Estimates of genetic parameters and expected gains from selection of yield traits in sugarcane families

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ABSTRACT

It is essential to have basic information on the genetic nature of variation of various metric traits in plantation crops for the proper planning of breeding strategies. The objective of this paper was to estimate the variability for five yield traits in sugarcane (*Saccharum* spp.) families. Eighteen controlled pollination families were evaluated in a randomized complete block trial having 16 plants per linear plot at Jaú Development and Research Station (DDD/APTA/SAA), in Jau city, Sao Paulo State, Brazil. In the second year, families were assessed and harvested six months after the first ratoon, and evaluated for the following characters: stalk height, stalk diameter, average Brix, stalk number and stalk weight. The results showed highly significant (p<0.01) genetic differences among families for most traits. The genotypic variance component accounted for 4.27, 3.55, 15.87, 3.32 and 51.68% of the phenotypic variance for stalk height, stalk number, stalk diameter, stalk weight and average Brix, respectively. Heritabilities at individual plant level for the above traits were 56.57, 76.59, 67.40, 72.73 and 54.11%, respectively. Negative significant genotypic and phenotypic correlations were found between Brix and stalk height ($r_g = -0.78**$, $r_p = -0.56**$) and stalk diameter ($r_g = -0.81**$, $r_p = -0.75**$). Selecting the best two families out of 18 families would result in a genetic gain of 4.92% and 10.82% for stalk height and stalk diameter, respectively. The best two selected individual seedlings within each family would result in a genetic gain of 18.61% and 16.94% with a total gain of 23.57 % and 27.76 % for these two traits, respectively.

KEY WORDS: *Saccharum* spp., heritability, genetic correlations, genetic variation, selection.

INTRODUCTION

The success of a sugarcane (*Saccharum* spp.) breeding program depends on the knowledge of the involved genetic aspects. These depend, partly, on the recognition of several characters considered important in the selection. Information on the genetic variability or heritability of traits being improved is extremely important and of vital importance for the prediction of the progress.

According to Paiva (1980), the success of a selection program depends on the available genetic variation in the population. It is of great interest, therefore, to determine the variability and inheritance of characters in order to arrive at the most appropriate methods for selecting young plants, thus reducing the selection cycle.

Estimation of genetic parameters for the most varied traits in sugarcane families was done by Brown et al.

(1968, 1969), Hogarth (1971a, 1971b), Hogarth and Bull (1990), Hogarth et al. (1981), Skinner et al. (1987), Cesnik and Vencovsky (1974), Chavanne and Mariotti (1984), Wu and Tew (1989) and more recently Bressiani (2001).

The objetive of the present work was to estimate the genetic variability, heritability coefficient, as well as the relative genetic gains for the yield traits in sugarcane families, in order to obtain necessary elements for the future choice of the more appropriate breeding methods of selection.

MATERIAL AND METHODS

The genetic material used in this study was 18 full-sib families obtained from controlled hand pollination seeds originated from different combinations of 10 commercial bi-parental clones phenotypically selected in the Copersucar collection.

Clones were hybridized at Experimental Station of Copersucar in Camamu city, State of Bahia, Brazil and the families were evaluated in the experimental field at Jaú Development and Research Station (DDD/APTA/SAA), established in Jaú city, State of São Paulo, at 22° 17'S latitude, 48° 34W' longitude and an altitude of 580m. The soil is clay textured dark red latosoil deep and flat with a well drained topography (hapludox). An Aw (Köppen) climate predominates in this region, with a defined dry season, annual mean temperature of 21.6ºC, average humidity of 70% with extremes of 77% in February and 59% in August. The mean annual rainfall is 1,344 mm.

For this evaluation, a trial in randomized block design was adopted with three replications and 16 plants per plot, spaced at 0,5 m x 1,4 m in double rows. Near to the family trial was installed a clone trial which followed a randomized block design with eighteen clones, three replications and 16 plants per plot. The dates and management procedures were similar to the family trial. The clone trial was performed in order to supply the estimate of the environmental variance among plants within plots ($\hat{\sigma}_{ew}^2$) (Bressiani, 2001).

