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Efficiency of selection within sugarcane families via simulated individual BLUP

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Abstract – *The aim of this study was to assess the efficiency of the simulated individual BLUP (BLUPIS) method in selecting genotypes within full-sib families of sugarcane in ratoon stage, through comparison with selection using the individual BLUP method. The optimal number of genotypes to be selected in the best families were established for mean stems mass, total soluble solids assay (BRIX), ton of stalks per hectare, and BRIX tons per hectare traits. Seventeen full-sib families were assessed in the Centre for Experimentation in Sugarcane, located in Oratórios, MG, Brazil. Mixed model methodology was used to predict the genotypic effects of each family and the genotypic values of each individual within family. BLUPIS method is efficient for individual selection. The optimal number of genotypes to be selected in the best family for obtaining higher efficiency of the BLUPIS method is 100 in the majority of cases.*

Key words: Saccharum *sp., best linear unbiased predictors (BLUP), BLUPIS, selection strategies, sugarcane breeding.*

INTRODUCTION

Individual selection at early stages in sugarcane (*Saccharum* sp.) breeding was initially based on mass selection methods (Mariotti et al. 1999), Australian sequential selection (between families, followed by mass selection) (Kimbeng and Cox 2003), and modified sequential selection (Bressiani et al. 2005). These last two methods use family information for selection and, therefore, are superior in relation to mass selection for traits with family mean heritability higher than individual plant heritability. Family selection has been proven to be essential in sugarcane breeding (Barbosa et al. 2004, Atkin et al. 2010, Stringer et al. 2011).

The optimal strategy for the selection of individuals in the early stages of sugarcane breeding would be through genotypic values predicted by BLUPI (Resende 2002). However, this method has not been used in sugarcane breeding due to the practical difficulties and uneconomical aspects of obtaining data from individual plants. Otherwise, sugarcane breeding strategies have relied on family selection (Atkin et al. 2010, Stringer et al. 2011).

A practical method that resembles BLUPI was proposed by Resende and Barbosa (2006). This selection method, called simulated individual BLUP (BLUPIS), aims to promote a dynamic allocation of the number of individuals selected per family, considering BLUP as the basis for the genotypic effects of these families. Additionally, according to the authors, by using the mean genotypic value of experimental plots within each progeny, BLUPIS method indicates in which replication the best individuals of each family are. BLUPIS method has been successfully applied in plant breeding (Resende et al. 2006, Oliveira et al. 2008, Farias Neto et al. 2009, Oliveira et al. 2011).

The aim of this study was to assess the efficiency of BLUPIS method in selecting genotypes within sugarcane full-sib families in ratoon stage, through comparison with selection using BLUPI method. In parallel, the optimal number of genotypes to be selected in the best family was established for four assessed traits.

MATERIAL AND METHODS

Experimental details

Seventeen sugarcane full-sib families were assessed.

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These families derived from crossings performed in 2003 at the Flowering and Crossings Station, located in Serra do Ouro, city of Murici (lat 9° 13' S, long 35° 50' W, and alt 450-500 m asl), AL, Brazil.

Seedlings obtained from each family were transplanted, in March 2004, at the Centre for Experimentation in Sugarcane (CECA), located in Oratórios, MG, Brazil (lat 20° 25' S, long 42° 48' W, and alt 494 m asl), of the Universidade Federal de Viçosa.

The trial was established in a randomized complete block design with six replications. Each experimental plot consisted in two rows spaced 1.40m apart, and plants were spaced 0.5 m apart, totalling 120 genotypes assessed per family. Due to eventual death of genotypes, the total final number of assessed genotypes was 1637.

Traits used to assess the efficiency of BLUPIS selection method were: mean stem mass (MSM), total soluble solids assay (BRIX), tons of stalks per hectare (TSH), and BRIX tons per hectare (TBH), assessed in April 2006, at ratoon stage.

