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# Genetic diversity of parental clones used in breeding programs of sugarcane

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**Abstract**
The present investigation aimed to assess the nature and magnitude of genetic divergence available in the Hybridization Block (E1) and National Hybridization Garden (E2) of ICAR-Sugarcane Breeding Institute, Coimbatore and to select the suitable diverse genotypes as parents for further utilization. Principal component and hierarchical cluster analyses were carried out in sixty eight genotypes with nine traits. In E1, the first three principal components explained about 73.45 per cent of the total variability and remaining six components accounted 26.55 per cent of variability. The PC 1 explained a maximum variability of 44.85 per cent followed by PC 2 and PC3. In E2, the first three principal components explained about 76.71 per cent of the total variability among the genotypes and the remaining six components described 23.29 per cent towards the total diversity. Nineteen clones *viz.,* Co 0314, Co 8371, Co 85019, Co 86010, Co 94008, Co 98010, Co 11015, Co 12014, Co 14002, CoSnk 05103, CoV 89101, CoV 92103, CoC 671, CoT 8201 Co 1148, CoH 119, SP 80-185, ISH 100 and ISH 2 were found promising in both the environments indicating their potential to perform under varied ecological situations. Twenty clones in E1 and 38 clones in E2 can be further exploited as trait specific donors and the traits cane height, cane diameter, cane weight should be given more emphasis for further selection.

**Key words**
Sugarcane, PCA, parental lines, diversity

## INTRODUCTION

Breeding for improved varieties are facilitated through the incorporation of new alleles into well adapted genetic background. The genetic variation provides greater opportunities in evolution of improved varieties with environmental stability. Accumulation of varied desirable genes into a genotype is important in any yield improvement programme. A good knowledge of the genetic diversity helps in selection of desirable clones for breeding program and in gene introgression. Genotypes are to be classified into clusters based on genetic divergence and the extent of genetic diversity need to be estimated so that the donors could be chosen from the clusters with a wide genetic divergence in hybridization programme. Multivariate methods are widely used in summarizing and describing the dissimilarity among the genotypes and among them Principal Component Analysis (PCA), Cluster analysis and discriminate analysis are also considered as useful (Oyelola, 2004). Cluster analysis is concerned with classifying earlier unclassified materials, whereas PCA can be used to find out the resemblance between the variables and classify the genotypes (Leonard and Peter, 2009). Large datasets are increasingly common and PCA is a technique used for reducing the dimensionality of such datasets, increase their interpretability and thereby to minimize the loss of information. The main objective of this study was to evaluate the genetic divergence among sugarcane parental clones through multivariate analysis and to classify them into clusters based on their similarity features regarding the traits under study and also to generate data on their performance for further utilization as donors in breeding programmes.

## MATERIALS AND METHODS

The present investigation was carried out with 68 sugarcane genotypes (**Table 1**) identified from different agro climatic zones of sugarcane and the experiments were performed at two environments *viz*., Hybridization plot (E1) of the East Chitrai Chavadi with black soil ( ECC :10.99 0N , 76.89 E ) and National Hybridization Garden (E2) with garden land soil (NHG : 11.0168 ° N, 76.9558 ° E ) during 2017 crop season at ICAR – SBI, Coimbatore. Each genotype was grown in two rows with aspacing of 120 cm between rows and 60 cm between plants and data recorded in five plants in each row. Standard agronomic package and practices were followed to raise a healthy crop. The analysis is based on the determination of the nine traits *viz*., Brix (%), Sucrose (%), cane length, cane diameter, single cane weight, estimated cane yield and estimated commercial cane sugar yield at 300 days and brix and sucrose (%) at 240 days. The quality parameters were recorded at both eighth and ten months to identify clones with early sugar accumulation for use in hybridization programmes. The descriptive statistics such as mean, standard deviation and coefficient of variation for all the nine traits were calculated, cluster analysis and PCA were done using Statistical Tool for agricultural Research (STAR) and R package.

## RESULTS AND DISCUSSION

The First order Statistical measures *viz*., maximum, minimum, sum, mean, Standard Deviation (SD) and Coefficient of Variation (CV) for the measured traits are shown in **Table 2**. In E1, the largest variation was observed for CCS (t/ha) with CV of 28.53 per cent followed by cane yield (kg/plot) with 25.13 per cent , single cane weight with 21.37 per cent, cane height with variation of 11.86 per cent and cane diameter with 8.21 per cent. The quality traits showed variation within the range of

**Table1. Parents utilized in the study**

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Co 0209 | T | 16 | Co 2000-10 | T | 31 | Co 99006 | T | 46 | SP 80-185 | EX | 61 | ISH 100 |
| 2 | Co 0240 | T | 17 | Co 2000-12 | T | 32 | Co 99008 | T | 47 | Co 1148 | ST | 62 | ISH 12 |
| 3 | Co 0310 | T | 18 | Co 8347 | ST | 33 | CoC 671 | T | 48 | BO 91 | ST | 63 | ISH 175 |
| 4 | Co 0312 | T | 19 | Co 8371 | T | 34 | CoSnk 03044 | T | 49 | Co 0118 | ST | 64 | ISH 176 |
| 5 | Co 0314 | T | 20 | Co 85002 | T | 35 | CoSnk 05103 | T | 50 | Co 0124 | ST | 65 | ISH 2 |
| 6 | Co 0320 | T | 21 | Co 85019 | T | 36 | CoSnk 14103 | T | 51 | Co 0232 | ST | 66 | ISH 229 |
| 7 | Co 0403 | T | 22 | Co 86002 | T | 37 | CoT 8201 | T | 52 | Co 0233 | ST | 67 | ISH 43 |
| 8 | Co 10026 | T | 23 | Co 86010 | T | 38 | CoTl 1153 | T | 53 | Co 05009 | ST | 68 | ISH 69 |
| 9 | Co 11004 | T | 24 | Co 86032 | T | 39 | CoV 09356 | T | 54 | CoH 110 | ST | | |
| 10 | Co 11012 | T | 25 | Co 94008 | T | 40 | CoV 89101 | T | 55 | CoH 119 | ST | | |
| 11 | Co 11015 | T | 26 | Co 94012 | T | 41 | CoV 92102 | T | 56 | CoLk 8102 | ST | | |
| 12 | Co 12006 | T | 27 | Co 97008 | T | 42 | CoV 92103 | T | 57 | CoLk 94184 | ST | | |
| 13 | Co 12009 | T | 28 | Co 97009 | T | 43 | CP 96-1252 | EX | 58 | CoM 0265 | T | | |
| 14 | Co 12014 | T | 29 | Co 97015 | T | 44 | CP 96-1662 | EX | 59 | CoM 88121 | T | | |
| 15 | Co 14002 | T | 30 | Co 98010 | T | 45 | SP 80-1842 | EX | 60 | CoPant 97222 | ST | | |

