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Multivariate Analysis in Sorghum

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Abstract: A total of 33 indigenous cultivars of sorghum [*Sorghum bicolor* (L.) Moench] were grown in replicated trial during rabi season of 1999 to assess genetic divergence based on ten developmental characters. The genotypes were grouped into five clusters. Amongst ten characters, grains/panicle paid maximum contribution towards genetic divergence. The inter-group distances were much longer than the intra-group distances. Cluster III was the largest with 11 genotypes and the cluster II was the smallest with 2 genotypes. Cluster III showed the maximum genetic distance (207.43) from cluster V. Simultaneous consideration of intercluster and intra cluster distances 7 genotypes of cluster I were genetically worthful to initiate the crossing programme for high heterotic effects in segregants. Cluster II exhibited the maximum intra cluster distance (3.15) and had considerable genetical divergence from rest of the clusters. Thus, 2 genotypes belonging to cluster II might be hybridized with the genotypes of other clusters for getting desirable improvement of specific traits in sorghum.

Key words: Sorghum, genetic diversity, genotypes, intercluster and intra cluster

Introduction

Genetic diversity is of turmoil awareness to the plant breeders in the selection of suitable genotypes with higher amount of heterotic effect in F_1s and broad spectrum of variability in segregating generations. With the development of advanced biometrical methods such as multivariate analysis (Rao, 1952) based on Mahalanobis (1936) D^2 statistics has been found to be a powerful tool to estimate the quantification of the magnitude of genetic divergence among the population (Murty and Arunachalam, 1966). The effectiveness to improve the unknown breeding lines with regard to placement in heterotic groups is possible by employing the level of genetic diversity in the population (Wenzel *et al.*, 1998). With the limits of fitness, the method of D^2 statistics has become effective in modeling the actual crosses with a view of getting desired genetic architecture in different crops (Bhutani *et al.*, 1983; Jagadev and Samal, 1991 and Biswas *et al.*, 1993). The technique has been used for realizing the genetic divergence in sorghum by Amiruzzaman *et al.* (1997) and Barhate *et al.* (2000). In Bangladesh context, the information on this aspect of sorghum is very scanty. An attempt in the present investigation has been made to assess the extent of divergence for grain yield and its components in 33 sorghum germplasms collected from different parts of Bangladesh.

Materials and Methods

A set of thirty three domestic sorghum [*Sorghum bicolor* (L.)] Moench) genotypes were grown at Hajee Mohammad Danesh Agricultural College field laboratory during rabi season of 1999. Each genotype was represented by 2 rows of 3m length with a spacing of 50X30 cm^2. Two guard rows along with the length of each replication were grown to avoid the border effect. Five randomly selected plants from each genotype in each replication were taken for recording observations on ten characters viz., days to 50% flowering, days to maturity, plant height (cm), tillers/plant, panicle length (cm), panicle weight (g), grains/panicle, 1000 grains weight, grain yield/plant (g) and fodder yield/plant (g).

Analysis of variance for the individual character and analysis of covariance for character pairs were carried out as described by Cochran and Cox (1957). Wilk criteria was used to test the significance of pooled differences (Singh and Chaudhari, 1977). Genetic divergence was estimated by multivariate analysis using Mohalanobis's D^2 statistics. The genotypes were grouped into different clusters by following Tocher's method (Rao, 1952).

Results and Discussion

Genetic divergence in the population, specially in respect of the characters in which important is sought for, is an indispensable pre-requisite for successful plant selection work. The germplasms under study were therefore, first of all examined for the variability present in the accessions in respect of yield and yield components. The analysis of variance showed highly significant differences among genotypes for all the characters studied. The pooled differences over characters were also significant (Wilk criteria $X^2 = 2540.58$). On the basis of D^2 values, the 33 genotypes were grouped into five clusters (Table 1). Cluster III was the largest having II genotypes followed by cluster V with 8, cluster I with 7, cluster IV with 5 and cluster II with 2 genotypes. The maximum intercluster distance was observed between cluster III and V (207.43) followed by cluster I and IV (198.35) while the minimum intercluster distance was found between cluster I and V (58.80). The intra cluster distance varied from 3.15 to 7.28 and the maximum intra cluster distance was found in cluster III with 11 genotypes. Thus, the genotypes of cluster III were highly heterogeneous. Arunachalam *et al.* (1984) and Mian and Bahl (1989) reported that the parents separated by D^2 values of medium magnitude generally showed higher heterosis. As regards, intercluster and intra cluster distances, 7 genotypes of cluster I and 5 genotypes of cluster IV may be incorporated in hybridization programme for exploiting heterosis with sustainable production. The genotypes of cluster III were genetically far away from the genotypes of cluster V but due to the highest intra cluster distance (7.28) in cluster III, there have been a little chance of exploiting heterosis while crossing programme to be initiated between cluster III and V. Cluster II comprised of 2 genotypes and intra cluster distance was minimum (3.15) and the cluster II was genetically diverged from other clusters. The results suggested that the genotypes of cluster II may be crossed with the genotypes of rest of the clusters for improving particular trait in sorghum.

