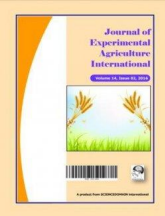

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Assessment of Genetic Variability and Heritability Analyses in Sugarcane Clones Obtained by Fuzz (True Seed) at Northern of Côte d'Ivoire

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Authors' contributions

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

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ABSTRACT

Sugarcane is the main sugar producing a crop in Côte d'Ivoire. However, improvement of this crop through breeding is limited due to the lack of genetic diversity. Therefore, genetic variability and diversity assessment are necessarily important for the sugarcane clones obtained by FUZZ (True Seed). The experiment was conducted with 47 sugarcane clones at Northern of Côte d'Ivoire (SUCAF CI), Ferkessédougou, during 2015-2016 to 2016-2017, following randomised complete block design (RCBD). Data were collected on different growth and yield contributing traits. %Flowering, Number of stem on 3 meters, stem diameter and %Brix exhibited a high genotypic coefficient of variation and phenotypic coefficient of variation. The medium phenotypic coefficient of

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variation (PCV) and genotypic coefficient of variation was observed for stem height. Based on the traits studied the stem height, stem diameter and % Brix have a high heritability value estimate excepted a number of stem on 3 meters and %Flowering showed low heritability. Number stem on 3 meters showed a negative correlation with stem diameter and positive correlation with %Brix. It was observed that stem height had a negative correlation with %Brix and positive correlation with %Flowering. Also, it was observed a negative correlation between %Brix and %Flowering. Results indicate that the genotypes should be selected on the basis of a number of stem on 3 meters, %Brix, stem diameter and %Flowering for future selection to get higher sugar yield.

Keywords: Sugarcane clone; genetic diversity; phenotypic diversity; heritability; SUCAF CI.

1. INTRODUCTION

The world's sugarcane cropped area in 2014 was over 27 million ha with a total cane production of 1900 million tons, making the world's average cane 70 tons per ha [1]. In the terms of cultivated area, sugarcane ranks the 7th place in the world, after wheat, maize, rice, soybean, barley and sorghum. Therefore, sugarcane (*Saccharum* spp.) contributes approximately 80% of the sugar to the world, greatly exceeding sugar beet as a source of sugar [2]. Today's commercial sugarcane cultivars are derived from hybridisation between the species *Saccharum officinarum* (2n = 80) with high sugar content (SC) and the wild species *Saccharum spontaneum* (2n=40- 128). The commercial cultivars have a chromosome number of 100-130 with 70-80% of the chromosomes derived from the *S. officinarum* species, 10-20% from *S. spontaneum* and 5-17% from a recombination of these two species [3, 4, 5]. The heterozygous and polyploidy natures of this crop have resulted in the 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 the most important sugar crop of tropical and subtropical countries for sugar production.

Patil et al. [6] showed in his work that in the sugarcane breeding program, the main objective is to obtain new cultivars that are more productive and have the best industrial characteristics. Tyagi and Singh [7] have shown in works that genotypic and phenotypic coefficients of variation along with heritability as well as genetic advance are essential to improve any trait of sugarcane, as this would help to know whether the objective desired can be achieved from the material.

Therefore, the objective of this study was to describe the nature and extent of genetic variability and phenotypic and genotypic variability of sugarcane clones obtained by FUZZ at northern of Côte d'Ivoire in some important traits.

2. MATERIALS AND METHODS

a) Experimental area

The study was conducted at the Experimental Station of the Sugar Complex of Ferké 2 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, with an average altitude 325 m above sea level. The climate prevailing in the study area is of the dry tropical type with two seasons; one dry season, from November to April and the other wet, from May to October. The rainfall pattern is unimodal and centred on the months of August-September which accumulate nearly half of the average annual rainfall height of about 1200 mm. To compensate for the water deficit of sugarcane, the water supply through irrigation approaches on average 700 mm [8].

The vegetation of Ferké 2 is a Guinean savanna (or sub-Sudanese) of wooded type, with variable levels containing small fragments of detached forests. The soils are predominantly ferritic, with shallow topsoil (40 to 60 cm) limited by indurations.

b) Plant materials

New genotypes have been developed from the bi-parental cross-breeding of fuzz (true seed) of Reunion origin at Reunion Island sugarcane breeding centre (eRcane). A large number of seedling clones was developed and year wise tested/screened under several selection stages, 1st stage, 2nd stage, 3rd stage [9]. The 1st stage is the seedling stage where the seeds are germinated in a greenhouse in terrines at 30°C (10 000 seedlings). Germination occurs within

three days. When the seedlings reach a height 5 cm, they are transplanted in nursery bags in a greenhouse. Automated irrigation system and bronzer regulate the temperature in the greenhouse has been installed. The plants remain in the greenhouse for 2 months. The best of 75% of the seedling is advanced for the next stage. At this stage, the seedling is classified by family according to their parent and the period of the cross. The 2nd stage is the line stage in the selection schema. In this stage after 2 months, the seedlings are pruned and transported for the transplantation. The transplantation is done in the line of 10 meters. At this stage, the seedling also is classified by family according to their parent and the period of the cross and the selection is done on the visual aspects of the cane, of the apparent absence of disease (sugarcane smut, Pokkha Boeing, Sugarcane leaf scald). In this stage, the best of 15% of seedling is advanced for the next stage. At stage 3, approximately 1000 to 700 seedling are planting in a single line of 3 meters. Periodic disease inspections are carried out. 10 stalks are harvested at randomly sampled per plot to determine sucrose content in the saccharimeter laboratory. Cane yield is estimated from a number of stalks, stalk height and stalk diameter. The Stage 4 are based on yield estimates, disease and pest data and visual evaluation of the genotypes in the field. The 3rd stage trial last 2 years and 10% of seedlings are advanced for the next stage. At stage 4, the selected genotypes are planted in 4 rows of 3 meters and 2 repetitions. The trial plots are harvested and sampled for sucrose content in plant and first ratoon crops. At harvest, the millable stalks in the plot are cut and weighed. Ten stalks are randomly chosen and analysed for sucrose content at the saccharimeter laboratory. The Stage 5 are based on the combined analysis of the data collected from the plant and first ratoon crops. The stage 4 trial last 3 years.

