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Early selection in sugarcane family trials via BLUP and BLUPIS procedures

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ABSTRACT. The objective of this study was to compare early selection in sugarcane families through the best linear unbiased prediction (BLUP) and simulated individual best linear unbiased prediction (BLUPIS) procedures. We tested 80 full-sib families in an incomplete block experimental design. Statistical analyses were performed using the mixed model methodology. The following traits were determined from the first rattoon: tons of stalks per hectare (TSH), percentage of soluble solids w/w in the juice (Brix), and tons of brix per hectare (TBH). Variance components were estimated by restricted maximum likelihood (REML), and the genotypic values of the families were predicted by BLUP and BLUPIS. The BLUPIS procedure suggested the selection of 30 families with a total of 344 individuals for TBH and gain with a selection intensity of 28%. The correlation between BLUPIS and true BLUP was 0.83, 0.93 and 0.91, for Brix, TSH and TBH, respectively, being validated with data from sugarcane. The BLUPIS procedure demonstrated an advantage in selecting families based on the total harvest of the plot, different from the BLUP procedure that requires the measurement of all individuals present in the plot.

Keywords: *Saccharum* spp., plant breeding, mixed models, family selection, full-sib families.

Seleção precoce em famílias de cana-de-açúcar via procedimentos BLUP e BLUPIS

RESUMO. O objetivo deste trabalho foi comparar a seleção precoce de famílias através da melhor predição linear não viesada (BLUP) correlacionando-se os resultados com o procedimento BLUP individual simulado (BLUPIS). Foram testadas 80 famílias de irmãos-germanos conduzidas a campo em delineamentos em blocos incompletos. As análises estatísticas foram realizadas utilizando os modelos mistos. As variáveis determinadas no ciclo de cana-soca foram: toneladas de colmos por hectare (TCH), porcentagem de sólidos solúveis no caldo da cana (Brix) e toneladas de brix por hectare (TBH). Os componentes de variância foram estimados utilizando a máxima verossimilhança restrita (REML) e os valores das famílias foram preditos pelos procedimentos BLUP e BLUPIS. O procedimento BLUPIS indicou a seleção de 30 famílias com um total de 344 indivíduos para a variável TBH e ganho com a seleção de 28%. A correlação entre o BLUPIS e BLUP foi de 0,83; 0,93 e 0,91 para Brix, TCH e TBH, respectivamente, sendo validado o procedimento BLUPIS com dados em cana-de-açúcar. O procedimento BLUPIS demonstra vantagem na seleção de famílias, pois se baseia na colheita total de parcela, diferente do procedimento BLUP que exige a mensuração de todos os indivíduos presente na parcela.

Palavras-chave: *Saccharum* spp., melhoramento vegetal, modelos mistos, seleção de famílias, famílias de irmãos-germanos.

Introduction

In sugarcane, selection is practiced in all phases of the breeding, in the choice of genitors, the choice of crosses, the selection of individuals derived from the crosses and in clonal selection. In the first phase of genetic breeding, experimental precision is very low due to the lack of replication and competition effects among the individuals. These factors contribute to reduced selection efficiency. When mass selection is used, it tends to be based on indirect production traits, with lower selective efficiency (KIMBENG; COX, 2003; SKINNER et al., 1987).

Family selection can be adopted when the selection traits have low heritability, like sugarcane productivity traits (JACKSON; MCRAE, 1998, 2001). This procedure consists of selecting the best families and rejecting the worst because higher genotypic value families tend to be more effective and indicate a higher proportion of promising genotypes (RESENDE; BARBOSA, 2006). The typical family selection schemes tend to be very unbalanced, due to differences in the numbers of seedlings per family and the number of times that the genitors are used in the crosses. Due to these

traits, the use of the best linear unbiased prediction (BLUP) procedure has been recommended (HENDERSON, 1975; KIMBENG; COX 2003; RESENDE, 2002).

BLUP is considered a preferred procedure because it offers more precision for various experimental conditions, and it maximizes the correlation between the true and predicted genotypic values and the predicted genotypic value relative to other methodologies, which is essential for the breeder (FURLANI et al., 2005; PIEPHO et al., 2008; RESENDE, 2002). One important characteristic of the BLUP procedure is the 'shrinkage' effect that shifts the results of the progeny in the direction of the observed mean; this is a desirable statistical property for an estimator with relatively high accuracy (COPAS, 1983).

