



Effects of inbreeding on the selection of sugar cane clones

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ABSTRACT - *The effects of inbreeding and of the selection of clones in families obtained through biparental, polycrossings and selfing (S_1) were evaluated. The families were represented in 89 clones and evaluated at the plant cane and ratoon stages. Results show that inbreeding depression in sugar cane is expressive for the trait tons of brix per hectare (TBH), tons of stalks per hectare (TSH), length, diameter and mean stalk weight, except for brix and number of stalks. The inbreeding influence on the traits TBH and TSH showed that selfing is not indicated for clone selection for commercial purposes, due to the high genetic load in the clones evaluated for yield per hectare. On the other hand, it was possible to select some productive inbred clones, suggesting an alternative form of using S_1 clones as parents in the process of reciprocal recurrent selection.*

Key words: *Saccharum spp.*, inbreeding depression, sugar cane breeding.

INTRODUCTION

The successful establishment of productive genotypes in any species depends on the capacity of choosing the best plants to be parents of the following generations. An identification of the crossings most capable of producing superior genotypes is especially desirable since genetic improvement programs for sugar cane take from 10 to 15 years from the moment of the hybridizations until the release of new varieties.

The crossing strategies sugar cane breeders most commonly used are biparental crossings, which involve one male (parent) and one female clone, or polycrossings where a bulk of pollen of various clones is formed to fertilize

a known female parent (Heinz and Tew 1987). However, in both crossing methods there may be an effect of inbreeding depression.

The possible occurrence of self-pollination in cross-pollination systems causes concern among sugar cane breeders. According to McIntyre and Jackson (2001) the plants obtained by self-pollination appear less vigorous than the true hybrid progeny and affect the performance of the families. In the case of self-pollinations, the genetic potential of the parents becomes questionable. An alternative to overcome this difficulty is the use of the emasculation technique with hot water (Machado et al. 1995). This process raises the cost of improvement programs, though.

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Despite selfing is considered the most intensive form of inbreeding, inbreeding depression does not occur with the same intensity among organisms. Some authors have come up with further important particulars regarding inbreeding effects on agronomical traits for sugar cane. Hogarth (1980) for example assessed the level of selfing visually, using the criterion of reduced vigor in a complete diallel with five parents. The level of selfing varied from 0-80%, depending on the specific crossing and direction of the crossing. Besides, the trait brix was not influenced by inbreeding depression, in one of the evaluated sites, while traits such as stalks per stool, tons of cane per hectare (TSH) and tons of brix per hectare (TBH) presented substantial inbreeding depression. Cassalet et al. (1996) mentioned that it is possible to segregate different traits in a particular variety without vigor loss by means of selfing and to find disease-resistant lines derived from susceptible parents. In relation to sugar yield, the segregation in superior plant lines was greater than in some varieties used as parents. Ethirajan et al. (1978) also recognized the potential contained in the selection of inbred plants to establish a genetic pool for the breeding of high quality sugar cane. Theoretically, it may be assumed that inbreeding helps to eliminate undesirable genes and fix genes of desirable loci and that the generated genotypes can be reliable donors with a predictable improved performance. Besides, the condition of ploidy in sugar cane could eventually mask some favorable traits within a variety that can be discovered by means of selfing (Cassalet et al. 1996).

Little research into the inbreeding effects in sugar cane has so far been done, principally in relation to Brazilian material. Even when considering the evidently high inbreeding depression for yield of stalks and components, the use of productive inbred clones for programs of recurrent selection is suggested in the formation of base populations in the hope of selecting well-performing inbred clones with base on the yield per hectare. In principle, the selfed progenies could be used to infer on the genetic load of their respective parents. The genetic load could be one more criterion for the prediction of crossings in sugar cane.

It is reckoned that some generations of selfing cause a "shock" in the loci that are bearers of deleterious (unfavorable) alleles and, consequently, eliminate these alleles in some inbred clones. The best materials selected would be designated to form base populations and would serve as parents, representing one more alternative to be implemented by sugar cane breeders.