Traits individually assessed in the plot were: mean stalk height (SH) in cm, mean stalk diameter (SD) in cm, number of stalks of each genotype (NS) and total soluble solids (BRIX). Assessment at the individual level was also necessary for the genetic values of each genotype (BLUPI method) to be estimated, providing the selection of the best genotype, as well as a comparison with the selection recommended by BLUPIS method.

By using the assessed traits, it was possible to estimate the MSM variable, expressed in kg, through the estimator proposed by Chang and Milligan (1992). This estimator is defined by: $MSM = d \times \pi \times SH \times \left(\frac{SD}{2}\right)^2 \times \frac{1}{1000}$, where d is the stalk specific density, the value of which is 1.0 g cm^{-3}, and π is expressed by approximate dimensionless value of 3.141593.

The TSH estimator of each individual was: $TSH = MSM \times NS \times \frac{10}{t_{au}}$, where t_{au} is the ground area that each individual explores, expressed in m². In this work, the t_{au} value was 0.7 m².

For the TBH characteristic, the TSH value of each individual was multiplied by the corresponding BRIX value.

Information at the plot level, necessary for application of BLUPIS method, was obtained through sampling of 14 random individuals of each plot per family. This number of individuals was adopted since the total number of individuals per family was low due to the high mortality rate in the experimental plots. Thus, through the means of the assessed variables in these individuals (SH, SD, NS and BRIX), it was possible to estimate the values at the plot level for MSM, BRIX, TSH and TBH, following previously described estimators.

Procedure for data analysis

Statistical analyses were performed using the mixed linear model methodology (Resende 2002) with aid of a computer program in genetics and statistics Selegen-Reml/Blup (Resende 2007a and b).

The applied linear mixed models were

1. y = Xr + Zg + e, where y is the vector of data; r is the vector of replication effects (assumed as fixed) summed to the general mean; g is the vector of genotypic effects of family (assumed as random); and e is the vector of errors or residuals (random effects). Capital letters represent the incidence matrices for these effects. This model is necessary for estimating the genotypic effects of each family based on plot means, which are essential for the usage of BLUPIS selection method.

2. y = Xr + Zg + Wp + e, where y is the vector of data; r is the vector of replication effects (assumed as fixed) summed to the general mean; g the is vector of individual genotypic effects (assumed as random); p is the vector of random plot effects; and e is the vector of errors or residuals (random effects). Capital letters represent the incidence matrices for these effects. This model was used as a mean to obtain the genotypic values (g) of each individual within the family necessary in the BLUPI selection method. The individual genotypic values were predicted by adjusting g to the model (2).

The variance components were obtained by the Restricted Maximum Likelihood (REML) method (Paterson and Thompson 1971), and were used to calculate the heritability at individual and family means levels, and also for obtaining the BLUP of the genotypic effects.

Simulated individual BLUP selection method (BLUPIS)

The BLUPIS method (Resende and Barbosa 2006) consists of dynamically determining the number of individuals to be selected in each family, with no individual assessment.

The expression which determines the number n_k of individuals to be selected in each family k is $n_k = (\hat{g}_k / \hat{g}_j)\, n_j$, where: $\hat{g}_j$ refers to the genotypic effect of the best family; $\hat{g}_k$ refers to the genotypic effect of the k-th family; and n_j

equals the number of selected individuals in the best family. In this paper, it was considered 50, 100, and 120 individuals selected in the best family, for each characteristic, with the aim of obtaining the best performance of BLUPIS method in comparison to BLUPI.

The number of individuals (r) to be selected from each plot is obtained from $r = \frac{(u + \hat{g}_k + \hat{g}_{plot_r})}{\sum (u + \hat{g}_k + \hat{g}_{plot_r})} \times n_k$, where: $\hat{g}_{parc_r}$ is the genotypic effect of each plot of each family; u is the general mean of each characteristic; and $\sum (u + \hat{g}_k + \hat{g}_{plot_r})$ refers to the sum of genotypic values ($u + \hat{g}_k + \hat{g}_{plot_r}$) of all plots of family k.

