

# Yield components in sugarcane families at four locations in the state of São Paulo, Brazil

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## ABSTRACT

The objective of this paper was to evaluate the genetic potential of 10 full-sib families of sugarcane (*Saccharum* spp.) planted at Experimental Stations in Jaú, Ribeirão Preto, Piracicaba and Pindorama using randomized complete blocks with three replications and 30 plants per plot. A total of 10 families was obtained from of a Copersucar germplasm breeding population in the state of Bahia. Yield components such as stalk height, stalk number, stalk diameter and average Brix were the studied traits. Except for stalk number in one location (Piracicaba), the results of the individual analysis showed genetic variations among families. Genetic variability was also detected among families for all traits. The joint analysis showed that locations effect and family x locations interaction were significant for all traits. Heritability varied among locations showing high values for stalk height and number in Piracicaba, suggesting great possibilities for genetic gain for these traits in this location. Stalk diameter and average Brix heritabilities were high, 96.02% and 94.88% respectively, among families at Pindorama, suggesting that an effort to increase both characters through family selection would be rewarding. Genotypic and phenotypic correlations among yield components in the joint analysis showed high negative correlations between stalk height and diameter.

**KEY WORDS:** *Saccharum* spp., Heritability, Genetic correlation, Family x Environment interaction.

## INTRODUCTION

Environmental effects are normally high on original seedlings population in sugarcane (*Saccharum* spp.) selection. In this situation, Skinner et al. (1987) agree that family selection would be appropriate. Heritability estimates obtained by them were very low for the majority of studied traits at the individual level, but very high at the family level, being these last ones more interesting for the study of progenies.

Many studies in several parts of the world have shown that genotype x environment interactions (GxE) or family x environment interactions are important in sugarcane and affect the way selection is carried out in breeding programs (Lo, 1987; Chavanne and Mariotti, 1989; Jackson and Hogarth, 1992; Jackson et al., 1995; Souza-Vieira and Milligan, 1999).

In Brazil, Bassinello (1991) evaluated the performance of location and families of seven sugarcane breeding populations in two contrasting environments. For the stalk weight component, the family x environment

interaction was significant, which demanded specific programs.

The sugarcane breeding program from the Instituto Agronômico, São Paulo State, Brazil, besides obtaining families by controlled pollination, involves evaluations and selections in seven different regions of the State, aiming the identification of genotypes with varied regional traits. The selection starts with Brix and is followed by other yield traits.

The present study aims at quantifying the genotype x environment interaction effect for yield components and Brix in the sugarcane and at estimating heritabilities. Attempts have also been made to determine the relationships among locations for the studied traits.

## MATERIAL AND METHODS

The material consisted of 10 full-sib families from controlled-pollinated seeds obtained from 10 randomized combinations of 14 parentals

phenotypically selected from the Copersucar<sup>1</sup> germplasm collection. The following families were used in the evaluation: SP80-4439 x SP82-6108, F174 x SP84-1192, SP80-4439 x SP80-185, SP84-1192 x RB855035, SP81-3251 x SP77-5181, SP81-5193 x SP77-5181, SP84-5124 x SP79-5099, SP85-5071 x SP80-1842, SP77-5181 x SP80-3390, SP83-2210 x IAC82-3092.

The family trials were set up at four experimental stations belonging to the Instituto Agronômico de Campinas (IAC), located in different sugarcane cultivation regions in the state of São Paulo, Brazil: a) The Jaú experimental station: latitude 22°17'S, longitude 48°37'W, altitude 580 m. The soil is dark red latosol, dystrophic, clay texture (hapludox), deep and flat with a well-drained topography. An Aw (Köppen) climate predominates in this region, with a defined dry season, annual mean temperature of 21.6°C, average humidity of around 70% with extremes of 77% in February and 59% in August. The mean annual rainfall is around 1,344mm; b) The Pindorama experimental station: latitude 21°13'S, longitude 48°56'W, altitude 560 m, with red-yellow podzolic soil TB eutrophic, medium texture (eutrudalf), deep, abrupt and well drained (Lepsch and Valadares, 1976). The climate is tropical, with a wet summer and a dry winter period. The monthly mean temperature varies from 16.6 to 28.9°C, and the annual mean rainfall is 1,390 mm. Precipitation for growth and production is usually favorable from October to April. Precipitation deficiencies and low temperatures occur from May to September; c) The Ribeirão Preto experimental station: latitude 21°12'S, longitude 47°52'W, altitude 621 m. Annual mean rainfall is 1,482 mm. The soil is dark red latosol, clay texture, deep and flat with a well-drained topography, hapludox. The monthly mean temperatures varies from 15.9 to 29.1°C; d) The Piracicaba experimental station: latitude 22°42'S and longitude 47°38'W, altitude 546m. Annual mean rainfall is 1257mm. The monthly mean temperature varies from 14.3 to 27.8°C (Ometto, 1991). Precipitation for growth and production is usually favorable from October to March. Precipitation deficiencies and low temperatures occur from April to September. Clayed alfissol and ultissol soils are typically found in the station.