In this setting, the present study had the objective of reaching conclusions on the inbreeding effects in the

selection process and of evaluating the viability of practicing selection of sugar cane clones in families derived from biparental crossings, polycrossings and selfings.

MATERIAL AND METHODS

Clones derived from biparental and polycrossings and families of selfing (S_1) were evaluated. The crossings were realized at the Universidade Federal de Alagoas - UFAL, in Murici, state of Alagoas, except for the selfings which were realized in COPERSUCAR, in Camamu, state of Bahia, in 1999. The obtained seeds were planted in the Centro de Pesquisa e Melhoramento da Cana-de-Açúcar (Research and improvement center for sugar cane) of the Universidade Federal de Viçosa, state of Minas Gerais (MG) in Oratórios - MG, (lat 20°25' S; long 42°48' W; alt 494 m asl; soil LVE).

The seedlings were obtained and transplanted according to a methodology described by Barbosa and Silveira (2000) and transplanted to the field in January 1999. The fully developed plants attained a height of approximately one meter and were cut without selection in July 1999. In February 2000 all clones in stools with at least 36 buds (12 stalks with three buds each) were sampled to form the experimental plot so the clones constituted a random sample of the families and mating systems.

The families were not completely balanced and different numbers of clones were utilized to represent them. The experiment was conducted in Fundão, on the experimental field of the Universidade Federal de Viçosa, MG. The clones were evaluated in two growth stages, plant cane and ratoons, totalling 289 clones. The data analysis was realized based on the mean of the two plant growth stages (plant cane and first ratoon) for all traits.

The experiment was set under an augmented block design (Federer 1956) with 20 replications and two common treatments, RB855536 and SP80-1816. The plots consisted of one 2 m long furrow and were spaced 1.40 m apart. Five hundred kg ha⁻¹ of the fertilizer mixture 05-20-20 was applied at planting. The following agronomical traits were assessed: brix (total soluble solids; an estimate of the sugar content), mean stalk length (SL) in meters, mean stalk diameter (SD) in millimeters, number of stalks (NS), and mean stalk weight (SW) in kilograms. Tons of stalks per hectare was expressed in $TSH = SPW \times 3,571458$, where SPW is the stalk plot weight; tons of brix per hectare was expressed by $TBH = (TSH \times \text{brix})/100$ and the estimated yield of stalks, given by $EY = \pi \times NS \times SL \times (SD/2)^2 \times d$, where EY is given in kilograms, considering a density $d =$

1.000 kg.m⁻³. Then all processable stalks per plot were counted. The length was measured from the stalk base to the first dewlap and the diameter was measured at the mean stalk height. In this case five measurements were carried out in five stalks sampled in the plot and the mean of these measures obtained were considered for the analysis of variance. Five readings of brix per plot were made on a manual refractometer for which the juice of the mean portion of the fifth internode, from the base upwards, was extracted with a small metal drill. The means of the brix readings were obtained for the analysis of variance. After these measurements, the stalks in the experimental plots were harvested and weighed on a 50 kg scale of the dynamometer type.

All traits were subjected to the analysis of variance according to Model (1) for the augmented block design.

$$Y_{ij} = m + t_i + t_{(ji)} + b_j + e_{ij} \quad (1)$$

where

Y_{ij} is the value observed in the experimental plot of the i^{th} regular treatment or of the i^{th} common treatment in the j^{th} block; m is the general mean; t_i is the fixed effect of the i^{th} common treatment (checks) with $i = 1, 2$; $t_{(ji)}$ is the random effect of the i^{th} regular treatment (family) in the j^{th} block, where $i = 1, 2, \dots, 289$; b_j is the fixed block effect where $j = 1, 2, \dots, 20$ and e_{ij} is the experimental error.