Families were assessed and harvested six months after the first ratoon. Tillerings from each shoot of seedlings were counted during each harvest conducted during the first ratoon.

Yield components such as stalk height, stalk number, stalk diameter, stalk weight and average Brix were evaluated. For the determination of the stalk height, a ruler was used to measure a sample of five stalks. For the measurement of the diameter, a universal pachymeter type was used to measure the same five stalks diameter, which was defined as stalk diameter. The average Brix was obtained through the reading of soluble solids of the sugarcane juice from each of the five stalks, which were removed to obtain "quantitative components", using a manual field refractometer, 0-32% scale, reading optical apparatus, used for measure the amount of soluble solids in a sugared cane juice.

The analysis using the statistical model below, considered all variable (except mean) as random effects:

$$Y_{ijk} = \mu + p_i + b_j + e_{ij} + d_{ijk}$$

where,

Y_{ijk}: observed value of the kth plant in the jth replication within the ith family;

μ: general mean;

p_i: effect of the ith family (i=1,2,…18)

b_j: effect of the jth replication (j=1,2,…3)

e_{ij}: experimental error associated with the ij^{th} plot and

d_{ijk}: effect the kth plant within the ij^{th} plot.

The estimates of the components of genotypic and phenotypic variances were obtained by the mathematical expected mean squares from the analyses of variances (Table 1), according to Vencovsky and Barriga (1992). Thus, the phenotypic variance due to differences among plants within the plots is:

$$\sigma_w^2 = \text{MSW}$$

where,

$\sigma_w^2 = \sigma_{gw}^2 + \sigma_{ew}^2$, which can be separated in genetic variance (σ_{gw}^2) and environmental variance (σ_{ew}^2) both among plants within plots.

Partioning the component σ_w^2 in σ_{gw}^2 and σ_{ew}^2, it is suggested to use information of the mean square within plot of the clone trial (Table 2) in order to supply the estimates of environmental variance within plots (σ_{ew}^2).

So, both environmental and genetic variances, among the plants within the plots can be obtained by the mean squares (Tables 3 and 4).

$$\hat{\sigma}_{ew}^2 = MSWC$$

$$\hat{\sigma}_{gw}^2 = MSW - MSWC$$

The estimates of the environmental variance among plots ($\hat{\sigma}_e^2$) and genotypic variance due to differences among families ($\hat{\sigma}_f^2$), were obtained through the expected mean square.

The total genotypic variance (σ_G^2), phenotypic variance based on families mean ($\sigma_{\bar{P}}^2$), and phenotypic variance based on individual plants (σ_p^2) were obtained through the expressions:

$$\hat{\sigma}_G^2 = \hat{\sigma}_f^2 + \hat{\sigma}_{gw}^2$$

$$\hat{\sigma}_{\bar{P}}^2 = \hat{\sigma}_f^2 + \frac{\sigma_e^2}{r} + \frac{\sigma_w^2}{rn}$$

$$\hat{\sigma}_P^2 = \hat{\sigma}_f^2 + \hat{\sigma}_e^2 + \hat{\sigma}_w^2$$

Heritability coefficients at individual plants level ($\hat{h}_i^2$), for selection within family ($\hat{h}_w^2$) and among families mean ($\hat{h}_f^2$), were estimated by following expressions (Vencovsky and Barriga, 1992) for the formulas:

$$\hat{h}_i^2 = \sigma_G^2 / \sigma_P^2$$
$$\hat{h}_w^2 = \hat{\sigma}_{gw}^2 / \hat{\sigma}_w^2$$
$$\hat{h}_f^2 = \hat{\sigma}_f^2 / \hat{\sigma}_{\overline{P}}^2$$

The coefficients of genotypic (CVg) variation were estimated using the following formula presented by Vencovsky (1987):

$$CVg(\%) = \frac{\sqrt{\sigma_f^2}}{\overline{x}}.100$$

Genetic gain from selection among families (G_f) and within family (G_w) levels was also computed using Falconer and Mackay's (1996) formula:

$$G_f = k_1 \hat{\sigma}_{\overline{P}} h_f^2$$
$$G_W = k_2 \hat{\sigma}_w h_w^2,$$

where,

k : selection differential in standard measure;

$\hat{\sigma}_{\overline{P}}$: estimates of phenotypic standard deviation of family means;

$\hat{\sigma}_w$: estimates of phenotypic standard deviation among plants within plots.

