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Multivariate Analysis in Advanced Sugarcane Clones

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ABSTRACT: Sugarcane breeding programmes require a thorough understanding of genotype performance and characteristic interrelationships. This experiment was aimed at improving selection efficiency. A field experiment was conducted at Regional Sugarcane and Rice Research Station, Rudrur, during *Eksali,* 2022-23. The clones of different maturity groups from Coimbatore and peninsular zones of different sugarcane research stations were planted in Randomized Block Design replicated thrice. In the present study, cluster analysis the maximum inter-cluster distance was recorded between clusters III and IV followed between clusters I and III and between clusters II and III. The greater the distance between two clusters, the greater the genetic diversity among those clusters lines. The PCA for the advanced lines exhibited a variance of 27.97 %, 18.37 %, 14.03 %, 11.46 %, and 7.71 % for the first five components and accounted for about 79.57 % of the total variation. Principal Components revealed characters *viz*., sucrose % at 10th month, sucrose % at 12th month, Brix % 10th month, purity % at 12th month and cane yield in PC1 and germination % at 30 days after planting (DAP), tillers at 120 DAP ('000/ha), Shoots at 240 DAP ('000/ha) and cane girth at 12th month were loaded in PC2, while single cane weight at 12th month, cane girth at 12th month, cane length at 12th month and CCS yield (t/ha) in PC3. In PC 4 & PC 5, Shoots at 240 DAP ('000/ha) and Cane yield (t/ha), germination % at 30 DAP and cane length at 12th month were positively loaded. The characters mentioned instantly contributed more towards variability and thus, cluster and principal component analysis will help breeders to identification of diverse parents that can be used for future breeding programs.

Keywords: Advanced clones, PCA, Principal Component Analysis, variability, canonical variant analysis.

INTRODUCTION

Sugarcane (*Saccharum officinarum* L.) is an important commercial crop in the tropics and warm sub-tropics. Telangana is one of the leading states in sugar and sugarcane production in India. As per 3rd Adv. Est.-2022-23, sugarcane is being cultivated in around 0.33 lakh ha, producing 2.64 million tons of cane with approximately 79.85 tons per hectare (E&S, DAC, New Delhi, *3rd Adv). Meanwhile, Tamilnadu has a productivity of 104.78 tons/ha. Thus, there is a wide gap between the Telangana and other states. This production potential can be achieved by adopting better high-yielding with quality clones.

In Telangana Present Status of cultivars are of an older generation and have various difficulties such as decreased production, inability to adapt to varied agro-ecologies, sensitivity to disease and insect pests, *etc.* Therefore, it is necessary to develop new clones for local adoption. Given this, varietal development is a dynamic process an effective breeding program requires an ongoing intake of gene sources. Information on the nature and magnitude of genetic variation is critical for every crop development initiative. To provide a trustworthy guide for selection, it is also necessary to understand the relative contribution and relationship of the component attributes to yield (Singh and Choudhary 1988).

Cluster analysis (CA) and Principal component analysis (PCA) are commonly utilized methods in many experimental procedures for improved data understanding since PCA aids in variable minimization and displays the association between variables (Mundaragi *et al.*, 2017). Furthermore, various studies show that multivariate statistical analyses, such as PCA and CA, are more effective in assessing genetic diversity in sugarcane cultivars (Arrey & Mih 2016); (Ahmed & Obeid 2010). The overall goal of this research is to improve selection efficiency. The results of the experiment could be used to establish an effective selection strategy for developing clones with the best commercial advantages, suitable for growing in various settings. The current research results will provide information that will be extremely useful in planning future plant breeding initiatives for the evaluation of high-yielding and higher-quality sugarcane varieties in the Telangana and peninsular zones of India.

