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Genetic diversity in sugarcane (*Saccharum* spp. Complex)

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Abstract

A quantitative assessment of genetic diversity for sixteen characters of sugarcane has been worked out by Mahalanobis D^2 statistics. The studies included thirty genotypes of sugarcane obtained from different ecogeographical regions of India, which showed that there was a substantial genetic diversity between the genotypes with inter cluster distance (D) values ranging from 4.29 to 13.99. Thirty genotypes were grouped into fifteen clusters. The clustering pattern revealed that genetic diversity was not necessarily associated with geographical diversity in this crop. The hybridization programme has been suggested on the basis of inter cluster divergence and cluster means for the character studied.

Keywords: genetic divergence, cluster distance, Mahalanobis D^2 statistics, hybridization

Introduction

Development of new varieties is mainly governed by the magnitude of genetic variability in the base material and the extent of variability for desired characters. Genetic variability and divergence are of great interest to the plant breeder as they play a vital role in framing a successful breeding programme. The genetically diverse parents are likely to produce high heterotic effects and larger frequency of better desirable segregants in subsequent generations. The choice of genetically diverse parents is important in hybridization programme to create variation for selection of useful recombinants. D^2 statistic developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among genotypes in any crop. Hence, an attempt has been made to study the genetic divergence in thirty genotypes of sugarcane.

Material and Methods

Thirty genotypes of sugarcane were grown in a randomized block design with three replications at Main Sugarcane Research Station, Navsari Agricultural University, Navsari-396 450 (Gujarat) during 2010-11 and 2011-12 by creating four environments. The gross plot size for each genotype was consisted of five rows each of six meter length with row to row spacing of 90 cm and the net plot was consisted of middle 3 rows each of 5 meter length with row to row spacing of 90 cm (excluding 0.5 m ring line at both ends of the plot). The two budded setts of sugarcane were planted in rows keeping 12 buds per meter row length. The crop was raised under irrigated conditions following all the recommended package of practices and fertilizer application for environment 1 and environment 3 (250 kg N + 125 kg P_2O_5 + 125 kg K_2O per ha) while for environment 2 and environment 4 half dose of recommended fertilizer (125 kg N + 62.5 kg P_2O_5 + 62.5 kg K_2O per ha) along with acetobacter treatment as a drenching @ 2.5 lit/ha for nitrogen fixation was followed. Observations were recorded on yield components and quality traits viz., germination % at 45 days, tillers at 120 days (000/ha), shoots at 240 days (000/ha), stalk height at 360 days (cm), stalk diameter at 360 days (cm), internodes/stalk at 360 days, stalk weight at 360 days (kg), number of millable canes/ha (NMC) at 360 days (000/ha), cane yield at harvest (t/ha), juice brix % at 360 days, sucrose % juice at 360 days, juice purity % at 360 days, CCS % at 360 days, fibre % cane at 360 days, pol % cane at 360 days and sugar yield at 360 days (t/ha). The mean performance of individual genotypes over four environments was pooled and used for statistical analysis. Wilks criterion (Rao, 1952) ^[9] was used for the simultaneous test of homogeneity of the mean values of sixteen characters. The data were computed for applying Mahalanobis's D^2 statistics among all the possible combinations of 30 genotypes grouped into different clusters following canonical root method described by Rao (1952) ^[9].

Results and discussion

Analysis of variance showed significant differences among the genotypes for all the 16

characters studied. The calculated generalized distance (D) values ranged from 4.29 to 13.99 indicating the existence of considerable amount of genetic diversity among the genotypes studied. Thirty genotypes were grouped into fifteen clusters. The results of the present study revealed that the distribution of genotypes into different clusters was at random and no relationship was observed between geographical origin and genetic diversity as the genotypes developed from the different geographic regions were included in the same clusters (Table-1). Many workers have been arrived at similar conclusion for example Pathak *et al.* (2000)^[8], Ravishankaran *et al.* (2003)^[10] and Sajjad and Khan (2009)^[11].

The maximum inter cluster distance was observed between cluster V and XV (13.99). The minimum inter cluster distance was between cluster II and cluster IV (4.29) followed by cluster IV and cluster VI (4.58) (Table 2). The intra cluster distance ranged from 0.00 to 5.60. The maximum intra cluster distance was observed for cluster I (5.60). Higher intra cluster distance indicates higher diversity among the genotypes. The results are conformation with the research were reported by Pathak *et al.* (2000)^[8], Ravishankaran *et al.* (2003)^[10], Singh *et al.* (2004)^[13], Bakshiram and Hemprabha (2005)^[2].

