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

Abstract:
Sugarcane is the main sugar producing crop in Côte d'Ivoire. However, improvement of this crop through breeding is limited due to lack of genetic diversity. Therefore, genetic variability and diversity assessment are necessarily important for the sugarcane clones obtained by FUZZ (True Seed). Experiment was conducted with 47 sugarcane clone at Northern of Côte d'Ivoire (SUCAF CI), Ferkessédougou, during 2016-17, following RCBD. Data were collected on different growth and yield contributing characters. Number of stem on 3 meter exhibited high genotypic coefficient of variation and phenotypic coefficient of variation. High phenotypic coefficients of variation (PCV) were also recorded for %Flowering, Nber_stem/3m and stem_diameter but moderate PCVs were recorded for %Brix. Low PCVs was observed for stem_Height. Based on the characters studied the Nber_stem.3m, % Flowering and % Brix have a high heritability value estimate while stem_diameter and stem_height have low heritability. Nber_stem/3m showed negative and weakly significant correlation with stem_diameter, stem_height, and positive weakly correlation observed with %Brix). There was also positive and weakly correlation of stem_height with %Flowering and negative and weakly correlation are observed between % Brix with %Flowering. A positive value of r shows that the changes of two variables are in the same direction, i.e. high values of one varable are associated with high values of other and vice versa. Results indicate that the genotypes should be selected on the basis of number of stem on 3 meter, %Brix, stem diameter and %Flowering for future selection to get higher sugar yield.

Keywords: Sugarcane clone, genetic diversity, phenotypic diversity, heritability, SUCAF CI

I. 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 (**Burleigh Dodds, *2018***). 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 (**Dahlquist, *2013***). Today's commercial sugarcane cultivars are derived from hybridization 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 chromosome number of 100-130 with 70-80% of the chromosome derived from the *S. officinarum* species, 10-20% from *S. spontaneum* and 5-17% from a recombination of these two species (**D'Hont, *2005*; D'Hont *et al., 1996*; Piperidis *et al., 2001***).

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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 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 varieties capable of producing high sugar yields per unit land area. To achieve this goal we need special varieties.

The improvement of modern cultivars could be achieved by identifying genes associated with important agronomic traits, such as sucrose content. To facilitate the selection of different cultivars for improved quality, it is necessary to evaluate existing germplasm and released varieties of sugarcane.

Therefore, sustainability of sugarcane cultivation in this country is threatened. To sustain sugarcane production and to improve the productivity, tolerance to biotic and abiotic stresses, nutrient management, and improved sugar recovery are of the major concerns. Development of varieties is important consideration that would be highly productive and tolerant against biotic and abiotic factors with the changing climate. Coefficients of variation with heritability as well as genetic advance are very essential to improve any trait of sugarcane because this would help in informing whether or not the desired objective can be achieved from the material (***Alam et al., 2017***). 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.

II. 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 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 centered 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 (**Péné *et al., 2012***).

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 ferrallitic, with shallow topsoil (40 to 60 cm) limited by indurations.

b) Plant materials

New genotypes have been developed from bi-parental cross breeding of fuzz (true seed) of Reunion origin at Reunion Island sugarcane breeding center (eRcane). The large number of

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seedling clones was developed and year wise tested/screened under several selection stages in single plant, 1st stage, 2nd stage and 3rd stage. Sugarcane planting was done in November 2015, and qualitative and quantitative traits factors 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 recognize 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)**.

Table1: Descriptors used for characterizing for the 5 traits of studied

Traits	Description
Nber_stem/3m	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

Forty-seven (47) genotypes used in this study were tested during 2 years (2015-16 and 2016-17) **Table 2**. All genotypes were planted compared with check commercial varieties SP70-1006.

