



## Genetic diversity studies in sweet sorghum [*Sorghum bicolor* (L.) Moench] based on quantitative traits

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**Abstract :** From the genetic diversity studies based on 17 morphological characters of 52 sweet sorghum genotypes it could be inferred that, the that the maximum contribution to the genetic divergence was accounted by sucrose per cent followed by plant height, juice weight, stay green trait, fresh cane weight, days to fifty per cent flowering, sucrose yield, brix per cent, millable cane weight, stem girth and juice volume. The constellation pattern of the fifty two genotypes was grouped into ten clusters indicated that the distribution of genotypes into different groups did not follow any defined pattern with regard to their origin. Clusters IV, V, VI, VII, VIII, and X may be useful for exploitation of hybrid vigour for traits like plant height, millable cane weight, juice yield and sucrose yield. The genotypes from these clusters may serve as potential genotypes to improve these traits. The genotypes from the selected clusters having outstanding mean performance may serve as potential genotypes for future breeding programme.

**Key Words :** Sweet sorghum, Diversity, Cluster, Dendrogram

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### INTRODUCTION

Sweet sorghum [*Sorghum bicolor* (L.) Moench] is a diploid species ( $2n = 20$ ) that is closely related to sugarcane, a polyploid species. An important crop in many parts of the world is grown for food, feed and industrial purposes. The first step in any plant breeding program is the study of genetic variability. Knowledge of the existing phenotypic and genetic variation and the association between such components and their heritability is of interest, not only from a theoretical point of quantitative inheritance of characters, but also of practical value for simultaneous selection of two or more traits and developing appropriate selection strategies (Kenga *et al.*, 2006). Therefore, under present investigation, effort was made to understand the quantum and nature of genetic variability present in a set of 52 elite sweet sorghum accessions.

### MATERIALS AND METHODS

For this study 52 accessions of sweet sorghum were

selected from sorghum gene bank at Department of Millets, Tamil Nadu Agricultural University, India. All the genotypes were evaluated during summer 2011. The experiment was laid out in a randomized block design (RBD) with two replications. The list of accessions taken for study is appended in Table A. Each genotype was sown in single row of 4m length with a spacing of 60 cm x 15 cm. The data were recorded on five random plants from each genotype in each replication for seventeen characters *viz.*, days to fifty per cent flowering, days to physiological maturity, plant height, stem girth, internode length, number of leaves, brix per cent, stay green trait fresh cane weight, millable cane weight, juice weight, juice volume, sucrose percentage, juice extractability percentage, cane yield, juice yield, sucrose yield.  $D^2$  analysis was carried out using all the twelve characters and generalized distance ( $D^2$ ) was calculated for each pair of genotypes. A method suggested by Tocher (Rao, 1952) was used to group the genotypes into different clusters based on the  $D^2$  values.

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**Table A : List of sweet sorghum accessions taken for genetic diversity studies**

Sr. No.	Accessions No.	Sr. No.	Accessions No.
1.	K05 22	27.	K05 235
2.	K05 27	28.	S03 238
3.	K05 29	29.	K05 244
4.	K05 30	30.	K05 240
5.	K05 51	31.	K05 242
6.	K05 53	32.	K05 247
7.	K05 56	33.	K05 264
8.	K05 60	34.	S03 263
9.	K05 69	35.	SS 265
10.	K05 144	36.	K05 267
11.	S03 146	37.	K05 273
12.	K05 154	38.	K05 278
13.	S03 155	39.	S03 281
14.	K05 156	40.	K05 289
15.	S03 173	41.	K05 291
16.	K05 176	42.	K05 296
17.	K05 181	43.	K05 302
18.	K05 183	44.	K05 303
19.	K05 184	45.	K05 311
20.	K05 190	46.	K05 312
21.	K05 192	47.	K05 365
22.	K05 199	48.	K05 SS 1143
23.	K05 200	49.	K05 SS 1173
24.	K05 201	50.	S03 479
25.	K05 224	51.	RSSV 9
26.	K05 226	52.	SSV 84

## RESULTS AND DISCUSSION

Using Tocher's method, 52 genotypes were grouped into clusters 10 clusters based on  $D^2$  values. Among 10 clusters, cluster I was the largest with 30 genotypes followed by cluster VIII with 14 genotypes. Cluster VI had 7 genotypes. Cluster IX and X had 3 genotypes each, respectively. Cluster II, III, IV and V had one genotype each. The clustering composition and the distribution of genotypes into different clusters are presented in Table 1. Fifty two sweet sorghum accessions were used to construct dendrogram based on Jaccard's coefficient and the results are presented in Fig. 1. Average values of intra and inter cluster D square distances are given in Table 2 and in Table 3 cluster mean value of 17 quantitative characters of sweet sorghum is given.

