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

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Abstract: Genetic divergence of 35 sorghum (*Sorghum bicolor* L.) genotypes was estimated using D^2 and principal component analysis for nine characters. The genotypes under study were grouped into 4 clusters. The cluster I contained the maximum number of genotype and the cluster III contained the minimum. The inter cluster distance in most of the cases were higher than the intra cluster distance indicating wider genetic diversity among the genotypes of different groups. The highest inter cluster distance between cluster III and IV followed by between III and V showing wide diversity among the groups. The highest intra-cluster distance was observed in cluster IV and lowest in cluster II. Days to maturity, number of tiller/plant and 1000 grain weight showed maximum contribution towards total divergence among the genotypes.

Key words: Genetic, divergence, sorghum

INTRODUCTION

Sorghum (*Sorghum bicolor* L.) is an important cereal crop in Bangladesh and ranks fifth among cereal crops^[1]. The crop is drought tolerant and moderately salt tolerant^[2] and it is the crop par excellence for dry areas^[3]. In Bangladesh, this crop is traditionally grown in the northern district and in the Chittagong Hill Tracts. Sorghum grain is mainly used for human food and feed for cattle. Moreover seeds are used for pop corn and preparing delicious food in our country. As the crop has potentiality to grow under adverse condition, minimum input and care, its cultivation can be extended in dry and saline areas. In Bangladesh, average yield of this crop is about 3 t ha⁻¹^[1]. Area and production of sorghum is gradually declining due to lack of good varieties.

Hybridization involving genetically diverse parents is known to provide an opportunity for bringing together gene constellations yield in desirable transgressive segregants in advanced generation^[4]. Knowledge of genetic diversity among plant populations and its quantitative assessment usually helps abreeder in choosing desirable parents for breeding program as

selection of parents on the basis of divergence analysis would be more effective. The utility of multivariate analysis and the use of generalized distance (D^2) as a quantitative measure of the genetic divergence are well illustrated^[5-7]. Some related results have been reported in sorghum by Arunachalam and Ram^[8], Chandrasekariah *et al.*^[9], Sisodia *et al.*^[10], Tiwari and Singhania^[11], Shanmugasundaram and Shubramanian^[12], Amiruzzaman *et al.*^[13]. In Bangladesh context the information on this aspect of sorghum is rare. The present study was therefore, undertaken to asses the extent of genetic diversity in 35 sorghum genotypes from abroad and Bangladesh. It will help in selecting suitable parent for future breeding program.

MATERIALS AND METHODS

Thirty five local and exotic genotypes of sorghum were grown in the experimental field of Plant Breeding Division, Bangladesh Agricultural Research Institute, Joydebpur, Gazipur during rabi 2002-2003. The seeds were sown in a RCB design with three replications and a spacing of 75 cm row to row and 25 cm plant to plant. The

size of each experimental plot was 3×3 m. N, P and K were applied as basal at the rate of 60-50-20 kg ha⁻¹. Two irrigations, one at seedling stage and another at vegetative stage were applied. Normal intercultural operations were done as and when necessary. Data were recorded from 10 plants randomly selected from the plot of each replication on days to flowering, days to maturity, plant height, number of tillers/plant, number of leaves/plant, panicle length, number of grain/panicle, 1000 grain weight and grain yield/plant. Genetic diversity was studied following Malanobis's^[14] generalized distance (D²) extended by Rao^[15]. Clustering of genotypes was done according to Tocher's Method^[15] and principal component analysis was done according to Rao^[16]. All the statistical analysis was carried out using GENSTAT-5 computer software.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating a considerable amount of genetic variability for the characters and therefore divergence analysis was carried out.

The genotypes of sorghum were grouped into five clusters based on D² values (Table 1). The distribution pattern indicated that the maximum number of genotypes were included in cluster I having 10 genotypes and the minimum number in cluster III having 2 two genotypes.

Genetic diversity is generally associated with geographical diversity but the former is not necessarily directly related with geographical distribution. Because in group I the genotype KCL is local and the rests are exotic. This indicated that the geographical and genetic distributions did not follow the same trend. This finding reported by Nadaf *et al.*^[17], Latif Akanda *et al.*^[18], Shewe *et al.*^[19], Shunmugam *et al.*^[20] and Surek and Korkut^[21]. Intra and inter cluster distances are presented in Table 2. The inter-cluster distances were higher than the average intra-cluster distances, which indicated wide genetic diversity among the genotypes of different groups than

those of same cluster. The highest inter cluster distance was observed between cluster III and IV (17.759) and followed by cluster III and V (13.077) and the lowest between I and II (3.793). The highest intra-cluster distance was observed for the cluster IV (5.417) and minimum for the cluster II (1.051). The maximum inter cluster distance between III and IV suggested that the cultivars from those clusters if chosen for hybridization program, they may give high heterotic F₁s and broad spectrum of variability in segregating generations. This finding supports with the findings of Samal and Jagadev^[22], Asawa^[23], Ahmed *et al.*^[24], Singh and Ramanujam^[25], Dumbre and Deshmukh^[26], Mian and Bahl^[27].