MATERIALS AND METHODS

The experimental material is sugarcane advanced lines consisting of 26 clones collected from promising clones of RSRRS, Rudrur, Coimbatore clones, and peninsular zones of different sugarcane research stations that belonged to different maturity groups and were planted in a randomized block design with three replications in the Regional Sugarcane and Rice Research Station, Rudrur, during 2022–23. The three-eyed setts of each genotype were planted in a 43.2 square meter size plot. Row-to-row distance was 1.2 meter. Setts were planted in the ridge and furrow method. Data were collected on seventeen different yield and quality characteristics, namely Germination % at 30 DAP, Tillers at 120 DAP ('000/ha), Shoots at 240 DAP ('000/ha), Number of millable canes (NMC) ('000/ha), Single cane weight at 12^{th} month, Cane length at 12^{th} month, Cane girth at 12^{th} month, Brix % 10^{th} month, sucrose % at 10th month, Purity % at 10^{th} month, CCS % 10^{th} month, BRIX % 12^{th} month, Sucrose % at the 12^{th} month, Purity % at the 12^{th} month, CCS % 12^{th} month, CCS yield (t/ha), and Cane yield (t/ha). Intercultural operations like weeding, earthen-up, and irrigation were done as per the required schedule.

Genetic diversity was studied following Mahalanobis (1936) D^2 statistics and clustering of genotypes was done based on D^2 values according to Tocher's method as described by Rao (1952). The principal component analysis method explained by Harman (1976) was followed in the extraction of the components. Principal Component Analysis was performed using Indostat software.

RESULTS AND DISCUSSIONS

The ANOVA revealed significant differences among all the sugarcane advanced lines for characters studied, which means the existence of variability among the lines. For the assessment of variation on a multivariate scale, Mahalanobis D^2 – statistic has proved to be a powerful technique (Murthy & Arunachalam 1966). It provides for measuring the genetic diversity in a respective population in relation to characters considered together (Mounika Korada *et al.*, 2021). Based on D^2 analysis, 26 sugarcane advanced lines were grouped into four clusters (Table 1). Cluster I was the largest comprising of fourteen lines followed by cluster II with 10 lines, cluster III and cluster IV have one line, indicating the existence of a high degree of heterogeneity among sugarcane advanced lines.

The intra and inter-cluster distance is given in Table 2. The inter-cluster distance was higher than the intra-cluster distance, implying more genetic divergence among the advanced lines. The maximum inter-cluster distance was recorded between III and IV (200.07) followed between cluster I and III (135.85) and between II and III (129.78). The greater the distance between two clusters, the greater the genetic diversity among those clusters lines. Such highly diverse, high-performing lines would be extremely useful in a recombination breeding program to obtain highly desirable progeny. The minimum inter-cluster was found between clusters II and III (70.50). These lines in respective clusters are genetically more similar. Therefore, crossing among the lines may not give desirable lines. The maximum intra-cluster distance was recorded in cluster II (40.48) followed by cluster I (28.70). As a result, selection within these clusters can be carried out based on the highest areas for desirable traits. These are recommended for inclusion in the sugarcane breeding programs.

The cluster mean for each seventeen characters is presented in Table 3. The data revealed that the highest cluster mean was observed in cluster I for brix % 10^{th} month, sucrose % at the 10^{th} month, CCS % 10^{th} month, sucrose % at the 12^{th} month, purity % at the 12^{th} month and CCS % in 12^{th} month as results, cluster I showed for maximum quality characters among all the clusters indicating the most promising lines for quality purpose. Cluster II showed the highest number of millable canes (NMC) ('000/ha), cluster III highest for germination % at 30 DAP, tillers at 120 DAP ('000/ha), shoots at 240 DAP ('000/ha) and purity % at 10^{th} month. Cluster IV recorded the highest for single cane weight at 12^{th} month, cane length at 12^{th} month, cane girth at 12^{th} month, brix % 12^{th} month, CCS yield (t/ha), and cane yield (t/ha). None of the clusters included lines with all of the desirable characters that could be selected and used directly. However, cluster I, III, and IV recorded desirable mean values for a maximum number of yield and quality characters thereby crossing between lines of clusters (I and IV, III, and IV) is necessary for the development of desirable lines for future purposes.

The contribution of each character to total divergence is presented in Table 3. The more diversity there is in a single character, the more it contributes to total genetic divergence. The results revealed that the contribution of the sucrose % at the 10th month was highest towards genetic divergence (42.77%) by taking 139 times ranking first, followed by single cane weight at 12^{th} month (20.62%) by 67 times, brix % 10^{th} month (15.08%) by 49 times and germination % at 30 DAP (6.15%) by 20 times. Zero contribution was observed in shoots at 240 DAP ('000/ha), number of millable canes (NMC) ('000/ha), CCS % 10^{th} month, purity % at the 12^{th} month, and CCS % 12^{th} month. The characters sucrose % at the 10^{th} month, single cane weight at the 12^{th} month, brix % 10th month, germination % at 30 DAP and sucrose % at 12^{th} month contribute nearly eighty percent towards total divergence. These above contributed characters are more consideration in crop improvement programs. The results are in conformity with the findings of Neetu *et al.* (2018) for single cane weight at the 12^{th} month and brix % 10^{th} month.

