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Genetic Divergence Studies for Cane Yield and Quality Attributes in Sugarcane (*Saccharum officinarum* L.)

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ABSTRACT

Genetic diversity among 25 sugarcane genotypes was estimated by using Mahalanobis D^2 statistic for sixteen characters. The analysis of variance revealed significant differences among all genotypes for the characters studied. Based on Tocher's method, twenty five genotypes were grouped into six clusters with maximum number of fifteen genotypes in cluster I followed by cluster VI with four genotypes, cluster II with three genotypes and clusters III, IV and V each comprising of single genotype. The character, per cent juice sucrose at 300 DAP showed maximum contribution towards genetic divergence followed by fibre per cent at 300 DAP, brix per cent at 300 DAP and single cane weight at harvest. Maximum inter cluster distances were recorded between clusters III and VI followed by clusters V and VI. Based on good *per se* performance for majority of yield contributing characters and juice quality characters, genotype 93 V 297 from cluster III, could be used in hybridization with genotypes 2002 V 48 and 2008 V 257 from cluster VI, genotype, 2010 V 32 from cluster II and genotypes 81 V 48, 83 V 15, 91 V 83, 2003 V 46 and 2007 V 127 from cluster I. Similarly, genotype, 2000 V 59 from cluster V, could be used in hybridization with genotypes 2002 V 48 and 2008 V 257 from cluster VI, genotype 2010 V 32 from cluster II and genotype 2009 V 127 from cluster IV to get superior hybrids.

Key words: *Divergence and quality attributes, Sugarcane.*

Sugarcane (*Saccharum officinarum* L.) is a major crop of tropical and subtropical regions of the world which is cross pollinated, grown as an important cash crop and is a sucrose storing member of tall growing perennial monocotyledonous grasses. India is the second largest producer of sugarcane in the world after Brazil. Across the world, 70 per cent sugar is manufactured from sugarcane and it is a major source of raw material for sugar industries and other allied group of by product industries. Diversity analysis helps in assessing the degree of diversity in order to identify genetically diverse genotypes for their use in breeding programmes. In sugarcane breeding programme the diversity of parents is always emphasized. More diverse the parent within a reasonable range, better the chances of improving economic characters under consideration in the resulting offspring (Agrawal and Kumar, 2017). In general, inclusion of diverse parents in hybridization programme will improve the chances of desirable segregants for yield and other characters in the progeny (Krishna *et al.,* 2018).

MATERIAL AND METHODS

The present investigation was conducted at the Sugarcane Research Station, Vuyyuru, Krishna District of Andhra Pradesh during 2017-18 cropping season. Experimental design consisted of twenty five promising sugarcane clones and was raised in randomized block design with three replications. Each clone was planted in two rows of five metres length spaced at distance of 80 cm between the rows with four three budded setts per meter as seed rate. Observations were recorded on plot basis on characters *viz.*, number of germinants at 35 DAP, shoot population at 120 DAP, stalk population at 240 DAP, number of millable canes at harvest and cane yield. Juice quality parameters like per cent brix, per cent CCS, per cent purity and per cent juice sucrose were recorded using sucrolyzer. CCS yield was estimated based on cane yield and CCS per cent. Data on length of millable cane, diameter of millable cane and single cane weight were recorded on 10 randomly selected canes in each plot and replication at harvest. The observations like specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) at 120 DAP were recorded on 5 randomly selected sugarcane leaves from each plant of each plot and replication. The analysis of genetic divergence was done using Mahalanobis D^2 (1928) statistic and genotypes were grouped into different clusters by Tocher's method described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed that significant differences among the genotypes for all the characters studied. Based on D^2 analysis all the 25 genotypes were grouped in to six clusters using Tocher's method (Singh and Chaudhary, 1977). However, with variable number of entries in each

Table 1. Clustering pattern of 25 genotypes of sugarcane (*Saccharum officinarum* L.) by Tocher's method.

Cluster	Number of genotypes	Genotypes
I	15	81 V 48, 83 V 15, 83 V 288, 86 V 96, 89 V 74, 91 V 83, 98 V 95, 98 V 100, 99 V 30, 2003 V 46, 2006 V 41, 2006 V 51, 2007 V 127, 2008 V 240, 2009 V 89
II	3	2008 V 52, 2010 V 32, 2010 V 146
III	1	93 V 297
IV	1	2009 V 127
V	1	2000 V 59
VI	4	82 V 12, 2002 V 48, 2005 V 96, 2008 V 257

Table 2. Average intra (diagonal) and inter cluster D^2 values of 25 genotypes of sugarcane (*Saccharum officinarum* L.).