Based on the intrablock analysis the adjusted means of the regular treatments were obtained and used to compose another analysis of variance, according to model (2).

$$Y_{ik} = m + t_k + c_{(ki)} + \varepsilon \quad (2)$$

where

Y_{ik} is the adjusted mean of the i^{th} clone of the k^{th} mating system; m is the general mean; t_k is the fixed effect of the k^{th} mating system ($k = 1, 2$ and 3); $c_{(ki)}$ is the random effect of the i^{th} clone in the k^{th} mating system and ε is the effective error.

The effective error was estimated according to the equation developed by Ferreira cited by Barbosa and Pinto (1998).

$$MS_e = 1 - \frac{1}{r} - \frac{r}{c(r-1)} - \frac{(r-2n)}{cn^2(r-1)} - \frac{b}{n^2} - \frac{b}{n^2} - \frac{b}{n^2} \quad MS_e$$

where

MS_e is the mean square of the effective error; MS_t is the mean square of the error of the intrablock analysis; r is the total number of regular treatments; c is the total number of common treatments; n is the total number of plots; b is the

number of blocks of the experiment and n_k is the number of plots per block ($k=1, \dots, b$).

Based on the estimates of the effective (experimental) error we tried to recover the interblock information. With the adjusted means of the regular treatments (intrablock analysis) a new sum of squares of treatments was determined so that the genetic parameters could be estimated with greater precision. The estimates of the genetic variances, heritabilities and coefficient of genetic and environmental variation regarding the three mating systems were obtained according to Cruz et al. (2004). The expressions of Knapp et al. (1985) were applied for the estimates of the confidence intervals (CI) for heritability.

A Tukey test was also realized to compare the means of the mating systems. The expected gain with selection (GS) of the clones in each mating system were estimated by $GS = h_s^2 \times ds$, where ds is the differential of selection ($ds = m_s - m_0$), m_s the mean of the selected clones and m_0 the mean of the target mating system of the selection. A criterion of selection of 15% was adopted and the clones were classified based on the traits TBH and TSH. All these analyses were processed by Genes software (Cruz 1997).

RESULTS AND DISCUSSION

In the analysis of variance presented in Table 1, significant variances were detected between clones for the traits Brix, mean stalk length (SL), mean stalk diameter (SD), and number of stalks (NS), indicating the existence of genetic variability among clones. For these same traits, there is genetic variability at the clone level among mating systems and clones within the respective mating systems with exception of trait NS, whose genetic variance of clones within the systems of polycrossing and selfing was not significant. The existence of significant differences between the systems of mating was verified for all traits.

For the mean stalk weight (SW), estimated stalk yield (EY), tons of Brix per hectare (TBH), and tons of stalks per hectare (TSH) no significant variance was detected at the level of clones or clones within each mating system. This lack of genetic variability may have been influenced by environmental factors, expressed in the high values of coefficients of environmental variation (CV_e%), according to the criterion of Gomes (1990).

Table 2 shows the evaluated trait means in relation to the different types of clone families (mating systems). In general, the clones derived from biparental crossings presented a similar performance to those derived from polycrossings, which in turn outmatched the selfed clones.

Table 1. Summary of the analysis of variance of the sugar cane mating systems based on the adjusted means of the regular treatments

Sources of variation	df	Mean square							
		BRIX	SL	SD	NS	SW	EY	TBH	TSH
Clone	288	1.30**	0.14**	9.65**	87.66*	0.20	263.20	170.29	3548.17
Mating systems	2	7.32**	4.89**	118.57**	570.13**	4.34**	5691.02**	3140.00**	68125.22**
Clone/Systems	286	1.25**	0.11**	8.89**	84.26*	0.17	225.24	149.53	3096.57
Clone/biparental	93	1.11**	0.09**	8.46**	90.56*	0.18	223.91	163.93	3365.91
Clone/polycrossing	90	1.40**	0.16**	7.42**	81.97	0.14	178.49	136.00	2816.82
Clone/selfing	103	1.26**	0.09**	10.57**	80.58	0.18	267.30	148.35	3097.85
Effective error	19	0.16	0.02	2.15	42.61	0.11	189.66	139.24	2805.40
General mean		21.00	2.30	26.04	22.95	1.26	29.18	22.01	104.33
CV _e (%)		1.75	5.14	5.18	26.14	23.68	43.38	49.27	46.67