Pollination were conducted in Camamu, Bahia State, at the Copersucar Experimental Station. Seeds were collected and germinated in polyethylene bags at the four experimental stations (locations) and taken to the field at the five leaf stage.

Seedlings were set out in a randomized complete blocks design with 10 treatments, three replications and 30 seedlings per plot spaced at 1.5 x 0.5 m in single rows. Families were assessed and harvested six months after the first ratoon. Tillering from each shoot of seedling were counted during each harvest conducted during the first ratoon.

Yield component determination such as stalk height and stalk number, stalk diameter, and average Brix were evaluated. For the determination of the stalk height component, a ruler was used to measure a sample of five stalks.

A pachymeter was used to measure the diameter of the same five stalks to obtain the stalk diameter. The average Brix was obtained through the reading of soluble solids of the sugarcane juice from each of the five stalks, using a manual refractometer.

Analyses were performed using the Genes Statistical Computer Program package developed by Universidade Federal de Viçosa, Brazil. For the joint analysis, the mathematical model used considered locations and families as random effects and was equivalent to the following equation described by Cruz and Regazzi (1994).

$$Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B/A_{jk} + e_{ijk}, \text{ where}$$

$Y_{ijk}$  = observed value of the  $i$ th family of the  $j$ th location in the  $k$ th replication;  $\mu$  general mean;  $G_i$  = effect of the  $i$ th family ( $i = 1, 2, \dots, 10$ ).  $A_j$  = effect of the  $j$ th location ( $j = 1, 2, \dots, 4$ );  $GA_{ij}$  = effects of the interaction of the  $i$ th family with  $j$ th, location;  $B/A_{jk}$  = effect of the  $k$ th replication within the  $j$ th location, and  $e_{ijk}$  = random error.

Variance and covariance components for the individual location analysis were calculated through the Expected Mean Square (EMS) and Expected Mean Covariance Product (EMCP) components given on the right side of the ANOVA table. (Table 1).

The phenotypic variance based on plot averages ( $\sigma_p^2$ ) and phenotypic variance based on individual plants ( $\sigma_p^2$ ) for the joint analysis they were obtained from the expressions:

$$\sigma_p^2 = \sigma_g^2 + \frac{\sigma_{ge}^2}{l} + \frac{\sigma_e^2}{lr}$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_{ge}^2 + \sigma_e^2$$

Individual ( $h_b^2$ ) and joint broad sense heritability

**Table 1.** Degree of freedom (d.f.), expected mean square (EMS) and expected mean covariance product (EMCP) for estimating components of variance, covariance and heritability for individual and joint analysis of 10 families of sugarcane established at four locations. São Paulo State, Brazil <sup>1/</sup>.

Sources of variation	d.f.	EMS	EMCP
Individual analysis			
Replications	r-1	-	-
Families	f-1	$\sigma_g^2 + r \sigma_g^2$	$\text{Cov}_{e(xy)} + \text{Cov}_{f(xy)}$
Residual	(r-1) (f-1)	$\sigma_e^2$	$\text{Cov}_{e(xy)}$
Joint analysis			
Replications/locations	(r-1)s	$\sigma_g^2 + f \sigma_r^2$	
Families (F)	f-1	$\sigma_e^2 + r \sigma_{ge}^2 + sr \sigma_g^2$	
Locations (L)	l-1	$\sigma_e^2 + r \sigma_{ge}^2 + f \sigma_r^2 + fr \sigma_e^2$	
F x L	(f-1) (l-1)	$\sigma_e^2 + r \sigma_{ge}^2$	
Residual (mean)	$\Sigma N_2$	$\sigma_e^2$	

<sup>1/</sup>  $\sigma_e^2$ : variance due to interaction of families and replications;  $\sigma_{ge}^2$ : variance due to interaction of families and locations,  $\sigma_g^2$ : variance due to differences among families;  $\text{Cov}_{e(xy)}$ : covariance due to interaction of families and replications, for traits x and y;  $\text{Cov}_{f(xy)}$ : covariance due to families for traits x and y. d.f.: degree of freedom, r: number of replications; f: number of families and  $\Sigma N$ : Sum of number of degrees of freedom for the individual analysis residuals.