The genetic gains expressed as a percent of the mean obtained from among and within families were estimated using the formula:

$$G_f \% = \frac{G_g}{\overline{x}}.100 \quad or \quad G_w \% = \frac{G_w}{\overline{x}}.100$$

where $\overline{x}$ is the general mean.

To determine the correlation among yield traits of sugarcane, genotypic ($r_{g(xy)}$) and phenotypic ($r_{p(xy)}$) correlations were worked out according to Kempthone (1966) as follows:

$$r_{g(xy)} = Cov_{g(xy)} / \sqrt{\sigma_{gx}^2 . \alpha_{gy}^2}$$

$$r_{p(xy)} = Cov_{p(xy)} / \sqrt{\sigma_{px}^2 . \sigma_{py}^2}$$

where $Cov_{g(xy)}$ and $Cov_{p(xy)}$: the genotypic and phenotypic covariances for traits x and y respectively; σ_{gx}^2 and σ_{px}^2: genotypic and phenotypic variances for trait x; σ_{gy}^2 and σ_{py}^2: genpotypic and phenotypic variances for trait y.

The significance of these correlations was tested using the table in Fisher and Yates (1971), for simple correlations at 5% and 1% probability. The genotypic and phenotypic correlations were tested with the error degrees of freedom.

RESULTS AND DISCUSSION

Genotypic variation

Table 3 shows the analyses of variance for the five sugarcane yield traits. Except for stalk height, high-significance differences among families were detected by the F test. This variability was an essential condition for establishing a genetic breeding program and it could be effectively exploited to increase sugarcane production.

The experimental coefficients of variation (CVe) obtained for stalk height (17.59%), stalk number (15.44%), stalk weight (14.85%) and average Brix (11.81%) (Table 3) may be considered low and indicate good experimental precision and good assessment criteria. These values agree with similar estimates by Brown et al. (1968), Cesnik and Vencovsky (1974), Chavanne and Mariotti (1984) and Bressiani (2001).

The genotypic variation coefficient, which expresses

Table 1. Degrees of freedom (d.f.), mean square (M.S.) and expected mean squares (E.M.S) of ANOVA for estimating components of variance in a controlled pollinated family trial of sugarcane.

Sources of variation	d.f.	M.S.	E.M.S. [1]	F test
Replications	r-1	MSR	-	MSR/MSE
Families	f-1	MSF	$\sigma_w^2 + n\sigma_e^2 + nr\sigma_f^2$	MSF/MSE
Residual	(r-1)(f-1)	MSE	$\sigma_w^2 + n\sigma_e^2$	MSE/MSW
Within families	rf(n-1)	MSW	σ_w^2	
TOTAL	rfn-1			

[1] σ_w^2: variance due to differences among plants within plots; σ_e^2: environmental variance among plots; σ_f^2: genotypic variance due to differences among families; r: number of replications; f: number of families and n: number of plants per plot.

the amount of existing genetic variation as a percentage of the general mean, was higher for stalk number (66.81%), than stalk weight (19.92%), stalk height (14.09%), average Brix (14.05%) and stalk diameter (7.60%). These results which agree with those of Silva et al. (2002) for the same traits confirmed for the variability in the species detected by family F test. The results also indicated that the breeding program for improved stalk number, stalk weight, stalk height and average Brix can be continued. The low genetic variability, as shown by the stalk diameter coeficient of genetic variation, demonstrates that it is necessary to increase the genetic variability in the worked population.

Table 4 shows the clone trial analysis of variance. Except for average Brix, significant differences among clones were detected by the F test for all yield traits. These results reinforce the variability observed in the family trial, an essential condition for establishing a genetic breeding program. Therefore, the main purpose of the clone analysis of variance was to supply the estimate for environmental variance among plants within plots.