Table2: All genotypes used in this study at 3rd stage of the selection scheme

Order	Genotypes	Pedigree	Order	Genotypes	Pedigree
1	RCI14/189	R 579 x R 97/0434	**25**	RCI13/153	R 579 x R 585
2	RCI14/188	R 96/2116 x Q 213	**26**	RCI13/151	R 96/2569 x R 585
3	RCI14/171	R 579 x R 585	**27**	RCI13/143	R 579 x BT 92/3586
4	RCI14/161	R 579 x R 585	**28**	RCI13/142	R 579 x BT 92/3586
5	RCI14/159	R 579 x R 585	**29**	RCI13/138	VMC 93/282 x R 01/6043
6	RCI14/158	R 579 x R 585	**30**	RCI13/13	R 579 x BT 92/3586
7	RCI14/155	R 579 x R 585	**31**	RCI13/122	R 99/2162 x R 585
8	RCI14/147	R 96/2116 x Q 213	**32**	RCI13/121	R 579 x BT 92/3586
9	RCI14/14	R 96/2116 x Q 213	**33**	RCI13/118	VMC 93/282 x R 01/6043
10	RCI14/131	R 579 x R 585	**34**	RCI13/1148	R 579 x BT 92/3586
11	RCI14/129	R 579 x R 585	**35**	RCI13/1135	R 96/2569 x R 585
12	RCI14/1139	R 579 x R 585	**36**	RCI13/1119	VMC 93/282 x R 01/6043
13	RCI14/1137	R 579 x R 585	**37**	RCI13/110	R 99/2162 x R 585
14	RCI14/1127	R 96/2116 x Q 213	**38**	RCI12/19	R 93/0136 x N 27
15	RCI14/1109	R 579 x R 585	**39**	RCI12/15	R 93/0136 x N 27
16	RCI14/1107	R 579 x R 585	**40**	RCI12/1130	R 582 x R 570
17	RCI14/1102	R 579 x R 585	**41**	RCI11/169	R 92/6545 x R 93/6683

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18	RCI14/11	NCo376 x N 27	**42**	RCI11/167	R 94/6113 x R 93/6885
19	RCI13/198	R 579 x R 585	**43**	RCI11/134	R 94/0142 x R 98/6092
20	RCI13/195	R 96/2569 x R 585	**44**	RCI11/114	R 89/2042 x R 97/2332
21	RCI13/194	R 582 x SP 70/1143	**45**	RCI11/112	R 94/6113 x R 93/6885
22	RCI13/187	R 579 x BT 92/3586	**46**	RCI11/1114	R 92/2401 x R 98/6092
23	RCI13/173	R 582 x R 01/6043	**47**	RCI13/16	R 92/2210 x R 91/2069
24	RCI13/17	R 579 x BT 92/3586			

c) Experimental design

The experimental design used at one-row screening stage was a randomized block with 2 replications comprising 47 genotypes were planted in November 2015, each being planted in single rows of 3 m long with 1.5 m of inter-row spacing. 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 SP70-1006.

d) Data collection and analysis

Data were collected on different growth and yield contributing characters. Intercultural operations like weeding, earthen-up, mulching, and irrigation were done as per required schedule.

The collected data were analyzed by R version 3.5.1 statistical software for variability and diversity analysis. Analysis of variance was performed using the Plant Breeding Statistical Program (PLABSTAT (Version 2N)).

- **Estimation of Genotypic and Phenotypic Variances**

Genotypic and phenotypic variances were calculated using the following formula (**Hill *et al., 1998*; Johnson *et al., 1955***): ***Genotypic variance*** $(\sigma^2 g) = \frac{GMS - EMS}{r}$

(1)

Where GMS is genotypic mean square, EMS is error mean square, r is number of replication, and ***phenotypic variance is*** $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$.

(2)

- **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 (**Johnson *et al., 1955;* Singh *et al., 1985***):

⇒ Genotypic coefficient of variation **(GCV)** $= (\sigma^2 g / \bar{X}) * 100$,

(3)

Where $\sigma^2 g$ is genotypic variance and $\bar{X}$ is population mean.

⇒ Phenotypic coefficient of variation **(PCV)** $= (\sigma^2 p / \bar{X}) * 100$,

Where $\sigma^2 p$ is phenotypic variance and $\bar{X}$ is population mean.

