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Darshana Patra
Department of Plant Breeding and Genetics, OUAT, Bhubaneswar, Odisha, India

PN Jagadev
Department of Plant Breeding and Genetics, OUAT, Bhubaneswar, Odisha, India

PK Nayak
Sugarcane Research Station (OUAT), Panipoila, Nayagarh, Odisha, India

Corresponding Author:
Darshana Patra
Department of Plant Breeding and Genetics, OUAT, Bhubaneswar, Odisha, India

Assessment of genetic divergence in sugarcane

Darshana Patra, PN Jagadev and PK Nayak

Abstract
Sugarcane is one of the important industrial multiproduct crop grown in India. The study of genetic diversity for twenty-two characters of sugarcane was carried out using Mahalanobis D^2 statistic. The genotypes of sugarcane obtained from different eco-geographical regions of India showed that there was a substantial genetic diversity between them with inter cluster distance (D) values ranging from 14.94 to 90.14. Forty-six genotypes were grouped into five clusters. The clustering pattern showed that the genetic diversity was not necessarily associated with its geographical diversity. These techniques help to quantify the variability available in used genetic materials and indicate groups of plants with similar or dissimilar genetic makeup.

Keywords: Genetic diversity, cluster distance, sugarcane, Mahalanobis D^2 statistic

Introduction
Sugarcane (Saccharum spp. complex) is an important industrial crop popular for its high concentrations of sugar, belonging to the family Poaceae, subfamily Panicoideae (Zan *et al*., 2020) [15]. Development of new lines mostly governed by the amount of genetic variability in the base material and the extent of variability for desired traits. Genetic diversity is important for sustainable production in crop species since greater losses of characteristics in any population may limit its chances of survival and requires greater human efforts for sucessful production. Due to evolution, minimal genetic diversity makes crops extremely susceptible to widespread biotic and abiotic stresses (Bisht *et al*., 2017) [2]. Genetically diverse parents are likely to give high heterotic effects with higher frequency of desirable segregants in advancing generations (Patil *et al*., 2017) [7]. The choice of genetically diverse parents is important in hybridization programme to create variation for selection of useful recombinants. D^2 statistics developed by Mahalanobis (1936) is a powerful tool to measure genetic divergence among genotypes in any crop. Hence, the investigation was made regarding the genetic divergence among the forty-six genotypes of sugarcane.

Materials and Methods
Forty-six genotypes of sugarcane were grown in a randomized block design with two replications at Sugarcane Research Station, Panipoila (Latitude - 19º54'- 20º32' N, Longitude - 84º29' - 85º27' E and altitude – 118m above mean sea level) is located at a distance of 12 km from the district headquarters, Nayagarh, Odisha University of Agriculture and Technology, Odisha during 2019-20 and 2020-21 by creating three environments. The plot size for each genotype was consisted of four rows each of six meter length with row to row spacing of 90 cm. The three 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. Observations were recorded on yield components and quality traits *viz*., germination % at 45 days, stalk height at 360 days (cm), stalk diameter at 360 days (cm), stalk weight at 360 days (kg), internodes/stalk at 360 days, internodal length at 360 days, tillers at 120 days (000/ha), shoots at 240 days (000/ha), number of millable canes/ha (NMC) at 300 days (000/ha), cane yield at harvest (t/ha), juice brix % at 300 and 360 days, sucrose % juice at 300 and 360 days, juice purity % at 300 and 360 days, CCS % at 300 and 360 days, fibre % cane at 360 days, pol % cane at 360 days and sugar yield i.e. CCS 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 oftwenty-two characters. The data were computed for applying Mahalanobis's D^2 statistics among all the possible combinations of forty-six genotypes grouped into different clusters following Tocher's method.

Results and Discussion

Analysis of variance showed significant differences among the genotypes for almost all the 22 characters studied.The calculated generalized distance (D) values varied between 14.94 to 90.14 indicating the existence of considerable amount of genetic diversity among the set of genotypes studied. Forty-six genotypes were grouped into five 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). Similar trends concluded by Pathak et. al. (2000) [8], Hapse *et al.* (2011) [4] and Sanghera *et al.* (2015) [11].

