, 23, 67-83. <https://dx.doi.org/10.1186%2F1297-9686-23-1-67>
- Oakey, H., Verbyla, A., Pitchford, W., Cullis, B. R., & Kuchel, H. (2006). Joint modeling of additive and non-additive genetic line effects in single field trials. *Theoretical and Applied Genetics*, 113, 809-819. <https://doi.org/10.1007/s00122-006-0333-z>
- Oakey, H., Verbyla, A. P., Cullis, B. R., Wei, X., & Pitchford, W. S. (2007). Joint modeling of additive and non-additive (genetic line) effects in multi-environment trials. *Theoretical and Applied Genetics*, 114, 1319-1332. <https://doi.org/10.1007/s00122-007-0515-3>
- Oliveira, R. A. de., Daros, E., Bessalho Filho, J. C., Zambon, J. L. C., Ido, O. T., Weber, H., Resende, M. D. V. de, & Zeni Neto, H. (2008). Seleção de famílias de cana-de-açúcar via modelos mistos. *Scientia Agraria*, 9(3), 269-274. <https://doi.org/10.5380/rsa.v9i3.11564>
- Pedroso, C. A., Benites, F. R. G., Barbosa, M. H. P., Resende, M. D. V., & Silva, F. L. (2009). Eficiência de Índices de seleção utilizando a metodologia REML/BLUP no melhoramento da cana-de-açúcar. *Scientia Agraria*, 10, 31-36. <https://doi.org/10.5380/rsa.v10i1.11711>
- Resende, M. D. V. de (2002). *Genetics, biometrics and statistics in breeding perennial plants*. Brasília, Brazil: Embrapa Informação Tecnológica.
- Resende, M. D. V. de (2007). *Software SELEGEN-REML/BLUP: Statistical system and genetic screening computed via mixed linear models*. Colombo, Paraná: Embrapa Florestas.
- Silva, G. M., Vidigal M. C. G., Vidigal Filho, P. S., Scapim, C. A., Daros, E., & Silvério, L. (2005). Genetic diversity among sugarcane clones (*Saccharum* spp.). *Acta Scientiarum Agronomy*, 27, 315-319. <https://doi.org/10.4025/actasciagron.v27i2.1851>
- Silva, F. L. da, Barbosa, M. H. P., Resende, M. D. V. de, Peternelli, L. A., & Pedrozo, C. A. (2015). Efficiency of selection within sugarcane families via simulated individual BLUP. *Crop Breeding and Applied Biotechnology*, 15, 1-9. <https://doi.org/10.1590/1984-70332015v15n1a1>

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