

Genetic Divergence Analysis in Sorghum (*Sorghum bicolor L.*)

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ABSTRACT

Genetic divergence on 20 genotypes of sorghum were studied through Principal Component Analysis, Non-Hierarchical Clustering Canonical Vector Analysis and D² statistics. The genotypes were grouped into four clusters. The cluster I contained the maximum number (11) and the cluster II contained the minimum number (2). The highest inter cluster distance (27.33) was estimated between cluster I and cluster III and that of the lowest (12.22) between cluster II and cluster III. The highest intra cluster distance (2.25) was calculated against the cluster I and the lowest (0.86) against cluster IV. The cluster I had the highest value (121.94 days) for days to maturity. The cluster II had the highest values for panicle length, 1000-grain weight and grain yield and the lowest value for number of tillers per plant. Early maturing and dwarf genotypes were included in cluster III. Therefore, crosses between genotypes belonging to cluster II with those of cluster III might produce high heterosis in regards to yield and earliness. On the basis of intercluster distance, cluster means and *per se* performance G4(BD4670), G6(BD4678), G8(BD4680) and G16(BD432) were identified as suitable for hybridization programme.

Key words: Genetic divergence, Cluster analysis, Sorghum.

INTRODUCTION

Sorghum (*Sorghum bicolor L.*) is popularly known as *jowar*, the most important food and fodder crop for dryland agriculture. With the production of about 68 million tons per year, sorghum ranks the fifth most important cereal crop in the world. It was originated in the North-Eastern quadrant of Africa, where high genetic variability was found in wild and cultivated species (Zeller, 2000). In India, sorghum grain has included in human either by breaking the grain for cooking it in the same way as rice or by grinding it into flour and preparing '*chapatis*'. It is also eaten as parched and popped grain to some extent. This grain is also fed by cattle, poultry and swine. Sorghum grain contains about 10-12 per cent protein, 3 per cent fat and 70 per cent carbohydrate; therefore, it is comparable to other grains in the feeding programme for dairy cattle, poultry and swine. Its industrial use has tremendous scope. Sorghum shows considerable differences in plant, panicle and grain characteristics which are greatly influenced by environment (Ezeaku *et al.* 1997). Genetic diversity is essential to meet the diverse goals such as producing cultivars with increased yield, wider adaptation, desirable quality, pest and disease resistance etc. Inclusion of more diverse parents (within a limit) in hybridization is supposed to increase the chance of obtaining maximum heterosis with broad spectrum of variability in segregating generations. Keeping this in view, an attempt was made in the present study to analyze genetic diversity among sorghum genotypes.

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MATERIALS AND METHODS

Twenty sorghum germplasm were collected from Bangladesh Agricultural Research Institute (BARI), Joydevpur, Gazipur and grown at Sher-e-Bangla Agricultural University farm, Dhaka during November 2007 to March 2008. Randomized Complete Block Design (RCBD) with three replications was followed for this experiment. The plant spacing was 75 x 25 cm. The unit plot was 5 meter long with 4 rows. NPK fertilizers with 15:15:15 were applied as a basal dose at the rate of 300 kg per hectare (Ezeaku and Mohammed, 2006). The standard agronomic practices were followed to raise a good crop. Data from ten randomly selected plant in each plot were recorded on ten characters viz., plant height (cm), days to 50% flowering (days), days to maturity (days), number of tillers per plant, panicle length (cm), 100-grain weight (g) and grain yield per plant (g) and subjected to Principal Component Analysis and D^2 - statistic, using Genestat 5, Rekase 4.1 software program and with the help of the book Statistical and Biometrical Techniques in Plant Breeding by J. R. Sharma (2006).

RESULTS AND DISCUSSION

The twenty sorghum genotypes were fallen into four clusters on the basis of cluster analysis (Table 1). Singh *et al.* 2001 grouped 46 genotypes of sorghum into eight clusters. Maximum number of genotypes (11) were included into cluster I, followed by clusters III with four, cluster IV with three and cluster II with two genotypes.

Table 1. Distribution of 20 genotypes of sorghum in four clusters

Cluster	Number of genotypes	Name of genotypes
I	11	G1(BD 4658), G2(BD 4660), G3(BD 4662), G8(BD 4680), G9(BD 4682), G10(BD 4687), G14(BD 4691), G15(BD 4718), G16(BD 432), G17(BD 9133) and G18(BD 9135)
II	2	G4(BD 4670) and G11(BD 4688)
III	4	G5(BD 4676), G7(BD 4679), G12(BD 4689) and G19(BD 9138)
IV	3	G6(BD 4678), G13(BD 4690) and G20(BD 9148)

The average inter and intra cluster distances are presented in Table 2. The inter cluster distances in all of the cases were larger than the intra cluster distance indicating presence of wider diversity among the genotypes. The intra cluster distance was highest in cluster I and lowest in cluster IV suggested that genotypes in cluster I were highly diverse (heterogeneous) than those of other clusters and the genotypes in the cluster IV were relatively homogeneous. The highest inter cluster distance (27.33) was estimated between cluster I and III followed by I and II, I and IV suggesting wide genetic diversity among them. The lowest inter cluster distance (12.22) was computed between cluster II and III suggesting genotypes in these clusters were genetically closely related to each other.