Variance components

The genotypic variance components among families (σ_f^2) accounted for 7.54, 4.64, 23.54 and 4.57%. and the genotype variance among plants within the plots (σ_{gw}^2) accounted for 92.46, 95.36, 76.46 and 95.43% of the total genotypic variance (σ_G^2) for stalk height, stalk number, stalk diameter and stalk weight, respectively (Table 5). The analysis of stalk number show similar value with stalk weight i.e. 95% of the σ_G^2. The analysis of these percentual values show the preponderance of the σ_{gw}^2 upon σ_f^2 for all characters.

In Argentina, Mariotti et al. (1999) evaluated 10 full-sib families and observed medium values related to 25% for stalk number, 44% for stalk height and 14% for stalk diameter. The authors highlight in full-sib families values close to 1.0 for the proportion $\sigma_f^2 : \sigma_{gw}^2$. They suggest a strong predominance of addictive effects in the determination of the genetic variability generated by the breeding process. In the same way, low values below 1 indicate different degrees of genetic effects, concerned to the other character, mainly for the stalk number and stalk diameter.

Table 2. Degrees of freedom (d.f.), mean square (M.S.) and expected mean square (E.M.S.) for estimating the variance due to differences among plants within plots in a clone trial of sugarcane [1].

Source of variation	d.f.	M.S.	EMS	F test
Replications	r-1	MSRC	-	MSRC/MSEC
Clones	c-1	MSC	-	MSC/MSEC
Residual	(r-1) (c-1)	MSEC	-	MSEC/MSWC
Within clones	rc (n-1)	MSWC	σ_{ew}^2	
TOTAL	rcn-1			

[1] σ_{ew}^2: variance due to differences among plants within plots; r : number of replications; c: number of clones and n: number of plants per plot.

Table 3. Degrees of freedom and mean squares from ANOVA, general mean, experimental (CVe) and genotypic (CVg) coefficients of variation for five yield traits, of 18 controlled pollination families of sugarcane.

Source of variation	d.f.	Stalk height	Stalk number	Stalk diameter	Stalk weight	Average Brix
Replications	2	0.1424	89.9803	0.4096	17.0771	40.1021
Families	17	0.5124	83.0724 [1]	1.9444 [1]	90.5876 [1]	309.3365 [1]
Residual	34	0.2598 [1]	25.3271	0.3574 [1]	22.3087	28.5811 [1]
Within plots	810	0.0971	35.8335	0.1441	43.2104	3.4650
General mean		1.6111	8.1505	2.2604	7.9480	18.6615
CVe(%)		17.5925	15.4366	5.9721	14.8565	11.8137
CVg(%)		14.0978	66.8097	7.6048	19.9209	14.0054

[1] p<0.01.

The proportions of the genetic variances among and within families in general indicated a smaller proportion of genetic variation among families σ_f^2 in relation to the total genetic variation σ_G^2. In addition the possible cause of this low rate $\sigma_f^2 : \sigma_{gw}^2$ compared with the literature, depends on the constitution of the population used in the breeding. There is the possibility that the clones used in the population base stem from combinations among parents of low genetic divergence.

Heritabilities

Heritability at the individual plant level (h_i^2) for stalk height and average Brix was around 50% (Table 6). These data did not agree with the Skinner et al. (1987) data review. They reported individual plant heritability values for stalk height of 21.10% in Hawaii, 24.00% in Argentina and 32.20% in Australia. For Brix average they reported values of 65.00% and 27.00% in Australia and Hawaii, indicating that these two traits had moderately high heritability estimates. It implies that there is genetic variability for stalk height and average Brix in the studied population. Heritability among family mean (h_f^2) for both traits i.e. stalk height and average Brix were 50.00% and 90.63%, respectively. Skinner et al. (1987) reported values of 84.0%, 40.0%, 54.0% and 24.0% for stalk height heritabilies among families in Australia, Hawaii, Fiji and Argentina, respectively. For Brix average, the reported values were 90.00% and 53.00% in Australia and Hawaii, respectively.