Table 1: Distribution of 46 sugarcane genotypes to different clusters on the basis of D^2 statistics

Clusters	No.of genotype (s)	Genotypes falling in the cluster
I	42	CoC 01061, CoA08323, CoC08336, 99NG 21, Co 86249, 86 V 96, CoOr11346, CoA08322, Co 06030, CoOr06346, CoA0 8321, PI 06376, CoOr05346, CoOr18346, 99NG 13, 99NG 07, 99NG 12, CoA92081, CoOr03151, Co 7508, 99NG 08, Co C09336, 99NG 16, Co 6907, CoOr17346, CoA06324, PC 31, Co 795, CoA07322, Co 87044, CoOr08346, Co 7219, Co Or13346, CoOr12346, CoOr04152, PC 36, CoC 08338, 99NG 17, CoOr10346, CoOr15346, CoC 08339, BP 14
II	1	CoOr03152
III	1	CoC 08337
IV	1	PI 09376
V	1	CoV 92102

The maximum inter cluster distance was observed between cluster IV and V (90.14). The minimum inter cluster distance was between cluster III and cluster IV (16.58) (Table 2). The intra cluster distance ranged from 0.00 to 14.94. The maximum intra cluster distance was observed for cluster I (14.94) which indicates higher diversity among the genotypes. Cluster IV and V showed the maximum distance of 90.14 followed by between cluster III and V (78.57). High value of inter cluster distance implied high amount of diversity between the clusters involved, hence, the genotypes from the cluster IV and V are more divergent than any other cluster. The magnitude of heterosis largely depends on the degree of genetic diversity in the parental lines (Ravishankaran *et al.*, 2013) [10]. Hence, the genotype belonging to the distinct cluster (IV and V) could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants.

Table 2: Intra cluster (in bold) and inter-cluster (D) genetic distances among five clusters of sugarcane

	Cluster I (42)	**Cluster II (1)**	**Cluster III (1)**	**Cluster IV (1)**	**Cluster V (1)**
Cluster I (42)	14.94	26.29	25.96	31.76	32.50
Cluster II (1)		0.00	40.47	69.92	23.53
Cluster III (1)			0.00	16.58	78.57
Cluster IV (1)				0.00	90.14
Cluster V (1)					0.00

The cluster means for the different characters (Table-3) showed that considerable difference existed between clusters for all characters. Cluster V had maximum mean value for cane yield, brix % at 360 days, pol % cane, CCS (t/ha), sucrose % juice at 360 days, CCS % at harvest and fibre % cane while cluster IV had maximum mean value for stalk diameter at 360 days, internodes/stalk at 360 days. Maximum mean value for stalk weight at 360 days was attained by cluster II, whereas, in that same cluster CCS (t/ha) was on fouth position. Cluster III had highest juice purity % at 360 days while it had second position for character internodes/stalk at 360 days. Cluster IV had maximum mean value for stalk diameter at 360 days, shoots at 240 days, NMC at harvest and second for stalk height at 360 days. Cluster V ranked first for stalk height at 360 days. Similarly, Singh *et al.* (2004) [13] found that single cane weight had the highest 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 I V for stalk diameter at 360 days, internodes/stalk at 360 days, sucrose % juice at 360 days, CCS % at harvest and fibre % cane. However, for stalk weight at 360 days cluster II and cluster V for germination % at 45 days as well as CCS (t/ha) and cluster V for stalk height at 360 days, whereas cluster IV 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. Ahmed and Obeid (2010) [1] showed higher inter cluster distance between cluster IV and V and low intra cluster distance within cluster VI and II. Also similar kind of results were reported by Kang *et al.* (2013) [5], Tahir *et al.* (2013) [14] and Chourasia *et al.* (2017) [3].