**T-Tropical, ST- Sub- tropical, Ex- Exotic, ISH- Interspecific hybrids**

**Table 2. Descriptive Statistics**

| | | E1 | | | | | E2 | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Traits** | **Harvest time (days)** | **Minimum** | **Maximum** | **Mean** | **SD** | **CV %** | **Minimum** | **Maximum** | **Mean** | **SD** | **CV %** |
| Cane yield (kg/plot) | 300 | 31.20 | 93.60 | 62.76 | 15.77 | 25.13 | 33.64 | 83.50 | 59.19 | 11.71 | 19.78 |
| Commercial cane sugar (t/ha) | 300 | 2.93 | 12.79 | 7.43 | 2.12 | 28.53 | 3.38 | 10.39 | 6.99 | 1.74 | 24.89 |
| Brix (%) | 300 | 16.22 | 22.40 | 19.32 | 1.55 | 8.02 | 16.12 | 24.00 | 19.43 | 1.49 | 7.67 |
| Sucrose (%) | 300 | 12.56 | 20.49 | 17.11 | 1.70 | 9.94 | 14.00 | 20.24 | 17.08 | 1.61 | 9.43 |
| Cane height (cm) | 300 | 165.00 | 300.00 | 213.69 | 25.34 | 11.86 | 115.00 | 270.00 | 197.81 | 27.04 | 13.67 |
| Cane diameter (cm) | 300 | 1.98 | 3.20 | 2.68 | 0.22 | 8.21 | 2.00 | 3.02 | 2.67 | 0.20 | 7.49 |
| Single cane weight (kg) | 300 | 0.68 | 2.05 | 1.17 | 0.25 | 21.37 | 0.58 | 1.89 | 1.13 | 0.21 | 18.58 |
| Brix (%) | 240 | 14.23 | 20.98 | 17.65 | 1.42 | 8.05 | 14.87 | 21.26 | 17.98 | 1.38 | 7.68 |
| Sucrose % 240 days | | 11.98 | 19.25 | 15.04 | 1.61 | 10.70 | 12.37 | 19.58 | 15.49 | 1.53 | 9.88 |

8.02 to 10.70 per cent. The minimum level of variation was observed for the trait brix at 300 days (CV 8.02 %). Wide range of means was observed for the traits studied in this environment. The genotype ISH 176 recorded the minimum sucrose of 11.98 per cent and the maximum was in Co 0314 (19.25 %) at 240 days. At 300 days, ISH 176 recorded a minimum of 12.56 per cent sucrose and the maximum of 20.49 per cent was recorded by Co 11015. The overall mean for sucrose at 300 days was 17.11 per cent and 38 clones recorded sucrose above the overall mean. The mean value for cane diameter was 2.68 cm with the minimum and maximum value of 1.98 cm and 3.20 cm were recorded by the genotypes ISH 176 and Co 98010, respectively. The short cane with 165 cm height was observed in ISH 229 and the tall growth was expressed by Co 2000-10 (300 cm) and an average total plant height was 213.69 cm. The genotype CoM 0265 recorded the highest single cane weight of 2.00 kg and four clones namely ISH 100, Co 8371, CoM 88121, CoT 8201 showed cane weight of 1.50 kg.

In E2, the largest variation was also observed for CCS (t/ha) with CV of 24.89 per cent followed by cane yield (kg/plot) with 19.78 per cent, single cane weight with 18.58 per cent, cane height with variation of 13.67 per cent, cane diameter with 7.49 per cent of variation. In E2 also the quality traits showed variation within the range of 8.02 to 10.70 per cent. The minimum level of variation was observed by the trait cane diameter at 300 days (CV 7.49 %). The genotype Co 1148 recorded the minimum sucrose of 12.37 per cent per cent and maximum was in Co 0314 (19.58 %) at 240 days. At 300 days, Co 1148 recorded a minimum of 14.00 per cent sucrose and the maximum of 20.24 per cent was recorded by CoC 671. The overall mean for sucrose at 300 days was 17.08 per cent and 30 clones recorded sucrose above the overall mean. The overall mean value for cane diameter was 2.68 cm with the minimum and maximum value of 2.00 cm and 3.02 cm. The clone ISH 43 expressed the tall growth (270 cm) and an average total plant height was 197.81 cm which was less than the average mean in E1. The cane thickness ranged from 2.00 to 3.02 cm and with the variation of 7.49 per cent. The maximum single cane weight observed was 1.89 kg in CoM 0265 and clones namely CoH 119, CoH 110, CoT 8201, CoSnk 14103, Co 99008, Co 0310, Co 0118 showed cane weight above 1.30 kg.