SL - mean stalk length; SD - mean stalk diameter; NS - number of stalks; SW - mean stalk weight; EY - estimated stalk yield; TBH - tons of brix per hectare and TSH - tons of stalks per hectare

* P < 0.05, ** P < 0.01

CV_e - Coefficient of experimental variation

Table 2. Means of the systems of mating of sugar cane for brix, mean stalk length (SL), mean stalk diameter (SD), number of stalks (NS), mean stalk weight (SW), estimated stalk yield (EY), tons of brix per hectare (TBH) and tons of stalks per hectare (TSH)

Traits	Mating systems		
	Biparental	Polycrossing	Selfing
BRIX	21.31a ¹	20.96b	20.77c
SL	2.48a	2.39b	2.06c
SD	26.95a	26.46a	24.86b
NS	24.93a	23.91a	20.36b
SW	1.41a	1.37a	1.03b
EY	35.59a	31.99a	21.03b
TBH	26.18a	24.81a	15.84b
TSH	124.56a	116.42a	75.70b

¹Means followed by the same letter in each line did not differ from each other in the Tukey test at 5% probability

Mettler and Gregg (1973) stated that selfing is the most intense form of inbreeding. Inbreeding may however also occur in bisexual species, when the mating plants have a relation of coancestry to each other. The inbreeding depression as well as the heterosis is quantified by the allelic frequencies in the population and by the effect of dominance (Falconer 1987). For the trait brix, the reduction in the mean of the selfed families (S_1) was about 2.5% and 0.09%, respectively, in relation to the clone mean of the families of biparental and polycrossings. This result suggests that the dominance effects must be of small magnitude for this trait.

For TBH and TSH however, which are rather important agronomical traits for the selection of sugar cane clones, the reduction in the mean of the S_1 families was around 39.50% and 36.15%, 39.22% and 34.98% in relation to the clone mean of the families of biparental and

polycrossings, respectively. Hogarth (1980), who analyzed some diallel crossings, stated that the trait brix was in fact not affected by the inbreeding depression, indicating that the genetic variance for brix is, possibly, mostly additive. On the other hand, it was observed that for TBH, TSH and the other traits most part of the genetic variance was due to dominance.

Among the family means the material of biparental crossing RB72454 x RB83102 stood out, principally regarding the traits brix, SL, EY, TBH and TSH (data not shown). Interestingly, other families with good attributes and performance stood out, as in the case of family SP70-1143 x ? for mean stalk length, CB45-3 x ? for number of stalks, estimated stalk yield and tons of stalks per hectare, RB751194 x SP70-1143 for mean stalk weight, RB83102 x ? for tons of stalks per hectare and tons of Brix per hectare. The selfed family SP88-819 however presented the worst performance, together with the selfed families SP88-754 and SP84-202.

The worst performance in some selfed families such as SP88-754, SP84-2029, and SP88-819 was possibly caused by the low frequency of favorable alleles for these traits. This fact was verified by Bastos et al (2003) when presenting estimates of the effects of general combining ability for TBH and TSH of small magnitude.

Assuming that no cross pollination had taken place, the selfing of the families RB72454 and SP81-1763 does not seem to have led to a high inbreeding depression, probably due to the higher frequency of favorable alleles of these parents. It must also be mentioned that in the two families where RB72454 was parent, the means were high for all traits, even when crossed with daughter RB855036, that is, having led to a certain level of inbreeding. RB72454

represented one of the most important parents used in genetic improvement programs of sugar cane in Brazil, having brought forth some of the nationwide most planted varieties. These results suggest that the frequency of favorable alleles is as important as heterosis to decide on the matings to be realized.

