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Genetic Variability Analysis of Foreign Sugarcane Varieties at Ferké 2 in Northern Côte d'Ivoire

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Authors' contributions

This work was carried out in collaboration between all authors. Author OOJDT performed the statistical analysis and wrote the first draft of the manuscript. Author KKD managed the analyses of the study, managed the literature searches and performed the manuscript writing. Authors OY and BBM designed the study and collected the data. Author PBC wrote the protocol and supervised the study. All authors read and approved the final manuscript.

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ABSTRACT

Aims: The study was to estimate and characterise the existing genetic variability of new candidate imported sugarcane varieties under Northern agro-climatic conditions of Côte d'Ivoire.
Study Design: A randomised complete block design with nine genotypes (clones) and four replications was used. The clones were planted in sandy-clay soil over an area of 95.68 m^2. Each clone was planted in a single row of 10 meters and in 6 rows with 1.5 m between rows (10 m x 6 x 1.5 m).
Place and Duration of Study: During 2014 and 2016 crop seasons, performance of seven new imported sugarcane clones with different origin were obtained from CIRAD Montpellier tested with two control varieties SP701006 and R579.
Methodology: Germination rate, plant height and tiller number per stool, individual stalk weight,

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tons of cane per hectare (TCH, t ha^{-1}) was determined and Pol% C was measured using a saccharimeter. The sucrose yield (TSH) was then calculated. At harvest, the rate of internodes attacked by *Eldana saccharina* was determined.

Results: Genotypes significantly differed for all the 6 traits indicating sufficient variability in the experimental material. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits studied, indicating that the apparent variation was not only genetic but also was influenced by the growing environment in the expression of the traits. In general, the quantitative trait was highly influenced by the environment. The GCV values were a bit lower ranging from 2.03% to 26.40% while the PCV values ranged from 3.21% to 53.70%. The traits TSH and Fiber showed high GCV and PCV. In the current study, the heritability ranged from 8.65% to 83.86%, while genetic advance as a percentage of the mean showed a wider gain ranging from 6.50% to 33.85%.

Conclusion: High estimates of heritability with high genetic advance were observed for TSH followed by Fiber, %Pol. Therefore, selection will be effective for these characters.

Keywords: Sugarcane; genetic variability; heritability; genetic advance; SUCAF CI.

1. INTRODUCTION

Sugarcane, a complex hybrid of *S. officinarum L., S. spontaneum* L., *S. barberi* Jeswiet and *S. sinese* Roxb. Amend. Jeswiet, is a globally important commodity crop worth $61 billion in 2013 according to FAOSTAT [1]. Present day sugarcane varieties are complex hybrids and complex polyploid derived from the inter-specific crosses involving *Saccharum officinarum* L. (2n = 80) and *S. spontaneum* L. (2n=40- 128) species [2]. The heterozygous and polyploidy natures of this crop have resulted in generation of greater genetic variability. The information on the nature and the magnitude of variability present in the genetic material is of prime importance for a breeder to initiate any effective selection program. However, it is most important sugar crop of tropical and subtropical countries for sugar production.

Breeding for higher yield and quality traits requires basic information on the extent of genetic variation in a population and its response to selection.

Generally, the main objective of sugarcane breeding is to develop special varieties capable of producing high sugar yields per unit land area. In Côte d'Ivoire, selection efforts so far have been made for increasing both cane and sugar yield and resistance to various biotic and abiotic stresses. To facilitate the selection of different cultivars for improved agro-technological quality, it is necessary to evaluate existing germplasm and released varieties of sugarcane.

Singh [3] showed in his work that in sugarcane, frequently aneuploid is impeded by its narrow gene pool, complex genome, poor fertility, caused by genetic recombination as well as long breeding selection cycle. The choice of the variety is one of the most important factors in sugarcane breeding and production. Different varieties have different yield potentials, pest and disease resistance and are bred for different ecological and economic conditions [4,5]. Therefore, the establishment of the adequate variety to be grown in a given region is of paramount importance. Normally, the choice of parental lines in sugarcane breeding programs has been defined on the basis of agronomic characters and pedigree records, using biparental crosses or polycrosses between elite genotypes. The lack of genealogy data and the inadequate identification of some genotypes may impair an accurate estimation of the genetic diversity among sugarcane accessions.