Sugarcane planting was done in November 2015, and qualitative and quantitative traits were measured during two separate seasons. The first season was November 2016 and coincided with 12-month-old plants. The second season was comprised of three successive time points, namely September 2017, and December 2017, and coincided with ratoon plants. The plan was to record data in the abovementioned time points in order to gain a detailed understanding of growth periods and to assess the difference between them and, consequently, to recognise critical stages for gaining the optimum yield.

Their numbers were reduced at each stage and only promising clones were promoted to the next selection stage on the basis of better stem diameter (mm), number of Stem on 3 meters, stem height (m), flowering rate % and Brix (Table 1).

The forty-seven (47) clones used in this study come from a population of 148 genotypes from the third stage of the selection scheme (Table 2) [9]. Selected genotypes from stage 3 are planted in 3 m row plots. It is at this stage that each clone receives a unique number, for example, RCI14/1-89: RCI is the name of crossing and testing country (R for Reunion Island and CI for Côte d'Ivoire), the year of the line was crossed (14 for 2014), number 1 is a 1st seed lot and the number 89 is the genotype position in ranking and in the trial. Forty-seven (47) genotypes used in this study were tested for 2 years (2015-16 and 2016-17) Table 2. All genotypes were compared with check commercial variety SP701006.

c) Experimental design

Several traits of 47 sugarcane clones obtained by Fuzz were evaluated in randomisation complete block design with 2 replications. The clones were planted in sandy-clay soil over an area of 2538 m^2. Each clone was planted in a single row of 3 meters and 6 rows with 1.5 m between rows (3m x 6 x 1.5). Split application of fertiliser was applied at 200 kg N, 100kg P_2O_5, and 300kg K_2O per hectare. All other cultural practices such as irrigation and weed control were adequately provided throughout the growth period of the cane. To avoid edge effects, the field trial was surrounded by a buffer zone 3 m wide and 30 m long planted with a commercial variety SP701006.

d) Data collection and analysis

Data were collected on different growth and yield contributing Traits. Intercultural operations like weeding, earthen-up, mulching, and irrigation were done as per required schedule. The collected data were analysed by R version 3.5.1 statistical software [10] for variability and diversity analysis. Mean comparisons among treatment mean were conducted by least significant difference (LSD) test at 5% levels of significance. Alam et al. [11] used the Plant Breeding Statistical Program (PLABSTAT (Version 2N)) for the Variance Analysis (ANOVA. The analysis of variance was used to derive variance components (Table 3) [12].

Table 1. Descriptive variable used for characterising the 5 traits of study

Traits	Description
Number of stem on 3 meters	Number of stem on 3 meters
Stem_height (m)	Stem height from ground level to the insertion of the top visible dewlap leaf (TVD)
Stem_diameter (mm)	Diameter of stem
Brix%	Brix is the total soluble solids in the aqueous solution from the stem as a percentage by weight (% w/w)
% Flowering	Flowering is the total apparent flowering

Table 2. All genotypes used in this study at the 3rd stage of the selection scheme

Order	Genotypes	Pedigree	Order	Genotypes	Pedigree
1	RCI14/1-89	R 579 x R 97/0434	**25**	RCI13/1-53	R 579 x R 585
2	RCI14/1-88	R 96/2116 x Q 213	**26**	RCI13/1-51	R 96/2569 x R 585
3	RCI14/1-71	R 579 x R 585	**27**	RCI13/1-43	R 579 x BT 92/3586
4	RCI14/1-61	R 579 x R 585	**28**	RCI13/1-42	R 579 x BT 92/3586
5	RCI14/1-59	R 579 x R 585	**29**	RCI13/1-38	VMC 93/282 x R 01/6043
6	RCI14/1-58	R 579 x R 585	**30**	RCI13/1-3	R 579 x BT 92/3586
7	RCI14/1-55	R 579 x R 585	**31**	RCI13/1-22	R 99/2162 x R 585
8	RCI14/1-47	R 96/2116 x Q 213	**32**	RCI13/1-21	R 579 x BT 92/3586
9	RCI14/1-4	R 96/2116 x Q 213	**33**	RCI13/1-18	VMC 93/282 x R 01/6043
10	RCI14/1-31	R 579 x R 585	**34**	RCI13/1-148	R 579 x BT 92/3586
11	RCI14/1-29	R 579 x R 585	**35**	RCI13/1-135	R 96/2569 x R 585
12	RCI14/1-139	R 579 x R 585	**36**	RCI13/1-119	VMC 93/282 x R 01/6043
13	RCI14/1-137	R 579 x R 585	**37**	RCI13/1-10	R 99/2162 x R 585
14	RCI14/1-127	R 96/2116 x Q 213	**38**	RCI12/1-9	R 93/0136 x N 27
15	RCI14/1-109	R 579 x R 585	**39**	RCI12/1-5	R 93/0136 x N 27
16	RCI14/1-107	R 579 x R 585	**40**	RCI12/1-130	R 582 x R 570
17	RCI14/1-102	R 579 x R 585	**41**	RCI11/1-69	R 92/6545 x R 93/6683
18	RCI14/1-1	NCo376 x N 27	**42**	RCI11/1-67	R 94/6113 x R 93/6885
19	RCI13/1-98	R 579 x R 585	**43**	RCI11/1-34	R 94/0142 x R 98/6092
20	RCI13/1-95	R 96/2569 x R 585	**44**	RCI11/1-14	R 89/2042 x R 97/2332
21	RCI13/1-94	R 582 x SP 70/1143	**45**	RCI11/1-12	R 94/6113 x R 93/6885
22	RCI13/1-87	R 579 x BT 92/3586	**46**	RCI11/1-114	R 92/2401 x R 98/6092
23	RCI13/1-73	R 582 x R 01/6043	**47**	RCI13/1-6	R 92/2210 x R 91/2069
24	RCI13/1-7	R 579 x BT 92/3586			

