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D^2 analysis in sugarcane

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ABSTRACT

Genetic divergence is an efficient tool for the selection of parents used in hybridization programme. In the present study, twenty sugarcane genotypes consisting of high yielding sugarcane varieties/clones and related species and genera were raised. These were evaluated for ten cane yield and sugar yield and its attributing characters using Mahalanobis D^2 analysis, to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped into five clusters. Maximum number of genotypes (11 genotypes) was grouped in cluster I. Cluster II consists of five genotypes followed by cluster III with two genotypes. Cluster IV and V were represented by one genotype each. The maximum inter cluster distance was observed between cluster I and cluster V followed by cluster II and V. The greater distance between the two clusters indicates wider genetic diversity between genotypes. Hence, the genotypes in cluster I *viz., Saccharum officinarum* cv. Badila, Co 6907, Co 8021, Co. Si 95071, CoC 671, Co 86032, CoC 92061, Co G 93076, Co 99012 and Co 99008, cluster II *viz.,* Co 8371, Co 99004, Co 7219 and CoC 90063 had wider diversity with *Erianthus arundinaceum* in cluster V and these lines may be utilized in further breeding programme. The intra cluster distance was maximum in cluster II (1060.89) followed by cluster I (1050.00) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the ten characters studied, maximum contribution was made by sugar yield (50.00%) followed by brix per cent (20.00%), cane yield (8.42%) and cane weight (5.26%). Hence, these characters should be given importance during hybridization and selection in the segregating population.

Keywords: sugarcane, genetic diversity, yield

Introduction

Sugarcane is widely grown in the tropical and subtropical areas of the world. India occupies number one position in the world sugar production. It is an important source of sugar and other sweeteners. This crop accounts for about sixty per cent of the world's requirement of sugar. Sugarcane is also a major source of by-products which provide raw materials for the distilleries, pulp and paper industries. This is a multipurpose crop providing food, fuel and fibre. Sugarcane is classified under the family of poaceae, sub family Panicoideae and tribe Andropogneae. Linnaeus named sugarcane as *Saccharum officinarum* L. *Saccharum* and related species are very promiscuous, readily intercross with related genera and thought to have been evolved as a polyploid complex in Andropogoneae. Classification by various workers differed in the number of species included in the genus. Mukherjee (1957) coined the term *Saccharum* complex to embrace the genus *Saccharum* L., *Erianthus* Micx., *Sclerostachya* A. Campus and *Narenga* Bor. Heinz (1987) reviewed the taxonomy of *Saccharum* thoroughly and include six species in the genus. They are (a) *Saccharum officinarum* L. (2n=80), (b) *Saccharum barberi* (2n=110-120), (c) *Saccharum sinense* (2n=80-124), (d) *Saccharum spontaneum* (2n=40-128), (e) *Saccharum robustum* (2n=60 and 80) and (f) *Saccharum edule* (2n=60-80). All the genera and *Saccharum* species hybridize to some extent and form a large breeding pool. Considering the utilization of this crop for various purposes, development of high yielding varieties is essential. The success of any breeding programme depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability.

Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable

combinations in the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme. Keeping this in view, the present study was focused to assess the genetic diversity of twenty, genotypes of sugarcane using Mahalanobis (1936) [5] D^2 statistics (Arunachalam, 1981) [1].

Materials and methods

Twenty sugarcane (*Saccharum* complex) genotypes with high and high sugar content (varieties/clones species and related genera) were raised. The experiment was laid out in randomized block design with two replications. The genotypes were raised in plot of 5 rows with each row of 5 metre length and 0.8 M distance between rows. The recommended agronomic practices were followed. They were evaluated for ten characters including cane yield and sugar yield attributing characters *viz.*, cane length, internode length, number of millable cane, cane thickness, single cane weight, brix per cent, sucrose per cent, commercial cane sugar per cent (CCS%), cane yield and sugar yield. The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) [5] and grouping of varieties into clusters was done following the Tochers method as detailed by Rao (1952) [6] and described by Singh and Chaudhary (1979).

Results and discussion

Analysis of variance showed significant differences for all the ten characters studied among the genotypes (Table 1). Based on D^2 value, twenty genotypes were grouped into five clusters (Table 2). Maximum number of genotypes (11 genotypes) was grouped in cluster I. Cluster II consists of five genotypes followed by cluster III with two genotypes. Cluster IV and V were represented by one genotype each. The overall composition of the clustering pattern showed that genotypes collected from the same origin were distributed in different clusters. Similar results were observed by Jose Marcelo *et al.* (1991) [4] and Cornide *et al.* (1999) [2].

The intra and inter cluster distance are presented in Table 3. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distanced was observed between cluster I and cluster V (57616.05) followed by cluster II and V (56018.68) indicating wider genetic diversity among the genotypes in these clusters. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. The minimum inter cluster distance was found between cluster I and II (1168.08). The genotypes in these clusters are genetically very close and hence, will not give fruitful results.