Varieties differed in morphological, cane and technological quality characters [6,7]. There was a need to evaluate introduced sugarcane varieties for morphological cane stalk characteristics for their identification, distinctiveness, uniformity and stability, use in breeding and selection of suitable ones for sugarcane production [8,9]. It was also known that there could be many genetic and environmental effects on the yield [10]. In view of the above, the present investigation was carried out with objective to evaluate introduced sugarcane varieties for morphological and technological characters at appropriate growth and development stage for their identification and selection for sugarcane production in Côte d'Ivoire.

2. MATERIALS AND METHODS

2.1 Description of the Study Area

The study was conducted at the Experimental Station of the Sugar estate of SUCAF Côte d'Ivoire in northern Côte d'Ivoire between 9°20' and 9°60' north latitude on the one hand, and, 5°22' and 5°40' west longitude. The climate prevailing in the study area is of dry tropical type with two seasons; one dry season, from November to April and the other wet, from May to October (Fig. 1). The average annual rainfall is 1200 mm and there is a diversity of soils whose majority is ferralitic and shallow (40 to 60 cm) because of induration [11,12]. The vegetation of Sugar estate of SUCAF CI is a Guinean savanna (or sub-Sudanese) of wooded type, with variable levels containing small fragments of detached forests. The soils are predominantly ferrallitic, with shallow topsoil (40 to 60 cm) limited by indurations. The area is characterized by average annual rainfall of 1160.75 mm with a mean minimum and maximum temperatures of 27.63°C and 30.78°C, respectively. Water demand of the crop is supplemented by sprinkler irrigation.

The subsoil of the Sugar estate of SUCAF CI consists of metamorphic and igneous Precambrian rocks (part of the basic complex dominated by granites and granitic gneisses). From the mineralogical point of view, there is a dominance of muscovite and biotite. The outcrops of granites and gneisses show that the degree of metamorphism seems to have been very variable. These outcrops are observed in a band parallel to the Bandama, but also in places in other areas of the zone.

2.2 Plant Material and Experimental Design

During 2014-15 and 2016-17 crop season's performance of seven new candidate imported sugarcane clones with different origin were obtained from CIRAD Montpellier (France) tested with two control varieties (SP701006 and R579) (Table 1). SP701006 was used for its high sugar content and R579 for its high cane tonnage per hectare.

Several traits of the 9 treatments (clones) were evaluated in the randomized complete block design with four replications. The clones were planted in sandy-clay soil over an area of 95.68 m^2. Each clone was planted in a single row of 10 meters and in 6 rows with 1.5 m between rows (10 m x 6 x 1.5 m).