- **Estimation of Genotypic and Phenotypic Variances**

Genotypic and phenotypic variances were calculated using the following formula [13,14]:

Genotypic variance ($\sigma^2 g$) =

$$\frac{Genotypic\ Mean\ Square - Error\ Mean\ Square}{number\ of\ replication\ (r)} \quad (1)$$

, and *phenotypic variance is* ($\sigma^2 p$) = $\sigma^2 g$ + $\sigma^2 e/r$. (2)

Where, σ^2e= Environmental Variance (error mean square) and r= replication

- **Estimation of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV).**

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were evaluated according to the methods as follows [13,15]:

⇒ Genotypic coefficient of variation $GCV\% = \sqrt{(\sigma^2 g/\bar{x})}$*100, (3)
Where $\sigma^2 g$ is genotypic variance and $\bar{X}$ is population mean.

⇒ Phenotypic coefficient of variation $PCV\% = \sqrt{(\sigma^2 p/\bar{x})}$*100,
Where $\sigma^2 p$ is phenotypic variance and $\bar{X}$ is population mean. (4)

Table 3. Derived variance components

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

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

- **Estimation of Heritability**

Broad-sense heritability (h^2) for mean values was calculated using PABSTAT [16], following the formula described by:

$$\text{Heritability } (h^2_b) = (\sigma^2g / \sigma^2p)*100, \quad (5)$$

- **Estimation of Genetic Advance.**

Genetic advance (GA) was estimated according to the methods illustrated [17, 18]:

$$\text{Genetic advance (GA)} = h^2_b \cdot K \cdot \sigma p, \quad (6)$$

Where h^2_b is heritability in broad sense, K=K is the selection differential value which is 2.06 at 5% selection intensity, and σp is phenotypic standard deviation.

$$GA\% = \frac{GA}{\bar{x}} * 100 \quad (7)$$

Where, $\bar{x}$ is mean of all traits studied.

- **Estimation of Correlation Coefficient.**

The genotypic and phenotypic correlation coefficients between growth and yield contributing character were calculated as follows:

$$\Rightarrow \text{ Genotypic correlation, } r_g(xy) = \frac{COV(g)1.2}{\sqrt{\sigma^2 g(1)\sigma^2 g(2)}} \quad (8)$$

$\text{Cov}(g)_{1.2}$ is genotypic covariance between the variables X and Y, $\sigma^{2(g)1}$ is genotypic variance of the variable X_1, and $\sigma^{2(g)2}$ is genotypic variance of the variable X_2.

$$\Rightarrow \text{ Phenotypic correlation, } r_p(xy) = \frac{COV(g)1.2}{\sqrt{\sigma^2 p(1)\sigma p(2)}} \quad (9)$$

$\text{Cov}(p)_{1.2}$ is phenotypic covariance between the variables X and Y, $\sigma^{2(p)1}$ is phenotypic variance of the variable X_1, and $\sigma^{2(p)2}$ is phenotypic variance of the variable X_2.

Randomisation Complete Block Design (RCBD) ANOVA was computed using the following model:

$$Y_{ij} = \mu + r_j + g_i + \varphi_{ij} \quad (10)$$

Where, Y_{ij} = the response of trait Y in the i^{th} genotype and the j^{th} replication
μ= the grand mean of trait Y
r_j = the effect of the j^{th} replication
g_i = the effect of the i^{th} genotype
φ_{ij} = experimental error effect

3. RESULTS AND DISCUSSION

a. Descriptive statistics

Statistical parameters such as mean, standard deviation, minimum, maximum, coefficient of variation (CV %) for different traits in this study are shown in Table 4. Among morphological traits such as Number of stem on 3 meters with CV%=22.58, had a higher variation while stem_diameter (mm) and stem_height (m) with CV%=11.25, 9.63 respectively, had a minimum variation. Among a phonological trait the% Flowering with CV%=77.02, had a higher variation while the technological quality Brix% had CV%=9.43. In order to avoid possible bias due to the shape of the curves, the classification proposed by Costa et al. [19] was also performed. However, the two methods showed a similar classification of the CV values for each response variable (data not shown). This result is in accordance with previous reports by Costa et al. [19] and Carvalho et al. [20], who concluded that, when the variable is normally distributed, both methods are equivalent.

b. Phenotypic Characterisation & Trait Distributions

The average Nber_stem / 3m in the second season (2017) was 62.14, which was significantly ($p<0.001$) higher than the Nber_stem / 3 m the first year (53). The stem_height was significantly ($p<0.001$) higher for the first season than the second season 3.01 and 2.76 respectively. In the

second season (2017), the genotypes of sugarcane were had a high Brix% than the first season (2016) 20.30 and 18.70 respectively. Contrary to these results, the average stem_diameter in the first season (2016) 24.14 mm was smaller than that of the second season (2017) 22.6 mm and this difference was significant ($p<0.05$). For the average %Flowering in the first season (2016) was 65.21, which was significantly ($p<0.001$) higher than the %Flowering the second year trial (41.15) Fig. 1.

c. Variance components and coefficient of variation

The analysis of variance for all Traits showed statistically highly significant ($p\leq 0.01$) among the genotypes (Table 5). Similar results were also found in case of a number of millable canes, individual cane weight, cane height, and sucrose [21]. These results indicated that there were greater variations among the genotypes that might support the design of a breeding program for sugarcane improvement.