The maximum intra cluster distance was observed in cluster II (1060.89) followed by cluster I (1050.00) indicating limited genetic diversity among genotypes representing these clusters. Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of improvement through intervarietal hybridization. The cluster IV and V considered of only one genotype hence, they lack intra-cluster distance (0.00).

Table 1: ANOVA for ten characters in 20 genotypes

Source	df	Cane length	Internode length	NMC	Cane thickness	Cane weight	Brix (%)	Sucrose (%)	CC (%)	Cane yield	Sugar yield
Replication	1	462.4000	0.8703	1199.0250	0.2890	0.397	2.4602	1.4251	1.5406	6227.0194	135.0930
Treatment	19	9241.6368*	26.2880*	4888.6039*	1.8192*	0.7563*	68.9751*	71.9812*	40.3744*	19711.2539*	360.0503*
Error	19	16.6105	0.229	9.7092	0.0037	0.0006	0.0719	0.1069	0.0854	64.7857	3.0485

*Significant at 1% level

Table 2: Distribution of sugarcane genotypes in different clusters

Cluster No.	No. of genotypes	Name of the genotypes
I	11	*Saccharum officinarum* cv. Badila
		Co 6907
		Co 8021
		CoSi 95071
		CoC 671
		Co 86032
		CoC 85061
		CoC 92061
		CoG 93076
		Co 99012
		Co 99008
II	5	Co 8371
		Co 99004
		Co 99006
		Co 7219
		CoC 90063
III	2	*Narenga porphyrocoma*
		Miscanthus sacchariflorus
IV	1	*Saccharum spontaneum*
V	1	*Erianthus arundinaceum*

Table 3: Average intra and inter cluster distance of various clusters in sugarcane

Clusters	I	II	III	IV	V
I	1050.00 (32.40	1168.08 (34.18)	2326.51 (152.54)	23545.29 (13.45)	57616.05 (240.03)
II		1060.89 (32.57)	23121.76 (152.06)	22982.14 (151.60)	56018.68 (236.68)
III			635.98 (25.22)	1709.10 (41.34)	25819.67 (160.69)
IV				0.00 (0.00)	17655.69 (132.88)
V					0.00 (0.00)

Table 4: Cluster mean and contribution of various characters towards divergence in sugarcane

Character/ cluster	Cane length (cm)	Internode length (cm)	Number of millable cane per plot	Cane thickness (cm)	Cane weight (kg)	Brix (%)	Sucrose (%)	Commercial cane sugar (%)	Cane yield per plot (kg)	Sugar yield per plot (kg)
I	200.96	8.01	169.64	2.93	1.59	20.30	16.96	11.56	270.64	31.24
II	189.40	7.55	152.90	2.94	1.66	18.45	14.92	9.86	252.65	25.06
III	72.25	12.45	297.75	0.40	0.04	6.02	2.18	0.47	12.84	0.06
IV	99.00	13.60	252.50	0.75	0.26	5.54	2.08	0.55	64.41	0.35
V	396.00	22.50	221.00	1.90	0.46	6.16	2.28	0.55	100.78	0.56
Grand mean	189.85	9.34	184.98	2.52	1.33	16.96	13.50	8.93	221.56	23.50
Contribution towards divergence (%)	2.11	0.53	4.21	3.68	5.26	20.00	1.58	4.21	8.42	50.00

The average cluster wise mean values for different characters are presented in Table 4. Which can be used to assess the superiority of clusters, which could be considered in the improvement of various characters through hybridization programme. Cluster I with eleven genotypes exhibited highest mean value for brix per cent (20.30), sucrose per cent (16.96), commercial cane sugar per cent (11.56), cane yield (270.64) and sugar yield (31.24) followed by cluster II in brix per cent (18.45), sucrose per cent (14.92), commercial cane sugar per cent (9.86), cane yield (252.65) and sugar yield (25.06). Also cluster II recorded maximum mean values for cane thickness (2.94) and cane weight (1.66) followed by cluster I in cane thickness (2.93) and cane weight (1.59). Cluster V exhibited superior mean performance for cane length (396.00) and internode length (22.50). The highest mean value for number of millable cane was recorded by cluster III (297.75) followed by cluster IV (252.50).

None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. However, cluster I recorded desirable mean value for brix per cent, sucrose per cent, commercial cane sugar per cent, cane yield and sugar yield. Hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Based on the *per se* performance of the best genotypes within the clusters, they may be used as potential parents in hybridization programme.

The contribution of each character to total divergence is presented in Table 4. Among the ten characters studied, sugar yield contributed maximum divergence (50.00%) followed by brix per cent (20.00), cane yield (8.42%) and cane weight (5.26%). The minimum percentage of contribution was observed in internode length (0.53) followed by sucrose per cent and cane length (2.11%). The characters sugar yield, brix per cent and cane yield contributed 78.42 per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

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