Among the 44 most productive clones with TBH above 35.40 and TSH above 166.03, 20, 18 and 6 resultant clones from biparental crossing, polycrossings and selfing, respectively, were detected (Table 3). This represented, respectively, 21.28, 19.78 and 5.77% of the clones evaluated within each mating system. The families RB72454 x RB83102 with six clones, RB72454 x RB855036, CB45-3 x ? and RB83102 x ?, each one with 5 clones presented outstanding performances.

Although with only two clones among the 44 selected, the selfed family RB72454 was classified as the third in relation to trait TBH, presenting values of 57.13 and 262.82 for TSH (Table 3). These values exceed the clone means, the mean of the selected clones and the mean of each one of the controls. This information once more confirms the superiority of genotype RB72454, which represents a parent of good general combining ability, based on the promising varieties and clones actually produced by sugar cane improvement programs in Brazil. Other selfed materials were also selected, three of which were SP88-754 S₁ clones and one an SP81-1763 S₁ clone.

The estimates of the genetic parameters obtained by the analysis of variance corresponding to the three types of clone families are presented in Table 4. Interestingly, the genetic variances were quite discrepant for the traits TBH and TSH - those of the families of biparental crossing were superior to those of polycrossing and selfing. However, the genetic variances for selfpollination were superior to the polycrossing. In fact, the traits TBH and TSH presented a high dominance that was not exploited by the polycrossings. On the other hand, the genetic variance among families of the different mating systems for Brix were of similar magnitudes, which reflects the greater importance of the component of additive variance for this trait in relation to TSH.

The gain with selection at a proportion of 15% of selected materials for the trait TBH and TSH should be more effective among the clones of the families of biparental crossings and selfing, despite the values of heritability were fairly small (Table 4). Although some heritabilities were of small magnitude, there will be gains with selection for the majority of the traits except in cases where the genetic variances were not significant (Table 1), principally EY and TBH for the polycrossings, whose estimates of genetic variance and heritability were negative. We

Table 3. Means of the 44 most productive clones and checks, evaluated for tons of brix per hectare (TBH) and their respective values of tons of stalks per hectare (TSH)

Families	TBH	TSH
RB83102 x ?	69.82	323.18
RB72454 x RB855036	60.30	272.28
RB72454 ⊗	57.13	262.82
RB72454 x RB855036	54.21	253.00
SP70-1143 x ?	51.13	228.89
SP70-1143 x ?	50.58	242.46
RB72454 x RB83102	49.02	217.82
RB855113 x ?	47.40	210.68
RB72454 x RB83102	47.27	217.46
RB855113 x ?	46.84	198.35
RB72454 x RB83102	46.23	218.71
RB72454 x RB855036	45.53	216.66
NA56-79 x ?	45.01	204.96
CB45-3 x ?	44.27	209.78
RB83102 x ?	43.18	198.00
RB751194 x SP70-1143	43.00	199.96
RB83102 x ?	42.79	191.57
CB45-3 x ?	42.70	198.53
RB72454 x RB855036	41.29	202.19
RB72454 x RB855036	40.92	183.53
RB751194 x SP70-1143	40.34	184.60
SP88-754 ⊗	40.28	187.28
RB8382 x SP79-2312	40.01	192.28
RB855113 x ?	39.83	174.25
RB72454 x RB83102	39.82	184.96
SP88-754 ⊗	39.34	188.00
RB751194 x SP70-1143	38.90	173.17
CB45-3 x ?	38.87	191.75
SP70-1143 x ?	38.85	180.14
RB83102 x ?	38.37	166.03
CB45-3 x ?	37.89	194.60
NA56-79 x RB91524	37.85	184.07
CB45-3 x ?	37.75	185.67
RB83102 x ?	37.52	174.07
SP88-754 ⊗	37.42	174.25
RB72454 ⊗	37.32	181.92
RB72454 x RB83102	37.23	172.64
RB751194 x SP70-1143	37.01	172.10
NA56-79 x RB91524	36.74	172.46
NA56-79 x RB91524	36.15	166.84
RB8382 x SP79-2312	36.05	167.46
SP81-1763 ⊗	35.62	168.89
NA56-79 x ?	35.41	167.28
RB72454 x RB83102	35.41	168.17
Mean SP80-1816 (checks)	26.40	116.92
Mean RB855536 (checks)	40.05	175.14
General mean of the clones (regular)	22.30	105.05
Means of selected clones	40.15	189.78