Table 4. Descriptive statistics for all traits studied

Parameters	Mean	Mini	Maxi	Variance	S.D	CV%
Nber_Stem/3 meter	57.57	34	93	168.99	13	22.58
Stem_Height	2.88	2.24	3.58	0.07	0.27	9.63
Stem_diameter	24.69	18	31.66	7.71	2.77	11.25
Brix%	19.51	14.2	24.4	3.38	1.84	9.43
%Flowering	53.18	0	100	1677.62	40.95	77.02

S.D: Standard deviation, CV%: Coefficient of variance

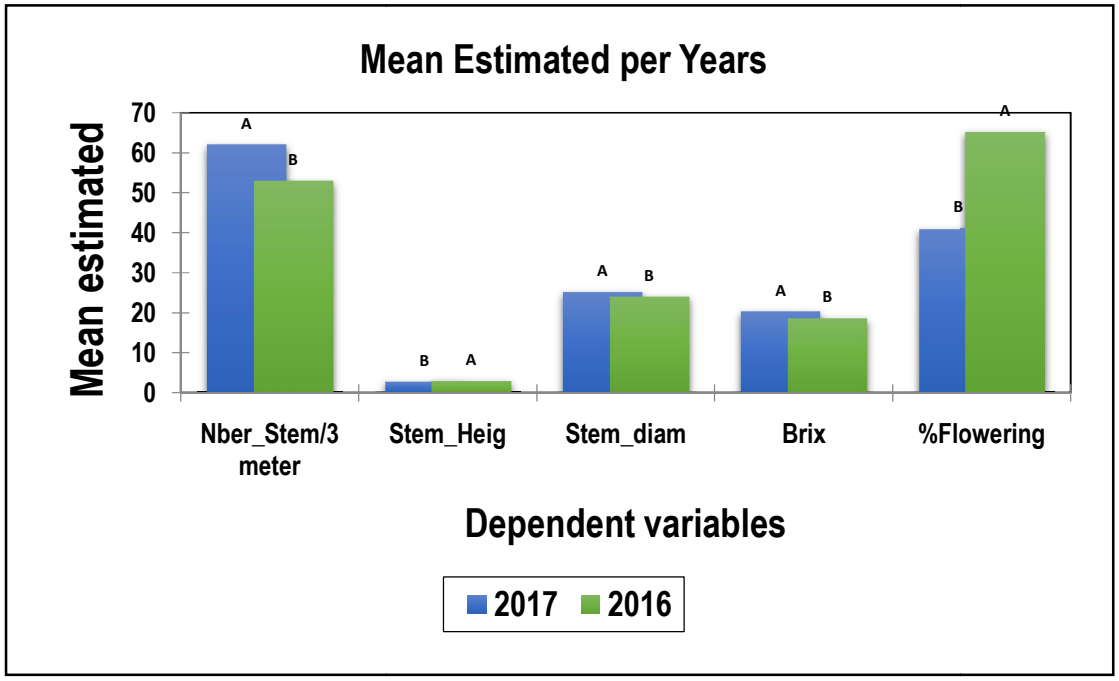

Fig. 1. Mean estimated per years for all traits studied

Table 5. Analysis of variances for 5 traits

Mean square (MS) and degree of freedom (DF) from ANOVA						
Sources	**df**	**Number of stem on 3 meters**	**Stem_ Height**	**Stem_ diameter**	**Brix**	**%Flowering**
Genotypes	46	58.0***	0.181***	10.93*	4.27**	74.5**
Replication	1	196.02**	1.44**	29.13*	62.56**	360.5**
Error	46	44.56	0.045	5.197	1.294	57.91

*Signification code: *p<.05. **p<.01. ***p<.001; df: degree of freedom*

Shivasubramanian and Menon [22] reported that the phenotypic coefficient variation (PCV) and genotypic coefficient of variation (GCV) values are ranked as low, medium, and high with 0 to 10%, 10 to 20%, and >20%, respectively (Table 6). Based on this classification, high genetic coefficient variation (GCV) were recorded for %Flowering (39.49), Number of stems on 3 meters (34.17), stem diameter (34.07) and Brix% (27.62), stem height (15.37), exhibited medium genetic coefficient variation GCV. High phenotypic coefficients of variation (PCV) were also recorded for %Flowering (83.69) followed by Number of stem on 3 meters (70.97), Stem diameter (47.05) and %Brix (33.08) but medium PCVs were recorded for stem height (17.73). The estimated phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits indicating a greater environmental influence on these traits for total variation. High GCV and PCV indicated that selection may be effective based on these Traits and their phenotypic expression would be a good indication of the genotypic potential [23]. Mean performance of different genotypes had a wider variation in performance values for different traits (Table 6).

d. 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 a selection [24]. The study showed high heritability for traits such as of Stem_Height (75.14) followed %Brix (69.70) and Stem diameter (52.45). Moderate heritability is observed for Number of stem on 3 meters (23.17) followed %Flowering (22.27). Heritability values are categorised as low (0–30%), moderate (30–60%), and high (60% and above) [25]. In the current study, the heritability ranged from 22.27% to 75.14%, while genetic advance as a percentage of the mean showed a wider gain ranging from 5.57% to 41.01% (Table 6). Based on this measure, the traits under study have high heritability value estimate (75.14%; 69.70% and 52.45%) was obtained for stem height, %Brix and Stem diameter respectively, and low heritability value estimated for (23.17% and 22.27%) stem diameter and stem height respectively. In case Ahmed et al. [26] and Songsri et al. [27] reported that better heritability values recorded point to the possibility of improvement in this parameter. It indicates that simple selection based on phenotype for these traits might be an effective method for sugarcane variety improvement selection program. High heritability coupled with low genetic advance was observed for Stem height followed by stem diameter and %Brix is indicative of non-additive gene actions' predominance which could be exploited through heterosis breeding. Sardana et al. [28] have shown in his work that high heritability may not necessarily lead to increased genetic gain unless sufficient genetic variability existed in the germplasm.

e. Pearson Correlation Coefficient

Correlation analysis of the data showed that most of the quantitative parameters correlated weakly with other quantitative parameters, whereas a negative correlation was observed for qualitative traits with other quantitative parameters, however, an association of the quantitative parameters with qualitative parameters was mostly low, or negative (Table 7).

