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Genetic divergence studies in first clonal stage of sugarcane (*Saccharum officinarum* L.)

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Abstract
The identification of diverse genotypes is an important consideration in sugarcane improvement. Mahalanobis' D^2 technique has been quite useful in determining the diversity in crop species. Knowledge on genetic divergence is therefore fundamental to identify and organize the available genetic resources aiming at the production of promising cultivars. In vegetatively propagated crops like sugarcane, development of improved genotypes with high heterotic expression for yield and quality characters is desired. The heterotic genotypes can be developed by utilization of diverse parents in hybridization. Proper exploitation of variability in a crop like sugarcane with a complex ploidy and a high level of heterozygosity is a complicated process. Breeding for higher cane yield and quality traits requires basic information on the extent of genetic variation in a population and its response to selection.

Keywords: Mahalanobis' D^2, genetic divergence, heterotic, diverse parents

Introduction
Globally, sugarcane is cultivated over an area of 24.10 m ha with an annual production of 1329.3 million tonnes and an annual productivity of 75.70 t/ha. In India, sugarcane is grown under diverse agro-climate situations covering an area of 5.2 m ha and production of 364.0 million tonnes of sugarcane with productivity of 70.39 t/ha (Anon., 2017) [2, 3]. Principal sugarcane growing states are Karnataka, Tamil Nadu, Maharashtra, Andhra Pradesh, Uttar Pradesh and Gujarat. In Karnataka sugarcane is grown in an area of 4.30 lakh hectare and production of 45.3 million tonnes of sugarcane with annual productivity of 93.80 t/ha (Anon., 2017) [2, 3]. In Cauvery Command Area sugarcane is grown in an area of 0.61 lakh hectare with the production of 77.10 lakh tonnes of sugarcane and productivity of 101.80 t/ha (Anon., 2017). In India 24.39 million tonnes of sugar is produced, but the projected requirement of sugar by 2030 is 36 million tonnes which has to be achieved from the existing cane area through improved varieties and management for cane yield and sugar recovery as further expansion in area is not possible.
Most of the sugarcane varieties in the world are breeds of *S. spontaneum* × *S. officinarum*. To reduce the negative effects of *S. spontaneum* and to retain the high sucrose producing ability of *S. officinarum* during crosses, a series of backcrosses were made between the inter-specific hybrids and *S. officinarum* parents. This led to the "noblization" of *Saccharum* spp. hybrids (Sreevastava *et al*., 1999) [10]. This was a major breakthrough in sugarcane varietal improvement programs in terms of improved sugar productivity, high disease resistance and high ratooning ability. Although noblization was highly successful but due to limits of the gene pool exploited during traditional breeding programs, very limited progress has been achieved in increasing sugar content.

Material and Methods
Fifty five genotypes selected from 2308 seedling nursery based on evaluation were planted in *eksali,* 2015. Each genotype was planted in two rows of 6.0 m length spaced at 90 cm apart (2R × 6m × 0.9m) with three budded setts per meter in augmented design with five blocks along with three checks *viz*., CoVC 99463, Co 86032 and Co 62175. All the recommended package of practices was adopted to raise the better crop stand.

Data recorded in First Clonal Generation (C_1) crop
Observations were recorded on the following traits for each genotype before and at the time of harvest in the settling nursery (C_1) crop.
1. Number of tillers/plot
2. Number of millable canes /plot
3. Millable cane length (cm)

4. Millable cane length (cm)
5. Cane diameter (cm)
6. Number of internodes
7. Internode length (cm)
8. Single cane weight (kg)
9. Pol per cent juice
10. Brix per cent juice
11. CCS per cent
12. CCS cane yield
13. CCS yield (t/ha)
14. Purity per cent
15. Cane yield (t/ha)
16. HRB Yield (t/ha)

Results and Discussion

Mahalanobis' generalized distances (D^2)

The D^2 values between any two clones were calculated as the sum of the squares of the differences between the uncorrelated mean values of all the 15 characters. As a consequence, each genotype produced 54 pair wise combinations and D^2 values were estimated for all the 55 genotypes.