( $h_x^2$ ) for each location were worked out for all characters using the formula suggested by Vencovsky and Barriga (1992), as follows:

$$h_b^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2}$$

$$h_x^2 = \frac{\sigma_g^2}{\sigma_p^2} \text{ where,}$$

$\sigma_g^2$ : genotypic variance;  $\sigma_e^2$ : environmental variance;  $\sigma_p^2$ : phenotypic variance, based on plot means.

The coefficients of genetics (CVg%) and experimental (CVe%) variations estimated for each trait in individual and joint analyses were obtained using the formulas presented by Vencovsky (1987):

$$\text{CV}_g(\%) = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \cdot 100$$

$$\text{CV}_e(\%) = \frac{\sqrt{\sigma_e^2}}{\bar{x}} \cdot 100$$

The genotypic  $rg_{(xy)}$  and phenotypic  $rp_{(xy)}$  correlations among pairs of location, for each trait under study, were obtained as suggested by Kempthorne (1966), using the following expressions.

$$rg_{(xy)} = \text{Cov}_{g(xy)} / \sqrt{\sigma_{gx}^2 \cdot \sigma_{gy}^2}$$

$$rp_{(xy)} = \text{Cov}_{p(xy)} / \sqrt{\sigma_{px}^2 \cdot \sigma_{py}^2} \quad \text{where,}$$

$\text{Cov}_{g(xy)}$  and  $\text{Cov}_{p(xy)}$ : genotypic and phenotypic covariance for traits x and y, respectively;  $\sigma_{gx}^2$  and  $\sigma_{px}^2$ : genotypic and phenotypic variances for trait x;  $\sigma_{gy}^2$  and  $\sigma_{py}^2$  genotypic and phenotypic variances for trait y.

The significance of these correlations was tested using the table in Fisher (1941) for simple correlations at the 5% and 1% levels of probability. The genotypic and phenotypic correlations were tested using the degrees of freedom from error.

## RESULTS AND DISCUSSION

### Individual analysis of variance for all locations

The four studied traits, with the exception of stalk number in Piracicaba, showed significant and highly significant differences ( $p < 0.05$  and  $p < 0.01$ ) in the

individual analysis of variance (Table 2). This suggests that differences were attributable to genetic causes and that selection within the sugarcane population included in this study is possible. Stalk height showed an average of 1.04 m/plant. The lowest height was found in Jaú with 0.96 m/plant, while the highest was found in Pindorama with 1.54 m/plant. In other words, 60% higher than Jaú value.

Stalk number of the four locations averaged 10.65 units/plant. The highest stalk number found in Jaú averaged 13.77 units/plant and the smallest, in Piracicaba, averaged 9.00 units/plant, a 53% difference.

Stalk diameter averaged 2.19 cm/plant. The location with the thickest stalk was Jaú, with 2.35 cm/plant, while the thinnest stalk was found in Piracicaba, with 1.97 cm/plant. In other words, a 19% variation in diameter.

The average Brix obtained from the sugar cane juice, from each of the five stalks, averaged 13.91% of soluble solids, in the four locations. The highest percentage of soluble solids was found in Piracicaba

(18.61%) and smallest value was found in Jaú (9.99%). In other words, a 86% difference.

Although the four experimental locations were in similar latitudes, longitudes and altitudes in the plateau region of São Paulo State, the performance of the families varied. This suggests that other environmental factors such as soil fertility, as well as soil type and structure may interfere in the family performances.

### Joint analysis of variance

The joint analysis of variance showed highly significant differences ( $p < 0.01$ ) among families for all traits (Table 3). These variations indicate good prospects for selections among families and for continuity in the sugarcane genetic breeding program.

The experimental coefficients of variation ( $CV_e$ %) showed higher values for stalk number and lower values for stalk diameter and average Brix. These values express the intrinsic properties of the traits.