The ideal procedure for the selection of individuals for cloning in the initial stages of the sugarcane improvement program is individual BLUP that simultaneously considers information from the individual, the family, the experimental design and the pedigree (BARBOSA et al., 2005; ATKIN et al., 2009). However, this information is not obtained when evaluating the families, which are analyzed based on the total harvest of the plots. Resende and Barbosa (2005) proposed a simulated individual BLUP procedure (BLUPIS), which represents the evolution of sequential selection in sugarcane. In this procedure, the progenies are evaluated based on the total harvest of plots, and the numbers of families that are above the experimental mean and the estimated numbers of individuals to be selected within each family are determined afterwards (RESENDE; BARBOSA, 2006).

The objective of this study was to compare early selection in the sugarcane family through BLUP and BLUPIS procedures. To reach these goals, the following steps were performed: i) estimation of compounds of variance and genetic parameters of the 80 families of full-sib families; ii) prediction of the genotypic values of the families through BLUP procedure, based on production traits, to determine relative genotypic value; iii) comparison of the BLUP and BLUPIS procedures.

Material and methods

Eighty full-sib families were tested in the field, in an experimental area in São Tomé city, Paraná state, Brazil. The region is located between the geographical co-ordinates 23°34'02.75" south latitude, and 52°38'53.87" west longitude, and has an average altitude of 450 meters. The experimental sugarcane was planted in March 2004, and manually harvested in March 2005. The number of stalks per plant (NSP) and Brix (%), which expresses the content of soluble solids in the juice, were determined from the first rattoons harvested in April 2006. The average mass of the plants (MP) was determined based on each individual as NSP x SW (kg), in which SW refers to the measured weight of one stalk per plant from ten plants in the plot referring to the family. The tons of stalks per hectare (TSH, mg ha^{-1}) was estimated as (SW x 10) x 0.7, in which 0.7 is the area for each plant in square meters, adapted from Chang and Milligan (1992) based on weight values measured in the field. The sugar yield per hectare (TBH, mg ha^{-1}) was calculated as (TSH x Brix) 100^{-1} (LEITE et al., 2009).

The experiment used an incomplete block design, with 80 full-sib families and five repetitions per family. Each experimental parcel was composed of 10 seedlings planted in rows with 0.50 m between plants and 1.40 m between rows.

Statistical analyses were performed using the mixed model methodology. Variance components were estimated by restricted maximum likelihood (REML), and the genotypic values of families were predicted by best linear unbiased prediction (BLUP) using Selegen-REML/BLUP (RESENDE, 2007) software. The mixed model associated with the full-sib family evaluation at individual level per plot was: $y = Xr + Za + Wp + Sf + Tb + e$, where y is the data vector, *r* is the repetition effect vector (assumed to be fixed) added to the general average; *a* is the additive genetic effect vector (assumed to be random); *p* is the parcel effect vector (random); *f* is the genetic effect of dominance associated to full-sib families (assumed to be random); *b* is the vector of the incomplete block effects (random); *e* is the vector of errors (random) and X, Z, W, S and T represent the incidence matrices for the effects of *r*, *a*, *p*, *f* and *b*, respectively.

Distributions and structures of means and variances:

$$y|r,V \sim N(Xr,V)$$

$$a|A,\sigma_a^2 \sim N(0,A\sigma_a^2)$$

$$p|\sigma_p^2 \sim N(0,I\sigma_p^2)$$

$$f|\sigma_f^2 \sim N(0,I\sigma_f^2)$$

$$b|\sigma_b^2 \sim N(0,I\sigma_b^2)$$

$$e|\sigma_e^2 \sim N(0,I\sigma_e^2)$$

Cov (a, p')=0; Cov (a, f')=0; Cov (a, b')=0, Cov (a, e')=0;

Cov (p, f')=0; Cov (p, b')=0; Cov (p, e')=0; Cov (f, b')=0;