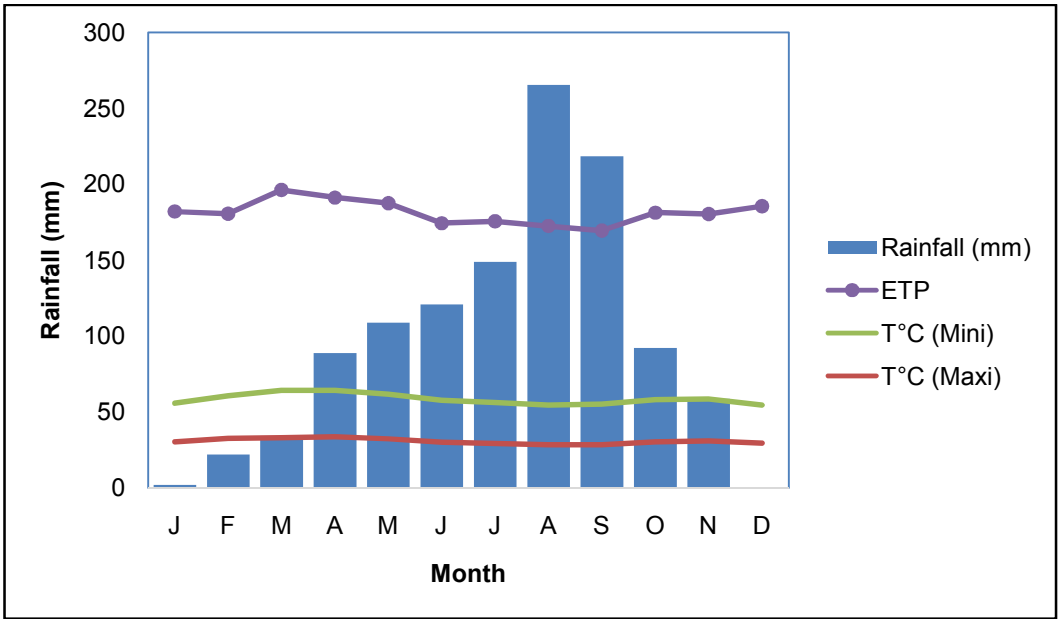

Fig. 1. Climate of Sugar estate of SUCAF CI on 4 years season (2014-2017)

Table 1. Studied clones' country of origin

Clones	Country of Origin
Kn88-260	Kenana Sugar Ltd (Soudan)
Kn89-21	Kenana Sugar Ltd (Soudan)
Kn89-24	Kenana Sugar Ltd (Soudan)
Q182	Queensland Sugar Research (Australia)
Q190	Queensland Sugar Research (Australia)
Q200	Queensland Sugar Research (Australia)
Q208	Queensland Sugar Research (Australia)
R579	CERF Reunion Island
SP701006	Brazil (Sao Paulo)

Split application of fertilizer was employed at the rate of 200 kg N, 100 kg P_2O_5, and 300 kg K_2O per hectare. All other cultural practices such as irrigation and weed control were adequately provided throughout the growth period of the cane.

2.3 Data Collection

Germination rate was determined one month after planting. Plant height and tiller number per stool, on the other hand, were taken at 2 months interval starting at the third month after planting. Plant fresh weights were used to determine individual stalk weight (kg stalk^{-1}), and tons of cane per hectare (TCH, t ha^{-1}) were calculated as the product of stalk number and stalk weight. Pol, a measure of the polarisation of the sugar solution, was measured using a saccharimeter. Sucrose yield (TSH, t sucrose ha^{-1}) was calculated as the product of TCH and SC (SC, sucrose content, %) divided by 1000 to convert kg sucrose to metric tons. The Purity is the ratio of sucrose contained in soluble solids. Normally sucrose is measured as %Brix and solid matter as %POL:

$$\boldsymbol{Purity} = \frac{(\boldsymbol{pol}\%)(\mathbf{100})}{\boldsymbol{brix}\%}. \quad (1)$$

The rate of internodes attacked by *Eldana saccharina* was determined at harvest. A sample of 30 sugarcane stalks was taken from 6 lines of each clone, at the rate of 5 canes per line. These canes were cut longitudinally and the internodes were observed to detect a possible attack of the borer (annular hole and reddish colouration of the pulp). The number of attacked internodes was reported as to the total number of internodes on each stalk to calculate the attack rate (%IA) as follows:

$$\%\mathbf{IA} = \frac{\boldsymbol{\Sigma}(\textbf{Internode attacked of 30 stalk})*\mathbf{100}}{\boldsymbol{\Sigma}(\textbf{Stalk internode of 30 stalk})}. \quad (2)$$

2.4 Data Analysis

The data collected were analysed using the JASP 0.8.6.0 version 2018 software [13]. Mean comparisons among treatment means were conducted by the least significant difference (LSD) test at 5% levels of significance. The analysis of variance was used to derive variance components (Table 2).

The data was subjected for analysis of variance [14]. The genotypic and phenotypic correlations were calculated by Kwon and Torrie [15] technic. The genetic advance in percentage of mean was calculated by using [16] formula:

$$Genetic\ variance\ (\sigma^2 g) = \frac{Genotype\ Mean\ Square - Error\ Mean\ Square\ (EMS)}{Number\ of\ Replication\ (r)} \quad (3)$$

$$Environmental\ Variance = Error\ Mean\ Square\ (EMS) \quad (4)$$

$$Phenotypic\ variance\ (\sigma^2 p) = \sigma^2 g + \sigma^2 e/r \quad (5)$$

$$GCV\% = \sqrt{(\sigma^2 g/\bar{x})}*100;\ PCV\% = \sqrt{(\sigma^2 p/\bar{x})}*100;\ ECV\% = \sqrt{(\sigma^2 e/\bar{x})}*100 \quad (6)$$

Where, GCV% = Genotypic Coefficient of variation; σ²g = Genotypic Variance; PCV % = Phenotypic Coefficient of variation; σ²p = Genotypic Variance; ECV % = Environmental Coefficient of variation; σ²e = Environmental Variance.