PCA is a powerful and well-recognized multivariate statistical technique widely used in identification of the least number of components, which provides information on maximum variability available for utilization out of the total variability (Anderson, 1972 ; Morrison, 1978) and also helps in ranking the genotypes on the basis of PC scores. In this design, the first component accounts for a large amount of the total variance and thereby each following component accounts for progressively smaller amounts of variance. Values with Eigenvalues more than 1 (Brejda *et al*., 2000 ; Jeffers, 1967) were taken into consideration, as it implies a minimum 10 per cent of the

**Table 3. Proportion of variance, cumulative proportion and Eigenvalues of sugarcane genotypes in E1**

**a.Principal Components, Eigenvalues and Proportion of variance**

| | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 | PC9 |
|---|---|---|---|---|---|---|---|---|---|
| Proportion of variance | 0.4485 | 0.2850 | 0.0995 | 0.0861 | 0.0362 | 0.0299 | 0.0087 | 0.0045 | 0.0017 |
| Cumulative proportion | 0.4485 | 0.7334 | 0.8330 | 0.9191 | 0.9553 | 0.9852 | 0.9938 | 0.9983 | 1.000 |
| Eigen values | 4.0361 | 2.5648 | 1.0957 | 0.6752 | 0.2256 | 0.2691 | 0.0780 | 0.0405 | 0.0149 |

**b.Contribution of different traits towards total variance- Eigenvectors**

| Traits | Harvest time (days) | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 | PC9 |
|---|---|---|---|---|---|---|---|---|---|---|
| Cane yield (kg/plot) | 300 | -0.2307 | 0.5037 | 0.2521 | -0.2099 | -0.2823 | 0.1931 | 0.0700 | 0.0725 | -0.6770 |
| Commercial cane sugar (t/ha) | 300 | 0.3730 | 0.3399 | 0.2112 | -0.2641 | -0.1521 | 0.3493 | 0.0968 | -0.0433 | 0.6889 |
| Brix (%) | 300 | -0.4143 | -0.2641 | 0.0018 | -0.1773 | 0.4265 | 0.1551 | 0.6745 | 0.2548 | -0.0363 |
| Sucrose (%) | 300 | -0.4262 | -0.2351 | 0.0089 | -0.1437 | 0.4628 | 0.1094 | 0.6632 | -0.1549 | -0.2287 |
| Cane height (cm) | 300 | -0.1195 | 0.2161 | -0.9086 | -0.3212 | -0.0882 | -0.0453 | 0.0097 | 0.0116 | -0.0131 |
| Cane diameter (cm) | 300 | -0.2168 | 0.2779 | -0.2267 | 0.03247 | 0.1377 | 0.3483 | 0.0019 | 0.0618 | -0.0108 |
| Single cane weight (kg) | 300 | -0.1797 | 0.5085 | 0.1190 | 0.0614 | 0.3862 | -0.7262 | 0.0520 | -0.0515 | 0.0964 |
| Brix (%) | 240 | -0.4311 | -0.2437 | -0.0222 | 0.1563 | -0.3676 | -0.1893 | 0.2234 | -0.7120 | -0.0450 |
| Sucrose (%) | 240 | -0.4183 | -0.2527 | 0.0107 | 0.1502 | -0.4359 | -0.3436 | 0.1955 | 0.6248 | 0.0424 |

**Table 4. Proportion of variance, cumulative proportion and Eigenvalues of sugarcane genotypes** in E2

**a. Principal Components, Eigenvalues and Proportion of variance**

| | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 | PC9 |
|---|---|---|---|---|---|---|---|---|---|
| Proportion of variance | 0.3724 | 0.2694 | 0.1253 | 0.0916 | 0.0621 | 0.0478 | 0.0272 | 0.0039 | 0.0004 |
| Cumulative proportion | 0.3724 | 0.6418 | 0.7670 | 0.8587 | 0.9208 | 0.9686 | 0.9957 | 0.9996 | 1.0000 |
| Eigen values | 3.3517 | 2.4243 | 1.1274 | 0.8245 | 0.5592 | 0.4300 | 0.2444 | 0.0351 | 0.0035 |

**b.Contribution of different traits towards total variance- Eigenvectors**

| Traits | Harvest time (days) | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 | PC8 | PC9 |
|---|---|---|---|---|---|---|---|---|---|---|
| Cane yield (kg/plot) | 300 | 0.3577 | 0.3697 | 0.3642 | -0.0318 | -0.1793 | 0.1991 | 0.4667 | -0.0358 | 0.5575 |
| Commercial cane sugar (t/ha) | 300 | 0.4808 | 0.1265 | 0.2579 | 0.1833 | -0.3681 | -0.0985 | 0.0891 | 0.0576 | -0.7045 |
| Brix (%) | 300 | 0.1247 | -0.2639 | 0.5433 | -0.6475 | 0.4090 | -0.1286 | 0.0088 | -0.0160 | -0.1278 |
| Sucrose (%) | 300 | 0.3809 | -0.3448 | 0.1209 | 0.1620 | -0.2481 | -0.4630 | -0.4967 | -0.0070 | 0.4154 |
| Cane height (cm) | 300 | 0.1694 | 0.2196 | -0.4989 | -0.7065 | -0.3974 | -0.1091 | -0.0718 | 0.0055 | 0.0029 |
| Cane diameter (cm) | 300 | 0.2809 | 0.3470 | -0.2934 | 0.1371 | 0.5581 | -0.5824 | 0.2119 | 0.0154 | 0.0002 |
| Single cane weight (kg) | 300 | 0.2668 | 0.4646 | 0.0520 | 0.0050 | 0.2989 | 0.4251 | -0.6624 | -0.0344 | -0.0163 |
| Brix (%) | 240 | 0.3881 | -0.3721 | -0.2854 | 0.0416 | 0.1303 | 0.2794 | 0.1494 | -0.7132 | -0.0421 |
| Sucrose (%) | 240 | 0.3884 | -0.3685 | -0.2682 | 0.0154 | 0.1670 | 0.3316 | 0.1279 | 0.6964 | 0.0442 |

variation. Superior Eigenvalues are considered as the best attributes in principal components. In the present study, PCA was performed using yield and quality related traits from 68 sugarcane clones. The proportion of variance, cumulative proportion and Eigenvalues in two different environments are provided in **Table 3 and Table 4**.