Cov (f, e')=0; Cov (b, e')=0, or else:

$$E = \begin{bmatrix} y \\ a \\ p \\ f \\ b \\ e \end{bmatrix} = \begin{bmatrix} Xr \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}; \text{ Var}$$

$$\begin{bmatrix} y \\ a \\ p \\ f \\ b \\ e \end{bmatrix} = \begin{bmatrix} V & ZA\sigma_a^2 & WI\sigma_p^2 & SI\sigma_f^2 & TI\sigma_b^2 & I\sigma_e^2 \\ A\sigma_a^2 Z' & A\sigma_a^2 & 0 & 0 & 0 & 0 \\ I\sigma_p^2 W' & 0 & I\sigma_p^2 & 0 & 0 & 0 \\ I\sigma_f^2 S' & 0 & 0 & I\sigma_f^2 & 0 & 0 \\ I\sigma_b^2 T' & 0 & 0 & 0 & TI\sigma_b^2 & 0 \\ I\sigma_e^2 & 0 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

$$V = Var(Y) = ZA\sigma_a^2 Z' + WI\sigma_p^2 W' + SI\sigma_f^2 S' + TI\sigma_b^2 T' + I\sigma_e^2,$$

where:

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

Mixed model equations:

$$\begin{bmatrix} X'X & X'Z & X'W & X'S & X'T \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'W & Z'S & Z'T \\ W'X & W'Z & W'W + I\lambda_2 & W'S & W'T \\ S'X & S'Z & S'W & S'S + I\lambda_3 & S'W \\ T'X & T'Z & T'W & T'S & T'T + I\lambda_4 \end{bmatrix}$$

$$\begin{bmatrix} \hat{r} \\ \hat{a} \\ \hat{p} \\ \hat{f} \\ \hat{b} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ S'y \\ T'y \end{bmatrix}$$

where:

$$\lambda_1 = \frac{\sigma_e^2}{\sigma_a^2} = \frac{1 - h^2 - p^2 - f^2 - b^2}{h^2}$$

$$\lambda_2 = \frac{\sigma_e^2}{\sigma_p^2} = \frac{1 - h^2 - p^2 - f^2 - b^2}{p^2}$$

$$\lambda_3 = \frac{\sigma_e^2}{\sigma_f^2} = \frac{1 - h^2 - p^2 - f^2 - b^2}{f^2}$$

$$\lambda_4 = \frac{\sigma_e^2}{\sigma_b^2} = \frac{1 - h^2 - p^2 - f^2 - b^2}{b^2}$$

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

Individual heritability coefficient in the narrow-sense; $p^2 = \frac{\sigma_p^2}{\sigma_a^2 + \sigma_p^2 + \sigma_f^2 + \sigma_b^2 + \sigma_e^2}$: coefficient of determination the effects of the parcel; $f^2 = \frac{\sigma_f^2}{\sigma_a^2 + \sigma_p^2 + \sigma_f^2 + \sigma_b^2 + \sigma_e^2}$: coefficient of determination the effects of the specific combining ability;

$b^2 = \frac{\sigma_b^2}{\sigma_a^2 + \sigma_p^2 + \sigma_f^2 + \sigma_b^2 + \sigma_e^2}$: coefficient of determination the effects of the blocks;

σ_a^2: variance of genetic additive; σ_f^2: variance of specific combining ability among full-sib families; σ_b^2: variance between blocks; σ_e^2: residual variance between plots and σ_e^2: residual variance.

The variance components were obtained by the REML method and used to calculate the heritability coefficient estimates at the individual level and at the level of full-sib family means.

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

$$\hat{\sigma}_e^2 = \left[y'y - \hat{r}'X'y - \hat{a}'Z'y - \hat{p}'W'y - \hat{f}'S'y - \hat{b}'T'y\right] / [N - r(x)]$$

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

$$\hat{\sigma}_{par} - \left[\hat{p}'\hat{p} + \hat{\sigma}_e^2 tr C^{33}\right] / s_1$$

$$\hat{\sigma}_f^2 = \left[\hat{f}'\hat{f} + \hat{\sigma}_e^2 tr C^{44}\right] / t$$

$$\hat{\sigma}_b^2 = \left[\hat{b}'\hat{b} + \hat{\sigma}_e^2 tr C^{55}\right] / s_2$$

where:

C^{22}, C^{33}, C^{44} and C^{55} are derived fron *C. C*: matrix of the coefficients of the mixed model equations; *tr*: matrix trace operator; *r(x)*: rank of the X matrix. *N*, *q*, s_1, *t* e s_2: total number of data, of parents, of parcel, of crossings and of blocks, respectively.