(4)

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- **Estimation of Heritability**

Broad-sense heritability (h^2) for mean values was calculated using PABSTAT (**Alam *et al., 2017***), following the formula described by:

Heritability **(h^2_b) = (σ^2g / σ^2p)*100,**

(5)

- **Estimation of Genetic Advance.**

Genetic advance (GA) was estimated accordance to the methods illustrated (**Nair *et al., 1998*; Fehr *et al., 1987***):

Genetic advance (GA) = $h^2_b \cdot K \cdot \sigma p$,

(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.

- **Estimation of Correlation Coefficient.**

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

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

(7)

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.

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

(8)

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.

III. 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 3**. Among morphological traits such as Nber_stem/3m 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., 2002*** was also performed. However, the two methods showed 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., 2002*** and **Carvalho *et al., 2003***, who concluded that, when the variable is normally distributed, both methods are equivalent.

Table 3: Descriptive statistics for all traits studied

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Parameters	Mean	Variance	S.D	CV%	Mini	Maxi
Nber_Stem/3 meter	57.57	168.99	13	22.58	34	93.0
Stem_Height	2.88	0.07	0.27	9.63	2.24	3.58
Stem_diameter	24.69	7.71	2.77	11.25	18	31.66
Brix%	19.51	3.38	1.84	9.43	14.2	24.4
%Flowering	53.18	1677.62	40.95	77.02	0.0	100

b. Phenotypic Characterization & 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 was 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 ($p<0.05$) **Figure1.**