PCA showed that out of nine components derived first three explained most of the total variations present in the gene pool. In E1, the first three principal components with Eigenvalue > 1 explained about 73.45 per cent of the total variability. The remaining six components accounted only 26.55 per cent variation. The PC 1 contributed maximum variability of 44.85 per cent followed by PC 2 with a phenotypic variability of 28.50 per cent and PC 3 had contributed 9 .00 per cent of the total variation. The important traits in PC 1 were due to variations among the genotypes for all the traits and had a negative factor loading value. PC 2 was related to diversity among the genotypes due to yield, single cane weight and commercial cane sugar. Zhou *et al*. (2015) investigated the principal component and cluster analysis for 111 accessions of Guitang sugarcane germplasm based on 9 quantitative traits, and reported that 74.42 per cent of cumulative variance for the first four principal components. Twenty four rice genotypes were studied for the thirteen grain quality traits and Principal Component Analysis was utilized to estimate the relative contribution of various traits for total variability. Four components were found to possess Eigenvalue more than 1 and accounted for 72.24 per cent of the variability of the genotypes and the relative contribution of grain quality ( Satya Sheela *et al*., 2019). In the present study, Eigenvalues gradually declined from PC1 to PC9. The Eigenvalues for remaining principal components were 2.56, 1.09, and 0.67 for PC2, PC3 and PC4 respectively (**Fig.1**).

The distribution of sugarcane genotypes in different groups clearly showed genetic diversity among genotypes (**Fig. 2 and Fig 3**). Scree plot depicted the percentage of variance associated with each PC obtained by drawing a graph between Eigenvalues and PC numbers in both the environments. In the present study, PC1 showed 44.85 per cent of variability with Eigen value of 4.03 which then declined gradually. Semi curve line is obtained after PC3 which formed a straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other PCs. Hence, the selection of lines from this PC would be useful for use in future breeding programs. Nachimuthu *et al*. (2014) reported the highest variability in PC1 with Eigenvalue more than 1.0 in 192 rice genotypes comprising traditional landraces and exotic genotypes. Kumar and Kumar (2021) in their Principal Component Analysis (PCA) study in linseed germplasm indicated that, five PCs contributed 84.68 per cent to the total variance amongst the genotypes assessed for agronomic traits which indicated the presence of genetic diversity and