The effect of location was significant on all traits,

**Table 2.** Results of ANOVA (mean square), general mean and experimental coefficients of variation ( $CV_e$ %) of stalk height (H), stalk number (N), stalk diameter (D) and average Brix (B) for 10 families of sugar cane established at four locations. São Paulo State, Brazil<sup>1/</sup>.

Locations	Traits <sup>2/</sup>	Mean square		General mean	$CV_e$ %
		Families	Residual		
Jaú	H	0.0831 <sup>4/</sup>	0.0143	0.9600	12.4637
	N	19.6741 <sup>4/</sup>	5.4320	13.7667	1.9297
	D	0.0514 <sup>4/</sup>	0.0092	2.3473	4.0852
	B	4.3433 <sup>4/</sup>	0.3490	9.9953	5.9103
Pindorama	H	0.1635 <sup>4/</sup>	0.0091	1.5398	6.1865
	N	13.6935 <sup>4/</sup>	1.5645	9.1800	13.6252
	D	0.0459 <sup>3/</sup>	0.0143	2.1643	5.5293
	B	2.7040 <sup>4/</sup>	0.6963	16.5770	5.0339
Ribeirão Preto	H	0.1398 <sup>4/</sup>	0.0120	1.4016	7.8033
	N	6.0006 <sup>4/</sup>	1.0117	10.6400	9.4534
	D	0.0568 <sup>4/</sup>	0.0023	2.2863	2.0781
	B	7.4183 <sup>4/</sup>	0.3796	10.4590	5.8909
Piracicaba	H	0.0353 <sup>3/</sup>	0.1310	1.2845	8.9189
	N	6.8574 <sup>5/</sup>	3.0760	9.0033	19.4802
	D	0.0803 <sup>4/</sup>	0.0143	1.9660	6.0643
	B	9.7040 <sup>4/</sup>	1.2266	18.6123	5.9504

<sup>1/</sup> Degrees of freedom related to families and residual were 2, 9 and 18 for replication, families and residual, respectively for all traits; <sup>2/</sup> The traits H, N, D and B are expressed in cm, unit, cm and percentage respectively; <sup>3/</sup>  $p < 0.05$ ; <sup>4/</sup>  $p < 0.01$ ; <sup>5/</sup> non significant.

indicating that they were affected by location variation under the conditions of the present study. The effect of family x location interaction was also significant

on all traits studied. According to Vencovsky (1987), the family x environment interaction reflects the difference in variability among families and the

**Table 3.** Estimate of genetics variance ( $\sigma_g^2$ ), environmental variance ( $\sigma_e^2$ ), phenotypic variance ( $\sigma_p^2$ ), broad sense heritability ( $h_b^2$ ), environment coefficient of variation (CVe%), genetic coefficient of variation (CVg%) and index of variation ( $\theta^{1/}$ ) for stalk height (H), stalk number (N), stalk diameter (D) and average Brix (B), of shoots of seedlings in sugarcane families in four locations, São Paulo State, Brazil.

Locations	Genetics parameters	Traits			
		H	N	D	B
Jaú	$\sigma_g^2$	0.2290	4.7474	0.0141	1.3315
	$\sigma_e^2$	0.0143	5.4320	0.0092	0.3490
	$\sigma_p^2$	0.2433	9.9060	0.02233	1.6805
	$h_b^2$	0.8277	0.7239	0.8210	0.9197
	CV <sub>e</sub> %	12.4600	16.9300	4.0900	5.9100
	CV <sub>g</sub> %	15.7600	15.8300	5.0600	11.5400
	$\theta^{1/}$	1.2700	0.9300	1.2400	1.9500
Pindorama	$\sigma_g^2$	0.0426	1.6630	0.0182	2.3463
	$\sigma_e^2$	0.0091	1.5645	0.0143	0.6963
	$\sigma_p^2$	0.0517	3.2275	0.0325	2.9309
	$h_b^2$	0.5144	0.8314	0.9602	0.9488
	CV <sub>e</sub> %	7.8000	9.4500	2.0800	5.8400
	CV <sub>g</sub> %	17.8300	12.1200	5.9000	14.6500
	$\theta^{1/}$	1.8900	1.2800	2.8400	2.4900
Ribeirão Preto	$\sigma_g^2$	0.0074	1.2604	0.0220	2.6165
	$\sigma_e^2$	0.0120	1.0117	0.0023	0.3796
	$\sigma_p^2$	0.0120	2.2157	0.0243	2.9911
	$h_b^2$	0.6283	0.5514	0.8231	0.8649
	CV <sub>e</sub> %	8.9200	14.4800	6.0600	5.9500
	CV <sub>g</sub> %	6.7000	12.4700	7.5400	8.6900
	$\theta^{1/}$	0.7500	0.6400	1.2400	1.4600
Piracicaba	$\sigma_g^2$	0.0515	4.0430	0.0105	0.6692
	$\sigma_e^2$	0.1310	3.0760	0.0143	1.2266
	$\sigma_p^2$	0.1825	7.1190	0.0248	1.8958
	$h_b^2$	0.9445	0.8858	0.6882	0.7425
	CV <sub>e</sub> %	6.1900	13.6200	5.5300	5.0300
	CV <sub>g</sub> %	14.7400	21.9000	4.7300	4.9300
	$\theta^{1/}$	2.3800	1.6100	0.8600	0.9800