Group constellation

Based on the D^2 values the genotypes were grouped into seven clusters (Table 1) using Tocher's method given by Rao (1952) [8]. Out of the 7 clusters, clusters I & VI were the largest, consisting of 22 and 13 genotypes respectively followed by cluster II and V with 6 genotypes each and cluster VII consisting of 4 genotypes, cluster III consisting of 3 genotypes and cluster IV was solitary with single genotype. The results revealed that the distribution of genotypes into different clusters was at random and independent of each other. The genotypes from same parentage had fallen in different clusters and the genotypes with different parentage had fallen in the same cluster.

Contribution of each character to the divergence

The per cent contribution of each character is estimated based on the number of times ranked and presented in table 2 and Fig. Among the total 1485 pair combinations, cane yield ranked first for 600 times and contributed 40.40% towards total divergence.

It was followed by millable cane (35.82%), number of tillers (20.20%), number of millable canes (2.83%), purity per cent cane (0.67%) and internode length (0.07%). The rest of the characters *viz*., HR Brix yield, CCS yield, pol per cent, number of internodes, cane diameter, Brix per cent, single cane weight, CCS per cent and CCS cane yield did not contribute much towards genetic divergence.

This suggested that breeder should give more emphasis on these characters for the purpose of further selection and choice of parents for hybridization.

Number of internodes and pol per cent had no contribution for genetic divergence indicating that parents used for the production of sugar cane hybrids were close to each other for these attributes.

Number of tillers per clump, single cane weight, cane yield per clump and quality character like Brix per cent contributed highest towards the total genetic divergence. Sreevastava *et al.,* (1999) [10] reported that contribution of sucrose per cent and purity per cent towards the genetic divergence in their study. Similar results were also reported by Guruprasad Hiremath (2012) [5] and Suresh Jaganur (2014) [11].

Intra-cluster distances

The average intra-cluster and inter-cluster D^2 and D values among seven clusters are furnished in table 3 and Figure 2. Average Intra-cluster distance values ranged from 13.45 (III) to 38.56 (VII), which was higher in cluster VII and lowest in cluster III. The intra-cluster distance values indicated that the cluster VII comprising four genotypes had highest genetic diversity (D=38.56) followed by clusters VI (D=37.63) comprising thirteen genotypes, clusters V (D=32.22) comprising six genotypes, clusters II (D=31.82) comprising six genotypes, cluster I (D=28.64) comprising twenty two genotypes, and cluster III (D=13.45) which comprised three genotypes. The cluster IV had no intra cluster distance as they were represented by a single genotype.

Inter-cluster distances

Average inter-cluster D^2 and D values furnished in table 3 and figure 2 revealed that the inter-cluster (D) distance ranged from 38.84 to 125.86. The inter-cluster D value was higher (125.86) between clusters IV and VI followed by cluster IV and VII with D value of 115.77. The cluster I and III were nearer to each other with an inter cluster distance of 38.84. Cluster IV formed a solitary cluster of a single genotype and it was the most diverse cluster. Cluster I which comprised 22 genotypes was closely related with cluster III with D values of 38.84 and farthest with cluster VI and VII with D values of 103.00, 86.25, respectively.

Table 1: Distribution of sugarcane genotypes under first clonal stage to different clusters

Cluster Number	Number of genotypes	Genotypes
I	22	CoVC14-09-04,CoVC14-45-02, CoVC 14-12-09, CoVC 14-12-23, CoVC 14-02-08, CoVC 14-12-03, CoVC 14-61-02, CoVC 14-06-04, CoVC 14-13-01, CoVC 14-62-24, CoVC 14-06-09, CoVC 14-31-05, CoVC 14-02-10, CoVC 14-45-03, CoVC 14-12-05, CoVC 14-61-14, CoVC 14-61-18, CoVC 14-35-02, CoVC 14-35-01, CoVC 14-12-27, CoVC 14-12-14 and CoVC 14-02-12.
II	6	CoVC 14-06-12, CoVC 14-42-03, CoVC 14-06-03, CoVC 14-12-02, CoVC 14-62-20 and CoVC 14-25-01.
III	3	CoVC 14-01-03, CoVC 14-62-27 and CoVC 14-42-04.
IV	1	CoVC 14-62-05
V	6	CoVC 14-62-26, CoVC 14-62-32, CoVC 14-29-02, CoVC 14-62-04, CoVC 14-62-02 and CoVC 14-26-02.
VI	13	CoVC 14-12-24, CoVC 14-42-05, CoVC 14-35-12, CoVC 14-02-04, CoVC 14-02-09, CoVC 14-31-03, CoVC 14-02-15, CoVC 14-62-31, CoVC 14-35-08, CoVC 14-62-21, CoVC 14-62-22, CoVC 14-35-05 and CoVC 14-62-28.
VII	4	CoVC 14-12-30, CoVC 14-12-25, CoVC 14-13-02 and CoVC 14-35-15.