A number of stem on 3 meters showed a negative correlation with stem diameter (r=-0.27**) and positive correlation with %Brix (r=0.21*). It was observed that stem height had a negative correlation with %Brix (r=0.34**) and positive correlation with %Flowering. Also, it was observed a negative correlation between %Brix and %Flowering (r=-0.46**).

f. Mean comparison

The clonal means for all agronomic traits considered in this study are shown in Table 8. In all the traits measured highly significant differences were observed among clones.

A number of stem on 3 meters. In all the sugarcane clones selected, RCI14/1109 (R579 x R585), RCI13/110 (R99/2162 x R585), RCI13/142 (R579 x BT92/3586), RCI13/16 (R 92/2210 x R 91/2069), RCI12/15 (R 93/0136 x N27) exhibited the highest number of stem on 3 meter while the selected clones RCI13/198 (R 579 x R 585), RCI14/171 (R 579 x R 585) represented the clones with a low number of stem on 3 meter. **Stem_height**. Among the clone selected, RCI14/161(R 579 x R 585), RCI13/142 (R 579 x BT 92/3586), RCI11/169 (R 92/6545 x R 93/6683), RCI13/195 (R 96/2569 x R 585), RCI11/167 (R 94/6113 x R 93/6885) showed the longest cane stem.

Stem_diameter. Of the selected genotypes, RCI14/171 (R 579 x R 585), RCI11/114 (R 89/2042 x R 97/2332), RCI13/110 (R 99/2162 x R 585), RCI12/1130 (R 582 x R 570), RCI13/118 (VMC 93/282 x R 01/6043) showed the largest stem diameter.

%Brix. Directly proportional to brix is percent pol or percent sucrose in the juice. The selected clones which exhibited higher %Brix value RCI14/131 (R 579 x R 585), RCI13/153 (R 579 x R 585), RCI14/1109 (R 579 x R 585), RCI12/15 (R 93/0136 x N 27), RCI11/112 (R 94/6113 x R 93/6885), RCI13/122 (R 99/2162 x R 585) consistently gave the highest percent sucrose in the juice. The low percentage brix were observed, RCI14/147 (R 96/2116 x Q 213), RCI14/1127 (R 96/2116 x Q 213), RCI14/188 (R 96/2116 x Q 213), RCI12/1130 (R 582 x R 570) and RCI14/14 (R 96/2116 x Q 213).

g. Divergence of genotypes

All the genotypes were clustered on the basis of agglomerative cluster analysis, where specifications were made based on cluster mean performance (Table 9) and grouping was made on average clustering method. Based on these two methods together the 47 genotypes were clustered into three groups named as cluster I, cluster II, and cluster III (Fig. 2). Cluster I included 16 genotypes, cluster II included 12 genotypes and 19 genotypes belonged to cluster I (Table 10).