Heritability (H^2) on Entry Mean Basis was calculated as:

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} \quad (7)$$

The expected Genetic Advance for each trait was calculated as:

$$GA = k\sqrt{Vp}H^2 \quad (8)$$

Where, K = 1.40 at 20% selection intensity for trait; σ²p = Phenotypic variance for trait; H^2 = Broad Sense Heritability of the trait; Genetic Advance as percentage of mean is calculated as:

$$GA\% = \frac{GA}{\bar{x}}100 \quad (9)$$

Table 2. Derived variance components

Source of variation	DF	Mean square	Expected mean square
Genotype	g-1	Msg	σ^2e+r σ^2g
Replication	r-1	Msr	σ^2e+g σ^2r
Error	(g-1) (r-1)	Mse	σ^2e

Where, r = number of replications; Msr = mean square due to replications; g = number of genotypes; Msg= mean square due to genotypes; Mse = mean square of error; σ^2g, σ^2r and σ^2e are variances due to genotype, replication and error

RCBD ANOVA was computed using the following model:

$$Yij = \mu + rj + gi + \varphi ij \quad (10)$$

Where, $\boldsymbol{Yij}$= the response of trait Y in the i[th] genotype and the j[th] replication
$\boldsymbol{\mu}$ = the grand mean of trait Y
$\boldsymbol{rj}$= the effect of the j[th] replication
$\boldsymbol{gi}$= the effect of the i[th] genotype
$\boldsymbol{\varphi ij}$= experimental error effect

3. RESULTS AND DISCUSSION

3.1 Variability for All Traits Studied

Statistical parameters such as mean, minimum and maximum mean ranges, standard deviation, coefficient of variation (CV %) for different traits in this study are shown in Table 3. Among quality traits such as Purity CV% = 2.55, %Pol CV% = 8.05 and Fiber CV%=7.90, had a lower/minimum variation while TCH, TSH and %IA with CV% =17.49, 19.20 and 47.26 respectively, had a higher/maximum variation. As the variables were normally distributed, the shape of the distribution was characterised by the mean.

3.2 Variance Components and Coefficients of Variation

The analysis of variance for all traits showed significantly high ($p<0.01$) amount of variability among the studied genotypes for all the characters, except for %IA (% internode attacked by *Eldana saccharina*) (Table 4). These indicate that there are wider variations among the studied genotypes which could possibly help to design better sugar cane improvement selection programs.

Estimates of variances and their components are given in Table 5. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all characters studied, indicating that the apparent variation was not only genetic but also was influenced by the growing environment in the expression of the traits. In general, the quantitative characters were highly influenced by the environment. The GCV values were a bit lower ranging from 2.03% to 26.40% while the PCV values ranged from 3.21% to 53.70% (Table 5). According to Deshmukh et al. [17], PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium. Based on this classification, high GCV and PCV values were observed for the TSH (26.40% and 28.83%, respectively), whereas moderate GCV and PCV values were observed for the Fiber (11.11% and 12.28%, respectively). Therefore, the study of GCV and PCV in sugarcane genotypes exhibited low to high variability for almost all characters (Table 5) indicating the existence of wider genetic variation [18,19,20,21,22].

Table 3. Descriptive statistics analysis for all 6 characters in 9 foreign sugarcane clones

Traits	Mean	Minimum	Maximum	SD	CV%
Purity	87.86	80.98	91.98	2.24	2.55
%Pol	14.83	11.62	17.1	1.19	8.05
Fiber	13.65	11.23	16.16	1.07	7.9
TCH	102.61	68.19	144.34	17.49	17.04
TSH	11.02	6.62	16.41	2.17	19.2
%IA	12.6	0.4	27.98	5.96	47.26

TCH: ton cane ha^{-1}; TSH: tone sucrose ha^{-1}; IA: percentage internode attacked by Eldana saccharina; SD: Standard deviation; CV%: Coefficient of variation