Maximum difference among the genotypes within the same cluster (intra cluster) was shown by cluster X (22.7) followed by cluster IX (19.71), VI (15.41), VIII (14.50) and I (14.29). Cluster II, Cluster III, Cluster IV, Cluster V, and Cluster VI had zero cluster distances. Diversity among the clusters varied with inter cluster D square values of 42.00 to 7.57. Inter

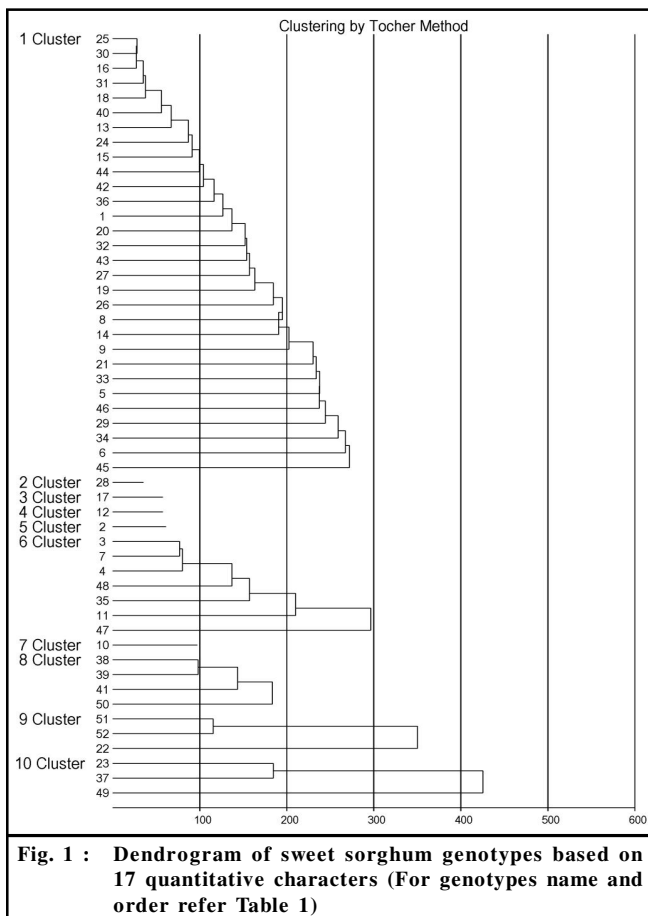
cluster distance, was the highest between cluster III and cluster X (42.00) followed by VII and X (40.10), and VIII and X (38.79), IV and X (37.45), II and X (37.40), V and X (35.21), I and X (34.91), IX and X (34.29), VII and IX (34.33), V and IX (34.32) and least between clusters II and III (7.57) followed by II and IV (7.82).

**Table 1 : Grouping of sweet sorghum genotypes into different clusters by Tocher's method**

Sr. No.	Cluster No.	Number of Genotypes	Genotypes
1.	I	30	K05 224, K05 240, K05 176, K05 242, K05 183, K05 289, S03 155, K05 201, S03 173, K05 303, K05 296, K05 267, K05 53, K05 22, K05 190, K05 247, K05 302, K05 235, K05 184, K05 226, K05 60, K05 156, K05 69, K05 192, K05 264, K05 51, K05 312, K05 244, S03 263, K05 311
2.	II	1	S03 238
3.	III	1	K05 181
4.	IV	1	K05 154
5.	V	1	K05 27
6.	VI	7	K05 29, K05 56, K05 30, SS 265, K05 1143, K05 365, S03 146
7.	VII	1	K05 144
8.	VIII	4	K05 278, S03 281, K05 291, S03 479
9.	IX	3	SSV 84, RSSV 9, K05 199
10.	X	3	K05 200, K05 273, K05 SS 1173