The mixed model associated to the full-sib families evaluation obtained with the total harvest per plot or observation per plot was: y = Xr + Za + Wf + Ub + e, where: y is the data vector, r is the

repetition effect vector (assumed as fixed) added to the general average; *a* is the additive genetic effect vector (assumed as random); *f* is the genetic effect of dominance associated to full-sib families (assumed as random); *b* is the vector of the incomplete block effects (random); *e* is the vector of errors (random) and X, Z, W and U represent the incidence matrices for the effects of *r*, *a*, *f* and *b*, respectively.

Distributions and structures of means and variances:

$$y \mid r, V \sim N(Xr, V);$$

$$a \mid A, \sigma_a^2 \sim N(0, A\sigma_a^2);$$

$$f \mid \sigma_f^2 \sim N(0, I\sigma_f^2);$$

$$b \mid I\sigma_b^2 \sim N(0, I\sigma_b^2);$$

$$e \mid I\sigma_e^2 \sim N(0, I\sigma_e^2).$$

Cov (a, f')=0: Cov (a, b')=0; Cov (a, e')=0
Cov (f, b')=0;Cov (f, e')=0; Cov (b, e')=0, or else:

$$E = \begin{bmatrix} y \\ a \\ f \\ b \\ e \end{bmatrix} = \begin{bmatrix} Xr \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}; \qquad \text{Var}$$

$$\begin{bmatrix} y \\ a \\ f \\ b \\ e \end{bmatrix} = \begin{bmatrix} V & \mathrm{ZA}\sigma_{\mathrm{a}}^2 & \mathrm{WI}\sigma_{\mathrm{f}}^2 & \mathrm{UI}\sigma_{\mathrm{b}}^2 & \mathrm{I}\sigma_{\mathrm{e}}^2 \\ \mathrm{A}\sigma_{\mathrm{a}}^2 Z' & \mathrm{A}\sigma_{\mathrm{a}}^2 & 0 & 0 & 0 \\ \mathrm{I}\sigma_{\mathrm{f}}^2 W' & 0 & \mathrm{I}\sigma_{\mathrm{f}}^2 & 0 & 0 \\ \mathrm{I}\sigma_{\mathrm{b}}^2 U' & 0 & 0 & \mathrm{UI}\sigma_{\mathrm{b}}^2 & 0 \\ \mathrm{I}\sigma_{\mathrm{e}}^2 & 0 & 0 & 0 & \mathrm{I}\sigma_{\mathrm{e}}^2 \end{bmatrix}$$

$$V = Var(Y) = ZA\sigma_a^2 Z' + WI\sigma_f^2 W' + UI\sigma_b^2 U' + I\sigma_e^2,$$

where:

A is the genetic additive relationship matrix between the individuals.

Mixed model equations:

$$\begin{bmatrix} X'X & X'V & X'W & X'U \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'W & Z'U \\ W'X & W'Z & W'W + I\lambda_2 & W'U \\ U'X & U'Z & U'W & U'U + I\lambda_3 \end{bmatrix};$$

$$\begin{bmatrix} \hat{r} \\ \hat{a} \\ \hat{f} \\ \hat{b} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ U'y \end{bmatrix},$$

where:

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

$$\lambda_2 = \frac{\sigma_e^2}{\sigma_f^2} = \frac{1 - h^2 - f^2 - b^2}{f^2};$$

$$\lambda_3 = \frac{\sigma_e^2}{\sigma_b^2} = \frac{1 - h^2 - f^2 - b^2}{b^2};$$

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

individual heritability coefficient in the narrow-sense;

$$f^2 = \frac{\sigma_f^2}{\sigma_a^2 + \sigma_f^2 + \sigma_b^2 + \sigma_e^2}:$$

coefficient of determination the effects of the specific combining ability;

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

coefficient of determination the effects of the blocks;

σ_a^2: variance of genetic additive; σ_f^2: variance of specific combining ability among full-sib families; σ_b^2: variance between blocks; and σ_e^2: residual variance.