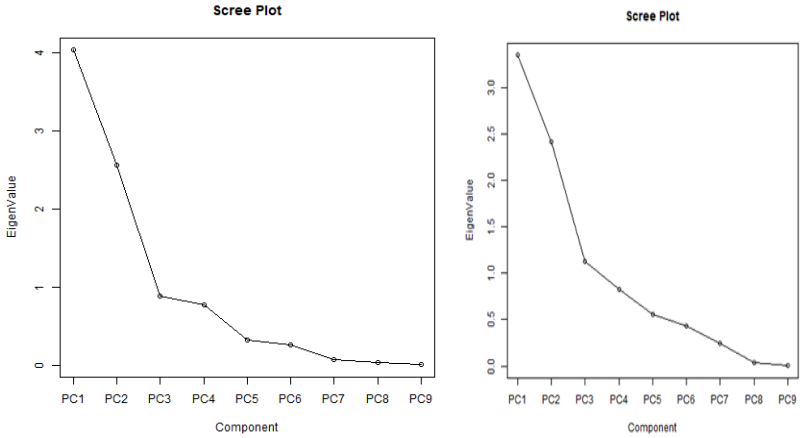


**Fig .1. Scree plot for different PCs (E1 and E2)**

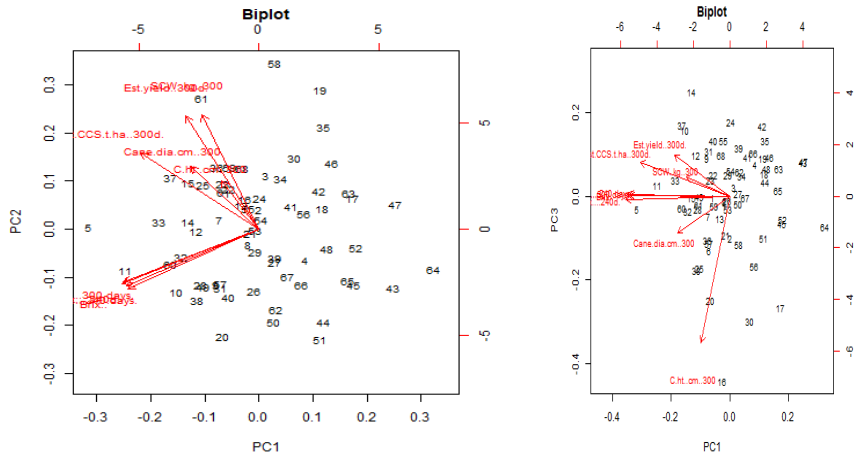


**Fig. 2. The Biplot of sugarcane genotypes for PC1 and PC2 (E1)**

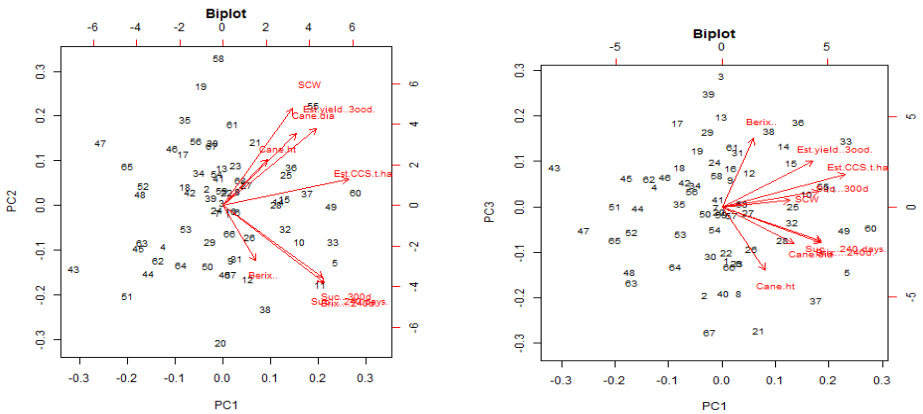


**Fig. 3. The Biplot of sugarcane genotypes for PC1 and PC2 (E2)**

genotypes with Eigenvalues more than 1 can be utilized in linseed breeding programmes. In our study cane height, cane diameter and single cane weight were contributing traits in PCs in both the environments. Tawadre *et al*. (2019) earlier observed that stalk height and stalk girth were the most effective variables contributing 28.64 and 17.98 per cent, respectively for PC1, whereas, cane yield (37.69 %), single cane weight (25.98 %) and plant height (10.49 %) were best explained by PC2. Similarly, it was identified that from the biplot axes PC1 and PC2, varieties such as Co Snk 07680, Co Snk 09227, Co Snk 09232, Co 2012-24, Co 2012-25, Co 2001-15 and Co Snk 081132 were found to be the highest for stalk diameter and plant height. Similar results were observed in interspecific hybrids of sugarcane (Karpagam and Alarmelu, 2016).

Principal component and hierarchical cluster studies with eight quantitative traits in 100 germplasm accessions of sorghum (*Sorghum bicolor* L. Monech) also revealed that 100 seed weight, plant height, leaf blade length and width were important traits depending upon their loading variables on a common principal axis and eight accessions were identified as superior genotypes for further utilization in breeding of high yielding sorghum varieties ( Kavithamani *et al*., 2019).

In E2, the first three principal components with Eigenvalue > 1 explained about 76.71 per cent of the total variability among the genotypes and the remaining six components accounted only 23.29 per cent towards the total diversity. The PC 1 explained the maximum variability of 37.24 per cent followed by PC 2 with a phenotypic variability of 26.94 per cent and PC3 had contributed 12.53 per cent to the total variation. The important traits in PC1 were due to variations among the genotypes for yield, and quality traits. PC 2 was related to variation among genotypes due to yield, single cane weight and cane diameter. PC1 showed 37.24 per cent variability with the Eigenvalue of 3.35. The Eigenvalues gradually decreased from PC1 to PC9. The Eigenvalues for remaining principal components were 2.42, 1.12, 0.82, 0.55, 0.43, 0.24, 0.03 and 0.0035 for PC2, PC3, PC4, PC5, PC 6, PC 7, PC 8 and PC 9 respectively. Eigen vectors of the PCs for different traits are presented in **Table 4**. The results showed that CCS t/ha had the highest positive value of 0.48 followed by sucrose % at 240 days (0.38) followed by single cane weight in (0.46) in PC2. Quality trait brix recorded the highest positive value (0.54) in PC3, cane diameter (0.55) in PC5, single cane weight (0.42) in PC6 and estimated cane yield (0.46) in PC 7, sucrose 240 (0.69) in PC 8 followed by yield (0.55) and sucrose (0.41) in PC9. Interspecific hybrid derivatives involving *Saccharum spontaneum, S. robustum and S. barberi* were characterized with twenty two qualitative traits (Karpagam and Alarmelu, 2017) and Principal Component Analysis (PCA) of qualitative traits revealed that the first nine principal components with Eigenvalue > 1 accounted for a cumulative variance of 62.40 per cent and the traits *viz*., cane diameter, dewlap color, and bud groove were identified as principal discriminatory characters which will be useful in preliminary screening and identification of interspecific hybrids. Thirty eight superior interspecific hybrids with high index score for agronomic traits and wider inter cluster distance were identified as pre breeding stocks and utilized in further backcross programmes In this study, we used the Principal Component Analysis (PCA) and identified five traits for phenotypic characterization of sugarcane, and there by to select superior clones in the breeding process. Kang *et al.* (2013), Ongala *et al.* (2016), Shahzad *et al.* (2016) and Mehrabeb *et al.* (2020) in their studies identified most of the yield traits to be significant in identifying the superior clones and their contribution to the selected traits.

The PC scores of each component in E1 contained positive values and in PC1, the positive value ranged from 1.039 in Co 86032 to 5.35 in ISH 176. In PC2 the positive value ranged from 0.0706 in Co 0314 to 4.55 in CoM 0265. In PC3 it ranged from 0.000318 in Co 0118 to 1.9577 in Co 12014. ISH 176 and CoV 89101 were identified as best clones for yield traits (**Table 5**).