Comparison between BLUPIS and BLUPI

For comparison between methods, linear regression analyses were used following the model: $y_i = \beta_0 + \beta_1 x_i + e_i$, where y_i is the number of genotypes selected by BLUPI method in the i^{th} family; x_i is the number of genotypes indicated for selection by the BLUPIS method in the i^{th} family; β_0 is the intercept; β_1 is the slope of the regression line; and e_i is the random error of the simple linear regression. Regression analyses were performed using the software Genes (Cruz 2006).

Through these regression analyses, it was possible to verify the efficiency of the BLUPIS selection method when compared to selection performed by the BLUPI method, as well as to verify the optimal number of genotypes to be selected in the best sugarcane family for each assessed characteristic.

RESULTS AND DISCUSSION

The values of the residual variation coefficients (CV_e) for MSM, TSH and TBH were of high magnitude, reflecting high plot and within-plot variations (Table 1). For MSM and TSH, similar values were found by Barbosa et al. (2005). For BRIX, the CV_e was of low magnitude, suggesting a high experimental accuracy for this characteristic.

The CV_e values are an inadequate parameter for assessing the quality of experiments, since they do not inform the selective accuracy and do not take into account genotypic variation level or number of replications (Resende and Duarte 2007). Resende (2002) states that an adequate statistic for assessing the quality of experiments would be that which simultaneously considers the experimental variation coefficient, the number of replications, and the genotypic variation coefficient. Such a parameter is the selective accuracy.

The selective accuracy values (Ac_{fam}) obtained were of high magnitude (> 0.74) (Table 1), according to the limiting values suggested by Resende and Duarte (2007), which provide family selection with great precision. Family selective accuracy values were 0.77, 0.79, 0.74, and 0.75, for MSM, BRIX, TSH, and TBH, respectively. Santos et al. (2014) to study the genetic control of resistance to rust in *Eucalyptus pellita* through inoculations under controlled conditions four full-sib families, found a high magnitude of the value of selective accuracy, concluding that it would be possible to obtain genetic gain with selection of resistant families for this disease.

Estimates of the narrow-sense individual heritabilities ($\hat{h}^2_a$) were of low magnitude, as expected for quantita-

Table 1. Estimates (according to model 2) of variance components and genetic parameters, for mean stalks mass (MSM), total soluble solids assay (BRIX), ton of stalks per hectare (TSH) and BRIX tons per hectare (TBH), of 17 full-sib families of sugarcane at the ratoon stage

Parameters[a]	MSM (kg)	BRIX (%)	TSH (t ha^{-1})	TBH (t ha^{-1})
$\hat{\sigma}^2_g$	0.01185	0.3340	251.81	10.635
$\hat{\sigma}^2_f$	0.0059	0.1670	125.905	5.3175
σ^2_{plot}	0.0172	0.3343	217.6695	8.1346
σ^2_{within}	0.2183	3.2314	8722.4475	327.8700
$\hat{h}^2_{mf}$	0.5988	0.6299	0.5461	0.5581
$\hat{h}^2_a$	0.0457 ± 0.0211	0.0895 ± 0.0296	0.0278 ± 0.0165	0.0312 ± 0.0175
Ac_{fam}	0.7738	0.7937	0.7390	0.7471
CV_{gi}(%)	10.3812	3.0355	14.0629	15.1153
CV_e(%)	17.8759	4.1368	27.2716	27.6060
General Mean	1.0486 kg	19.0389 %	112.8396 t ha^{-1}	21.5751 t ha^{-1}

[a] Individual genotypic variance ($\hat{\sigma}^2_g$); genotypic variance between families ($\hat{\sigma}^2_f$); environmental variance between plots (σ^2_{plot}); residual variance within plot (σ^2_{within}); family mean heritability ($\hat{h}^2_{mf}$); narrow-sense individual heritability ($\hat{h}^2_a = \hat{\sigma}^2_g / (\hat{\sigma}^2_f + \sigma^2_{plot} + \sigma^2_{within})$; selection accuracy of families (Ac_{fam}); coefficient of genotypic variation (CV_{gi} %) and coefficient of residual variation (CV_e %).

tive traits. However, their standard errors were of low magnitude, indicating that these heritability values were statistically different from zero, enabling the selection of superior individuals. This significance in genetic effect was also confirmed by the deviance analysis using the likelihood ratio test (Peternelli et al. 2011). Estimates of $\hat{h}^2_a$ were 0.05; 0.09; 0.03 and 0.03, for MSM, BRIX, TSH and TBH, respectively. After adjustment (as done by the BLUP procedure) of the individual phenotypic values for environmental plot effects, the heritability for within-family selection was higher.