Heritabilities for the other traits such as stalk diameter, stalk weight and stalk number were relatively high, i.e. 67.40, 72.73 and 76.59% at individual plant level (h_i^2), 66.13, 73.23 and 76.96% within families level (h_w^2) and 80.99, 53.65 and 58.78% among family mean (h_f^2), respectively. These highly significant heritability estimates coupled with the large amount of variation observed within the sugarcane population

Table 4. Degrees of freedom and mean squares from ANOVA, general mean, experimental (CV_e) and genotypic (CV_g) coefficient of variation for five yield traits of 18 clones of sugarcane.

Source of variation	d.f.	Stalk height	Stalk number	Stalk diameter	Stalk weight	Average Brix
Replications	2	2.1862 [2/]	22.0289 [3/]	0.0595 [3/]	110.3962 [3/]	20.4796 [3/]
Clones	17	1.2327 [1/]	137.4196 [2/]	1.6194 [2/]	84.5567 [2/]	47.3732 [3/]
Error	34	0.2619 [2/]	14.6147 [2/]	0.1411 [2/]	30.4191 [2/]	39.9834 [2/]
Within clones	810	0.0358	8.2545	0.0486	11.5642	3.7136
Mean		1.8524	8.0301	2.6463	8.3369	18.2170
CVe(%)		6.9065	11.9019	3.5498	16.5390	8.6777
CVg(%)		14.0978	66.8097	7.6048	19.9209	14.0054

[1/] p<0.05; [2/] p<0.01; [3/] ns.

Table 5. Estimates of genotypic and phenotypic components of variances for five yield traits of 18 controlled pollination families of sugarcane.

Traits	Components[1/]							
	$\hat{\sigma}_f^2$	$\hat{\sigma}_e^2$	$\hat{\sigma}_w^2$	$\hat{\sigma}_{gw}^2$	$\hat{\sigma}_{ew}^2$	$\hat{\sigma}_G^2$	$\hat{\sigma}_{\bar{P}}^2$	$\hat{\sigma}_P^2$
Stalk height	0.0050	0.0090	0.0972	0.0613	0.0358	0.0663	0.0100	0.1172
Stalk number	1.3420	0.5837	35.8335	27.5790	8.2545	28.9210	2.2831	37.7592
Stalk diameter	0.0294	0.0118	0.1441	0.0955	0.0486	0.1249	0.0363	0.1853
Stalk weight	1.4902	1.1612	43.2104	31.6462	11.5642	32.6266	2.7775	44.8618
Average Brix	5.1992	1.3953	3.4650	-0.2486	-3.7136	5.4428	5.7365	10.0595

[1/] $\hat{\sigma}_f^2$: genotypic variance due to differences among families; $\hat{\sigma}_e^2$: environmental variance among plots; $\hat{\sigma}_w^2$: phenotypic variance due to differences among plants within plots; $\hat{\sigma}_{gw}^2$: genetic variance among plants within plots; $\hat{\sigma}_{ew}^2$: environmental variance among plants within plots; $\hat{\sigma}_G^2$: total genotypic variance; $\hat{\sigma}_{\bar{P}}^2$: phenotypic variance based on families means and $\hat{\sigma}_P^2$: phenotypic variance based in individual plants.

suggest that an effort to increase yield traits through family selection would be rewarding, as reported by Cesnik and Vencovsky (1974) and Wu and Tew (1989).

Expected genetic gains

Expected genetic gains for the yield traits, at different levels of selection intensity are shown in Table 7. If the best six families were selected and planted on sites similar to that used in the experimental trial, a genetic gain among families for stalk height and stalk diameter of 3.23% and 7.11%, respectively, could be

Table 6. Heritabilities coefficients for five yield traits of 18 controlled pollination families of sugarcane.

Traits	Heritabilities[1]		
	h_i^2	h_w^2	h_f^2
Stalk height	0.5657	0.6306	0.5000
Stalk number	0.7659	0.7696	0.5878
Stalk diameter	0.6740	0.6613	0.8099
Stalk weight	0.7273	0.7323	0.5365
Average Brix	0.5411	0.0681	0.9063

[1] h_i^2: individual plants level; h_w^2: within families level and h_f^2: among families mean.