<sup>1/</sup>  $\theta = CVg\% / CVe\%$  (Index of variation).

correlation among materials for different traits. Kageyama (1980) points out that for selection purposes, the correlations among materials from different locations allows inferences about the efficiency of indirect selection, i.e., selection in one traits and genetic gain in another.

### Genetic and environmental parameters

The genetic coefficient of variation which expresses the amount of existing genetic variation as a percentage of the general mean was higher for the average Brix% in Pindorama (14.65%) than at Jaú (11.54%), Ribeirão Preto (8.69%) and Piracicaba (4.93%) locations. These results confirm the significance of differences among families (Table 4) and characterizes Pindorama as the most suitable environment for the expression of the genetic variability in the population. For height, number and diameter of the stalks, Pindorama (17.83%), Piracicaba (21.90%) and Ribeirão Preto (7.54%), respectively are the best locations for genetic variability expression for these traits alone in this population.

The experimental coefficients of variation (CVe%) obtained for height, number and diameter of the stalks and average Brix (Table 4) may be considered low indicating good experimental precision and good assessment criteria. The (CVe%) for stalk height in Jaú (12.46%), stalk number in Pindorama (13.62%) and Piracicaba (19.48%) locations indicated the satisfactory precision level of the experiments.

The family variance components were always higher than those for the environmental effects (Table 4)

except for the joint analysis (Table 6).

The relationship between the genetic and the experimental coefficients of variation represented by the index of variation, showed high values for all traits in Pindorama, with an average of 2.12, followed by the Piracicaba, Jaú and Ribeirão Preto locations with averages values of 1.45, 1.34, 1.02 respectively (Table 3). The joint analysis (Table 5) showed values of 1.00, 0.93, 0.84, 0.82 for average Brix, height, diameter and number of stalks, respectively. According to Vencovsky (1987), values equal or higher than 1.0 are favorable to selection. For the studied sugarcane population the obtained results showed possibilities for genetic gain for the studied traits.

### Heritability

Broad sense heritability estimated for stalk height, stalk number, stalk diameter and average Brix (Table 4) varied among locations, showing higher values for stalk height and stalk number in Piracicaba, suggesting great possibilities for genetic gain for these characters and the existence of large genetic variability for both traits in this population.

Heritability for stalk diameter and average Brix were highest (96.02% and 94.88%) among families in Pindorama. The highly significant heritability estimates coupled with the large amount of variation observed among sugarcane families in the Pindorama population, suggest that an effort to increase both stalk diameter and average Brix through family selection would be feasible.

**Table 4.** Results of ANOVA (mean square) of the joint analysis variance for stalk height (H), stalk number (N), stalk diameter (D) and average Brix (%) (B) of shoots of seedlings in sugarcane families established in the Jaú, Pindorama, Ribeirão Preto and Piracicaba locations, São Paulo State, Brazil.

Sources of variation	d.f.	Characters			
		H <sup>1/</sup>	N <sup>1/</sup>	D <sup>1/</sup>	B <sup>1/</sup>
Replications/locations	8	0.0060	3.5000	0.0083	1.3604
Families (F)	9	0.1995 <sup>2/</sup>	28.3400 <sup>2/</sup>	0.1233 <sup>2/</sup>	11.8361 <sup>2/</sup>
Locations (L)	3	1.8365 <sup>2/</sup>	45.8600 <sup>2/</sup>	0.8486 <sup>2/</sup>	564.5882 <sup>2/</sup>
F x L	27	0.0741 <sup>2/</sup>	5.9600 <sup>2/</sup>	0.0371 <sup>2/</sup>	3.9019 <sup>2/</sup>
Residual (mean)	72	0.0121	2.7700	0.0100	0.6629
Mean		1.2960	10.6000	2.1900	13.9100
Coefficients of variation		8.4900	15.6300	4.5600	5.8500

<sup>1/</sup> The traits H, N, D and B are expressed in cm, unit, cm and percentage, respectively; <sup>2/</sup> p<0.01.