The variance components were obtained by the REML method and used to calculate the heritability estimates at the individual level and at the level of full-sib family means.

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

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

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

$$\hat{\sigma}_f^2 = \left[\hat{f}'\hat{f} + \hat{\sigma}_e^2\, tr\, C^{33}\right] / s_1$$

$$\hat{\sigma}_b^2 = \left[\hat{b}'\hat{b} + \hat{\sigma}_e^2\, tr\, C^{44}\right] / s_2$$

where:

C^{22}, C^{33} e C^{44} are derived fron *C.* matrix of the coefficients of the mixed model equations; *tr*: matrix trace operator; *r(x)*: rank of the X matrix. *N*, *q*, s_1, e s_2: total number of data, of parents, of crossings and of blocks, respectively.

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

The BLUPIS algorithm used to generate real genotypic values for non-evaluated individuals, considering individual i from family j, was $u + g_{ij} = u + g_j + g_{i/j}$, in which u is the general mean; g_{ij} is the genotypic effect of the individual ij; g_j is the genotypic effect of the family j; and $g_{i/j}$ is the genotypic effect within the family of the individual ij. This procedure, denominated 'simulated individual BLUP (BLUPIS)', was determined dynamically. The number of individuals n_k selected in each family k is given by $n_k = (\hat{g}_k / \hat{g}_j) n_j$, in which $\hat{g}_j$ refers to the genotypic value of the best family and n_j is equal to the number of individuals selected in the best family. The determination of n_j involves the concept of effective population size. Alternatively, this expression can be given as $n_k = [1 - (\hat{g}_j - \hat{g}_k)/(\hat{g}_j)] n_j = (\hat{g}_k / \hat{g}_j) n_j$. The latter expression shows that n_k depends on the differences among the genotypic effects of the two families as a proportion of the best family's genotypic effect. The method automatically eliminates the families with negative genotypic effects, i.e., those below the general mean of the experiment (RESENDE; BARBOSA, 2006).

The correlations between the BLUPIS and BLUP procedures were calculated based on the number of potential clones identified by both methodologies, as described in the formula: $r_{blupis;\ blup} = Cov_{(blupis;blup)} / \sigma_{blupis}\,\sigma_{blup}$, in which: $Cov_{(blupis;\ blup)}$: covariance between *blupis* and *blup*; σ_{blupis}: standard deviation for the variable *blupis*; and σ_{blup}: standard deviation for the variable *blup*.

Results and discussion

The estimates of the individual heritability coefficient in the restricted sense ($\hat{h}_a^2$) for Brix, TSH and TBH (Table 1) indicated that only the Brix had a significant magnitude (0.45 ± 0.04); for the traits TSH and TBH, the individual heritability coefficient in the restricted sense was of moderate magnitude (0.22 ± 0.03). These estimates were accurate, as demonstrated by their respective standard errors. However, considering the respective heritability coefficient in the restricted sense (< 0.50) and the family level heritability coefficient (> 0.70), it may still be advantageous to use family information to select for these traits because the heritability coefficient of the mean of the families was > 0.73 (RESENDE, 2002). In this study, the average familial heritability coefficients for Brix, TSH and TBH were of high magnitude, varying between 0.73 and 0.87, as estimated with the BLUP procedure (Table 1). These results suggest that there is genetic variability among full-sib families and that it is possible to select the best families through individual selection. Kimbeng and Cox (2003) report that several researchers and simulation studies show that a combination of family and individual clone selection is a practical and efficient selection method for the first phase of selection.

Another important factor for selection is the presence of genetic variability in the test population. The Brix variable exhibited a genetic variance of 5.04% (Table 1). For TSH and TBH, the genetic variance was more than 10% (CVg > 10), indicating that the selection based on TSH and TBH traits can be efficient due to the presence of high genetic variability (OLIVEIRA et al., 2005; RESENDE, 2002). The presence of genetic variability for the variables TSH and TBH was indicated because the respective CVgs (%) were higher than 10% (18.95, 36.02 and 36.43%, respectively).