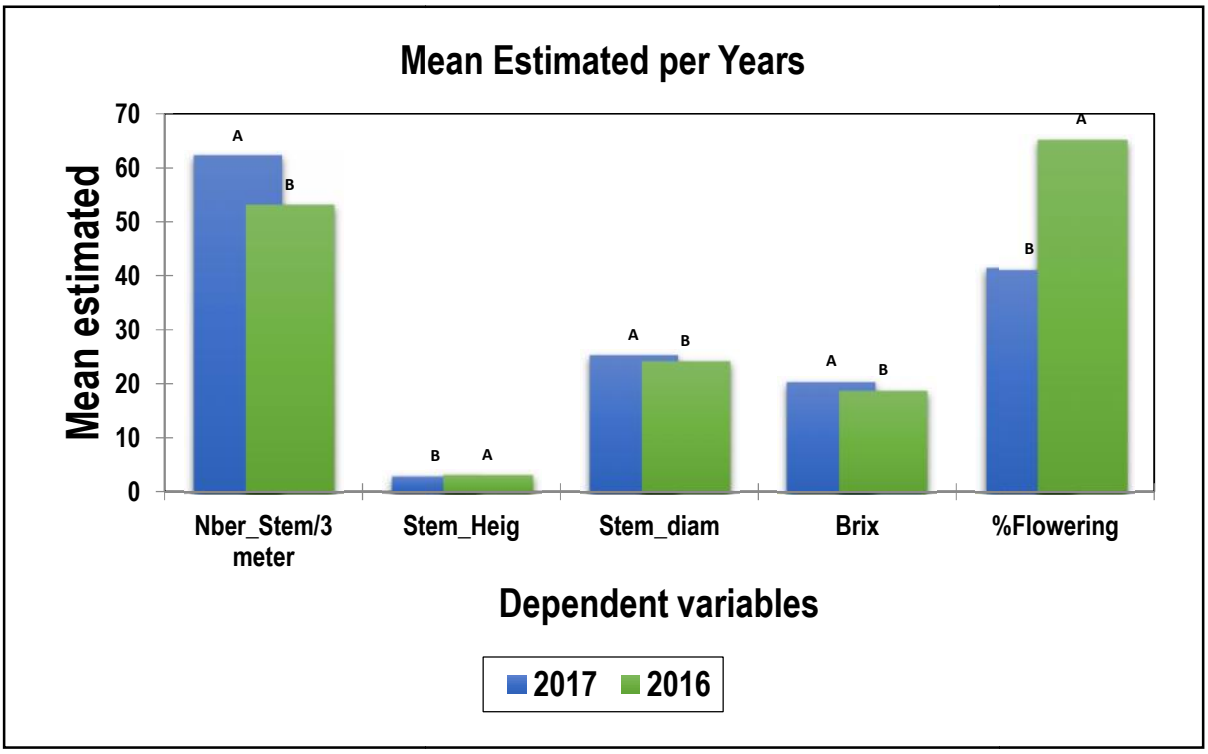

Figure 1: Mean estimated per years for all traits studied

c. Genetic and phenotypic coefficient variance components

The analysis of variance for all characters showed statistically highly significant ($p\leq 0.01$) among the genotypes (Table 4). Similar results were also found in case of number of millable canes, individual cane weight, cane height, and sucrose (**Chaudbary, *2001***). These results indicated that there were greater variations among the genotypes that might support the design of a breeding program for sugarcane improvement.

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Table 4: Analysis of variances for 5 traits

		Mean square (MS) and degree of freedom (DF) from ANOVA				
Sources	**DF**	**Nber_Stem/3m**	**Stem_Height**	**Stem_diameter**	**Brix**	**%Flowering**
Genotypes	46	258.15***	0.08***	9.92*	4.30**	2544.47**
Replication	1	2056.79**	1.36**	24.18*	59.74**	14911.05**
Error	46	42.61	0.047	5.30	1.35	529.35

As stated, the PCV (phenotypic coefficient of variation) and GCV (genotypic coefficient of variation) values are ranked as low, medium, and high with 0 to 10%, 10 to 20%, and >20%, respectively (***Shivasubramanian et al., 1973***) (**Table 5**). High GCV were recorded for Nber_stem/3m (187.20), % flowering (1894.62) and stem_diameter (9.36), Brix% (7.56) and stem_Height (0.17), exhibited low GCV. High phenotypic coefficients of variation (PCV) were also recorded for %Flowering (2890.02), Nber_stem/3m (261.21) and stem_diameter (30.82) but moderate PCVs were recorded for %Brix (14.48). Low PCVs are observed for stem_Height (2.60). High genotypic coefficient of variation and phenotypic coefficient of variation (187.20 and 1894.62) and (261.21 and 2890.02) were found in Nber_stem/3m and %Flowering respectively. The estimated phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits indicating greater environmental influence on these traits for total variation. High GCV and PCV indicated that selection may be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential (***Singh et al., 1994***). Mean performance of different genotypes had wider variation in performance values for different traits (**Table 5**).

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

Traits	**Mean**	**σp**	**Msg**	**σ^2g**	**σ^2p**	**σ^2e**	**Heritability (h^2_b)**	**GCV%**	**PCV%**	**GA**	**GA%**
Nber_Stem/3m	57.57	13	258.15	101.77	129.07	42.61	71.67	187.20	261.21	19.19	33.34
Stem_Height	2.88	0.27	0.08	0.005	0.04	0.07	6.67	0.17	2.60	0.04	1.29
Stem_diameter	24.69	2.77	9.92	2.31	4.61	5.3	30.35	9.36	30.82	1.73	7.02
%Brix	19.51	1.84	4.3	1.475	2.15	1.35	52.21	7.56	14.48	1.98	10.14
%Flowering	53.18	40.95	2544.47	1007.56	127.23	529.35	65.56	1894.62	2890.02	55.30	103.99

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 selection (***Singh and Rai, 1981***). The characters of Nber_stem/3m, %Brix and % Flowering showed high heritability, moderate heritability observed for stem_diameter and low heritability are observed for stem_height. Heritability values are categorized as low (0–30%), moderate (30–60%), and high (60% and above) (***Robinson et al., 1949***). In the current study, the heritability ranged from 6.67% to 71.67%, while genetic advance as a percentage of the mean showed a wider gain ranging from 1.29% to 103.99% (**Table 5**). Based on this measure, the traits under study have high heritability value estimate (71.67%; 65.56% and 652.21%) was

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obtained for Nber_stem.3m, % Flowering and %Brix respectively, and we are observed low heritability value estimated for (30.35% and 6.67%) stem_diameter and stem_height respectively. It indicates that simple selection based on phenotype for these traits might be effective method for sugarcane variety improvement selection program.