Table 7. Expected gains from different levels of selection and percentage of the mean, among (G_f) and within (G_w) families selection and total (G_{f+w}) for five different traits in 18 controlled pollination families of sugarcane.

Traits	Selection level[1]			From selection			In percent of the mean		
	N	K_1	K_2	G_f	G_w	G_{f+w}[2]	G_f	G_w	G_{f+w}
Stalk height	2	1.585	1.5250	0.0792	0.2998	0.3790	4.92	18.61	23.53
	4	1.271	1.2010	0.0635	0.2361	0.2996	3.95	14.66	18.61
	6	1.042	0.9620	0.0521	0.1891	0.2412	3.23	11.74	14.97
	8	0.851	0.7600	0.0425	0.1494	0.1919	2.64	9.27	11.91
	10	0.681	0.5770	0.0340	0.1134	0.1474	2.11	7.04	9.15
Stalk number	2	1.585	1.5250	1.4077	7.0255	8.4332	17.27	86.20	103.47
	4	1.271	1.2010	1.1288	5.5329	6.6617	13.85	67.88	81.73
	6	1.042	0.9620	0.9255	4.4318	5.3573	11.35	54.38	65.73
	8	0.851	0.7600	0.7558	3.5012	4.2570	9.27	42.96	52.23
	10	0.681	0.5770	0.6048	2.6581	3.2629	7.42	32.61	40.03
Stalk diameter	2	1.585	1.5250	0.2446	0.3828	0.6274	10.82	16.94	27.76
	4	1.271	1.2010	0.1961	0.3015	0.4976	8.68	13.34	22.02
	6	1.042	0.9620	0.1608	0.2415	0.4023	7.11	10.68	17.79
	8	0.851	0.7600	0.1313	0.1908	0.3221	5.81	8.44	14.25
	10	0.681	0.5770	0.1051	0.1448	0.2499	4.65	6.41	11.06
Stalk weight	2	1.585	1.5250	1.4251	7.3409	8.7660	17.93	92.36	110.29
	4	1.277	1.2010	1.1428	5.7813	6.9241	14.38	72.74	87.12
	6	1.042	0.9620	0.9369	4.6308	5.5677	11.79	58.26	70.05
	8	0.851	0.7600	0.7652	3.6584	4.4236	9.63	46.03	55.66
	10	0.681	0.5770	0.6123	2.775	3.3898	7.70	34.95	42.65
Average Brix	2	1.585	1.5250	3.4405	0.1923	3.6338	18.44	1.04	19.48
	4	1.271	1.2010	2.7589	0.1522	2.9111	14.78	0.82	15.60
	6	1.042	0.9620	2.2618	0.1219	2.3837	12.12	0.65	12.77
	8	0.851	0.7600	1.8472	0.0963	1.9435	9.90	0.52	10.42
	10	0.681	0.5770	1.4782	0.0731	1.5513	7.92	0.39	8.31

[1] n: Number of families/individuals within families and k_1, k_2: selection differential in standard measure (after Becker, 1984); [2] G_{f+w}: Total genetic gain ($G_f + G_w$).

achieved. When only the two best families (i.e. two families out of 18 families) were selected, for stalk height and stalk diameter with a selection intensity of 11.11% the gain in production was 7.92 cm and 24.46 mm, which is 4.92% and 10.82% greater than the overall family means. Even smaller increases than these would result in appreciable improvement if the planting is large enough.

On the other hand, if the best two individuals were selected within families, assexually multiplied and planted at the same site, the genetic gain for stalk height and stalk diameter would be about 18.61% and 16.94%, respectively. For stalk number, stalk weight and Brix average the gains would be 86.20%, 92.36 and 1.04%, respectively. Considering combined selection among and within families the total genetic gains would be 23.53%, 27.76% for stalk height, stalk diameter, and 19.48% for average Brix, respectively.

Correlations

Genotypic and phenotypic correlations between stalk height and others characters like stalk diameter and average Brix were generally significant (Table 8). Families with high stalk height and high stalk diameter often exhibited average Brix with negative, highly significant coefficient of correlation value.