Table 2. Average intra (Diagonal) and inter cluster distances (D^2) for 20 genotypes of sorghum

Cluster	I	II	III	IV
I	2.25	23.63	27.33	22.13
II		1.26	12.22	18.36
III			1.11	22.23
IV				0.86

The results presented in Table 3 showed that the mean value of cluster I had the highest mean for days to maturity (121.94 days) indicating late maturing genotypes were included in this cluster and cluster IV also contained late maturing genotypes. Cluster II had the highest values for panicle length, 1000-grain weight and grain yield and the lowest for number of tillers per plant. Early maturing and dwarf genotypes were included in cluster III but were with maximum number of tiller.

Table 3. Cluster means for seven characters of 20 genotypes of sorghum

Characters	Clusters			
	I	II	III	IV
Plant height (cm)	136.64	170.33	119.77	145.39
Days to 50% flowering	97.27	101.92	73.67	97.46
Days to maturity	121.94	120.75	105.00	121.50
No. of tillers per plant	5.73	4.75	8.34	5.42
Panicle length (cm)	19.63	21.41	14.24	18.75
1000-grain weight (g)	1.81	2.22	1.98	1.81
Grain yield per plant (g)	88.74	108.25	72.67	85.57

A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, reflecting in the relative position (Figure 1).

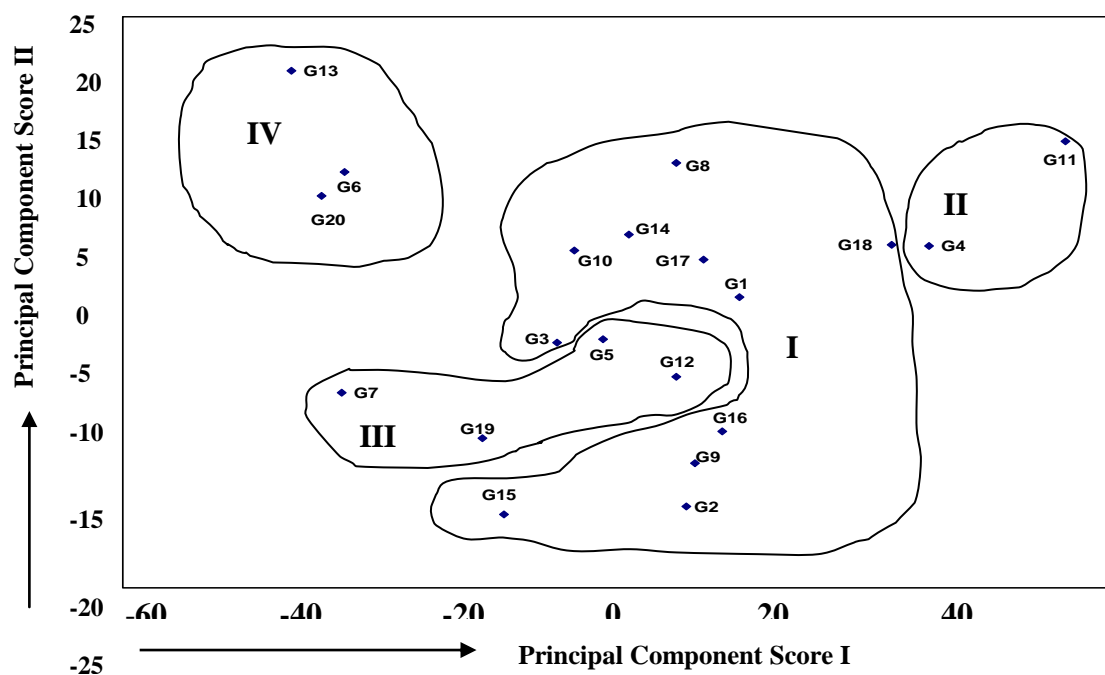


Figure 1. Scattered diagram of 20 genotypes of sorghum based on their principal component scores super imposed with respective clustering

As per scatter diagram the genotypes were apparently distributed into four clusters. It was also revealed that the genotypes of cluster III was more diverse from the genotypes under cluster II.

The canonical variate analysis displayed that the vectors (I and II) for panicle length, 1000-grain weight and grain yield per plant were contributed maximum towards divergence because both the vectors were positive across two axes (Table 4).

Table 4. Relative contribution of the seven characters to the total divergence of 20 genotypes of sorghum

Characters	Vector-I	Vector-II
Plant height (cm)	0.67134	-0.20947
Days to 50% flowering	0.33593	-0.54612
Days to maturity	0.13993	-0.51631
No. of tillers per plant	-0.03191	0.06229
Panicle length (cm)	0.09471	0.01508
1000-grain weight (g)	0.00527	0.01036
Grain yield per plant (g)	0.63785	0.62216

It is assumed that maximum percentage of heterosis is manifested in cross combination involving the genotypes belonging to the most distant clusters. In the present study, the maximum distance existed between cluster I and III. Therefore, the crosses between the genotypes belonging to cluster III with those of cluster I might produce high heterosis in terms of yield and earliness. On the basis of intercluster distance, cluster means and *per se* performance G4, G6, G8 and G16 were identified as suitable for hybridization programme.

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