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	24.87	51.19	43.72	39.43	43.49	84.67
Cluster II		34.86	100.13	53.96	90.64	73.87
Cluster III			0.00	36.77	34.78	154.61
Cluster IV				0.00	44.97	98.01
Cluster V					0.00	126.78
Cluster VI						53.32

Table 3. Contribution of different characters towards genetic divergence among 25 genotypes of sugarcane (*Saccharum officinarum* L.)

S.No	Source	Contribution %	Times Ranked 1st
1	Number of germinants at 35 DAP	0.33	1
2	Shoot population at 120 DAP	0.33	1
3	Stalk population at 240 DAP	0.33	1
4	Number of millable canes at harvest	0.67	2
5	Length of millable cane at harvest (cm)	1.00	3
6	Diameter of millable cane at harvest (cm)	3.67	11
7	Single cane weight at harvest (kg)	6.33	19
8	Per cent brix at 300 DAP	11.33	34
9	Per cent juice sucrose at 300 DAP	49.67	149
10	Per cent CCS at 300 DAP	0.01	0
11	Per cent purity at 300 DAP	3.00	9
12	Per cent fibre at 300 DAP	11.67	35
13	CCS yield at harvest (kg $plot^{-1}$)	4.67	14
14	Specific leaf area (SLA) at 120 DAP (cm2 g^{-1})	1.33	4
15	SPAD chlorophyll meter reading (SCMR) at 120 DAP	2.67	8
16	Cane yield at harvest (kg $plot^{-1}$)	3.00	9

cluster revealing considerable amount of genetic diversity in the material studied. The distribution of 25 genotypes into 6 clusters (Table 1) were at random with maximum number of fifteen genotypes in cluster I followed by cluster VI with four genotypes, cluster II with three genotypes while cluster III, cluster IV and cluster V having single genotype each.

Average intra and inter cluster distance values among six clusters were presented in Table 2 and the maximum intra cluster D^2 value was 53.32 for cluster VI followed by 34.86 for cluster II, 24.87 for cluster I and zero for cluster III, cluster IV and cluster V. The high intra cluster distance in cluster VI indicated the presence of wide genetic diversity among the genotypes *viz.*, 82 V 12, 2002 V 48, 2005 V 96 and 2008 V 257. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied.

The maximum inter cluster D^2 value was observed between clusters III and VI (154.61) followed by clusters V and VI (126.78) indicating wide genetic diversity between clusters. Based on these studies, crosses could be made between genotypes with high index of specific character by cluster III (93 V 297) and cluster V (2000 V 59) with cluster VI (2002 V 48 and 2008 V 257) to obtain new desirable recombinants with maximum hybrid vigour in sugarcane. Lower inter cluster distances observed between clusters III and V (34.78) and clusters III and IV (36.77) which might indicate the close relationship between the genotypes of these clusters.

The per cent contribution towards genetic divergence by all the 16 characters is presented in Table 3. The trait, juice sucrose per cent at 300 DAP (49.67) showed maximum contribution towards genetic divergence due to genetic dissimilarity among genotypes for this trait followed by fibre per cent at 300 DAP (11.67), brix per cent at 300 DAP (11.33), single cane weight at harvest (6.33), CCS yield (4.67), diameter of millable cane at harvest (3.67), purity per cent at 300 DAP (3.00), cane yield at harvest (3.00), SPAD chlorophyll meter reading (SCMR) at 120 DAP (2.67), specific leaf area (SLA) at 120 DAP (1.33), length of millable cane at harvest (1.00), number of millable canes at harvest (0.67), number of germinants at 35 DAP (0.33), shoot population at 120 DAP (0.33), stalk population at 240 DAP (0.33) and CCS per cent at 300 DAP (0.01).