In E2, the positive value ranged from 1.03 in Co 85019 to 3.50 in CoC 671. In PC2 the positive value ranged from 0.078 in Co 0310 to 4.23 in CoM 0265. In PC3 it ranged from 0.0039 in Co 94008 to 2.52 in Co 0310. The genotypes Co 98010 and CoV 89101 appeared in PC1 and PC2. Clones Co 200012, Co 85002, Co 12014, Co 1148, CoLk 8102, CoM 0265, ISH 175, ISH 176 and CoV 89101 were identified for yield traits.

The pattern of expression of genotypes in each PCs and environment varied. In E1 the genotypes Co 98010 and CoV 89101 appeared in PC1 and PC2. The clone Co 85019 appeared in all the three PCs in E2. Nineteen clones were common in their expression in both the environments which indicated the similarity among them which may be due to parents involved in their evolution. Twenty clones selected on this basis of positive PC score with Eigenvalues >1.0 in PC1 and PC2 of E1 and 38 clones from PC1, PC2 and PC3 in E2 can be exploited as parents in hybridization programme.

Agglomerative Hierarchical Cluster analysis (AHC) grouped the 68 genotypes into five clusters both in E1 and E2 environments (**Fig. 4 and Fig. 5**). Wide ranges of mean values among the clusters were found for different traits in both the environments (**Table 8**) and grouping of genotypes into different clusters confirmed the presence of variation among genotypes. In E1, the cluster strength ranged from seven genotypes (Cluster I and Cluster IV) to 26 genotypes in Cluster II. In E2, it varied from eleven genotypes (Cluster IV) to 19 genotypes in Cluster I. Cluster I had the maximum mean values for yield, cane diameter and single cane weight, while Cluster II had the maximum mean value for cane height in E1. In E2 cluster III had the high mean values for all the traits

except for cane height and SCW, while cluster II had the highest mean for cane height and SCW. The clusters IV and V showed the minimum values for most of the traits which included mostly exotic clones, interspecific hybrids and sub- tropical clones studied in both E1 and E2. The cluster III had genotypes which were superior for quality traits in both E1 and E2 **(Table 6 and Table 7**).

**Table 5. Clones selected on basis of PC score in each component having positive Eigenvalues and >1.0 in each PC'S**

**Environment I**

| PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|
| Co 0312 | Co 0310 | Co 11012 | Co 0240 | Co 11004 |
| Co 2010 -12 | Co 0320 | Co 12014 | Co 85002 | Co 97008 |
| Co 8347 | Co 14002 | Co 86032 | Co 85019 | |
| Co 8371 | Co 8371 | Co 98010 | CoC 671 | |
| Co 98010 | Co 86002 | CoV 89101 | CoSnk 05103 | |
| CoSnk 05103 | Co 86010 | CoV 92103 | CoV 89101 | |
| CoSnk 14103 | Co 94008 | CoH 119 | | |
| CoV 92103 | Co 98010 | | | |
| CP 96-1254 | CoSnK 03044 | | | |
| CP 96-1662 | CoT 8201 | | | |
| SP 80-1842 | CoV 92103 | | | |
| SP 80-185 | SP 80-185 | | | |
| Co 1148 | CoM 0265 | | | |
| BO 91 | CoM 88121 | | | |
| Co 0232 | ISH 100 | | | |
| Co 0233 | ISH 69 | | | |
| CoLk 8102 | | | | |
| ISH 175 | | | | |
| ISH 176 | | | | |
| ISH 2 | | | | |
| ISH 229 | | | | |

**Environment II**

| PC1 | PC2 | PC3 |
|---|---|---|
| Co 0314 | Co 12009 | Co 0310 |
| Co 11012 | Co 2010-12 | Co 12014 |
| Co 11015 | Co 8371 | Co 2010-12 |
| Co 12014 | Co 85019 | Co 8371 |
| Co 14002 | Co 86010 | Co 97015 |
| Co 85019 | Co 98010 | Co 99006 |
| Co 94008 | CoSnk 05103 | ISH 100 |
| Co 97009 | CoV 09356 | |
| Co 99008 | SP 80-185 | |
| CoC 671 | Co 1148 | |
| CoSnK 14103 | CoLk 8102 | |
| CoT 8201 | CoM 0265 | |
| CoTl 1153 | ISH 100 | |
| Co 0118 | ISH 2 | |
| CoH 119 | ISH 43 | |
| CoPant 97222 | | |