Table 4. Estimates of the genetic parameters, based on the analysis of variance for brix, mean stalk length (SL), mean stalk diameter (SD), number of stalks (NS), mean stalk weight (SW), estimated stalk yield (EY), tons of brix per hectare (TBH) and tons of stalks per hectare (TSH)

Estimates	Traits							
	BRIX	SL	SD	NS	SW	EY	TBH	TSH
$\hat{\sigma}_b^2$	0.95	0.07	6.30	47.94	0.08	34.25	24.68	560.51
$\hat{\sigma}_{pl}^2$	1.24	0.15	5.27	39.36	0.03	-	-*	11.42
$\hat{\sigma}_a^2$	1.10	0.07	8.42	37.97	0.08	77.64	9.11	292.45
h_{ab}^2	0.85	0.81	0.75	0.53	0.43	0.15	0.15	0.17
*CI _b	0.73 to 0.93	0.64 to 0.91	0.52 to 0.89	0.12 to 0.79	-0.07 to 0.74	-0.59 to 0.62	-0.60 to 0.62	-0.57 to 0.63
h_{apl}^2	0.89	0.90	0.71	0.48	0.24	-	-	0.01
*CI _{pl}	0.78 to 0.95	0.81 to 0.95	0.45 to 0.87	0.02 to 0.77	-0.44 to 0.66	-1.00 to 0.52	-0.93 to 0.54	-0.88 to 0.55
h_{aa}^2	0.87	0.81	0.80	0.47	0.42	0.29	0.06	0.09
*CI _a	0.76 to 0.94	0.64 to 0.91	0.62 to 0.91	0.01 to 0.76	-0.08 to 0.74	-0.33 to 0.68	-0.75 to 0.58	-0.69 to 0.59
GS _b	1.07	0.26	2.55	7.02	0.24	3.44	2.50	14.26
GS _{pl}	1.47	0.32	3.02	7.14	0.15	-	-	0.33
GS _a	1.14	0.32	3.79	7.01	0.21	7.40	1.05	8.00
CV _{gb}	4.56	11.05	9.49	28.96	20.48	18.30	20.03	20.34
CV _{gpl}	5.32	15.37	8.52	25.17	12.91	0.00	0.00	2.71
CV _{ga}	5.05	12.91	11.67	30.26	26.92	41.90	19.05	22.59
CV _{gb} /CV _e	2.43	2.06	1.71	1.06	0.87	0.42	0.42	0.45
CV _{gpl} /CV _e	2.78	2.96	1.56	0.96	0.56	0.00	0.00	0.06
CV _{ga} /CV _e	2.62	2.06	1.98	0.94	0.85	0.64	0.26	0.32

$\hat{\sigma}^2$ - Genetic variance among family-within clones of biparental crossings (b), polycrossing (pl) and selfing (a)

h^2 - Heritability in the broad sense in relation to family-within clones of biparental crossings (b), polycrossing (pl) and selfing (a)

CI - Confidence interval for the respective heritabilities ($\alpha=0.05$), according to methodology presented by Knapp et al. (1985)

GS - Expected gain with selection within the families of biparental crossings (b), polycrossing (pl) and selfing (a)

CV_g - Coefficient of genetic variation between the clones within the families of biparental crossings (b), polycrossing (pl) and selfing (a)

CV_e - Coefficient of experimental variation

*Negative estimates of genetic variance, broad-sense heritability, gain of selection and coefficient of variation were considered to be zero

underline that the traits brix, SL, SD, and NS did not present an inferior limit of the negative confidence interval, while SW, EY, TBH, and TSH presented a confidence interval for heritability with a negative inferior limit at 5% probability. This could affect the gains with selection for these traits in this selection phase in which replications of the regular treatments could not be made owing to the restricted number of plantlets.