Table 2: Contribution of each character to the divergence in first clonal stage of sugarcane

Sl. No.	Characters	Number of ranked First	Per cent Contribution
1	Cane yield (t/ha)	600	40.40
2	Millable cane length (cm)	532	35.82
3	Tiller number	300	20.20
4	NMC	42	2.83
5	Purity per cent	10	0.67
6	Internode length (cm)	1	0.07
7	HRB Yield (t/ha)	0.00	0.00
8	CCS yield (t/ha)	0.00	0.00
9	Number of internodes	0.00	0.00
10	Cane diameter (cm)	0.00	0.00
11	Brix per cent juice	0.00	0.00
12	Single cane weight (kg)	0.00	0.00
13	Pol per cent juice	0.00	0.00
14	CCS per cent	0.00	0.00
15	CCS cane yield	0.00	0.00
Total		1485	100

Table 3: Average intra and inter cluster D^2 values along with their D values (in parenthesis) for 7clusters formed in first clonal stage of sugarcane

Cluster number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	820.42 (28.64)	2050.54 (45.28)	1508.71 (38.84)	1517.51 (38.96)	2392.34 (48.91)	10608.66 (103.00)	7438.70 (86.25)
Cluster II		1012.57 (31.82)	2061.52 (45.40)	5043.54 (71.02)	4498.78 (67.07)	6279.68 (79.24)	3083.97 (55.53)
Cluster III			180.97 (13.45)	3197.13 (56.54)	5559.14 (74.56)	13192.90 (114.86)	6403.97 (80.02)
Cluster IV				0.00	1992.90 (44.64)	15840.60 (125.86)	13402.75 (115.77)
Cluster V					1038.38 (32.22)	10044.64 (100.22)	11076.06 (105.24)
Cluster VI						1416.07 (37.63)	4815.48 (69.39)
Cluster VII							1487.22 (38.56)

Cluster II was closely related to cluster I, VII, and V with respective distances of 45.28, 55.53 and 67.07 respectively and it was farthest with cluster IV and VI with D value of 71.02 and 79.24. Cluster III was in close proximity with cluster III with D value of 38.84 whereas, it was more diverse from clusters V, VII and VI with D values of 74.56, 80.02 and 114.86, respectively.

Nearest clusters to the IV was I with D value of 38.96 whereas the farthest clusters VI with D values of 125.86. Cluster V was closely related to cluster IV with D value of 44.64 and it was farthest with cluster VII with D value of 105.24. Cluster VI was nearer to the cluster VII with D value of 69.39 and it was farthest with cluster IV with D value of 125.86. Cluster VII was nearer to the cluster II with D value of 55.53 and farthest to cluster IV with D value of 115.77 (Table 4).

Cluster mean analysis

When clusters means of all the characters was analysed, considerable differences between clusters was evident in table 5. The higher mean value for number of tiller / plot was observed in cluster VII (103.00) followed by cluster VI (100.23), while less number of tillers (35.00) was exhibited by the genotypes of cluster IV.

The cluster means for number of millable canes/ plot ranged from 23.00 (IV) to 81.50 (VII) represented by cluster IV and cluster VII, respectively.

Higher values than the general mean of 59.69 were recorded in the clusters VI and VII. The higher mean value for millable cane length was observed in cluster V (237.83) followed by cluster VI (223.08), while cluster III was exhibited by the genotypes with less millable cane length.

Genotypes with low cane diameter (2.70 cm) was found respectively in cluster IV and cluster V while, higher means were noticed in cluster VI (3.35) and cluster II (3.17), respectively. The cluster means for number of internodes ranged from 16.20 (III) to 21.00 (IV). More number of internodes was observed in cluster IV and less in cluster III. The clusters V exhibited more number of internodes than its general mean 18.24.