The clusters contributing maximum to the divergence were given greater emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization^[28]. Based on the cluster means (Table 3) the important clusters are IV for panicle length, number of grain/plant, 1000 grain weight and grain yield/plant, III for the lowest mean values of days to flowering, days to maturity and highest. Cluster I have the highest mean values for number of tiller/plant and number of leaves/plant and cluster V has also the highest mean values for number of tiller/plant. It could be concluded that early maturing, dwarf cultivar from cluster I, highest cultivar with the highest panicle length, number of grain/plant, bold grain and gain yield/plant I could be selected as parents for hybridization program.

Group constellation were also independently developed by using principal component analysis (PCA) to verify grouping obtained through D² statistics in two dimensional Z₁-Z₂ chart (Table 4).

Contribution of the characters towards divergence of the genotypes the results of PCA revealed that in vector I (Z₁) the important characters responsible for genetic divergence in the major axis of differentiation were days to flowering (0.0190), days to maturity (0.130), plant height (0.0219), number of tiller/plant (0.9334) and 1000 grain weight (0.1075) (Table 4). In vector II (Z₂) which was second axis of differentiation, days to maturity (0.1744), number of tiller/plant (11.030), number of grain/plant

Table 1: Distribution of 35 genotypes in five clusters in sorghum

Cluster No.	No. of genotypes/varieties	Genotypes/varieties
I	10	BSV-41, BSV-42, BSV-53, BSV-57, BSV-61, BSV-697, BSV-720, KCL, BSV-45, BSV-4
II	7	BSV-5, BSV-50, BSV-58, BSV-62, BSV-33, BSV-34, BSV-69
III	2	BSV-698, BSV-23
IV	8	BSV-25, BSV-46, BSV-2, BSV-13, BSV-14, BSV-32, BSV-11, BSV-16
V	8	BSV-3, BSV-24, BSV-75, BSV-81, BSV-6, BSV-8, BSV-17, BSV-18,

Table 2: Average intra (bold) and inter- cluster distances for 35 genotypes of sorghum

Cluster	I	II	III	IV	V
I	2.49	3.79	8.66	9.12	4.51
II		1.05	5.11	12.72	8.30
III			2.13	17.75	13.07
IV				5.41	5.14
V					2.53

Table 3: Cluster mean values for yield and yield contributing characters of sorghum

Characters	I	II	III	IV	V
Days to flowering	111.2	110.8	100.3	102.7	108.3
Days to maturity	151.3	153.4	137.2	148.7	152.3
Plant height (cm)	143.2	137.9	126.9	153.5	148.1
No. of tiller/plant	2.8	2.6	2.5	2.7	2.8
No. pf leaves/plant	22.0	20.9	20.1	21.4	21.2
Panicle length (cm)	26.8	25.7	22.0	31.2	28.7
No. of grains/panicle	2938.5	2208.2	1190.7	4792.2	3883.1
1000 grain wt. (g)	22.6	22.2	25.8	24.9	22.5
Grain yield/plant (g)	185.1	125.7	74.3	316.3	242.4

Table 4: Latent vectors for nine characters in sorghum

Characters	Vector-I (Z ₁)	Vector-II (Z ₂)
Days to flowering	0.01	-0.11
Days to maturity	0.13	0.17
Plant height (cm)	0.02	-0.00
No. of tiller/plant	0.93	11.03
No. pf leaves/plant	-0.02	-0.31
Panicle length (cm)	-0.05	-0.13
No. of grains/panicle	-0.00	0.00
1000 grain wt. (g)	0.10	0.76
Grain yield/plant (g)	-0.01	-0.10

(0.0068) and 1000 grain weight (0.7624) were important. The PCA analysis revealed that the vectors (vector I and II) for days to maturity, number of tiller/plant and 1000 grain weight were positive. Such results indicated that those three characters contributed maximum towards divergence. The greater divergence in the present materials due to these three characters will offer a good scope for improvement of yield through rational selection of parents for producing heterotic sorghum hybrid.

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