Table 1: Clustering pattern among twenty six advanced sugarcane clones.

Cluster No.	No. of lines (genotypes)	Names of lines (genotypes)
I	14	RDRS-273(23), RDRS-12(25), RDRS-122(26), RDRS-269(13), RDRS-268(12), RDRS-19(24), RDRS-260(4), RDRS-253(17), RDRS-270(20), RDRS-262(6), RDRS-246(14), RDRS-272(22), RDRS-271(21), and RDRS-263(7)
II	10	RDRS-259(3), RDRS-124(18), RDRS-267(11), RDRS-257(1), RDRS-125(19), RDRS-252(16), RDRS-266(10), RDRS-258(2) RDRS-265(9) and RDRS-264(8)
III	1	RDRS-245(15)
IV	1	RDRS-261(5)

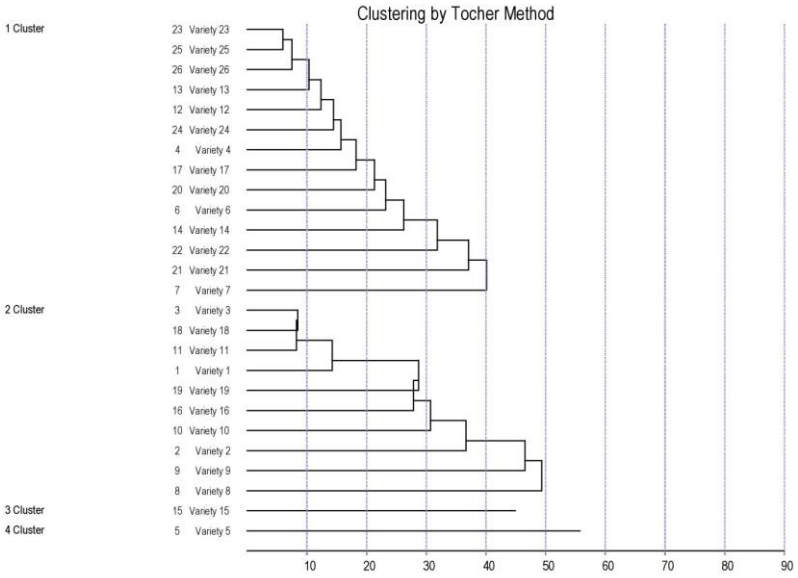

Fig. 1. Clustering by Tocher method for twenty six advanced sugarcane clones.

Table 2: Intra (diagonal) and Inter clusters D2 values of 26 advanced sugarcane clones.

Cluster	I	II	III	IV
I	**28.70**	96.60	135.85	108.11
II		**40.48**	70.50	129.78
III			**0.00**	200.07
IV				**0.00**

Table 3: Cluster mean values estimated by Tocher's method from 26 advanced sugarcane clones and % contribution of genetic divergence.

Sr. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Times ranked 1st	% Contribution
1.	GER	52.19	49.82	64.22	52.22	20	6.15
2.	Tillers at 120 ('000/ha)	126.84	112.35	130.32	113.50	1	0.31
3.	Shoots 240 ('000/ha)	93.88	91.47	110.26	88.50	0	0
4.	NMC ('000/ha)	64.41	65.59	55.40	57.10	0	0
5.	SCW at 12m (kg)	1.42	1.42	1.23	2.08	67	20.62
6.	Cane girth at 12m (cm)	2.98	2.97	3.49	3.54	2	0.62
7.	cane length at 12m (cm)	253.28	268.20	249.30	301.43	10	3.08
8.	BRIX % 10	19.21	17.94	16.63	19.20	49	15.08
9.	SUCROSE% 10th	17.28	15.72	15.01	16.94	139	42.77
10.	PURITY% 10th	89.97	87.68	90.23	88.25	7	2.15
11.	CCS % 10th	12.05	10.83	10.48	11.71	0	0
12.	BRIX % 12th	20.88	19.86	19.53	21.10	4	1.23
13.	SUCROSE % 12th	19.21	17.87	17.69	18.79	15	4.62
14.	PURITY % 12th	92.04	89.98	90.55	89.09	0	0
15.	CCS % 12 th	13.53	12.47	12.37	13.04	0	0
16.	CCS t/ha	12.29	11.62	8.45	15.49	10	3.08
17.	Cane Yield (t/ha)	90.79	93.43	68.12	118.71	1	0.31