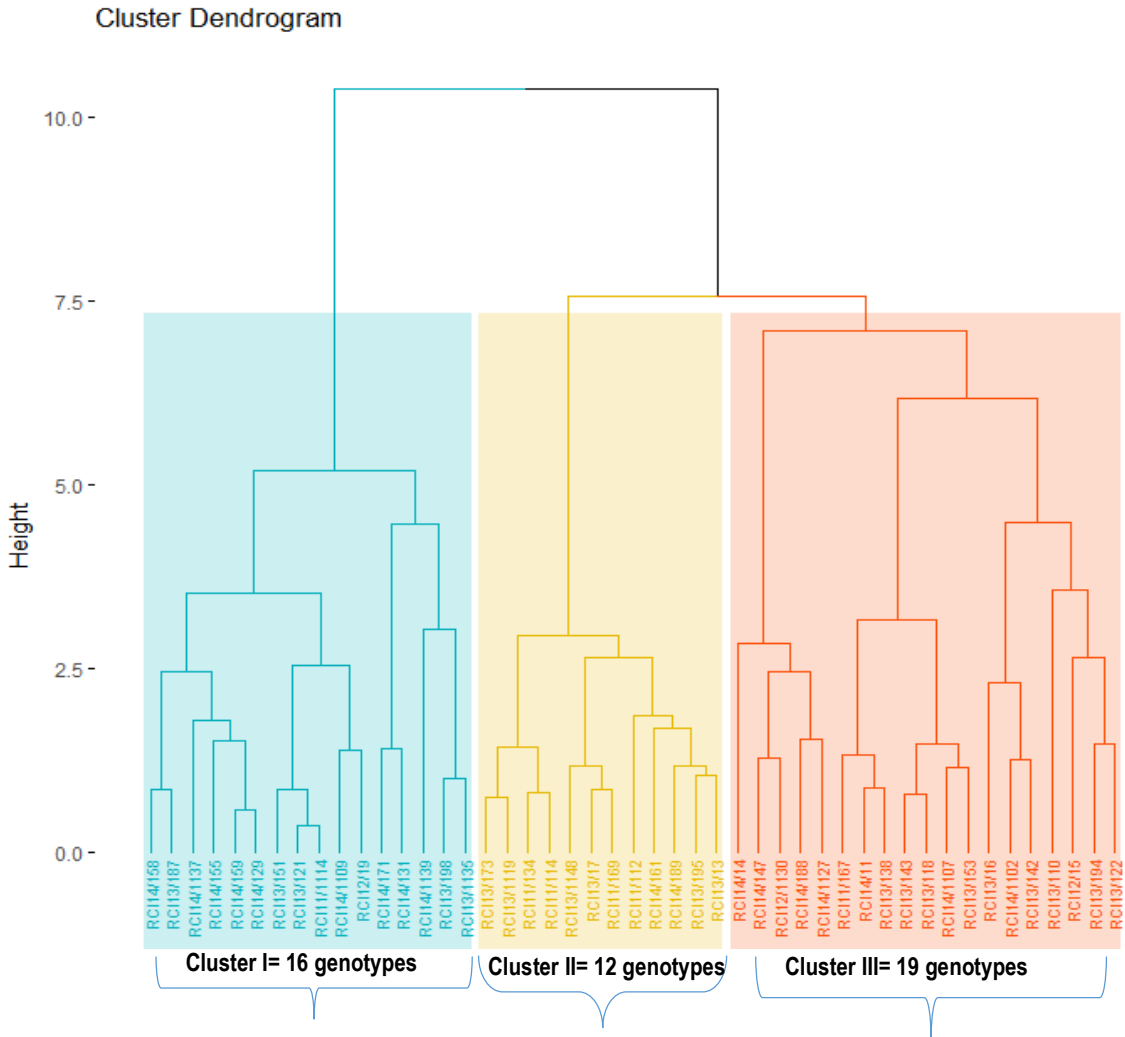

Fig. 2. Dendrogram based on the mean performance of variables among 47 sugarcane clones.

Table 6. Component for variances, heritability in a broad sense (h^2_b), and genetic advance (GA) for 5 traits of sugarcane

Traits	Mean	Msg	σ^2g	σ^2p	σ^2e	Heritability (h^2b)	GCV%	PCV%	GA	GA%
Number of stem/3m	57.57	58	6.72	29	44.56	23.17	34.17	70.97	11.06	19.21
Stem_Height	2.88	0.181	0.07	0.09	0.045	75.14	15.37	17.73	0.16	5.57
Stem_diameter	24.69	10.93	2.86	5.46	5.197	52.45	34.07	47.05	3.33	13.5
%Brix	19.51	4.27	1.49	2.13	1.294	69.7	27.62	33.08	1.96	10.03
%Flowering	53.18	74.5	8.29	37.25	57.91	22.27	39.49	83.69	21.81	41.01

Msg: Genotype Mean Square; σ^2g: genotypic variance; σ^2p: Phenotypic variance, σ^2e: Environment variance; GCV%: Genotypic coefficient of variance; PCV%: phenotypic coefficient of variance; GA%: Genetic variance.

Table 7. Correlation coefficient matrix among different 5 traits

Parameters		Number of stem on 3 meters	Stem_Heig	Stem_diam	%Brix	%Flowering
Number of stem on 3 meters	Pearson r	1				
Stem_Height	Pearson r	-0.10	1			
Stem_diameter	Pearson r	-0.27**	0.09	1		
%Brix	Pearson r	0.21*	-0.34**	0.03	1	
%Flowering	Pearson r	-0.07	0.30**	0.05	-0.46**	1

*Signification code : *p<0.05. **p<0.01. ***p<0.001;*

Table 8. Mean performances of sugarcane clone obtained by Fuzz for 5 traits

Genotypes	Pedigree	Nber_Stem/3 M	Stem_Height	Stem_diameter	%Brix	%Flowering
RCI13/1-10	R 99/2162 x R 585	77^{ab}	$3.08^{abcdefgh}$	28.83^{abc}	18.35^{fghi}	86.84^{ab}
RCI13/1-38	VMC 93/282 x R 01/6043	$60^{defghij}$	$2.91^{abcdefghijklm}$	$26.5^{abcdefghi}$	19.89^{bcdefg}	90.76^{ab}
RCI13/1-73	R 582 x R 01/6043	52.5^{hijkl}	$3.09^{abcdefgh}$	27.16^{abcde}	18.73^{efgh}	96.29^{a}
RCI13/1-42	R 579 x BT 92/3586	77^{ab}	3.23^{ab}	$23.33^{defghijkl}$	19.54^{bcdefg}	61.72^{abc}
RCI14/1-102	R 579 x R 585	73^{abcd}	$3.10^{abcdefg}$	$25.66^{abcdefghij}$	18.96^{efgh}	69.78^{ab}
RCI12/1-5	R 93/0136 x N 27	76^{abc}	$2.66^{hijklmn}$	$26.66^{abcdefgh}$	21.51^{abcd}	51.97^{abcdef}
RCI11/1-67	R 94/6113 x R 93/6885	41^{lmn}	3.12^{abcde}	$26.25^{abcdefghij}$	20.51^{abcdef}	75.13^{ab}
RCI13/1-6	R 92/2210 x R 91/2069	76.5^{abc}	$3.05^{abcdefghi}$	18.91^{l}	20.05^{bcdefg}	84.75^{ab}
RCI13/1-94	R 582 x SP 70/1143	75^{abc}	$2.80^{cdefghijklmn}$	$25.66^{abcdefghij}$	19.30^{defg}	83.98^{ab}
RCI13/1-95	R 96/2569 x R 585	$57.5^{efghijk}$	3.18^{abcd}	$24.50^{cdefghijk}$	18.61^{efghi}	87.69^{ab}
RCI13/1-119	VMC 93/282 x R 01/6043	54.50^{ghijk}	$2.91^{abcdefghijklm}$	27.0^{abcdef}	18.97^{efgh}	80.18^{ab}
RCI14/1-61	R 579 x R 585	54^{ghijkl}	3.28^{a}	$25.83^{abcdefghij}$	19.38^{cdefg}	52.34^{abcdef}
RCI14/1-89	R 579 x R 97/0434	45^{klmn}	3.11^{abcdef}	$24.83^{bcdefghijk}$	19.54^{bcdefg}	93.26^{a}
RCI11/1-12	R 94/6113 x R 93/6885	44.5^{klmn}	$3.04^{abcdefghij}$	$25.0^{abcdefghijk}$	21.5^{abcd}	74.09^{ab}
RCI13/1-7	R 579 x BT 92/3586	$61^{defghij}$	$3.02^{abcdefghijk}$	$25.66^{abcdefghij}$	18.79^{efgh}	58.69^{abcd}