e. Correlation Coefficient

The phenotypic and genotypic correlations for all component characters are indicated in **Table 6**. Breeders always look for genetic variation among traits to select desirable types as some of these characters are highly correlated among themselves, so that the analysis of the relationship among these traits and their correlation with sugar yield is essential to establish selection criteria (***Singh, 2000***). Nber_stem/3m showed negative and weakly significant correlation with stem_diameter (r=-0.26, p=0.024), stem_height (r=-0.23, p=0.009), and positive weakly correlation observed with %Brix (r=0.19, p=0.054). There was also positive and weakly correlation of stem_height with %Flowering (r=0.33, p<0.001) and negative and weakly correlation are observed between % Brix with %Flowering (r=-0.44, p<0.001). A positive value of r shows that the changes of two variables are in the same direction, i.e. high values of one variable are associated with high values of other and vice versa.

Table 6: Correlation coefficient matrix among different 5 traits

Parameters		Nber_Stem/3 meter	Stem_Height	Stem_diameter	%Brix	%Flowering
Nber_Stem/3 meter	Pearson's r	—				
	p-value	—				
Stem_Height	Pearson's r	**-0.23**	—			
	p-value	**0.024**	—			
Stem_diameter	Pearson's r	**-0.26**	0.04	—		
	p-value	**0.009**	0.694	—		
%Brix	Pearson's r	**0.19**	**-0.32**	0.02	—	
	p-value	**0.054**	**0.002**	0.836	—	
%Flowering	Pearson's r	-0.074	**0.33**	0.05	**-0.44**	—
	p-value	0.476	**< .001**	0.611	**< .001**	—

f. Mean comparison

The clonal means for all agronomic traits considered in this study are shown in **Table 7.** In all the traits measured highly significant differences were observed among clones.

Nber_stem/3m. 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 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.

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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).

274 **Table 7:** Mean performances of sugarcane clone obtained by Fuzz for 5 traits