It was moreover verified that the coefficient of genetic variation was slightly superior in the selfed families for trait TSH. This increase may be ascribed to the mean performance of the selfed families in relation to the others since this estimator depends on the genetic variance and the general mean of the trait.

The distributions of frequencies of each trait are presented in Figure 1. Generally speaking, there was no great difference among the mating systems for the trait brix and NS in the distribution of frequencies. Inbreeding depression in selfing becomes evident as one obtains

higher values for the traits SL, SD, SW, EY, TBH and TSH (Figure 1). The frequency of these values tends to be lower than those of the biparental and polycrossings. According to Hogarth et al. (1971a, b) and Bastos et al. (2003) the additive as much as the non-additive genetic variance is important for yield-related traits, with exception of the NS.

One theory explains this inbreeding depression by the fact that sugar cane has a high genetic load, i.e., the unfavorable alleles are not expressed in the plant due to the dominance, but could be expressed in the descendance and would bring forth plants with low performance, reducing the probability of identifying superior genotypes.

Ethirajan et al. (1978) indicated the potential of the selection of inbred clones to form genetic pools. In our present study, it was verified that it is possible to select some inbred clones of good performance in this population (Table 3). We propose the use of inbred and productive clones as one more alternative for the formation of base populations for programs of reciprocal recurrent selection.