Among the clusters, Cluster IV showed high mean value for fresh cane weight (0.88 kg), millable cane weight (0.64 kg), cane yield (53.24 t/ha) and sucrose yield (1.5 t/ha). Cluster VIII showed high mean value for juice weight (0.22 kg), juice volume (0.24 l), juice extraction percentage (44.77) and juice yield (18.61 t/ha). Cluster X had higher mean value for stay green trait (3.47) and days to fifty per cent flowering (72.67). Cluster V showed the high mean value for internode length (20.50). Cluster VII showed the high mean value for plant height (292.95 cm) and brix percentage (22.50). Cluster VI showed the high mean value for number of leaves (11.35 cm). Cluster X had lowest mean value for internode length (14.71 cm), number of leaves (9.22), fresh cane weight (0.33 kg), millable cane weight (0.17 kg), juice weight (0.06 kg), juice volume (0.07 l), cane yield (13.89 t/ha), juice yield (5.22 t/ha) and for sucrose yield (0.16 t/ha). Cluster VII had lowest mean value for stay green trait (1.25). Cluster V had lowest mean value for days to physiological maturity (89) and for stem girth (1.28) and for sucrose per cent (1.95). Cluster IV had lowest mean value for juice extraction percentage (27.50). Cluster VI had lowest mean value for brix percentage (16.44) and sucrose yield (0.16 t/ha).

The bolded numbers are the highest and lowest mean



**Fig. 1 : Dendrogram of sweet sorghum genotypes based on 17 quantitative characters (For genotypes name and order refer Table 1)**

values

The per cent contribution of each character towards divergence is presented in Table 4. It was observed that maximum contribution of traits towards genetic divergence was made by sucrose per cent (46.61%), plant height (15.31%), juice weight (13.88 %), stay green trait (4.45 %), fresh cane weight (3.09 %), days to fifty per cent flowering (2.19%), sucrose yield (2.64%), days to physiological maturity (1.96%), brix per cent (1.43 %), millable cane weight (1.36%), stem girth (1.21 %) and juice volume (1.14). Traits like number of leaves (0.60%), internode length (0.38), juice yield (0.38 %) and cane yield (0.15%) contributed little to genetic divergence.

The hierarchial cluster analysis of quantitative traits with 52 selected accessions formed ten clusters which indicated the existence of high level of genetic diversity among the genotypes. The cluster analysis suggested the resolution of fifty two genotypes into ten clusters following Tocher's method of clustering, indicating wide diversity in the experimental material for majority of the characters.

The success in obtaining highly heterotic hybrids and creating greater variability for efficient selection of useful recombinants in a breeding programme depends to a large extent on the degree of divergence between the parents

Cluster	Genotype	1	2	3	4	5	6	7	8	9	10		
1 Cluster	25	X											
	30		X										
	16			X									
	31				X								
	18					X							
	40						X						
	13							X					
	24								X				
	15									X			
	44										X		
2 Cluster	20										X		
	32										X		
	43										X		
	3 Cluster	27										X	
		19										X	
		26										X	
		8										X	
		4 Cluster	14										X
			9										X
			21										X
33												X	
5												X	
46												X	
29											X		
34											X		
6											X		
45											X		
5 Cluster	28										X		
	6 Cluster	17										X	
		12										X	
		7 Cluster	2										X
			3										X
			7										X
			48										X
			35										X
			11										X
			47										X
8 Cluster			10										X
	38											X	
	39											X	
	41										X		
	50										X		
	9 Cluster	51										X	
		52										X	
		22										X	
		10 Cluster	23										X
			37										X
49												X	

Table 3: Cluster mean values for 17 characters in 52 genotypes of sweet sorghum

Cluster	Days to 50% flowering	Days to 50% physiological maturity	Days to 50% flowering	Stem weight (g)	No. of leaves	Stay green trait	Brix %	Plant height (cm)	Variable among genotypes (g)	Juice weight (kg)	Volume (litre)	Sucrose %	Juice extraction %	Cane yield (t/ha)	Juice yield (t/ha)	Sucrose yield (t/ha)
I	55.33	101.72	270.37	1.61	17.57	19.06	19.06	0.62	0.72	0.73	0.77	6.18	37.79	37.77	10.83	0.66
II	55.50	107.00	263.73	1.63	15.33	20.20	20.20	0.65	0.71	0.72	0.73	10.32	29.57	37.37	10.77	1.11
III	57.00	101.50	287.25	1.57	15.71	21.20	21.20	0.66	0.73	0.75	0.76	11.63	35.77	35.72	12.50	1.75
IV	53.50	107.00	273.75	1.77	17.33	21.75	21.70	0.83	0.67	0.77	0.78	10.20	27.87	33.37	17.59	1.50
V	55.50	89.00	262.75	1.28	20.50	17.75	18.60	0.61	0.30	0.72	0.73	1.95	39.82	25.00	10.00	0.20
VI	50.25	95.50	252.39	1.37	19.05	23.71	16.77	0.75	0.27	0.65	0.67	3.35	27.37	22.77	5.29	0.16
VII	53.00	105.00	292.25	1.69	20.38	17.25	22.50	0.77	0.78	0.75	0.76	2.37	32.55	70.00	13.00	0.37
VIII	57.00	100.63	275.07	1.82	19.37	22.55	18.33	0.78	0.56	0.22	0.27	7.22	17.77	76.57	18.67	0.77
IX	50.50	98.50	279.72	1.92	17.88	17.80	17.30	0.68	0.75	0.76	0.77	10.23	37.35	37.72	13.77	1.36
X	72.67	107.00	157.08	1.37	17.77	37.77	15.80	0.33	0.77	0.65	0.67	3.73	38.02	19.89	5.22	0.16