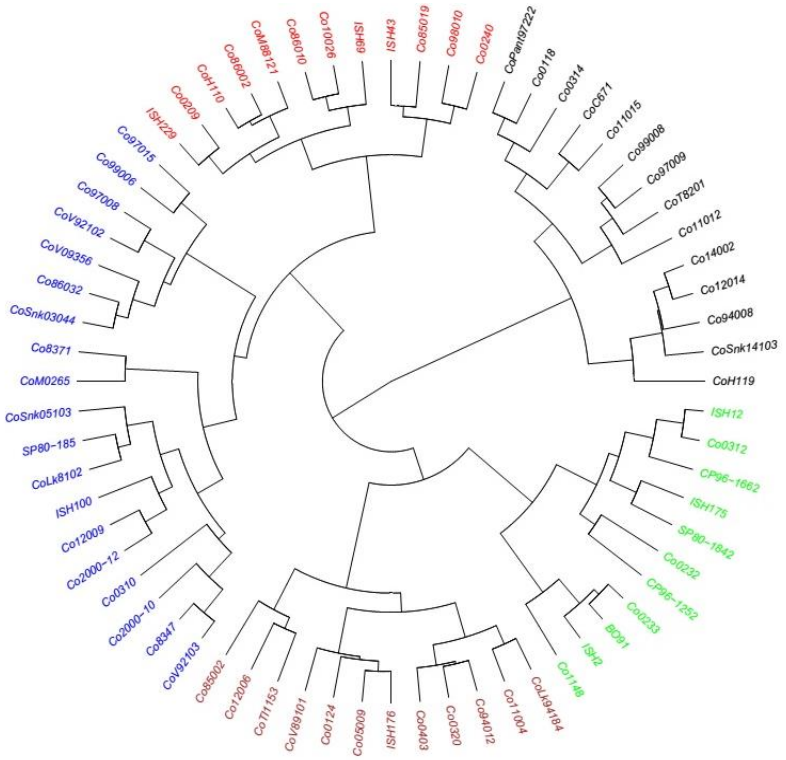


**Fig. 4. Clustering of genotypes in E1**

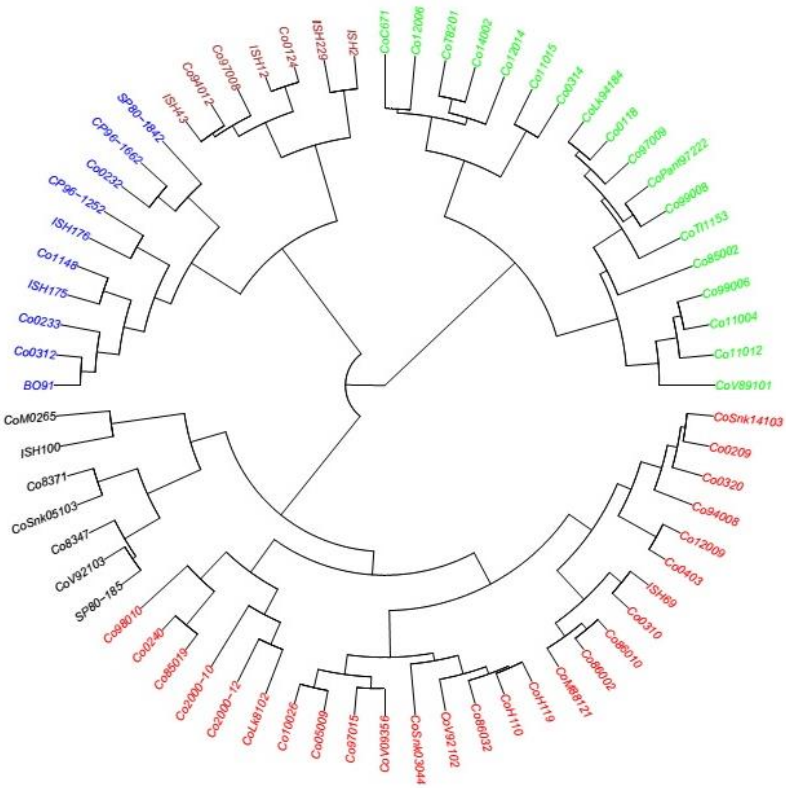


**Fig. 5. Clustering of genotypes in E2**

Cluster I in E1 comprised 26 genotypes out of which 22 were from tropical zone of the country and three from sub-tropical region. No exotic hybrids clustered with them. These clones had a high mean values for CCS and quality traits at 300 days. Cluster I was found to be superior for cane yield, cane thickness and single cane weight at 10 months of age. Cluster one in E2 consisted of 19 genotypes collected from different parts of the country and one exotic variety SP 80-185 (SauPaulos, Brazil) clustered with these clones. This variety should have close similarity with the genotypes of this group with which it had clustered together .These clones had tall to medium tall and medium thick to thick canes. They have also showed the mean values greater than the grand mean for sugar quality. Cluster three had fourteen genotypes of which ten are high quality types. Accessions in this cluster had the mean values greater than the grand mean for quality. Cluster four contained 11 clones of which three clones, CP 96-1252, CP 96-1662 and SP 80-1842 were exotic and three were interspecific hybrids and the clones might share common ancestral parents in their genealogical history which could be the reason for their clustering together. Among the five clusters Cluster III was found to be superior for cane yield and sucrose at 240 and 300 days. Sumbele *et al*. (2021) in their cluster analysis also showed that the accessions from different series were grouped in the same cluster despite their different geographic origin and also accessions from the same geographic origin were found in different clusters.

The number of individuals in each group varied in both the environments. Earlier studies (Silva *et al*., 2005; Lopes *et al*., 2008) reported variation in the number of groups and genotypes within each group according to environment. The variability for cane height, cane diameter and single cane weight were found out by PCA. In clustering method also the highest variation for all these traits was observed and therefore the genotypes were grouped into different clusters. The genotypes with high values of cane weight, cane diameter, cane yield and its component traits and quality in any cluster in both the environments can be used as donors in hybridization. These results of genetic diversity study were in accordance with the findings of Kang *et al.* (2013) and Khan *et al*. (2019). The genotypes in Clusters I, II and III in E1 and E2 are expected to produce the maximum heterosis and are also likely to produce potential recombinants with desired traits. The parental lines in IV and V need improvement by incorporating more desirable alleles through population improvement. The characters cane height, cane diameter, cane weight contributing the maximum to the divergence from the study should be given more emphasis for the purpose of further selection and choice of parents for hybridization.