**Table 5.** Genetic ( $\sigma_g^2$ ), environmental ( $\sigma_e^2$ ), phenotypic ( $\sigma_p^2$ ), variances genotype x environment variance ( $\sigma_{ge}^2$ ), broad sense heritability ( $h_b^2$ ), genetic coefficient of variation (CVg%), environment coefficient of variation (CVe%) and index of variation ( $\theta$ )<sup>1/</sup> for stalk height (H), stalk number (N), stalk diameter (D) and average Brix (B) of shoots of seedlings in sugar cane families at four locations, São Paulo State, Brazil.

Genetic parameters	Traits			
	H	N	D	B
$\sigma_g^2$	0.0010	1.8600	0.0072	0.6612
$\sigma_e^2$	0.0121	2.7700	0.0100	0.6629
$\sigma_p^2$	0.0317	5.5900	0.0253	1.3242
$\sigma_{ge}^2$	0.0186	0.9600	0.0081	0.9717
$h_b^2$	0.6287	0.7897	0.6994	0.6703
CVg %	7.8800	12.8300	3.8600	5.8500
CVe %	8.4900	15.6300	4.5600	5.8500
$\theta$ <sup>1/</sup>	0.9300	0.8200	0.8400	1.0000

<sup>1/</sup> $\theta = CVg\%/CVe\%$  (Index of variation).

**Table 6.** Genotypic (rg) and phenotypic (rp) correlation among Jaú (1), Ribeirão Preto (2), Piracicaba (3) and Pindorama (4) locations, for height, number, diameter of the stalk and average Brix, São Paulo State, Brazil.

Stalk height					Stalk number				
Location	Correlation type	2	3	4	Location	Correlation type	2	3	4
1	Rg	0.37	0.33	0.50	1	Rg	0.54	0.99 <sup>2/</sup>	0.81 <sup>2/</sup>
	Rp	0.32	0.24	0.44		Rp	0.42	0.63	0.65 <sup>1/</sup>
2	Rg	-	0.80 <sup>2/</sup>	0.33	2	Rg	-	0.34	0.50
	Rp	-	0.61	0.31		Rp	-	0.23	0.43
3	Rg	-	-	0.00	3	Rg	-	-	0.84 <sup>2/</sup>
	Rp	-	-	0.00		Rp	-	-	0.59

  

Stalk diameter					Average Brix				
Location	Correlation type	2	3	4	Location	Correlation type	2	3	4
1	Rg	0.17	0.89 <sup>2/</sup>	0.62	1	Rg	0.63	0.41	0.24
	Rp	0.15	0.73 <sup>1/</sup>	0.46		Rp	0.59	0.37	0.20
2	Rg	-	0.23	0.05	2	Rg	-	0.71 <sup>1/</sup>	-0.06
	Rp	-	0.20	0.04		Rp	-	0.64 <sup>1/</sup>	-0.05
3	Rg	-	-	0.79 <sup>1/</sup>	3	Rg	-	-	0.13
	Rp	-	-	0.59		Rp	-	-	0.10

<sup>1/</sup> p<0.05; <sup>2/</sup> p< 0.01.

### Correlations

High and significant genotypic and phenotypic correlations between the Jaú and Piracicaba (Table 6) was found for stalk diameter ( $rg = 0.89^{**}$ ;  $rp = 0.73^*$ ) and stalk number ( $rg = 0.99^{**}$ ,  $rp = 0.63$ ); however, there was a low correlations for stalk height ( $rg = 0.33$ ;  $rp = 0.24$ ) and average Brix ( $rg = 0.41$ ;  $rp = 0.37$ ). The high correlation of the genetic material in the locations indicated that a single breeding program could satisfactorily serve both locations. This assertion is valid for stalk diameter and stalk number, which can be checked by the genetic correlation among locations (Vencovsky and Barriga, 1992).