The influence of Brix on stalk height and stalk diameter is not evident on the field. Collected data suggest that selection for high stalk height and for high stalk diameter have varying effects on Brix. A positive genotypic and phenotypic association between average Brix with another important yield trait was not evident.

The lack of significance of the genotypic and phenotypic association of stalk height with stalk number and stalk weight, stalk number with stalk diameter and stalk diameter with stalk weight implies low genetic gain in all of these traits even if selection is undertaken on only one trait

Breeding strategy

Based on the results of this experiment it is possible to develop a program for sugarcane improvement. According with Zobel and Tarbert (1984) the "family plus within – family selection" method is the predominant form of selection used in most advanced generation tree improvement programs. This method consists of selecting the best families along with the individuals within those families. Consequently, this method will be adopted for improving stalk diameter, stalk height and average Brix. Since there is no significant genetic correlation among the three characters, indirect selection is not applicable in this instance. For this purpose "tandem selection" should be employed, e.g. the stalk diameter will be improved first. When a desired diameter level has been obtained, breeding efforts will be concentrated on Brix and stalk height. However, if the intention is to improve stalk diameter and Brix simultaneously, then an independent culling method would be recommended.

Table 8. Estimates of genotypic (r_g) and phenotypic (r_p) correlation coefficients based and individual plants among five yield traits of 18 sib families of sugarcane.

Traits		Stalk Number	Stalk diameter	Average Brix	Stalk weight
Stalk height	r_g	0.2646	0.8441 [2/]	-0.7798 [2/]	0.4305
	r_p	0.1597	0.6553 [2/]	-0.5553 [1/]	0.4469
Stalk number	r_g		0.0958	-0.2103	0.8801 [2/]
	r_p		0.0188	-0.1016	0.8231 [2/]
Stalk diameter	r_g			-0.8104 [2/]	0.1543
	r_p			-0.7545 [2/]	0.1209
Average Brix	r_g				-0.1969
	r_p				-0.1128

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RESUMO

Variabilidade genética, correlações e ganhos esperados com a seleção de caracteres de produção em famílias de cana-de-açúcar

Informações básicas sobre a natureza genética da variação de caracteres em qualquer cultura são essenciais para um planejamento estratégico de melhoramento genético. O presente trabalho teve por objetivo estimar a variabilidade dos caracteres de produção em famílias de cana-de-açúcar (*Saccharum* spp*.)*. Dezoito famílias obtidas de polinização controlada foram plantadas sob o delineamento de blocos ao acaso com 16 plantas por parcela linear em áreas experimentais da Unidade de Pesquisa e Desenvolvimento de Jaú (DDD/ APTA/SAA), estabelecido no município de Jaú, SP, em solo Latossolo Vermelho Escuro, álico, textura argilosa, profundo, com topografia plana e drenada. Na cana soca, seis meses após a colheita, foram obtidos os seguintes caracteres: altura media dos colmos, número médio de colmos, diâmetro médio do colmo, peso médio da touceira e Brix médio. Os resultados obtidos mostraram diferenças genéticas significativas entre famílias para a maioria dos caracteres estudados. Os componentes de variâncias genéticas contribuíam com 4,27, 3,55, 15,87, 3,32 e 51,68% da variância fenotípicas para altura, número, diâmetro, peso do colmo e Brix médio, respectivamente. Estimativas de herdabilidade ao nível de planta individual para os caracteres acima foram 56,57, 76,59, 67,40, 72,73 e 54,11%. Correlações genotípicas e fenotípicas negativas altamente significativas foram observadas entre Brix médio com altura (r_g= -0,78**, r_{p} =-0,56**) e com diâmetro do colmo (r_g= -0,81**, r_p = -0,75**). A seleção de duas melhores famílias resultou em um ganho genético de 4,92% e 10,82% para altura e diâmetro do colmo, respectivamente, e a seleção das duas melhores plântulas dentro de cada família selecionada resultou em um ganho genético de 18,61% e 16,94% com um ganho total de 23,53% e 27,76% para esses dois caracteres, respectivamente.

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