Table 4: The nearest and farthest clusters from each cluster based on 'D' values (Indicated in parenthesis) in first clonal stage of sugarcane

Cluster Number	Nearest cluster with D value	Farthest cluster with D value
I	III (38.84)	VI (103.00)
II	II (45.28)	VI (79.24)
III	I (38.84)	VI (114.86)
IV	I (38.96)	VI (125.86)
V	IV (44.64)	VII (105.24)
VI	VII (69.39)	IV (125.86)
VII	II(55.53)	IV (115.77)

Table 5: The mean values of 15 characters for seven clusters formed in sugarcane genotypes in first clonal stage

Sl. No.	Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1	Tiller number	53.68	72.33	57.33	35.00	52.83	100.23	103.00
2	NMC	40.68	59.17	44.67	23.00	40.67	81.46	81.50
3	Millable cane length (cm)	198.55	187.17	167.67	213.00	237.83	223.08	171.75
4	Cane diameter (cm)	2.91	3.17	2.90	2.70	2.70	3.35	3.10
5	Number of internodes	18.07	17.32	16.20	21.00	18.68	18.15	16.43
6	Internode length (cm)	11.37	10.40	10.67	9.00	13.90	13.26	10.43
7	Single cane weight (kg)	0.98	1.04	0.73	1.10	1.03	1.44	1.02
8	Pol per cent juice	18.92	18.72	17.42	15.21	17.03	17.92	19.05
9	Brix per cent juice	20.07	20.17	19.17	16.00	18.42	19.27	20.13
10	CCS per cent	13.49	13.27	12.20	10.90	12.05	12.70	13.60
11	CCS cane yield	0.13	0.14	0.09	0.12	0.13	0.18	0.14
12	CCS yield (t/ha)	5.01	7.68	3.70	2.55	4.75	13.56	10.47
13	Purity per cent	94.29	92.44	90.55	95.06	92.39	92.89	94.61
14	Cane yield (t/ha)	36.98	56.71	30.14	23.43	39.21	106.83	76.68
15	HRB Yield (t/ha)	7.46	11.56	5.80	3.75	7.28	20.57	15.46

Cluster mean for internode length varied from 9.00 cm in cluster IV to 13.90 cm in cluster V. Low cluster mean for single cane weight (0.73) was found in cluster III while, higher cluster means were noticed in clusters VI (1.44) and IV (1.10). Pol per cent varied from 15.21 (IV) to 19.05 (VII).

The superior clusters for pol per cent over their general mean (17.91) were I, II, VII and VI. The genotype with low cluster means for Brix per cent was found in cluster IV (16.00) while, high cluster mean was noticed in cluster II (20.17).

The highest and lowest cluster mean values for CCS per cent were observed in cluster VII (13.60) and IV (10.90), respectively. Higher mean values than the overall mean were observed in clusters I and VII.

Cluster mean for CCS cane yield varied from 0.09 in cluster III to 0.18 in cluster VI. Cluster VI exerted highest cluster mean for CCS yield (13.56 t/ha) while lowest mean (2.55 t/ha) was recorded in cluster IV. Low cluster mean for purity per cent was found in cluster III (90.55) while higher cluster mean was recorded in cluster IV (95.06).

Low cluster mean for cane yield was observed in cluster IV (23.43 t/ha) while higher cluster mean value was noticed in cluster VI (106.83 t/ha). Highest cane yield was observed in clutser VI while lowest cane yield was noticed in cluster IV. Cluster mean for HR Brix yield varied from 3.75 t/ha in cluster IV to 20.57 t/ha in cluster VI.

From the foregoing results it was evident that genetic variability existed in the sugarcane clones tested, but this variability should be further increased by divergent crosses to raise the probability of finding superior clones. Crosses between divergent genotypes increase the heterotic effect (Silva *et al.*, 2002) [9] and avoid future problems with inbreeding depression (Ferreira *et al.*, 2005) [4], which improves the chances to select superior clones in the segregating populations derived from these divergent crosses. The crosses between the most divergent with the highest yielding clones would improve the variability.

Pratap and Singh (2002) [7] suggested that varieties belonging to different clusters having maximum distance should be selected for hybridization for generating the highest possible variability in yield and quality traits.

In general it could be concluded from the present investigation that, clusters VII and VI were superior for important characters *viz*., cane yield, CCS cane yield and CCS yield and quality attributes and clones included in these diverse clusters hold good as parents for obtaining potential hybrids through creating large variability for desirable characters and these observation are in close confirmity with earlier sugarcane studies of Srivastava *et al*., (1999), Ahmed and Obeid (2010) [1], Guruprasad Hiremath (2012) [5] and Kasayya (2016) [6].