Table 1. Estimations of variance compounds and genetic parameters for Brix, TSH (mg ha^{-1}) and TBH (mg ha^{-1}).

Parameters [1]	Brix		TSH		TBH	
σ_a^2	2,067		955,853		42,788	
σ_{plot}^2	0.486		743,715		31,298	
σ_d^2	0.648		421,654		19,820	
σ_{bl}^2	0.005		88,281		3,205	
σ_e^2	1,330		2093,991		94,006	
σ_y^2	4,537		4303,493		191,117	
$\hat{h}_a^2$	0.456	±0.044	0.222	±0.031	0.224	±0.031
$\hat{h}_m^2$	1,027		0,614		0,639	
c_{plot}^2	0,107		0,173		0,164	
c_{fam}^2	0,143		0,098		0,104	
c_{bloc}^2	0,001		0,021		0,017	
σ_p^2	1,038		566,207		24,599	
$\hat{h}_{mf}^2$	0,878		0,739		0,742	
Ac_{fam}	0.937		0.860		0.861	
VC_g(%)	5,047		36,027		36,437	
VC_e(%)	4,210		47,900		48,084	
VCr	1,199		0.752		0.758	
General means	20,188		66,049		13,612	

[1]Individual heritability coefficient in the restricted sense ($\hat{h}_a^2$), individual heritability coefficient in the broad sense ($\hat{h}_m^2$), heritability coefficient of the mean of the families in the broad sense ($\hat{h}_{mf}^2$), additive genetic variance (σ_a^2), variance between plots (σ_{plot}^2), genetic variance of dominance between families (σ_d^2), variance between b.

These results highlight the possibility of selecting families based on these traits, due to the presence of genetic variability. The selection of superior families based on production traits, such as selection for TSH and TBH, is a strategy that has been used in initial stages and allows a greater genetic gain (KIMBENG; COX, 2003) with advantages for the evaluation of the performance of the families together with robust BLUP estimates (ATKIN et al., 2009; COX et al., 1994), and individual clone selection in the first rattoon was shown to be an efficient method for obtaining new sugarcane cultivars (PEDROZO et al., 2011).

The number of families indicated for selection for Brix was 44; these families had genotypic values above the general mean (20.19) and therefore the potential for higher precocity and early harvest. The selection of these 44 families would enable a gain of 3.47%, considering that these families represent 57.5% of those evaluated. For TSH, we identified 30 families with genotypic values above the general mean of 66.05 (mg ha^{-1}). These families correspond to 37.5% of the total of families evaluated. For TBH variable, the gain with the selection of the 30 above-mean families (13.61 mg ha^{-1}) would be approximately 28%. Of these, 29 families present higher values (Table 2). Overall, family selection tends to be more effective at identifying genotypes that have significant potential to affect quantitative traits (KIMBENG; COX, 2003).

Table 2. The genotypic values of 80 full-sib families of sugarcane determined via BLUP and relative genotypic value determined via BLUPIS for the variables Brix, TSH (mg ha^{-1}) and TBH (mg ha^{-1}).