Genotypes	Pedigree	Nber_Stem/3 M	Stem_Height	Stem_diameter	%Brix	%Flowering
RCI13/110	R 99/2162 x R 585	77 ab	3.08 abcdefgh	28.83 abc	18.35 fghi	86.84 ab
RCI13/138	VMC 93/282 x R 01/6043	60 defghij	2.91 abcdefghijklm	26.5 abcdefghi	19.89 bcdefg	90.76 ab
RCI13/173	R 582 x R 01/6043	52.5 hijkl	3.09 abcdefgh	27.16 abcde	18.73 efgh	96.29 a
RCI13/142	R 579 x BT 92/3586	77 ab	3.23 ab	23.33 defghijkl	19.54 bcdefg	61.72 abc
RCI14/1102	R 579 x R 585	73 abcd	3.10 abcdefg	25.66 abcdefghij	18.96 efgh	69.78 ab
RCI12/15	R 93/0136 x N 27	76 abc	2.66 hijklmn	26.66 abcdefgh	21.51 abcd	51.97 abcdef
RCI11/167	R 94/6113 x R 93/6885	41 lmn	3.12 abcde	26.25 abcdefghij	20.51 abcdef	75.13 ab
RCI13/16	R 92/2210 x R 91/2069	76.5 abc	3.05 abcdefghi	18.91 l	20.05 bcdefg	84.75 ab
RCI13/194	R 582 x SP 70/1143	75 abc	2.80 cdefghijklmn	25.66 abcdefghij	19.30 defg	83.98 ab
RCI13/195	R 96/2569 x R 585	57.5 efghijk	3.18 abcd	24.50 cdefghijk	18.61 efghi	87.69 ab
RCI13/1119	VMC 93/282 x R 01/6043	54.50 ghijk	2.91 abcdefghijklm	27 abcdef	18.97 efgh	80.18 ab
RCI14/161	R 579 x R 585	54 ghijkl	3.28 a	25.83 abcdefghij	19.38 cdefg	52.34 abcdef
RCI14/189	R 579 x R 97/0434	45 klmn	3.11 abcdef	24.83 bcdefghijk	19.54 bcdefg	93.26 a
RCI11/112	R 94/6113 x R 93/6885	44.5 klmn	3.04 abcdefghij	25 abcdefghijk	21.5 abcd	74.09 ab
RCI13/17	R 579 x BT 92/3586	61 defghij	3.02 abcdefghijk	25.66 abcdefghij	18.79 efgh	58.69 abcd
RCI13/118	VMC 93/282 x R 01/6043	44 klmn	2.77 defghijklmn	27.25 abcde	20.22 bcdefg	86.047 ab
RCI13/13	R 579 x BT 92/3586	53.50 hijkl	3.02 abcdefghijk	25.41 abcdefghijk	20.36 bcdefg	45.00 bcdefg
RCI12/19	R 93/0136 x N 27	69.50 bcdef	2.98 abcdefghijkl	22.66 efghijkl	20.67 abcde	15.24 cdefg
RCI14/11	NCo376 x N 27	67 bcdefg	2.83 bcdefghijklmn	22.50 fghijkl	20.02 bcdefg	83.12 ab
RCI14/171	R 579 x R 585	36.50 n	3.11 abcdef	29.50 a	20.48 abcdef	0.0 g
RCI11/114	R 89/2042 x R 97/2332	48 jklmn	3.01 abcdefghijkl	29.33 ab	18.15 ghij	83.67 ab
RCI11/134	R 94/0142 x R 98/6092	48.5 jklmn	2.97 abcdefghijkl	26.16 abcdefghij	18.91 efgh	86.53 ab
RCI14/158	R 579 x R 585	58.5 efghij	2.76 defghijklmn	26.50 abcdefghi	19.93 bcdefg	15.44 cdefg