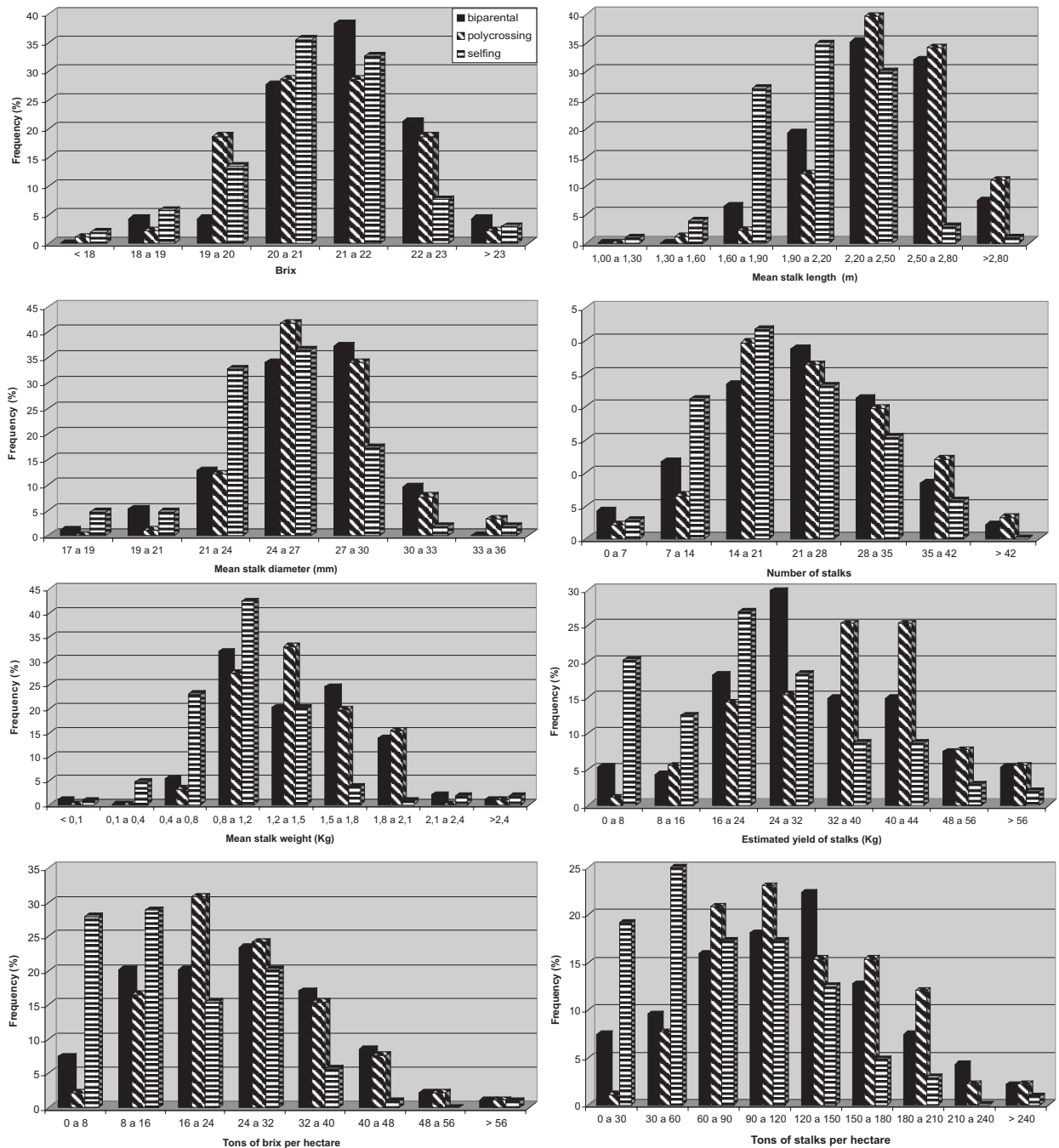


Figure 1. Frequency distribution of the eight evaluated traits in the clones from biparental mating, polycrossing and selfing

Once the heterotic groups are defined, the best families of each group would be subjected to a generation of selfing (S_1) and the best progenies selected. These selected inbred

clones would return to their respective heterotic groups and would be intercrossed, thus creating hybrid families and in the future, commercial clones.

CONCLUSIONS

1. Biparental and polycrossing are favorable for the selection of clones in sugar cane improvement.
2. Selfing is not indicated for the use in the selection of clones for commercial purposes due to the high genetic load existing in the evaluated clones for yield per hectare.
3. The inbreeding depression in sugar cane was expressive in the traits tons of brix per hectare, tons of stalks per hectare, length, diameter and mean stalk weight, besides the estimated stalk yield.
4. It was possible to select some inbred clones of good performance which can be recommended for the use as parents in programs of reciprocal recurrent selection.

Efeitos da endogamia e seleção de clones de cana-de-açúcar

RESUMO - *Avaliou-se os efeitos da endogamia e da seleção de clones em famílias de irmãos completos (IC), meios irmãos (MI) e obtidas por autofecundação (S_1). As famílias foram representadas por 289 clones avaliados em cana-planta e soca. Há evidência de que a depressão por endogamia em cana-de-açúcar é acentuada nas características toneladas de brix por hectare (TBH), toneladas de colmos por hectare (TCH), comprimento, diâmetro e peso médio de colmos, à exceção de brix e número de colmos. Embora esteja evidente a influência da depressão por endogamia nas características TBH e TCH, neste trabalho, os clones provenientes de autofecundação apresentaram ganhos com a seleção comparáveis àqueles observados para as famílias IC. Foi possível selecionar alguns clones endogâmicos produtivos, sugerindo de maneira alternativa, a utilização de clones S_1 como genitores no processo de seleção recorrente recíproca.*

Palavras-chave: *Saccharum* spp., depressão endogâmica, melhoramento de cana-de-açúcar.

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