Selection via BLUPIS and BLUPI procedures

The selection of individuals via BLUPI procedure was carried out from the classification of the predicted genotypic value of all the assessed individuals, taking as a basis the

Table 2. Genotypic effects ($\hat{g}_j$), number of genotypes to be selected (n_k) by the BLUPIS method, and the number of genotypes selected through individual genotypic values predicted via BLUPI, for mean stalks mass (MSM) and total soluble solids assay (BRIX), considering the number of genotypes to be selected in the best family (n_j), equal to 50, 100 and 120, of sugarcane at the ratoon stage

Families	$\hat{g}_j$	(n_j = 50)		(n_j = 100)		(n_j = 120)	
		BLUPIS (n_k)	BLUPI	BLUPIS (n_k)	BLUPI	BLUPIS (n_k)	BLUPI
MSM							
97	0.1026	50	85	100	89	120	89
14	0.0966	47	84	94	108	113	109
44	0.0697	34	32	68	72	82	81
116	0.0677	33	7	66	62	79	77
22	0.0567	28	7	55	51	66	71
78	0.0328	16	1	32	12	38	17
19	0.0138	7	1	13	26	16	49
62	0.0078	4	0	8	3	9	4
33	-0.0052	0	2	0	5	0	6
112	-0.0052	0	0	0	7	0	14
82	-0.0151	0	0	0	1	0	2
98	-0.0231	0	0	0	0	0	0
121	-0.0351	0	0	0	0	0	4
123	-0.0391	0	0	0	0	0	0
76	-0.0561	0	0	0	0	0	0
48	-0.0750	0	0	0	0	0	0
109	-0.1938	0	0	0	0	0	0
Total selected		219	219	436	436	523	523
BRIX							
78	0.4175	50	87	100	94	120	99
121	0.3240	39	53	78	78	93	87
33	0.2768	33	61	66	89	80	93
116	0.2589	31	6	62	48	74	55
123	0.2495	30	20	60	58	72	69
98	0.2464	30	3	59	38	71	54
22	0.1414	17	21	34	62	41	74
44	0.1162	14	7	28	34	33	47
19	0.0931	11	8	22	28	27	47
112	0.0899	11	0	22	2	26	11
109	-0.0382	0	0	0	0	0	0
76	-0.1064	0	0	0	0	0	1
97	-0.1064	0	0	0	0	0	0
48	-0.2303	0	0	0	0	0	0
62	-0.3227	0	0	0	0	0	0
14	-0.6670	0	0	0	0	0	0
82	-0.7426	0	0	0	0	0	0
Total selected		266	266	531	531	637	637

same number of genotypes indicated for selection via the BLUPIS method (Tables 2 and 3).

For MSM, and considering the total number of selected genotypes, selection rates (total number of selected individuals in the best families divided by 1637) were approximately 13, 27, and 32% for n_j equal to 50, 100, and 120, respectively. For BRIX, selection rates were 16, 32, and 39%, respectively (Table 2).