RCI13/122	R 99/2162 x R 585	63.5 cdefghi	2.61 klmn	23.33 defghijkl	21.35 abcd	71.31 ab
RCI11/169	R 92/6545 x R 93/6683	54.50 ghijk	3.21 abc	23.16 defghijkl	18.74 efgh	70.89 ab
RCI14/1137	R 579 x R 585	56.50 fghijk	2.86 abcdefghijklmn	23.66 defghijk	20.86 abcde	5.00 fg
RCI14/147	R 96/2116 x Q 213	60.50 defghij	2.87 abcdefghijklmn	22.66 efghijkl	16.98 hij	93.83 a
RCI13/1148	R 579 x BT 92/3586	50.50 ijklm	3.06 abcdefghi	25 abcdefghijk	18.88 efgh	56.75 abcde

RCI14/1109	R 579 x R 585	83.5 a	2.69 efghijklmn	20.83 kl	21.65 abc	0.53 g
RCI13/151	R 96/2569 x R 585	65 bcdefgh	2.83 bcdefghijklmn	23 defghijkl	20.33 bcdefg	1.35 g
RCI14/1127	R 96/2116 x Q 213	76.5 abc	2.73 efghijklmn	22.33 ghijkl	16.89 hij	90.58 ab
RCI13/187	R 579 x BT 92/3586	55 ghijk	2.86 abcdefghijklmn	25.83 abcdefghij	18.81 efgh	14.75 cdefg
RCI13/153	R 579 x R 585	50 jklm	2.75 efghijklmn	22 ijkl	21.67 ab	73.39 ab
RCI11/1114	R 92/2401 x R 98/6092	59.5 efghij	2.69 fghijklmn	25.08 abcdefghijk	19.38 cdefg	20.17 cdefg
RCI12/1130	R 582 x R 570	51 ijklm	2.74 efghijklmn	27.5 abcd	16.4 ij	73.42 ab
RCI13/143	R 579 x BT 92/3586	60 defghij	2.67 ghijklmn	23.165 defghijkl	19.89 bcdefg	58.31 abcde
RCI14/1107	R 579 x R 585	49 jklmn	2.77 defghijklmn	23.66 defghijk	19.53 bcdefg	79.41 ab
RCI14/131	R 579 x R 585	49.5 jklmn	2.70 efghijklmn	24.33 cdefghijk	22.73 a	1.78 g
RCI14/188	R 96/2116 x Q 213	56 ghijk	2.82 bcdefghijklmn	21.83 jkl	16.76 hij	93.39 a
RCI14/1139	R 579 x R 585	48.5 jklmn	3 abcdefghijkl	22.83 efghijkl	19.93 bcdefg	11.11 efg
RCI14/129	R 579 x R 585	51.5 ijklm	2.48 n	24.83 bcdefghijk	20.76 abcde	7.40 fg
RCI13/198	R 579 x R 585	38.5 mn	2.93 abcdefghijkl	26.83 abcdefg	18.18 ghij	13.75 defg
RCI13/121	R 579 x BT 92/3586	70 bcde	2.61 jklmn	21.83 jkl	20.42 bcdefg	0.0 g
RCI14/14	R 96/2116 x Q 213	50.5 ijklm	2.59 lmn	24.33 cdefghijk	15.91 j	97.22 a
RCI14/155	R 579 x R 585	53.5 hijkl	2.49 mn	22.16 hijkl	20.87 abcde	2.5 g
RCI13/1135	R 96/2569 x R 585	50.5 ijklm	2.90 abcdefghijklmn	25.33 abcdefghijk	18.14 ghij	0.0 g
RCI14/159	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