3.3 Heritability and Genetic Advance

Heritability values are helpful in predicting the expected progress to be achieved through the process of selection; high heritability coupled with high genetic advance is an indicator of a greater proportion of the additive genetic variance and consequently a high genetic gain is expected from selection [23]. In the current study, the heritability ranged from 8.65% to 83.86%, while genetic advance as a percentage of the mean showed a wider gain ranging from 1.79% to 33.85% (Table 5). According to Singh [24], heritability values greater than 80% are very high, values 60 to 79% are moderately high, values from 40 to 59% are medium and values less than 40% are low. Therefore, the traits under study (Table 5) fall into the high category since heritability >80%. Johnson et al. [25] classified genetic advance as a percentage of the mean; values 0 to 10% are low, 10 to 20% are moderate and 20% and above are high. Based on this measure, the traits under study have high heritability value estimate (83.86%; 81.87% and 69.18%) was obtained for TSH, Fiber and %Pol respectively, and we observed low heritability for Purity (39.71%). Genetic advance as percent of mean was recorded as high as 33.85 for Purity followed by Fiber (14.07) and %Pol (11.22); whereas, for rest of the characters genetic advance was moderate to low (Table 5).

Shift in the gene frequency towards superior side under selection pressure is termed as genetic advance and is generally expressed as percentage of mean (genetic gain). Johnson et al. [25] found it more useful to estimate heritability values together with genetic a dvance in predicting the ultimate choice of the best genotypes by selection. However, high genetic gain along with high heritability showed most effective condition for selection.

3.4 Association among Characters

The phenotypic and genotypic correlations of qualitative with quantitative component characters are indicated in Table 6. Sugar yield is the result of many characters which are interdependent. Breeders always look for genetic variation among traits to select desirable types as some of these characters are highly correlated among themselves and with yield, so that the analysis of the relationship among these characters and their correlation with sugar yield is essential to establish selection criteria [26]. Correlation among the 6 traits studied is shown in Table 6. A positive and high significant correlation was founded between TSH and Purity (*r = 0.49, p=.0001*), %Pol (r = *0.39, p=.0001*), negative correlation with Fiber (*r = -0.49, p=.0001*) and high correlation with TCH (*r = 0.86, p=.0001*). A negative correlation was observed between %IA, Purity and TSH (*r = -0.46, p=.0001; r = -0.26, p=.006; r = -02.9, p=.002*) respectively.

Table 4. Analysis of variance (ANOVA) for 6 characters in 9 foreign sugarcane clones

		Mean squares					
Sources	**df**	**%Purity**	**%POL**	**%Fiber**	**TCH**	**TSH**	**%IA**
Genotype	8	17.48***	9.08***	9.72***	2520.30***	35.51***	57.70
Replication	3	1.16	0.48	0.65	975.70***	9.48**	32.22
Error	72	4.81	0.91	0.51	94.14	1.63	41.85

*Signification code: * p < .05. ** p < .01. *** p < .001; TCH: ton cane ha^{-1}; TSH: tone sucrose ha^{-1}; IA: percentage internode attacked by Eldana saccharina, df= degrees of freedom*

Table 5. Genetic variability and heritability parameters for all traits studied across 9 foreign sugarcane clones

Parameters	**Mean**	**Msg**	**σ^2g**	**σ^2p**	**σ^2e**	**GCV%**	**PCV%**	**H^2**	**G.A%**
Purity	87.86	17.48	3.168	7.98	4.81	2.03	3.21	39.71	1.79
%Pol	14.84	9.08	2.043	2.95	0.91	9.63	11.58	69.18	11.22
Fiber	13.66	9.72	2.30	2.81	0.51	11.11	12.28	81.87	14.07
TCH	102.61	250.3	39.04	133.18	94.14	6.09	11.25	29.31	4.62
TSH	11.02	35.51	8.47	10.1	1.63	26.40	28.83	83.86	33.85
%IA	12.60	57.7	3.96	45.81	41.85	15.79	53.70	8.65	6.50

TCH: ton cane ha^{-1}; TSH: tone sucrose ha^{-1}; %IA: percentage internode attacked by Eldana saccharina W. Msg= Mean Square Genetic

Table 6. Correlation analysis for all characters studied across 9 foreign sugarcane clones