Genotypes	Pedigree	Nber_Stem/3 M	Stem_Height	Stem_diameter	%Brix	%Flowering
RCI13/1-18	VMC 93/282 x R 01/6043	44^{klmn}	2.77^{defghijklmn}	27.25^{abcde}	20.22^{bcdefg}	86.047^{ab}
RCI13/1-3	R 579 x BT 92/3586	53.50^{hijkl}	3.02^{abcdefghijk}	25.41^{abcdefghijk}	20.36^{bcdefg}	45.00^{bcdefg}
RCI12/1-9	R 93/0136 x N 27	69.50^{bcdef}	2.98^{abcdefghijkl}	22.66^{efghijkl}	20.67^{abcde}	15.24^{cdefg}
RCI14/1-1	NCo376 x N 27	67^{bcdefg}	2.83^{bcdefghijklmn}	22.50^{fghijkl}	20.02^{bcdefg}	83.12^{ab}
RCI14/1-71	R 579 x R 585	36.50^{n}	3.11^{abcdef}	29.50^{a}	20.48^{abcdef}	0.0^{g}
RCI11/1-14	R 89/2042 x R 97/2332	48^{jklmn}	3.01^{abcdefghijkl}	29.33^{ab}	18.15^{ghij}	83.67^{ab}
RCI11/1-34	R 94/0142 x R 98/6092	48.5^{jklmn}	2.97^{abcdefghijkl}	26.16^{abcdefghij}	18.91^{efgh}	86.53^{ab}
RCI14/1-58	R 579 x R 585	58.5^{efghij}	2.76^{defghijklmn}	26.50^{abcdefghi}	19.93^{bcdefg}	15.44^{cdefg}
RCI13/1-22	R 99/2162 x R 585	63.5^{cdefghi}	2.61^{klmn}	23.33^{defghijkl}	21.35^{abcd}	71.31^{ab}
RCI11/1-69	R 92/6545 x R 93/6683	54.50^{ghijk}	3.21^{abc}	23.16^{defghijkl}	18.74^{efgh}	70.89^{ab}
RCI14/1-137	R 579 x R 585	56.50^{fghijk}	2.86^{abcdefghijklmn}	23.66^{defghijk}	20.86^{abcde}	5.00^{fg}
RCI14/1-47	R 96/2116 x Q 213	60.50^{defghij}	2.87^{abcdefghijklmn}	22.66^{efghijkl}	16.98^{hij}	93.83^{a}
RCI13/1-148	R 579 x BT 92/3586	50.50^{ijklm}	3.06^{abcdefghi}	25^{abcdefghijk}	18.88^{efgh}	56.75^{abcde}
RCI14/1-109	R 579 x R 585	83.5^{a}	2.69^{efghijklmn}	20.83^{kl}	21.65^{abc}	0.53^{g}
RCI13/1-51	R 96/2569 x R 585	65^{bcdefgh}	2.83^{bcdefghijklmn}	23^{defghijkl}	20.33^{bcdefg}	1.35^{g}
RCI14/1-127	R 96/2116 x Q 213	76.5^{abc}	2.73^{efghijklmn}	22.33^{ghijkl}	16.89^{hij}	90.58^{ab}
RCI13/1-87	R 579 x BT 92/3586	55^{ghijk}	2.86^{abcdefghijklmn}	25.83^{abcdefghij}	18.81^{efgh}	14.75^{cdefg}
RCI13/1-53	R 579 x R 585	50^{jklm}	2.75^{efghijklmn}	22^{ijkl}	21.67^{ab}	73.39^{ab}
RCI11/1-114	R 92/2401 x R 98/6092	59.5^{efghij}	2.69^{fghijklmn}	25.08^{abcdefghijk}	19.38^{cdefg}	20.17^{cdefg}
RCI12/1-130	R 582 x R 570	51^{ijklm}	2.74^{efghijklmn}	27.5^{abcd}	16.4^{ij}	73.42^{ab}
RCI13/1-43	R 579 x BT 92/3586	60^{defghij}	2.67^{ghijklmn}	23.165^{defghijkl}	19.89^{bcdefg}	58.31^{abcde}
RCI14/1-107	R 579 x R 585	49^{jklmn}	2.77^{defghijklmn}	23.66^{defghijk}	19.53^{bcdefg}	79.41^{ab}
RCI14/1-31	R 579 x R 585	49.5^{jklmn}	2.70^{efghijklmn}	24.33^{cdefghijk}	22.73^{a}	1.78^{g}
RCI14/1-88	R 96/2116 x Q 213	56^{ghijk}	2.8^{2bcdefghijklmn}	21.83^{jkl}	16.76^{hij}	93.39^{a}
RCI14/1-139	R 579 x R 585	48.5^{jklmn}	3.0^{abcdefghijkl}	22.83^{efghijkl}	19.93^{bcdefg}	11.11^{efg}
RCI14/1-29	R 579 x R 585	51.5^{ijklm}	2.48^{n}	24.83^{bcdefghijk}	20.76^{abcde}	7.40^{fg}
RCI13/1-98	R 579 x R 585	38.5^{mn}	2.93^{abcdefghijkl}	26.83^{abcdefg}	18.18^{ghij}	13.75^{defg}
RCI13/1-21	R 579 x BT 92/3586	70^{bcde}	2.61^{jklmn}	21.83^{jkl}	20.42^{bcdefg}	0.0^{g}
RCI14/1-4	R 96/2116 x Q 213	50.5^{ijklm}	2.59^{lmn}	24.33^{cdefghijk}	15.91^{j}	97.22^{a}
RCI14/1-55	R 579 x R 585	53.5^{hijkl}	2.49^{mn}	22.16^{hijkl}	20.87^{abcde}	2.5^{g}
RCI13/1-135	R 96/2569 x R 585	50.5^{ijklm}	2.90^{abcdefghijklmn}	25.33^{abcdefghijk}	18.14^{ghij}	0.0^{g}
RCI14/1-59	R 579 x R 585	52^{hijkl}	2.64^{ijklmn}	24^{defghijk}	19.59^{bcdefg}	0.0^{g}
Mean		57.57	2.88	24.69	19.51	53.18
P>F		< 0.0001	0.001	0.011	< 0.0001	< 0.0001
$LSD_{5\%}$		2.77	0.08	0.94	0.47	9.8