For TSH and TBH, families 14, 19, 48, 82, 98, 109, and 112 had negative values for the genotypic effect (Table 3). Therefore, these families did not contribute to the indication of genotypes to be selected by the BLUPIS method. This method automatically eliminates families with a negative genotypic effect, i.e., those which present genotypic effect lower than the general mean of the experiment. This is reasonable when the very low probability of obtaining a

Table 3. Genotypic effects ($\hat{g}_j$), number of genotypes to be selected (n_k) by the BLUPIS method and the number of genotypes selected through individual genotypic values predicted via BLUPI, for ton of stalks per hectare (TSH) and BRIX tons per hectare, considering the number of genotypes to be selected in the best family (n_j), equal to 50, 100 and 120, of sugarcane at the ratoon stage

Families	$\hat{g}_j$	(n_j = 50)		(n_j = 100)		(n_j = 120)	
		BLUPIS (n_k)	BLUPI	BLUPIS (n_k)	BLUPI	BLUPIS (n_k)	BLUPI
TSH							
44	20.4909	50	84	100	84	120	84
76	7.4657	18	3	36	20	44	26
97	7.3701	18	22	36	68	43	85
116	7.0853	17	11	35	36	41	46
78	6.9897	17	19	34	52	41	63
62	6.8414	17	9	33	31	40	40
22	5.0303	12	0	25	2	29	2
123	1.8504	5	0	9	2	11	2
121	1.4008	3	12	7	25	8	32
33	1.1879	3	0	6	0	7	1
14	-0.8325	0	0	0	1	0	3
82	-5.2292	0	0	0	0	0	0
112	-6.6189	0	0	0	0	0	0
48	-8.2534	0	0	0	0	0	0
98	-9.5212	0	0	0	0	0	0
19	-10.5969	0	0	0	0	0	0
109	-24.6605	0	0	0	0	0	0
Total selected		160	160	321	321	384	384
TBH							
44	4.0937	50	84	100	84	120	84
78	1.7617	22	31	43	86	52	100
116	1.7310	21	17	42	51	51	62
76	1.4548	18	4	36	21	43	30
97	1.2520	15	10	31	35	37	49
22	1.0845	13	0	26	3	32	3
62	1.0408	13	3	25	12	31	16
121	0.6129	7	19	15	42	18	54
123	0.4985	6	0	12	2	15	5
33	0.2781	3	0	7	1	8	2
14	-0.8595	0	0	0	0	0	0
112	-1.0837	0	0	0	0	0	2
82	-1.6381	0	0	0	0	0	0
48	-1.7004	0	0	0	0	0	0
98	-1.8046	0	0	0	0	0	0
19	-1.9730	0	0	0	0	0	0
109	-4.7487	0	0	0	0	0	0
Total selected		168	168	337	337	407	407

superior clone in these families is considered (Resende and Barbosa 2006).

Selection rates for n_j equal to 50, 100, and 120 for TSH were approximately 16, 32, and 39%, respectively, and for TBH, these rates were 19, 38, and 45%.

The number of selected individuals by family decreased progressively and slowly from 100 or 120 for the best family, to zero for the null genetic-effect family. These results reflect the importance of the BLUPIS procedure in dynamically allocating the number of selected individuals per family, at the expense of the acceptance, a priori, of fixed selection proportions within families, as practiced in Australia (Kimbeng and Cox 2003).

For TSH and TBH, family 44 indicated the maximum number of selected individuals (n_k), as a result of its outstanding genotypic effect in relation to other families. This fact suggests indication of the parents involved in this crossing for performing a recurrent selection program aimed at the accumulation of alleles favorable for these traits.

The distribution of the numbers of individuals to be selected from each family via BLUPIS and BLUPI methods were similar (Table 4). This result reveals that the methods are close in this respect; thus, BLUPIS is efficient for showing the number of individuals to be selected in each plot. For other traits, this distribution was performed in the same manner, considering the mean genotypic values of experimental plots within each family (data not shown).

Efficiency of the BLUPIS selection method

BLUPIS was compared to BLUPI through linear regression $y_i = \beta_0 + \beta_1 x_i + e_i$ as defined before. These methods will be considered equivalent if $\beta_0 = 0$ and $\beta_1 = 1$ statistically, and if the determination coefficient is above 70%. This enables the same number of individuals selected by BLUPI to be selected by this alternative method.