Based on Mahalanobis' D^2 analysis it can be inferred that maximum divergence exists between clusters III and VI followed by clusters V and VI. In selecting genotypes for initiating any breeding programme one should also consider the *per se* performance of those genotypes for yield and yield contributing characters along with genetic diversity. It was evident that the cluster III recorded highest mean values for cane yield as well as for juice quality characters indicating the superiority of genotype, 93 V 297 for both yield and quality traits. The cluster III had the maximum genetic distance with cluster VI followed by cluster II and cluster I. Cluster V comprising of single genotype 2000 V 59 has also recorded good mean values for yield and quality. The cluster V recorded the maximum genetic distance with cluster VI followed by cluster II and cluster IV. Based on good *per se* performance for majority of yield contributing characters and juice quality characters, genotype, 93 V 297 from cluster III may be used in hybridization with genotypes 2002 V 48 and 2008 V 257 from cluster VI, genotype, 2010 V 32, from cluster II and genotypes, 81 V 48, 83 V 15, 91 V 83, 2003 V 46 and 2007 V 127, from cluster I. Similarly genotype, 2000 V 59 from cluster V could be used in hybridization with genotypes, 2002 V 48 and 2008 V 257, from cluster VI, genotype, 2010 V 32, from cluster II and genotype, 2009 V 127, from cluster IV to get superior hybrids. The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence in sugarcane has been studied by Srivastava *et al*. (1999), Pathak *et al.* (2000), Ravishankaran *et al.* (2003), Singh *et al.* (2004), Silva *et al.* (2005), Muhammad and Ahmad (2007), Mali *et al.* (2009), Ahmed and Obeid (2010), Tahir *et al*. (2013), Brasileiro *et al.* (2014), Sanghera *et al*. (2015), Tena *et al.* (2016), Agrawal and Kumar (2017), Patil *et al.* (2017) and Krishna *et al.* (2018).

LITERATURE CITED

Agarwal R K and Kumar B 2017 Variability, heritability and genetic advance for cane yield and its contributing traits in sugarcane clones under waterlogged condition. *International Journal of Current Microbiology and Applied Sciences*. 6(6): 1669-1679.

Ahmed A O and Obeid A 2010 Genetic divergence among sugarcane genotypes (*Saccharum* spp.) for cane yield attributes and quality determinants. *African Journal of Agicultural Research*. 5(16): 2103-2107.

Brasileiro B P, Marinho C D, Costa P M A, Moreira E F A, Peternelli L A and Barbosa M H P 2014 Genetic diversity in sugarcane varieties of Brazil based on the Ward-modified location model clustering strategy. *Genetics and Molecular Research*. 13(1): 1650-1660.

Krishna B, Kamat D N, Kumari J and Prakash D 2018 Genetic divergence of sugarcane under waterlogging conditions. *International Journal of Pure and Applied Bioscience.* 6(1): 210-218.

Mahalanobis P C 1928 A statistical study at Chinese head measurement. *Journal of Asiatic Society of Bengal*. 25: 301-307.

Mali S C, Patel A I, Patel D U and Patel C L 2009 Variability, correlation, path analysis and genetic divergence in sugarcane. *Research on Crops*. 10(2): 343-350.

Muhammad K and Ahmad F K 2007 Divergence in sugarcane (*Saccharum officinarum* L.) based on yield and quality traits. *Pakistan Journal of Botany*. 39(5): 1559-1563.

Pathak A D, Natarajan U S and Kulshreshtha N 2000 Divergence studies among sugarcane (*Saccharum* spp.). *Annual Agricultural Research*. 21(3): 410-412.

Patil P P, Patil S S and Patel D U 2017 Genetic diversity in sugarcane (*Saccharum* spp. complex). *Journal of Pharmacognosy and Phytochemistry*. 6(6): 570-573.

Rao C R 1952 *Advanced Statistical Methods in Biometrical Research.* John Wiley and Sons INC., New York. 357-363.

Ravishankaran C R, Klakarni R S, Ramappa B N and Prakash P 2003 Genetic diversity among sugarcane (*Saccharum* spp.) accessions. *Environment & Ecology*. 21(4): 951-954.

Sanghera G S, Tyagi V, Kumar R, Thind K S and Sharma B 2015 Genetic variability, association and their dissection through path analysis for cane yield and its component traits in early maturing sugarcane clones. *Journal of Science*. 5(1): 28-34.

Silva C M, Vidigal M CG, Filho P S V, Scapim C A, Daros E and Silverio L 2005 Genetic diversity among sugarcane clones (*Saccharum* spp.). *Acta Scientiarum Agronomy*. 27(2): 315-319.

Singh R K and Chaudhary B D 1977 *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi: 215-218.

Singh P K, Kumar S and Singh J 2004 Genetic divergence in *saccharum* spp. germplasm under subtropics. *Indian Sugar*. 53(1): 903-906.

Srivastava H M, Srivastava S, Kumar R and Mishra G P 1999 Genetic diversity among interspecific hybrids of sugarcane. *Sugar Technology* 1(1/2): 19-22.

Tahir M, Rahman H, Ali A and Khalid M 2013 Genetic divergence in sugarcane genotypes. *American Journal of Experimental Agriculture*. 3(1): 102-109.

Tena E, Mekbib F and Ayana A 2016 Heritability and correlation among sugarcane (*Saccharum* spp.) yield and some agronomic and sugar quality traits in Ethiopia. *American Journal of Plant Sciences*. 7: 1453-1477.

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