GER-Germination % at 30 DAP (Days after planting), Tillers at 120 DAP ('000/ha), Shoots 240 DAP ('000/ha), Number of millable canes (NMC) ('000/ha), Single cane weight at 12th month, Cane length at 12th month, Cane girth at 12th month, Brix % 10th month, Sucrose % at 10th month, Purity % at 10th month, CCS % 10th month, BRIX % 12th month, Sucrose % at 12th month, Purity % at 12th month, CCS % 12th, CCS yield (t/ha), and Cane yield (t/ha).

Principal component analysis (PCA) was carried out to determine the relative contribution of the characteristics to overall variability and to give a direction for trait selection. The primary goal of PCA was to reduce the total variation caused by the variables under consideration to a small number of factors. The component qualities that were mostly responsible for the retrieved PCs were then identified.

The principal component analysis results for the 17 characters presented in (Table 4 and Fig. 2) were the Eigen values, % variance, % cumulative variance, and factor loading of different characters. In canonical variant analysis, the number of variable is produced to a linear function called canonical vector which account for most of the variation produced by these characters. The 7 vectors accounted for 90.51 % of the total variability produced by all sugarcane advanced clones for yield. The results indicated that all the characters showed loading on PC1 which contributed to 27.97 % of the total variation having an Eigen value of 4.756 with the highest loadings coming from sucrose % at the 10th month, sucrose % at the 12th month, Brix% 10th month, purity % at 12th month and cane yield with values of 0.405, 0.380, 0.376, 0.365 and 0.285 respectively.

The least contribution came from cane girth at the 12th month with a value of 0.027, while purity % at the 10th month (-0.327), cane length at the 12th month (-0.115), number of millable canes (- 0.069) had the higher negative values. and also, the PC2 which contributed to 18.37% of the total variability with Eigen value of 3.124 showed maximum positive loadings on germination % at 30 DAP (0.411), Tillers at 120 DAP ('000/ha) (0.318), Shoots at 240 DAP ('000/ha) (0.289) and cane girth at 12th month (0.274), while CCS% 12th month (-0.471), number of millable canes ('000/ha) (- 0.286), single cane weight at 12th month (- 0.261) had the higher negative values. The PC3 which contributed to 14.03 % of total variability with an Eigen value of 2.386 showed maximum positive loadings on single cane weight at the 12th month, cane girth at the 12th month, cane length at the 12th month, and CCS yield (t/ha) with the corresponding values of 0.491, 0.488, 0.373 and 0.278, respectively with the highest negative values on cane yield (t/ha) (-0.332) and sucrose % at 12th month (-0.204). The PC4 which contributed to 11.46 % of the total variability with an Eigen value of 1.950 showed maximum positive loadings on Shoots 240 ('000/ha) (0.481), with the least value of -0.479 from CCS % at the 10th month. The PC5 which contributed to 7.71% of the total variability with an Eigen value of 1.312 showed maximum loading factors on Cane yield (t/ha), germination % at 30 DAP, and cane length at the 12th month of 0.403, 0.322, and 0.276, respectively with the least values of -0.517 and -0.260 for number of millable canes and Brix% 12th month, respectively.

Principal component 6 which contributed to 7.36 % of the total variability with an Eigen value of 1.252 showed maximum positive loadings on Tillers at 120 DAP ('000/ha) (0.414), CCS % at 10th month (0.405) and number of millable canes ('000/ha) (0.353) while sucrose % at 12th month (- 0.236) and cane girth at 12th month (-0.166) had higher negative values. The variation in the PC7 is 3.57 with an Eigenvalue of 0.607 showing positive loadings on germination % at 30 DAP (0.220), with the least value of -0.294 from a number of millable canes ('000/ha).