Critical analysis of inter cluster distance indicated that cluster V and XV showed the maximum distance of 13.99 followed by between cluster V and XIV (13.36). High value of inter cluster distance points out towards high amount of diversity between the clusters involved, hence, the genotypes from the cluster V and XV are more divergent than any other cluster. The magnitude of heterosis largely depends on the degree of genetic diversity in the parental lines. Hence, the genotype belonging to the distinct cluster (V and XV) could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants.

The comparison of cluster means for the different characters (Table-3) indicated considerable difference existed between clusters for all characters. Cluster XV had maximum mean value for cane yield, stalk diameter at 360 days, internodes/stalk at 360 days, juice brix % at 360 days, pol % cane and CCS (t/ha), cluster XIV had maximum mean value for sucrose % juice at 360 days, CCS % at harvest and fibre % cane. Cluster XI had maximum mean value for stalk diameter at 360 days and second for germination % at 45 days and third ranking for stalk weight at 360 days and fibre % cane. Maximum mean value for stalk weight at 360 days was attained by cluster IX, whereas, in that same cluster CCS (t/ha) was on third position. Cluster VII had highest germination % at 45 days as well as juice purity % at 360 days while it had second position for character

internodes/stalk at 360 days. Cluster VI ranked first for stalk height at 360 days, whereas cluster V attained maximum shoots at 240 days and NMC at harvest. Singh *et al.* (2004)^[13] reported that single cane weight had the higher contribution in the genetic divergence of the materials examined. The clustering pattern could be utilized in crossing for recombination which may generate highest variability for various traits. The superior genotypes for breeding programme can also be selected on the basis of cluster means and to increase yield by inter crossing the genotypes of cluster XV for cane yield, stalk diameter at 360 days, internodes/stalk at 360 days, juice brix % at 360 days, pol % cane and CCS (t/ha), cluster XIV for sucrose % juice at 360 days, CCS % at harvest and fibre % cane, for stalk diameter cluster XI. However, for stalk weight at 360 days cluster IX and cluster VII for germination % at 45 days as well as juice purity % at 360 days and cluster VI for stalk height at 360 days, whereas cluster V for shoots at 240 days and NMC at harvest. Silva *et al.* (2005)^[12] observed that the number of stalks per plot and the brix were the characteristics that most contributed for the genetic variability. Singh *et al.* (2004)^[13] observed higher inter cluster distance which was observed between cluster VI and VII followed by V and VII. Ahmed and Obeid (2010)^[11] reported higher inter cluster distance between cluster IV and V while intra cluster distance within cluster VI and II was very low. These techniques help to quantify the amount of variability available in used genetic materials and also indicate groups of crop plants with similar or dissimilar genetic makeup. Also similar kind of results were reported by Hapse *et al.* (2011)^[4], Kumar and Kumar (2012)^[5] and Tahir *et al.* (2013)^[14].

In the present investigation germination % at 45 days (20.23 %), tillers at 120 days (13.10 %), stalk weight at 360 days (17.70 %) and CCS (t/ha) (11.72 %) were the main contributors to the total divergence (Table 4). Stalk height at 360 days, internodes/stalk at 360 days, stalk diameter at 360 days, fibre % cane, NMC at harvest, cane yield (t/ha), juice brix % at 360 days, juice purity % at 360 days, contributed moderately, whereas, sucrose % juice at 360 days, CCS % at harvest exhibited small contribution. However, characters shoots at 360 days had negligible contributors towards total divergence. Such type of results were reported by Bhakta (2010)^[3] and Patel (2012)^[12]

On the basis of above results and discussion, it can be concluded that hybridization between genotypes of variable clusters may produce wide spectrum of variation in the progenies.

Table 1: Distribution of 30 sugarcane genotypes to different clusters on the basis of D² statistics.