All regression parameter estimates (β_0 and β_1), except in three situations, were not statisti-

Table 4. Distribution of the number of genotypes to be selected (n_k) by the BLUPIS method, and selected through individual genotypic values predicted via BLUPI within repetitions, for mean stalks mass (MSM) considering the number of individuals to be selected in the best family (n_j), equal to 50, 100 and 120, of sugarcane at the ratoon stage

Families	(n_j = 50)												(n_j = 100)												(n_j = 120)											
	BLUPIS (n_k)						BLUPI						BLUPIS (n_k)						BLUPI						BLUPIS (n_k)						BLUPI					
	Repetition						Repetition						Repetition						Repetition						Repetition						Repetition					
	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6
97	8[a]	8	8	8	8	8	13	17	11	14	13	17	17	17	17	17	17	17	13	18	13	14	14	17	20	20	20	20	20	20	13	18	13	14	14	17
14	8	8	8	8	8	8	13	11	15	17	13	15	16	16	16	16	16	16	19	17	17	20	17	18	19	19	19	19	19	19	19	17	18	20	17	18
44	6	6	6	6	6	6	5	4	7	7	6	3	11	11	11	11	11	11	10	13	11	12	13	13	14	14	14	14	14	14	13	13	12	13	16	14
116	5	6	5	6	5	6	1	2	1	1	1	1	11	11	11	11	11	11	11	15	9	10	8	9	13	13	13	13	13	13	12	18	11	11	11	14
22	5	5	5	5	5	5	0	1	2	0	3	1	9	9	9	9	9	9	7	10	7	9	9	9	11	11	11	11	11	11	10	12	11	12	14	12
78	3	3	3	3	3	3	0	1	0	0	0	0	5	5	5	5	5	5	3	6	1	1	1	0	6	6	6	6	6	6	3	6	1	1	4	2
19	1	1	1	1	1	1	0	0	1	0	0	0	2	2	2	2	2	2	3	7	3	5	4	4	3	3	3	3	3	3	7	11	8	10	6	7
62	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	0	0	1	1	0	1	1	1	1	2	2	2	1	0	1	1	0	1
33	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	1	1	1	2	1	0
112	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	1	1	4	2	3	3
82	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0
98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
121	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	1
123	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
109	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

[a] Rounded integer number of genotypes indicated for selection in each replication by the BLUPIS method.

cally different from zero and from unity, respectively (Table 5). There was optimal concordance between the BLUPI and BLUPIS methods for all equations in all traits. Therefore, values of n_j equal to or higher than 50 are adequate for efficient use of the BLUPIS method.

For the dataset considered in this work, the selection of 100 genotypes in the best family provided the best results for β_0, β_1 and R^2 statistics, considered simultaneously. So, n_j equal to 100 maximized the efficiency of the BLUPIS method.

According to results presented by Vencovsky (1978), with an n_j equal to 100, it is possible to reach 99% of the maximum representation of a full-sib family. For a n_j equal to 50, this representation would be 98%. Resende and Barbosa (2006) stated that increasing sampling within the family from n_j equal to 50 contributed nearly nothing to adding different genotypes in the sample. This means that many genotype means and few extreme genotypes (including superior genotypes) are added when increasing the sample from this n_j value. Thus, these authors stated that 50 individuals from the best family, mass-selected for several restrictive traits, are sufficient to retain the best individuals of the progeny.

Considering the results presented in Table 5 and in Figure 1, it can be verified that the higher efficiency of the BLUPIS selection method, as compared to the BLUPI selection of the best individuals via predicted genotypic values, occurred when there was selection of 100 genotypes in the best family. In other words, the maximum concordance between genotypes selected by the two methods occurred when n_j equaled 100 in six situations out of eight cases (four traits in two growth stages).

BLUPIS was efficient in the indication of the number of individuals to be selected by each experimental plot (Table 4). Such results were also reported in *Stylosanthes* (Resende et al. 2006) and coconut (Farias Neto et al. 2009). However, the results obtained in this work are relevant only for this research, and it is necessary to assess a larger number of experiments for possible indications of the optimal number of individuals to be selected in the best full-sib family. If using BLUPIS suggests an optimal sample size of 100, then it would be a great misuse of time and resources, as 50 seedlings can give 98% of the variation within a family. Thus, the use of n_j equal to 50 or 100 should be studied in other experiments with a larger number of families.