The genotypic and phenotypic correlation coefficients obtained for Jaú and Pindorama were high and significant for stalk number ( $rg = 0.81^{**}$ ,  $rp = 0.65^*$ ) and medium for stalk height ( $rg = 0.50$ ,  $rp = 0.44$ ) and stalk diameter ( $rg = 0.62$ ,  $rp = 0.46$ ). The highest values, however, were smaller than those found for the coefficients between Jaú and Piracicaba. As in the previous analysis, these results characterized the interaction for stalk number, indicating that, for these traits, only one breeding program, at one location, will satisfy the needs of the other locations involved. The genotypic and phenotypic correlations between Jaú and Ribeirão Preto were high for average Brix and medium for stalk height and stalks diameter.

High genetic correlation between Piracicaba and Pindorama was found for stalk number ( $rg = 0.84$ ), stalk diameter ( $rg = 0.79$ ) and low for average Brix

( $rg = 0.13$ ). These results indicate a small interaction for stalk number and stalk diameter and that selection at one location could satisfy the needs of the other location.

In the joint analysis, the genotypic ( $rg$ ) and phenotypic ( $rp$ ) correlation (Table 7) among the yield components, showed a high negative correlation between stalk height and stalk diameter ( $rg = -0.86$ ,  $rp = -0.76$ ), and medium value of negative correlation between stalk number and stalk diameter ( $rg = -0.48$ ,  $rp = -0.42$ ). Positive and highly significant correlation was observed between stalk height and average Brix with values of  $rg = 0.89$  and  $rp = 0.64$ .

### CONCLUSIONS

The genetic coefficient of variation was higher for average Brix in Pindorama location, characterizing it as the most suitable environment for the expression of genetic variability in this family population.

The high broad sense heritability estimates coupled with the large amount of variation observed among the population families in Pindorama suggest that an increase in both stalk diameter and average Brix through family selection would be possible.

The high genotypic and phenotypic correlation among Jaú, Piracicaba and Pindorama locations for stalk diameter and stalk number respectively, indicates that,

**Table 7.** Genotypic ( $rg$ ) and phenotypic ( $rp$ ) correlations for stalk height (H), stalk number (N), stalk diameter (D) and average Brix components considering the mean for the four locations São Paulo State, Brazil.

Characters	Correlations (type)	N	D	B
H	$rg$	0.33	-0.86 <sup>2/</sup>	0.89 <sup>2/</sup>
	$rp$	0.29	-0.76 <sup>2/</sup>	0.64 <sup>1/</sup>
N	$rg$	-	-0.48	0.29
	$rp$	-	-0.42	0.08
D	$rg$	-	-	-0.68 <sup>1/</sup>
	$rp$	-	-	-0.44

<sup>1/</sup>  $p < 0.05$ ; <sup>2/</sup>  $p < 0.01$ .



for these traits, a single breeding program, in one location, will attend the region satisfactorily.

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## RESUMO

### **Comportamento de famílias de cana-de-açúcar em relação aos componentes de produção em quatro locais de seleção no Estado de São Paulo, Brasil**

O objetivo deste trabalho foi avaliar o potencial genético de 10 famílias de irmãos germanos de cana-de-açúcar (*Saccharum* spp.) plantadas nas Estações Experimentais de Jaú, Ribeirão Preto, Piracicaba e Pindorama. Os experimentos foram instalados em campo obedecendo ao delineamento de blocos ao acaso com três repetições e 30 plantas por parcela. As famílias foram obtidas de cruzamentos em uma população básica de germoplasma da Copersucar no Estado da Bahia. Componentes de produção tais como altura do colmo, quantidade de colmo por touceira, diâmetro do colmo e Brix médio foram os caracteres estudados. Exceto quantidade de cana por touceira (Piracicaba), os resultados de análises individuais mostraram variações genéticas entre famílias e locais bem como a interação famílias x locais foram altamente significativos para todos os caracteres. Nas análises individuais foram observadas variações genéticas entre famílias para todos os caracteres. Os valores das herdabilidades variaram entre locais, mostrando altos valores para altura do colmo e quantidade de colmos por touceira em Piracicaba, sugerindo grandes possibilidades de ganho genético para estes caracteres neste local. Diâmetro do colmo e Brix médio entre famílias em Pindorama, 96,02% e 94,88% sugerindo que altos ganhos poderiam ser obtidos através da utilização desse tipo de seleção. Correlações genotípicas e fenotípicas entre

componentes de produção para a análise conjunta mostraram correlações altamente negativas entre altura e diâmetro do colmo.

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