**Table 6. Hierarchical cluster grouping in sugarcane genotypes ( E1)**

| Cluster | Members in each cluster | Clones |
|---|---|---|
| 1 | 7 | Co 8347, Co 8371, CoSnk 05103, CoV 92103, SP 80-185, CoM 0265, ISH 100 |
| 2 | 26 | Co 0209, Co 0240, Co 0310, Co 0320, Co 0403, Co 10026, Co 12009, Co 2000-10, Co 2000-12, Co 85019, Co 86002, Co 86010, Co 86032, Co 94008, Co 97015, Co 98010, CoSnk 03044, CoSnk 14103, CoV 09356, CoV 92102, Co 05009, CoH 110, CoH 119, CoLk 8102, CoM 88121, ISH 69 |
| 3 | 18 | Co 0314,Co 11004, Co 11012, Co 11015, Co 12006, Co 12014 Co 14002, Co 85002, Co 97009, Co 99006, Co 99008, CoC 671, CoT 8201, CoTl 1153, CoV 89101, Co 0118, CoLk 94184, CoPant 97222 |
| 4 | 7 | Co 94012, Co 97008, Co 0124, ISH 12, ISH 2, ISH 229, ISH 43 |
| 5 | 10 | Co 0312, CP 96-1252, CP 96-1662, SP 80-1842, Co 1148, BO 91, Co 0232, Co 0233, ISH 175, ISH 176 |

**Table 7. Hierarchical cluster grouping in sugarcane genotypes (E2)**

| Cluster | Members in each cluster | Clones |
|---|---|---|
| 1 | 19 | Co 0310, Co 12009, Co 2000-10, Co 2000-12, Co 8347, Co 8371, Co 86032, Co 97008, Co 97015, Co 99006, CoLk 8102, CoM 88121, CoSnk 03044, CoSnk 05103, CoV 09356, CoV 92102, CoV 92103, ISH 100, SP 80-185 |
| 2 | 12 | Co 0209, Co 0240, Co 10026, Co 85019, Co 86002, Co 86010 Co 98010, CoH110, CoM 0265, ISH 229, ISH 43, ISH 69 |
| 3 | 14 | Co 0118, Co 0314, Co 11012, Co 11015, Co 12014, Co 14002, Co 94008, Co 97009, Co 99008, CoC 671, CoH 119, CoPant 97222, CoSnk 14103, CoT 8201 |
| 4 | 11 | BO 91, Co 0232, Co 0233, Co 0312, Co 1148, CP 96-1252, CP 96-1662, ISH 12, ISH 175, ISH 2, SP 80-1842 |
| 5 | 12 | Co 0124, Co 0320, Co 0403, Co 05009, Co 11004, Co 12006, Co 85002, Co 94012, CoLk 94184, CoTl 1153, CoV 89101, ISH 176 |

**Table 8. Cluster mean for traits**

| Traits | Harvest time (Days | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V |
|---|---|---|---|---|---|---|
| | | | Environment (1) | | | |
| Cane yield (kg/plot) | 300 | 79.76 | 68.14 | 65.07 | 41.02 | 47.91 |
| Commercial cane sugar (t/ha) | 300 | 8.11 | 7.97 | 8.70 | 4.82 | 5.09 |
| Brix (%) | 300 | 17.22 | 19.20 | 21.07 | 19.38 | 17.88 |
| Sucrose (%) | 300 | 14.83 | 17.04 | 19.05 | 16.99 | 15.49 |
| Cane height (cm) | 300 | 212.57 | 225.12 | 211.94 | 190.71 | 204.00 |
| Cane diameter (cm) | 300 | 2.77 | 2.76 | 2.72 | 2.67 | 2.34 |
| Single cane weight (kg) | 300 | 1.51 | 1.25 | 1.15 | 1.03 | 0.85 |
| Brix (%) | 240 | 16.27 | 17.45 | 19.28 | 17.89 | 16.02 |
| Sucrose (%) | 240 | 13.60 | 14.67 | 17.01 | 15.20 | 13.38 |
| | | | Environment (2) | | | |
| Cane yield (kg/plot) | 300 | 64.84 | 59.63 | 71.03 | 43.96 | 49.96 |
| Commercial cane sugar (t/ha) | 300 | 7.24 | 6.56 | 9.46 | 4.63 | 6.31 |
| Brix (%) | 300 | 19.65 | 18.39 | 19.75 | 18.70 | 20.41 |
| Sucrose (%) | 300 | 16.62 | 16.04 | 18.75 | 15.68 | 18.18 |
| Cane height (cm) | 300 | 186.05 | 218.67 | 206.07 | 182.82 | 199.67 |
| Cane diameter (cm) | 300 | 2.67 | 2.80 | 2.81 | 2.43 | 2.59 |
| Single cane weight (kg) | 300 | 1.18 | 1.28 | 1.25 | 0.89 | 0.98 |
| Brix (%) | 240 | 16.96 | 18.08 | 19.36 | 16.89 | 18.88 |
| Sucrose (%) | 240 | 14.38 | 15.62 | 17.11 | 14.24 | 16.38 |

The genotypes grouped into same cluster indicates the lowest degree of divergence and recombinants are not expected from the cross combinations. The selection of genotypes as donors based on these results will produce more genetic diversity and will open the scope for additional enhancement of the cultivars in crop improvement programmes for both tropical and sub - tropical regions of the country.

Breeding in sugarcane greatly depends on genetic diversity existing in the hybridization pool and the choice of parents used in hybridization programmes. Thus increase in the genetic diversity of parental clones will be helpful to create new variability for use. Both PCA and clustering methods recorded the same level of variability between genotypes. Nineteen clones *viz.,* Co 0314, Co 8371, Co 85019, Co 86010, Co 94008, Co 98010, Co 11015, Co 12014, Co 14002, CoSnk 05103, CoV 89101, CoV 92103, CoC 671, CoT 8201 (Tropical), Co 1148, CoH 119 (Sub-tropical), SP 80-185, ISH 100 and ISH 2 were promising for both yield and quality traits in both the environments indicating their potential to perform under varied ecological situations and can be studied further to ascertain their stability. These clones may be utilized in the recombination breeding programmes to develop high yielding new varieties and also to combat with the climate change.

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