The present study used the number of selected individuals from selected families as a criterion to compare BLUPIS and BLUPI, as these numbers might imply different sets of clones. For BLUPI, the clones are selected by their own predicted genetic effects, so all selected clones are determined; for BLUPIS, the number only determines how many clones should be selected, and the clones still have to be chosen based on individual phenotypes of the main correlated trait with production. Such an approach approximately coincides with the within-family selection component for BLUPI, thus, the methods can, in fact, lead to the selection of almost the same set of clones.

Obviously, the accuracy of all traits in individual seedlings is not high; therefore, BLUPI itself needs to be validated. However, there is no other option for quantitative traits; one must rely on within-family phenotypes to predict the within-family component of the genotypic value of an individual. It is therefore reasonable to select potential clones to enter into clone trials when there is high accuracy and sufficient

Table 5. Estimates of the regression constant ($\hat{\beta}_0$) and linear regression coefficient ($\hat{\beta}_1$), and p-values (P) associated with the hypotheses H_0 :$\beta_0 = 0$ and H_0 :$\beta_1 = 0$, and determination coefficients (R^2), associated with regressions between the total number of genotypes selected in each full-sib family of sugarcane through the individual genotypic value via BLUPI, and the total number of genotypes to be selected in each family via BLUPIS, for the assessed traits, considering the number of individuals to be selected in the best family (n_j), equals to 50, 100 and 120, of sugarcane at the ratoon stage

Traits[a]	n_j	$\hat{\beta}_0$	$\hat{\beta}_1$	P ($\hat{\beta}_0 = 0$)	P ($\hat{\beta}_1 = 1$)	R^2
MSM	50	-4.1246	1.3202	0.3809	0.1478	72.52
	100	0.6217	0.9758	0.8054	0.6771	95.12
	120	4.4820	0.8543	0.2341	0.0528	91.02
BRIX	50	-4.4128	1.2820	0.4150	0.2469	66.67
	100	0.8777	0.9719	0.8415	0.7739	87.22
	120	4.2716	0.8860	0.3760	0.2094	87.38
TSH	50	-4.0040	1.4254	0.1715	0.0299	81.16
	100	1.7340	0.9082	0.6766	0.4890	76.64
	120	4.2581	0.8115	0.4426	0.2073	68.21
TBH	50	-4.4161	1.4469	0.1552	0.0277	80.60
	100	0.8523	0.9570	0.8672	0.7863	71.56
	120	3.5221	0.8529	0.5825	0.3776	64.94

[a] Mean stalks mass (MSM); total soluble solids assay (BRIX); ton of stalks per hectare (TSH) and BRIX tons per hectare.

precision to identify the best clones for commercial planting.

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Eficiência da seleção dentro de famílias de cana-de-açúcar via BLUP individual simulado

Resumo – *A eficiência do método BLUP individual simulado (BLUPIS) na seleção de genótipos dentro de famílias de irmãos germanos de cana-de-açúcar no estágio de cana soca, comparada com a seleção utilizando o método BLUP individual, foi avaliada. O número ótimo de genótipos a serem selecionados na melhor família foi estabelecido para as características massa media de colmos, teor de sólidos solúveis totais (BRIX), tonelada de colmos por hectare e tonelada de BRIX por hectare. Foram avaliadas dezessete famílias de irmãos germanos no Centro de Experimentação em Cana-de-açúcar, localizado em Oratórios, MG, Brasil. A metodologia de modelo misto foi utilizada para predizer os efeitos genotípicos de cada família e os valores genotípicos de cada individuo dentro de família. O método BLUPIS mostrou-se eficiente para a seleção individual. O número ótimo de genótipos a serem selecionados na melhor família para obter a maior eficiência do método BLUPIS foi 100, na maioria dos casos.*

Palavras-chave: Saccharum *sp., melhor preditor linear não-viesado (BLUP), BLUPIS, estratégias de seleção, melhoramento de cana-de-açúcar.*

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