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

Table 9. Cluster mean performance for all 5 traits

Traits	Cluster I	Cluster II	Cluster III
Nber_Stem/3 meter	54.09	43.9	62.5
Stem_Heig	3.04	2.96	2.91
Stem_diam	24.45	24.3	22.25
Brix	18.29	19.35	19.71
%Flowering	97.58	1.5	4.16

Tables 10. Clusters of 47 sugarcane clones based on all traits studied

Cluster I (16 genotypes)		Cluster II (12 genotypes)		Cluster III (19 genotypes)	
Genotypes	**Pedigree**	**Genotypes**	**Pedigree**	**Genotypes**	**Pedigree**
RCI14/1-58	R 579 x R 585	RCI13/17-3	R 582 x R 01/6043	RCI14/1-4	R 96/2116 x Q 213
RCI13/1-87	R 579 x BT 92/3586	RCI13/1-119	VMC 93/282 x R 01/6043	RCI14/1-47	R 96/2116 x Q 213
RCI14/1-137	R 579 x R 585	RCI11/1-34	R 94/0142 x R 98/6092	RCI12/1-130	R 582 x R 570
RCI14/1-55	R 579 x R 585	RCI11/1-14	R 89/2042 x R 97/2332	RCI14/1-88	R 96/2116 x Q 213
RCI14/1-29	R 579 x R 585	RCI13/1-148	R 579 x BT 92/3586	RCI14/1-127	R 96/2116 x Q 213
RCI14/1-31	R 579 x R 585	RCI13/1-7	R 579 x BT 92/3586	RCI11/1-67	R 94/6113 x R 93/6885
RCI13/1-98	R 579 x R 585	RCI11/1-12	R 94/6113 x R 93/6885	RCI14/1-1	NCo376 x N 27
RCI14/1-59	R 579 x R 585	RCI14/1-61	R 579 x R 585	RCI13/1-38	VMC 93/282 x R 01/6043
RCI13/1-51	R 96/2569 x R 585	RCI14/1-89	R 579 x R 97/0434	RCI13/1-43	R 579 x BT 92/3586
RCI13/1-21	R 579 x BT 92/3586	RCI13/1-95	R 96/2569 x R 585	RCI13/1-18	VMC 93/282 x R 01/6043
RCI11/1-114	R 92/2401 x R 98/6092	RCI13/1-3	R 579 x BT 92/3586	RCI14/1-107	R 579 x R 585
RCI14/1-109	R 579 x R 585	RCI11/1-69	R 92/6545 x R 93/6683	RCI13/1-53	R 579 x R 585
RCI12/1-9	R 93/0136 x N 27			RCI13/1-6	R 92/2210 x R 91/2069
RCI14/1-71	R 579 x R 585			RCI14/1-102	R 579 x R 585
RCI14/1-139	R 579 x R 585			RCI13/1-42	R 579 x BT 92/3586
RCI13/1-135	R 96/2569 x R 585			RCI13/1-10	R 99/2162 x R 585
				RCI12/1-5	R 93/0136 x N 27
				RCI13/1-94	R 582 x SP 70/1143
				RCI13/1-22	R 99/2162 x R 585

4. CONCLUSION

The study indicated that there is wide genetic variability among the tested sugarcane clones for all Traits. Moreover, the results showed high GCV for %Flowering (39.69 followed by stem diameter (34.07), number of stems on 3 meters (34.17) and %Brix (27.62), while stem height (15.37) showed medium GCV. High phenotypic coefficients of variation (PCV) was also recorded for %Flowering (83.69) followed by a number of stem on 3 meters (70.97), stem diameter (47.05) and %Brix (33.08) but medium PCVs was recorded for stem height (17.73). The study indicated that high heritability for stem height (75.14) followed by %Brix (69.70) and stem diameter (52.45), also we observed moderate heritability for a number of stem on 3 meters (23.17) and %Flowering (22.27). The 47 genotypes were clustered into three groups named as cluster I, cluster II, and cluster III. Cluster I included 16 genotypes, cluster II included 12 genotypes and 19 genotypes belonged to cluster I.

However, selection of candidate sugarcane clones should also be performed considering those Traits with high values of heritability because they magnify the genetic advance to progenies.

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CONFLICTS OF INTERESTS

The authors declare that there are no conflicts of interest regarding the publication of the paper.

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