In the present investigation stalk weight at 360 days (15.24%), cane yield (14.54%), brix % at 300 days (11.45%), NMC (8.12%) and CCS % at 300 days (7.15%) were the main contributors to the total divergence (Table 3). CCS % at 360 days, internodal length at 360 days, stalk height at 360 days, fibre % cane, tillers at 120 days, juice brix % at 360 days, CCS (t/ha) contributed moderately, whereas stalk diameter at 360 days, internodes/stalk at 360 days, germination % at 45 days, sucrose % juice at 300 and 360 days, pol % at 360 days, juice purity % at 300 and 360 days exhibited small contribution. However, characters shoots at 240 days had negligible contributors towards total divergence. Such type of results were reported by Patil (2017) [7]. 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 3: Cluster means and relative contribution to D2 values of 22 characters in sugarcane

Sl. no.	Characters	Cluster I (42)	ClusterII (1)	ClusterIII (1)	ClusterIV (1)	ClusterV (1)	Mean	Contribution to D^2 values (%)
1	Germination per cent at 45DAP	42.99	39.92	42.54	39.05	49.86	42.87	1.06
2	Plant height (cm)	2.25	2.27	2.17	2.37	2.44	2.3	4.00
3	Cane Girth (cm)	2.32	2.12	2.24	2.45	2.23	2.27	1.74
4	Single Cane Weight (kg)	1.31	1.36	1.2	1.12	1.35	1.26	15.24
5	Number of internodes per cane	23.63	23.55	23.95	26.7	23.75	24.31	1.64
6	Internodal length (cm)	13.31	13.32	14.39	12.9	13.27	13.43	5.41
7	Number of tillers at 120DAP	113.28	103.12	117.21	103.68	118.95	111.24	3.00
8	Number of shoots at 240DAP	86.64	75.12	89.39	95.18	91.12	87.49	0.19
9	Number of millable canes	81.93	71.45	86.18	90.26	88.62	83.68	8.12
10	Cane Yield (t/ha)	87.91	75.65	87.35	83.58	98.3	86.55	14.54
11	CCS per cent at 10 monthss	19.88	20.63	19.49	19.16	20.77	19.98	7.15
12	Brix per cent at 10 months	26.66	26.86	25.58	25.46	27.72	26.45	11.45
13	Sucrose per cent at 10 months	24.4	25.09	23.75	23.44	25.47	24.43	2.00
14	Purity per cent at 10 months	62.5	64.83	63.32	62.57	63.28	63.3	3.00
15	CCS per cent at 12 months	20.05	20.84	19.62	19.35	20.89	20.15	5.45
16	Brix per cent at 12 months	26.72	26.95	25.64	25.51	27.78	26.52	2.10
17	Sucrose per cent at 12 months	24.56	25.29	23.87	23.62	25.59	24.58	1.10
18	Purity per cent at 12 months	67.69	70.5	69.36	68.49	67.89	68.78	0.61
19	CCS (t/ha) at 12 months	10.35	9.57	9.83	9.16	12.49	10.28	2
20	Pol per cent at 12 months	22.74	23.5	22.37	21.97	23.49	22.81	1.16
21	Fibre per cent at 12 months	21.76	20.61	20.91	22	21.84	21.42	4.5
22	Juice extraction at 12 months	46.5	47.16	46.76	46.9	47.56	46.97	4.54

Conclusion

As the demand of white sugar is continuously increasing owing to the rising population, breeders are prompt to enhance both cane productivity and sugar recovery by developing potential sugarcane clones through improvement. It is one of the cheapest technologies for boosting cane production, productivity and sugar recovery and this proceeds via choosing genetically diverse parents and selection of transgressive genotypes from segregating populations to evolve a new tailored variety. In the present study, divergence analysis was used to determine the genetic diversity among a set of sugarcane lines existing in India. All the forty six genotypes of sugarcane were grouped into five clusters based on D^2 statistics. Most of the clones remained in cluster 1 which indicates the low divergence due to the narrow genetic basis of these clones or the selection pressure put on these clones in previous clonal selection cycles. The clustering and genetic distance also gives a notion regarding development of the diverse genetic pool for successful breeding programme. The identified genotypes based on higher D^2 value are more diverse and hence can be used as parents for comprehensive hybridisation programme.

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