Characters		%Purity	%POL	%Fiber	TCH	TSH	%IA
%POL	Pearson's r	**0.71**	—				
	p-value	**.0001*** **	—				
%Fiber	Pearson's r	-0.09	0.12	—			
	p-value	0.308	0.205	—			
TCH	Pearson's r	0.1	-0.12	**-0.57**	—		
	p-value	0.27	0.215	**.0001*** **	—		
TSH	Pearson's r	**0.49**	**0.39**	**-0.49**	**0.86**	—	
	p-value	**.0001*** **	**.0001*** **	**.0001*** **	**.0001*** **	—	
%IA	Pearson's r	**-0.46**	**-0.26**	0.1	-0.14	**-0.29**	—
	p-value	**.0001*** **	**.006*** **	0.302	0.142	**.002*** **	—

*Signification code: * P < .05. ** P < .01. *** P <.001; TCH: ton cane ha^{-1}; TSH: tone sucrose ha^{-1}; %IA: rate of internode attacked by Eldana saccharina*

Table 7. Summary of mean values for all 9 foreign sugarcane clones for all characters studied

Genotypes	%Purity	%POL	%Fiber	TCH	TSH	%IA
Q208	89.57^{a}	15.82^{a}	14.12^{ab}	107.54^{cd}	12.54^{b}	11.77^{ab}
SP701006(C)	88.56^{ab}	15.31^{a}	13.48^{bc}	110.78^{bc}	12.35^{b}	13.03^{ab}
Q200	88.24^{ab}	15.52^{a}	14.56^{a}	98.46^{d}	11.05^{b}	7.99^{b}
Q190	87.80^{bc}	14.07^{b}	12.84^{c}	115.78^{b}	11.77^{b}	14.54^{ab}
Q182	89.26^{a}	15.49^{a}	14.01^{ab}	81.73^{e}	9.32^{c}	13.88^{ab}
R579 (C)	87.66^{bc}	14.96^{a}	11.88^{d}	127.54^{a}	13.92^{a}	11.86^{ab}
Kn89-21	87.14^{bc}	14.12^{b}	14.50^{a}	96.20^{d}	9.72^{c}	12.69^{ab}
Kn89-24	85.83^{c}	13.17^{c}	13.16^{c}	99.98^{cd}	9.37^{c}	15.74^{a}
Kn88-260	86.67^{bc}	15.06^{a}	14.35^{a}	85.49^{e}	9.19^{c}	11.92^{ab}
P>F	.003	.003	.000	.000	.000	.001
Mean	87.86	14.83	13.65	102.61	11.02	12.60
CV%	1.37	5.86	6.59	14.12	15.61	17.38
$LSD_{5\%}$	1.62	0.73	0.55	9.13	1.13	4.70

Means followed by the same letter (a,b,c,d) do not differ significantly at 5% level probability along the columns

Most of the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficient indicating the masking of the efficiency of the environment which modified the expression of a character thereby reducing the phenotypic expression [27,28]. All characters observed for quantitative data showed positive genotypic and phenotypic correlations with the sugar yield (ton sucrose ha^{-1}, i.e. sugar yield) (Table 6).

3.5 Mean Comparison

Presented in Table 7 are the mean comparisons for all characters studied. Highest cane yield (TCH) was recorded by R579 followed by SP701006. Highest sugar yield (TSH: 13.92) was recorded for R579. However, the Queensland Sugar Research (Australia) varieties Q208, Q182, Q200, Q190, and gave the highest %Purity of 89.57, 89.26, 88.24 and 87.80% respectively. For the sugar yield (TSH), all Queensland Sugar Research (Australia) varieties Q208, Q190 and Q200, were highest with 12.52, 11.77 and 11.05 tons ha^{-1} respectively.

4. CONCLUSION

It can be concluded from the results of this study that high heritability coupled with high genetic advance was observed for the characters TSH (ton sucrose ha^{-1} or sugarcane yield), followed by Fiber percent, Pol percent (%polarization of sugar solution). This indicated that these characters are governed by additive gene action and selection for these characters will be useful in choice of best genotype.

Accordingly, based on the research data and user's selection criterion, candidate varieties Q208, Q182, Q200, and Q190 of the Queensland Sugar Research (Australia) were recommended for commercial production.

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COMPETING INTERESTS

The authors declare that there are not conflicts of interest regarding the publication of the paper.

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