Clusters	No. of genotypes	Genotypes
I	16	Co 07006, Co 07020, CoSnk 07103, CoJn 07094, Co 85004, Co 07009, Co 07003, Co 07010, CoM 07083, Co 86032, CoJn 07093, Co 94008, Co 07007, Co 07008, Co 07015, PI 07132
II	1	CoSnk 07101
III	1	CoN 07073
IV	1	CoJn 07092
V	1	Co 07012
VI	1	CoSnk 07105
VII	1	Co 07017
VIII	1	CoVC 07061
IX	1	2005 N 699
X	1	CoSnk 07104
XI	1	MS 07081
XII	1	CoN 95132
XIII	1	PI 07131
XIV	1	Co 99004
XV	1	CoN 07072

Table 2: Intra and inter-cluster (D) values for 30 genotypes of sugarcane

Cluster	Group-1	Group-2	Group-3	Group-4	Group-5	Group-6	Group-7	Group-8	Group-9	Group-10	Group-11	Group-12	Group-13	Group-14	Group-15
I	5.6	6.2	6.59	7.24	6.98	8.59	8.62	6.51	8.92	7.21	8.45	7.76	8.3	9.35	11.55
II		0	6.77	4.29	8.02	4.92	4.68	6.66	8.12	6.24	6.58	7.23	7.19	8.38	9.11
III			0	6.12	4.84	8.68	8.94	5.4	9.96	8.86	9.73	9.63	8.82	11.16	11.92
IV				0	8.02	4.58	5.91	7.09	9.77	7.71	8.12	8.31	8.24	8.72	9.36
V					0	10.5	10.37	7.53	11.59	9.81	10.92	11.09	10.54	13.36	13.99
VI						0	6.33	7.02	10.09	6.54	8.22	7.46	7.84	7.72	9.25
VII							0	8.72	7.84	6.37	5.51	8.25	8.23	9.28	7.17
VIII								0	9.58	6.03	9.06	8.01	8.49	9.42	12.17
IX									0	6.66	6.27	6.75	8.07	9.52	7.73
X										0	5.83	5.69	7.18	8.49	9.23
XI											0	8.55	7.56	9.52	6.17
XII												0	6.16	6.1	8.94
XIII													0	7.45	8.47
XIV														0	9.46
XV															0

Table 3: Cluster means for sixteen characters in 30 genotypes of sugarcane.

Clusters	Germination % at 45 days	Tillers at 120 days (000/ha)	Shoots at 240 days (000/ha)	Stalk height (cm) at 360 days	Stalk diameter (cm) at 360 days	Internodes /stalk at 360 days	Stalk weight (kg) at 360 days	NMC at harvest (000/ha)	Cane yield (t/ha)	Juice brix % at 360 days	Sucrose % juice at 360 days	Juice purity % at 360 days	CCS %	Fibre % cane	Pol % cane	CCS (t/ha)
I	56.27	178.81	152.63	255.57	2.45	23.82	1.21	115.24	120.14	21.28	19.69	92.58	13.92	15.02	14.77	16.71
II	69.71	189.73	160.09	287.50	2.46	21.89	1.21	116.55	124.64	21.34	19.86	93.05	14.07	15.01	14.89	17.52
III	56.23	211.30	184.19	272.33	2.63	24.15	1.28	128.47	130.7	20.15	18.61	92.41	13.14	14.93	13.98	17.17
IV	65.92	206.90	181.09	282.75	2.51	24.94	1.15	125.68	127.6	21.88	19.87	90.82	13.92	15.05	14.9	17.78
V	62.32	207.39	191.78	231.83	2.45	22.69	1.14	133.70	123.94	20.36	19.02	93.41	13.49	14.77	14.31	16.73
VI	69.16	177.49	153.97	310.67	2.59	23.40	1.18	124.15	127.39	21.16	19.29	91.22	13.55	14.47	14.57	17.27
VII	74.80	195.07	166.91	276.17	2.49	26.71	1.21	115.13	131.29	20.56	19.23	93.55	13.65	15.01	14.42	17.93
VIII	55.76	176.22	151.30	282.00	2.64	25.47	1.26	118.79	133.12	19.56	18.04	92.21	12.73	14.35	13.64	16.92
IX	60.73	179.77	159.60	273.17	2.27	26.25	1.47	121.10	130.31	21.23	19.65	92.56	13.89	14.76	14.78	18.08
X	63.58	160.83	143.59	266.83	2.44	26.57	1.24	112.39	125.62	20.11	18.5	92.01	13.05	14.24	14.02	16.35
XI	71.65	165.33	145.19	244.08	2.68	25.74	1.35	117.71	131.86	21.08	19.38	91.92	13.66	15.07	14.52	18.01
XII	50.60	163.76	142.28	288.92	2.26	26.32	1.26	117.65	121.87	22.24	20.62	92.72	14.59	14.11	15.65	17.77
XIII	55.25	156.60	138.35	288.00	2.58	24.35	1.28	125.62	128.19	20.92	19.45	92.66	13.76	15.22	14.55	17.64
XIV	48.80	144.45	127.44	304.58	2.56	26.48	1.26	110.16	131.27	22.4	20.85	93.06	14.77	15.38	15.56	19.39
XV	68.73	181.91	159.84	264.75	2.68	26.73	1.42	127.10	137.24	22.53	20.76	92.16	14.64	14.56	15.66	20.09
Mean	61.97	179.70	157.22	275.28	2.51	25.03	1.26	120.63	128.35	21.12	19.52	92.42	13.79	14.80	14.68	17.69