Conclusion

Most significant point that emerged from the present divergence investigation is that the clusters IV and VI not only exhibited highest inter-cluster distances between them but also moderate and farthest inter cluster distance values with all other clusters. The genotypes of these two clusters and also the genotypes of other superior cluster like VII could be beneficially employed in future breeding programmes to improve cane and sugar yield. From the results of present investigation it can be concluded a clones included in distant clusters IV, VI, and VII can be used for hybridization programme to yield desirable recombinants.

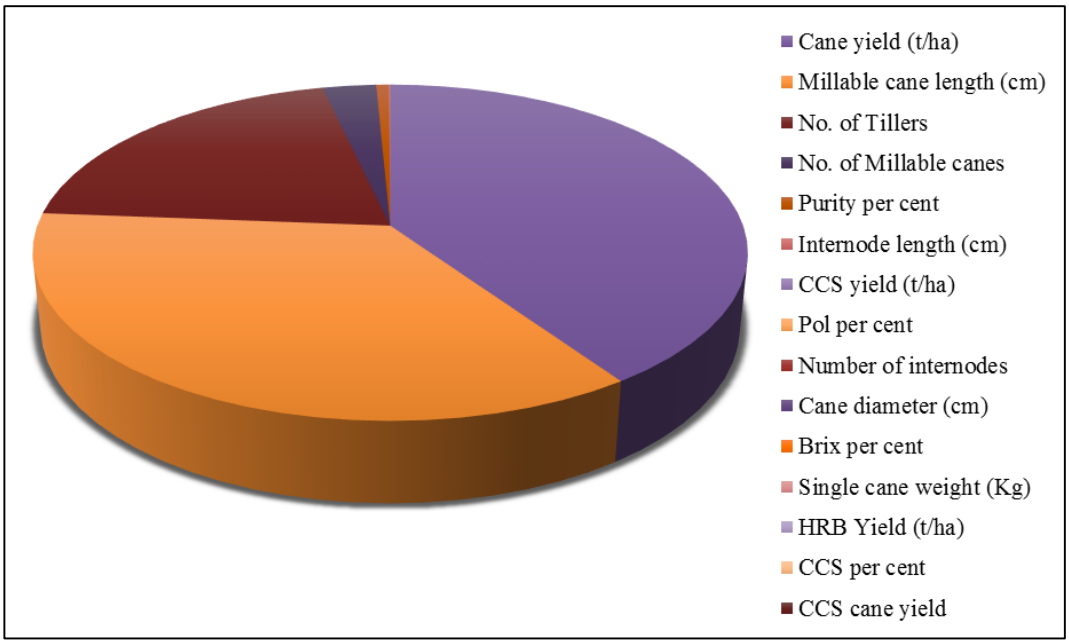

Fig 1: Contribution of each trait to the genetic divergence in in first clonal stage of sugarcane genotype