Genetic variability is a measure of the tendency of individual plants in a population to vary from each other due to the differences in the individuality expression. In the present study, the PCA for the advanced lines exhibited a variance of 27.97 %, 18.37 %, 14.03 %, 11.46 %, and 7.71 % for the first five components and accounted for about 79.57 % of the total variation. A scree plot displaying the variance described by the 17 PCs was shown in Fig. 3. Similarly results obtained by Zhou *et al.* (2015) reported principal component analysis for 111 accessions of Guitang sugarcane germplasm based on 9 quantitative traits, wherein they observed 74.42% of the cumulative variance for first four principal components. Smiullah *et al.* (2013) described genetic diversity assessment for ten genotypes using PCA and their study revealed a cumulative variance of 67.3% for the first two components.

In view of above, Principal Components revealed characters viz., sucrose % at 10th month, sucrose % at 12th month, Brix % 10th month, purity % at 12th month and cane yield in PC1 and germination % at 30 DAP, Tillers at 120 DAP ('000/ha), Shoots at 240 DAP ('000/ha) and cane girth at 12th month were loaded in PC2, while single cane weight at 12th month, cane girth at 12th month, cane length at 12th month and CCS yield (t/ha) in PC3. In PC 4 &PC 5, Shoots at 240 DAP ('000/ha) and Cane yield (t/ha), germination % at 30 DAP and cane length at 12th month were positively loaded. The characters mentioned instantly contributed more towards variability and thus, the characters should be given more attention in selection for hybridization. The contribution of the main characters for variance is easily identified by the characters loaded on PC1 as it explained maximum variance is, therefore, first and foremost considered in selection for hybridization followed in accordance by characters in the other vectors. Finally, principal component analysis revealed that sucrose % at 10th month, sucrose % at 12th month, Brix% 10th month, purity % at 12th month, cane yield, germination % at 30 DAP, Tillers at 120 DAP ('000/ha), Shoots at 240 DAP ('000/ha), cane girth at 12th month, single cane weight at 12th month, cane length at 12th month and CCS yield (t/ha) are the major contributors to the total variability and thus, the characters can be utilized in further crop improvement. The results of the principal components analysis corroborated with results obtained by Muhammad *et al*. (2018); Baloch *et al*. (2017); Smiullah *et al*. (2013) ; Tahir *et al*. (2013).

Table 4: Studies on Principal component for 26 advanced sugarcane clones for 17 characters.

Sr. No.	Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7
1.	GER	0.074	0.411	0.117	0.125	0.322	0.279	0.220
2.	Tillers at 120 DAP ('000/ha)	0.228	0.318	0.004	0.079	-0.252	0.414	0.111
3.	Shoots 240 DAP ('000/ha)	0.029	0.289	0.095	0.481	-0.147	0.303	-0.038
4.	NMC ('000/ha)	-0.069	-0.286	-0.138	0.174	-0.517	0.353	-0.294
5.	SCW at 12m (Kg)	0.077	-0.261	0.491	-0.194	-0.022	0.074	-0.077
6.	Cane girth at 12m (cm)	0.027	0.274	0.488	-0.078	-0.142	-0.166	0.094
7.	cane length at 12m (cm)	-0.115	-0.262	0.373	0.031	0.276	0.304	0.144
8.	BRIX % 10	0.376	-0.122	-0.085	-0.273	0.037	0.157	0.153
9.	SUCROSE% 10th	0.405	-0.032	-0.076	0.202	0.107	-0.129	-0.086
10.	PURITY% 10th	-0.327	0.187	-0.193	-0.242	0.235	0.005	-0.192
11.	CCS % 10th	0.087	0.184	-0.139	-0.479	0.133	0.405	-0.204
12.	BRIX % 12th	0.277	0.033	0.088	-0.456	-0.260	0.059	0.145
13.	SUCROSE % 12th	0.381	0.007	-0.204	-0.032	-0.257	-0.236	0.099
14.	PURITY % 12th	0.365	-0.072	0.163	0.197	0.195	-0.192	0.079
15.	CCS % 12 th	0.113	-0.471	0.084	0.087	0.157	0.286	-0.055
16.	CCS t/ha	0.218	0.188	0.278	-0.011	0.061	-0.115	-0.806
17.	Cane Yield (t/ha)	0.285	-0.065	-0.332	0.117	0.403	0.107	-0.117
	Eigene Value (Root)	4.756	3.124	2.386	1.950	1.312	1.252	0.607
	% Var. Exp.	27.976	18.377	14.036	11.469	7.717	7.362	3.575
	Cum. Var. Exp.	27.976	46.353	60.389	71.859	79.576	86.938	90.513