The cluster means of different characters are presented in Table 3. Cluster IV had the highest mean values for days to 50% flowering, days to maturity and plant height. On the contrary, cluster I had the lowest mean values for days to 50% flowering and days to maturity. The highest mean values for panicle length and panicle weight were scored by the cluster II but the highest mean value for grains/ panicle (3622) was obtained in the cluster I. Moreover, cluster I had the highest grain yield/plant and fodder yield/plant. Endang *et al.* (1971) stated that clustering pattern offered a better scope in choosing parents for hybridization to generate variability for effective selection of various economic traits in advanced generation. Therefore, the results suggested that days to 50% flowering, days to maturity and grains/panicle were the influential traits for improving yield potential and the genotypes of cluster I were economically worthful.

The contribution of the characters towards genetic divergence was assumed by the cluster means. The contribution paid by a particular character to the genetic divergence is presented in Table 4. The canonical analysis revealed that positive high values were for panicle weight, grains/panicle and grain yield/plant for both vector I and vector II. The results indicated that these characters

Table 1: Composition of clusters based on D^2 statistics in sorghum

Clusters	No. of Genotypes	Included Populations
I	7	SB02, SB04, SB07, SB15, SB17, SB24, SB28
II	2	SB22, SB32
III	11	SB01, SB06, SB08, SB09, SB11, SB12, SB13, SB16, SB19, SB26, SB31
IV	5	SB03, SB18, SB20, SB29, SB30
V	8	SB05, SB10, SB14, SB21, SB23, SB25, SB27, SB33

Table 2: Average intra and intercluster D^2 values for five clusters in sorghum

Clusters	I	II	III	IV	V
I	**4.37**	158.14	85.72	198.35	56.80
II		**3.15**	166.59	104.70	129.26
III			**7.28**	99.52	207.43
IV				**5.65**	83.56
V					**0.00**

The values of bold indicate intra-cluster distance

Table 3: Cluster means for ten characters of 33 sorghum genotypes

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Tillers. /plant	Panicle length (cm)	Panicle weight (g)	Grains /panicle	1000-grains weight (g)	Grain yield /plant (g)	Fodder yield /plant (g)
I	101	142	126	1.5	23.75	53.28	3622	22.84	120.89	235.73
II	105	144	135	1.2	29.44	62.37	2505	24.05	69.95	140.59
III	99	139	123	2.0	21.95	48.69	1426	20.68	56.46	115.64
IV	107	148	140	1.7	28.16	55.60	1930	21.25	68.30	136.05
V	102	145	131	1.7	25.80	50.32	2956	23.20	114.73	258.16

Table 4: Relative contributions of ten characters to the total divergence in sorghum

Characters	Vector I	Vector II
Days to 50% flowering	-0.245	-0.340
Days to maturity	-0.458	-0.085
Plant height	0.502	-0.252
Tillers/plant	-0.123	-0.181
Panicle length	-0.235	0.094
Panicle weight	0.391	0.407
Grains/panicle	0.484	0.574
1000-grain weight	-0.217	-0.133
Grain yield/plant	0.409	0.385
Fodder yield/plant	0.246	0.492

Negative (-) sign stand for direction. Positive (+) sign indicates increasing weight towards divergence and negative (-) sign indicates decreasing weight towards divergence.

have exerted maximum load towards genetic divergence. Sisodia *et al.* (1983) reported that days to flowering, panicle length and grains/panicle contributed maximum to the genetic divergence while Tiwari and Singhania (1989) reported that duration of flowering, plant height. whorls/rachis and length of rachis were the important components for genetic divergence in sorghum.

As regards, intercluster and intra cluster distances and cluster means of the important yield components like days to 50% flowering, grains/panicle and grain yield./plant, the 7 genotypes, SB02, SB04, SB07, SB15, SB17, SB24 and SB28 under cluster I were identified as prospective parents for increasing yield potential. Besides, the 2 genotypes, SB22 and SB32 of cluster II were suitable for improving special trait through hybridization programme in sorghum.

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