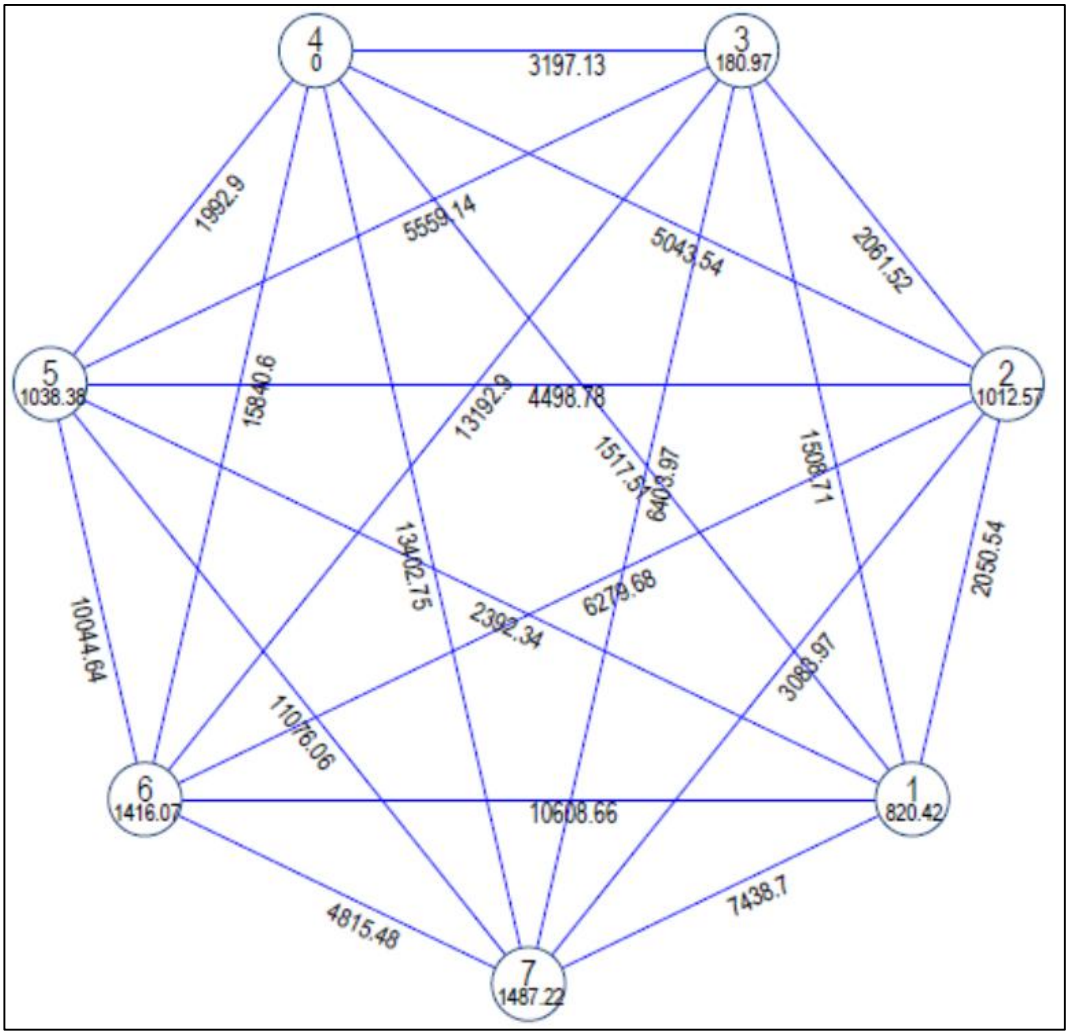

Fig 2: Average intra and inter cluster D^2 values for 7clusters formed in first clonal stage of sugarcane

References

1. Ahmed AO, Obeid A. Investigation on variability, broad sensed heritability and genetic advance in sugarcane (*Saccharum* spp.). International. J Agric. Sci 2012;2(9):839-844.
2. Anonymous 2017. http//www. faostat. com
3. Anonymous 2017. http//www. indiastat. Com
4. Ferreira FM, Barbosa MHP, Castro RDDE, Peternelli LA, Cruz CD. Effects of inbreeding on the selection of sugarcane clones. Crop Breeding and Applied Biotech 2005;5(2):174-182
5. Guruprasad Hiremath. Morphological traits and DNA markers assay based diversity in selected clones of sugarcane. M.Sc. (Agri). Thesis, Univ. Agric. Sci., Bangalore 2012, 197 pp.
6. Kasayya. Genetic investigation in mid-late maturing sugarcane (*Saccharum officinarum*) clones isolated for cauvery command area. M. Sc.(Agri). Thesis, Univ. Agric. Sci., Bangalore 2016, 107 pp.
7. Pratap Singh, Singh VP. Genetic divergence in sugarcane germplasm. Indian Journal of Agricultural Sciences. 2002;72(4):252-253.
8. Rao CR. Advanced statistical methods in biometrical Research. John Wiley and Sons Int. New York 1952, 357-363.
9. Silva MDA, Goncalves PDS, Landell MGDA, Bressiani JA. Estimates of genetic parameters and expected gains from selection of yield traits in sugarcane families. Crop Breed. Appl. Biotechnol 2002;2(4):569-578.
10. Sreevastava HM, Sangeeta Srivastava, Rajesh Kumar, Misra GP. Genetic Divergence among Interspecific Hybrids of Sugarcane. Sugar Technol 1999;1(12):19-22.
11. Suresh Jaganur. Evaluation of elite clones of sugarcane (*Saccharum officinarum*) for cane yield, quality traits and rationing ability. M.Sc (Agri). Thesis, Univ. Agric. Sci., Bangalore 2014, pp 85.