	Brix			TSH			TBH	
Families	Gv[1]	$g_{relative}$ [2]	Families	Gv	$g_{relative}$	Families	Gv	$g_{relative}$
6219	22.23	1.00	449	171.48	1.00	449	36.65	1.00
5222	22.04	0.64	1910	137.79	0.68	1910	29.32	0.68
435	21.89	0.59	6645	118.43	0.50	6645	25.39	0.51
4426	21.73	0.53	5811	114.89	0.46	5811	23.74	0.44
4948	21.68	0.51	1417	112.05	0.44	4341	22.95	0.41
4419	21.55	0.47	6114	105.51	0.37	1417	22.27	0.38
232	21.51	0.45	4341	105.35	0.37	1217	21.01	0.32
2715	21.50	0.45	1217	99.40	0.32	6114	20.64	0.31
3528	21.47	0.44	435	90.72	0.23	435	20.04	0.28
4341	21.44	0.43	6013	90.56	0.23	1727	19.07	0.24
4846	21.44	0.43	578	90.13	0.23	4426	18.97	0.23
2822	21.42	0.42	1727	89.92	0.23	4419	18.40	0.21
4929	21.30	0.38	4426	87.45	0.20	578	17.84	0.18
4620	21.28	0.38	4419	85.80	0.19	6013	17.67	0.18
2812	21.27	0.37	1340	84.73	0.18	6219	17.64	0.18
4130	21.21	0.35	4422	81.57	0.15	1340	17.56	0.17
6748	21.21	0.35	1714	81.00	0.14	4422	17.36	0.16
1527	21.20	0.35	3946	80.07	0.13	6147	16.63	0.13
6645	21.16	0.34	6147	78.51	0.12	2812	16.61	0.13
6143	21.14	0.33	6219	78.35	0.12	3946	16.51	0.13
449	21.13	0.33	4331	78.17	0.12	4331	15.98	0.10
4422	21.12	0.32	491	77.58	0.11	1714	15.88	0.10
2146	21.09	0.31	6542	76.86	0.10	6542	15.70	0.09
514	21.07	0.31	2812	76.36	0.10	497	15.38	0.08
4921	21.06	0.30	497	72.83	0.06	491	15.30	0.07
524	20.99	0.28	2146	70.40	0.04	2146	14.95	0.06
1727	20.98	0.27	4620	67.91	0.02	4620	14.58	0.04
6147	20.89	0.24	566	67.27	0.01	4929	14.17	0.02
2432	20.84	0.23	4537	66.49	0.01	2835	14.07	0.02
2433	20.75	0.20	2835	66.32	0.01	566	13.84	0.01
497	20.73	0.19	-	-	-	1835	13.09	0.04
154	20.72	0.18	-	-	-	1837	10.84	0.04
1217	20.62	0.15	-	-	-	5222	9.10	0.03
1910	20.59	0.14	-	-	-	2146	11.03	0.02
4331	20.44	0.09	-	-	-	4537	12.28	0.02
1340	20.39	0.07	-	-	-	-	-	-
2835	20.38	0.07	-	-	-	-	-	-
2324	20.36	0.06	-	-	-	-	-	-
1835	20.34	0.05	-	-	-	-	-	-
1923	20.34	0.05	-	-	-	-	-	-
3224	20.30	0.04	-	-	-	-	-	-
3518	20.24	0.02	-	-	-	-	-	-
5811	20.24	0.02	-	-	-	-	-	-
5140	20.24	0.02	-	-	-	-	-	-

[1]Genotypic value; [2] $n_j = 50$, number of selected individuals within the best family; $n_k =$, where refers to the predicted genotypic value of family *k* and to the genotypic values of the best family (number 1 in the ranking).

Of the number of families with positive genotypic values predicted by BLUPIS, 44, 28 and 30 families contributed to the selection of specific individuals for Brix, TSH and TBH, representing 53, 35 and 37% of the tested families, respectively. An additional advantage to the selection of these individuals is in the possibility of directing the selection to quantitative traits with low heritability coefficients because the first phase of the selection originated from directed crosses.

To determine the number of clones, we estimated the relative genotypic values ($g_{relative}$) of

the families. Based on this value, we were able to determine the number of individuals to be selected within each family (Table 3). For the variables Brix, TSH and TBH, the number of individuals were 390, 299 and 326, respectively. The numbers of individuals indicated by BLUPIS were 467, 343 and 344 for Brix, TSH and TBH, respectively.

Table 3. The number of selected individuals within the sugarcane families determined via BLUP and BLUPIS procedures, for the variables Brix, TSH (mg ha^{-1}) and TBH (mg ha^{-1}), based on 80 full-sib families.