GER-Germination % at 30 DAP (Days after planting), Tillers at 120 DAP ('000/ha), Shoots 240 DAP ('000/ha), Number of millable canes (NMC) ('000/ha), Single cane weight at 12th month, Cane length at 12th month, Cane girth at 12th month, Brix % 10th month, Sucrose % at 10th month, Purity % at 10th month, CCS % 10th month, BRIX % 12th month , Sucrose % at 12th month, Purity % at 12th month, CCS % 12th, CCS yield (t/ha), and Cane yield (t/ha).

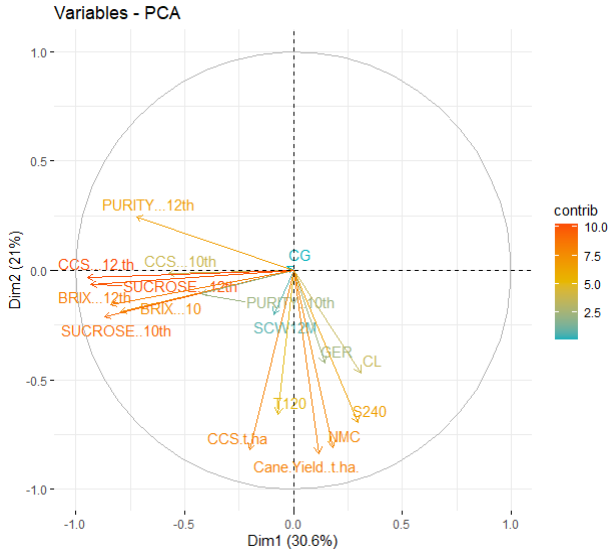

Fig. 2. PCA graph for the 17 characters of principal component analysis.

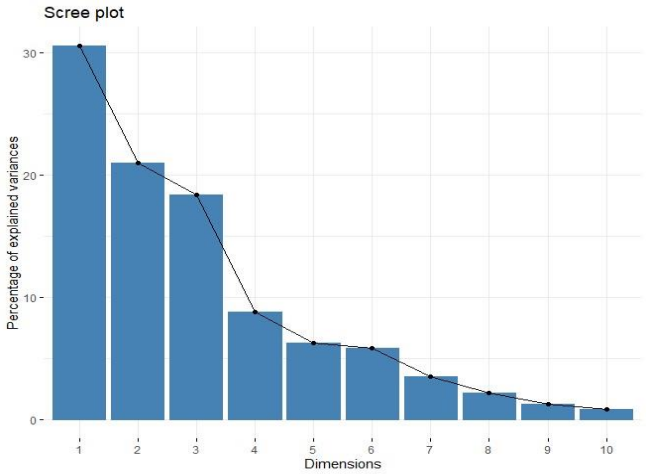

Fig. 3. Scree plot indicating the percent variance detailed by each Principal component.

CONCLUSIONS

In cluster analysis the maximum inter-cluster distance was recorded between III and IV followed between cluster I and III and between II and III. The greater the distance between two clusters, the greater the genetic diversity among those clusters lines. Such highly diverse, high-performing lines would be extremely useful in a recombination breeding program to obtain highly desirable progeny. Principal Components analysis identified the importance of traits like germination % at 30 DAP, Tillers at 120 DAP ('000/ha), Shoots at 240 DAP ('000/ha), cane girth at 12th month, single cane weight at 12th month, cane length at 12th month, sucrose % at 10th month, sucrose % at 12th month, Brix% at 10th month, purity % at 12th month, cane yield that can be beneficial for the improvement of cane yield as well as quality in sugarcane by breeders. These traits need to be given due consideration in sugarcane breeding programs targeted for cane yield with quality. Hence multivariate analysis such as cluster and principal component analysis will help breeders to identification of diverse parents that can be used for future breeding programs in the Telangana state as well as the peninsular zones of India.

FUTURE SCOPE

The research helps to generate high yielding and sucrose canes, which benefit the farmers. Further research and utilization of identified clusters and significant traits are recommended for future sugarcane crop improvement.

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Conflict of Interest. None.

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