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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 8) 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 (Figure 2). Cluster I included 16 genotypes, cluster II included 12 genotypes and 19 genotype belonged to cluster I (Table 9).

Table 8: 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

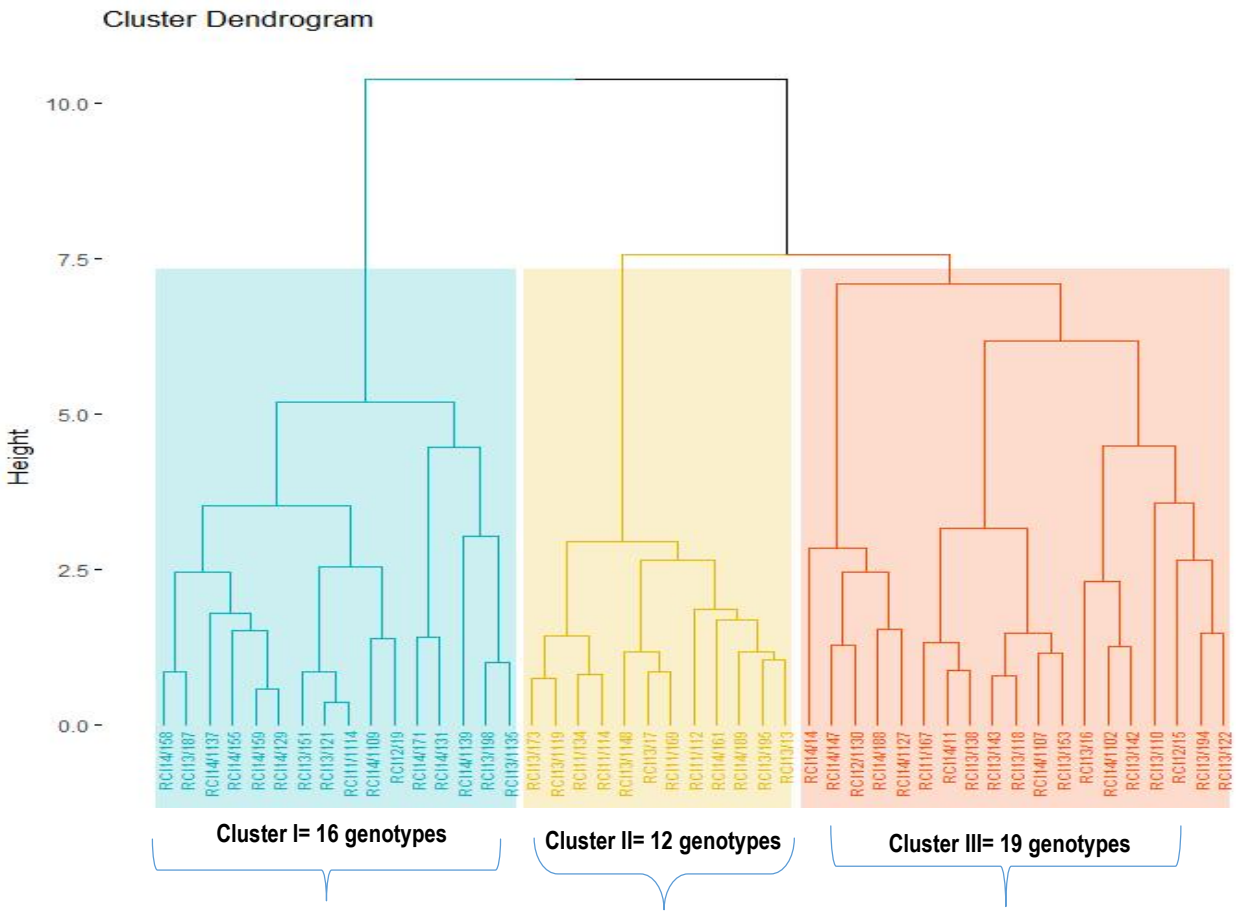

Figure 2: Dendrogram based on mean performance of variables among 47 sugarcane clones.

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Tables 9: 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**
RCI14/158	R 579 x R 585	RCI13/173	R 582 x R 01/6043	RCI14/14	R 96/2116 x Q 213
RCI13/187	R 579 x BT 92/3586	RCI13/1119	VMC 93/282 x R 01/6043	RCI14/147	R 96/2116 x Q 213
RCI14/1137	R 579 x R 585	RCI11/134	R 94/0142 x R 98/6092	RCI12/1130	R 582 x R 570
RCI14/155	R 579 x R 585	RCI11/114	R 89/2042 x R 97/2332	RCI14/188	R 96/2116 x Q 213
RCI14/129	R 579 x R 585	RCI13/1148	R 579 x BT 92/3586	RCI14/1127	R 96/2116 x Q 213
RCI14/131	R 579 x R 585	RCI13/17	R 579 x BT 92/3586	RCI11/167	R 94/6113 x R 93/6885
RCI13/198	R 579 x R 585	RCI11/112	R 94/6113 x R 93/6885	RCI14/11	NCo376 x N 27
RCI14/159	R 579 x R 585	RCI14/161	R 579 x R 585	RCI13/138	VMC 93/282 x R 01/6043
RCI13/151	R 96/2569 x R 585	RCI14/189	R 579 x R 97/0434	RCI13/143	R 579 x BT 92/3586
RCI13/121	R 579 x BT 92/3586	RCI13/195	R 96/2569 x R 585	RCI13/118	VMC 93/282 x R 01/6043
RCI11/1114	R 92/2401 x R 98/6092	RCI13/13	R 579 x BT 92/3586	RCI14/1107	R 579 x R 585
RCI14/1109	R 579 x R 585	RCI11/169	R 92/6545 x R 93/6683	RCI13/153	R 579 x R 585
RCI12/19	R 93/0136 x N 27			RCI13/16	R 92/2210 x R 91/2069
RCI14/171	R 579 x R 585			RCI14/1102	R 579 x R 585
RCI14/1139	R 579 x R 585			RCI13/142	R 579 x BT 92/3586
RCI13/1135	R 96/2569 x R 585			RCI13/110	R 99/2162 x R 585
				RCI12/15	R 93/0136 x N 27
				RCI13/194	R 582 x SP 70/1143
				RCI13/122	R 99/2162 x R 585

IV. Conclusion

The study indicated that there is wide genetic variability among the tested sugarcane clones for all characters. Moreover, the results showed high GCV for Nber_stem/3m (187.20) and % flowering (1894.62), while stem_diameter (9.36), Brix% (7.56) and stem_Height (0.17) showed low GCV. High phenotypic coefficients of variation (PCV) was also recorded for %Flowering (2890.02), Nber_stem/3m (261.21) and stem_diameter (30.82) but moderate PCVs was recorded for %Brix (14.48). Low PCVs are observed for stem_Height (2.60). 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 genotype belonged to cluster I.

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

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