Table 4 : Per cent contribution of different characters towards divergence

Sr. No.	Characters	Times ranked first	Percentage contribution (%)
1.	Days to 50% flowering	29	2.19
2.	Days to physiological maturity	26	1.96
3.	Plant height (cm)	203	15.31
4.	Stem width(cm)	16	1.21
5.	Internode length(cm)	5	0.38
6.	No. of leaves	8	0.60
7.	Stay green trait	59	4.45
8.	Brix %	19	1.43
9.	Fresh cane weight (kg)	41	3.09
10.	Millable cane weight (kg)	18	1.36
11.	Juice weight(kg)	184	13.88
12.	Juice volume (Litre)	19	1.43
13.	Sucrose %	618	46.61
14.	Juice extraction %	39	2.94
15.	Cane yield (t/ha)	2	0.15
16.	Juice yield (t/ha)	5	0.38
17.	Sucrose yield (t/ha)	35	2.64

chosen (Murthy and Tiwari, 1965). For exploiting heterosis as a means of increasing production, it is necessary to utilize parents with maximum genetics divergence. The more diverse in the parents more are the chances of pronounced heterotic effects and increased spectrum of variability in the segregating generation.

The mean performance of juice weight, juice volume, juice extraction percentage and juice yield were highest for cluster IV. Cluster VIII showed high mean value for juice weight, juice volume, juice extraction percentage and juice yield. Cluster X had higher mean value for stay green trait and days to fifty per cent flowering. Cluster V showed the high mean value for number of days to physiological maturity and internode length. Cluster VII showed the high mean value for plant height and brix percentage. Cluster VI showed the high mean value for number of leaves. Thus, the various genotypes in different clusters which recorded outstanding mean performance for different traits, may be used as potential parents and could be utilized in hybridizing programme of sweet sorghum for improving the yield and performance of trait of interest. For developing varieties and hybrids with high juice and sucrose content genotypes of cluster IV (K05 154) and genotypes of VIII (K05 278, K05 291, S03 281 and S03 479) can be used.

The constellation pattern of the fifty two genotypes was grouped into ten clusters indicated that the distribution of genotypes into different groups did not follow any defined

pattern with regard to their origin. This might be due to free exchange of genetic stocks among the different regions. Though the cluster grouped the genotypes with greater similarity for quantitative characters, they did not necessarily include the genotype from the same source of origin.

Clustering pattern of genotypes of the same habitat into different clusters could be due to different genetic nature of parents from which they were derived or due to the selection pressure applied on same characters in selection process. Distribution of genotypes of same geographical regions into different clusters indicated that geographical location has no influence on the genetic architecture of the variety.

Several authors have suggested that the crossing between the genotypes of clusters with high inter cluster would yield good segregants for selection (Rao, 1972; Prasad Rao *et al.* 1989, Vidyabhushanam *et al.*, 1989). Hybridization programme of genotypes belonging to clusters IV, V, VI, VII, VIII, and X may be useful for exploitation of hybrid vigour for traits like plant height, millable cane weight, juice yield, sucrose yield. The genotypes from the selected clusters having outstanding mean performance may serve as potential genotypes for future breeding programme.

In addition to general features of variation and divergence, this study also provides the information on the potent characters that contributes to the divergence between the genotypes. It was found that the maximum contribution to the genetic divergence was accounted by sucrose per cent followed by plant height, juice weight, stay green trait, fresh cane weight days to fifty per cent flowering, sucrose yield, brix per cent, millable cane weight, stem girth and juice volume.

The low contribution to genetic divergence by other characters may be due to selection towards uniformity in these characters.

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