Brix			TSH			TBH		
Families	Nº [1]	Nº [2]	Families	Nº [1]	Nº [2]	Families	Nº [1]	Nº [2]
154	5	3	435	9	12	435	11	14
435	31	29	449	39	50	449	39	50
449	44	50	491	10	5	491	9	4
491	15	19	497	5	3	497	4	4
497	13	17	566	1	1	566	9	1
524	6	1	578	8	11	578	12	9
566	1	1	1217	10	16	1217	9	16
578	6	11	1340	9	9	1340	16	9
1217	17	25	1417	19	22	1417	16	19
1340	11	11	1714	6	7	1714	4	5
1417	13	13	1727	12	11	1727	11	12
1714	3	2	1910	17	34	1910	17	34
1727	16	18	2146	5	2	2146	5	3
1835	5	6	2812	9	5	2812	9	6
1910	17	30	3946	8	7	2835	8	1
2146	5	3	4331	6	6	3946	8	6
2731	7	5	4341	13	19	4331	5	5
2812	7	7	4419	6	9	4341	15	20
2835	6	4	4422	4	7	4419	10	10
3425	8	5	4426	6	10	4422	4	8
3946	6	16	4620	2	1	4426	7	12
4130	3	1	5811	20	23	4620	3	2
4331	8	11	6013	9	12	4929	3	1
4341	6	30	6114	18	19	5811	19	22
4419	1	1	6147	9	6	6013	9	9
4422	12	15	6219	6	6	6114	15	15
4426	9	11	6542	9	5	6147	9	7
4620	12	14	6645	24	25	6219	9	9
4921	3	3				6542	9	5
4929	6	6				6645	22	26
4948	2	2						
5811	20	20						
6013	9	11						
6114	19	20						
6143	3	6						
6147	11	11						
6645	24	29						
Total	390	467		299	343		326	344

[1]Number of individuals indicated by the selection via BLUP procedure; [2]Number of individuals indicated by the selection via BLUPIS procedure.

In this study, high correlations were observed between BLUP and BLUPIS for the variables Brix, TSH and TBH, confirming the high precision of clone indication via the BLUPIS procedure. The values were $r^2 = 0.83^{**}$ for Brix, $r^2 = 0.93^{**}$ for TSH and $r^2 = 0.91^{**}$ for TBH. Correlations were significant in all cases. For TSH and TBH, it was verified that the selection through BLUPIS indicated only 13 and 5% of below mean individuals, respectively, leading to a coincidence among individuals in excess of 87% (Table 4).

Table 4. Estimated coefficients of correlation, coincidence, corrected coincidence and proportions of indicated individuals between the individual BLUP and BLUPIS selection methodologies, based on 80 full-sib sugarcane families.

Estimations	Brix	TSH	TBH
Correlation BLUP vs. BLUPIS	0.83**	0.93**	0.91**
[1]Coincidence BLUP vs. BLUPIS	0.85	0.87	0.95
[2]Corrected coincidence BLUP vs. BLUPIS	0.71	0.81	0.85
[3]Proportion BLUPIS	0.15	0.13	0.05

*, **Significant at 5 and 1%, respectively. [1]Number of coincident individuals between two selection methodologies. [2]Coincidence of the same selected individuals between two selection methodologies. [3]Proportion of individuals indicated by BLUPIS below the general mean.

These results indicate high precision for the selection of individuals within the best families via simulated individual BLUP procedure (BLUPIS) and confirm the results obtained by Resende and Barbosa (2006). Therefore, the best families can be exploited through individual selection, considering the expressive genotypic value of these hybridizations. This is desirable because it produces a higher probability of selecting individuals with these traits that can be fixed by vegetative propagation (BARBOSA et al., 2004).

The corrected coincidence between the BLUP and BLUPIS selection procedures was verified to be above 0.81. For the family selection aiming to increase TBH, the coincidence was 0.85, which indicates a high probability of selecting the potentially ideal individuals for this characteristic using the BLUPIS procedure. The main advantage of this procedure is its ability to estimate the genotypic values of the families based on the total harvest of the plots. This differs from the BLUP procedure, which requires the measurement of all individuals present in the plot (RESENDE; BARBOSA, 2005). These results indicate that the combination of full-sib family selection with the BLUPIS procedure and individual clone selection in the rattoon is efficient and may provide an improvement in resource use for obtaining new sugarcane cultivars. These results confirm those obtained by Pedrozo et al. (2011) by studying families and environments.

Conclusion

The use of BLUP or individual BLUPIS enables increased selection efficiency to advance the clonal selection phases. However, BLUPIS is operationally easier than family selection, with its use of individual information. Therefore, it can be considered appropriate to recommend the use of BLUPIS in sugarcane improvement programs.

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