Table 4: Contribution of different characters towards diversity in sugarcane

Sr. No.	Characters	Number of times ranked first	Contribution (%)
1	Germination % at 45 days	88	20.23 %
2	Tillers at 120 days (000/ha)	57	13.10 %
3	Shoots at 240 days (000/ha)	0	0.00 %
4	Stalk height (cm) at 360 days	42	9.66 %
5	Stalk diameter (cm) at 360 days	21	4.83 %
6	Internodes /stalk at 360 days	29	6.67 %
7	Stalk weight (kg) at 360 days	77	17.70 %
8	NMC at harvest (000/ha)	6	1.38 %
9	Cane yield (t/ha)	8	1.84 %
10	Juice brix % at 360 days	14	3.22 %
11	Sucrose % juice at 360 days	4	0.92 %
12	Juice purity % at 360 days	9	2.07 %
13	CCS % at harvest	2	0.46 %
14	Fibre % cane	19	4.37 %
15	Pol % cane	8	1.84 %
16	CCS (t/ha)	51	11.72 %

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References

- Ahmed AO, Obeid A. Genetic divergence among sugarcane genotypes for cane yield attributes and quality determinants. African J Agri. Res. 2010; 5(16):2103-2107.
- Bakshiram, Hemaprabha G. Genetic divergence of sugar yield and its components in flowering type of *Saccharum*

- officinarum* (L.). Agri. Sci. Digest. 2005; 25(2):118-120.
3. Bhakta RS. A Ph.D. thesis on Genetic evaluation in sugarcane (*Sachharum* spp. Complex) submitted to Navsari Agricultural University, Navsari, 2010.
 4. Hapse RS, Repale JM, Deshmukh RB. Genetic divergence in sugarcane (*Saccharum officinarum* spp.). Proc. Of 10th Joint Conv. Of STAI and DSTA, 2011, 240-244.
 5. Kumar S, Kumar D. Genetic diversity in sugarcane germplasm under sub-tropics. Scholarly J Agri. Sci. 2012; 2(8): 186-189.
 6. Mahalanobis PC. On generalized distance in statistics. Proc. Nat. Ins. India. 1936; 2:49-55.
 7. Patel DC. A. M.Sc. (Agri) thesis on “Genetic study for cane yield, sugar yield and their components in sugarcane (*Saccharum* spp. complex) submitted to Navsari Agricultural University, Navsari, 2012.
 8. Pathak AD, Natarajan US, Kulshreshtha N. Divergence studies among interspecific hybrids of sugarcane (*Saccharum* spp.). Ann. Agric. Res. 2000; 21(3):410-412.
 9. Rao CR. Advanced statistical methods in biometrical research. John Willey and Sons Inc. New York, 1952, 390.
 10. Ravishankaran CR, Kulkarni RS, Ramappa BN, Prakash P. Genetic diversity among sugarcane (*Saccharum* spp.) accessions. Environment and Ecology. 2003; 21(4):951-954.
 11. Sajjad M, Khan FA. Genetic diversity among sugarcane cultivars in Pakistan. American-Eurasian J Agric & Environ. Sci. 2009; 6(6):730-736.
 12. Silva CM, Goncalnes Vidigal MC, Vidigal FPS, Scapim CA, Daros E, Silverio L. Genetic diversity among sugarcane clones (*Saccharum* spp.) Acta Scietiarum Agronomy, 2005; 27(2):315-319.
 13. Singh PK, Kumar S, Singh J. Genetic divergence in *Saccharum* spp. germplasm under sub tropics. Indian Sugar. 2004; 53(11):903-906.
 14. Tahir M, Rahman H, Gul R, Ali A, Khalid M. Genetic divergence in sugarcane genotypes. American J. of Expt. Agriculture. 2013; 3(1):102-109.