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Research Article

Genetic diversity analysis in in rabi sorghum (*Sorghum bicolor* L. Moench) local genotypes

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Abstract :
Mahalanobis D^2 statistics was applied to assess the divergence among the 50 local collections and 4 popular cultivars of rabi sorghum. The analysis of variance revealed significant differences among the genotypes for all the traits studied. The 54 genotypes were grouped into 8 clusters where, cluster I was largest containing 15 genotypes followed by cluster V with 10 genotypes, cluster IV with 9 genotypes. The inter cluster distance was maximum between cluster VII and VIII followed by cluster III and VII and cluster V and VIII. Based on the inter cluster distance and the *per se* performance, the genotype RSV 1037 in the cluster VIII can be utilized in further breeding programme as a parent. Seed yield contributed maximum to divergence (94.2%), plant height (3.49%) and days to 50% flowering (2.10%).

Key words:
Rabi sorghum, Genetic Divergence, D^2 statistics

Introduction

Sorghum is the third most important cereal crop cultivated extensively in India after wheat and rice. The area under rabi sorghum is fairly consistent over many years but the progress in productivity is much slower compared to kharif season. Hybridization involving genetically diverse parents is known to provide an opportunity for bringing together gene constellations resulting in desirable transgressive segregants in advanced generations. However, postulation of rational criteria for identification of such parents is still a live problem in plant breeding. To consider geographic diversity among the parents as an index of genetic diversity has been acclaimed and equally disclaimed in numerous reports. However, reports on genetic diversity among the rabi sorghum is very limited. In the present study, D^2 analysis has been applied to assess the diversity among the 54 rabi sorghum local genotypes, to identify the divergent types suitable for hybridization programme. Diversity analysis provides information on deciding choice of parents from distantly related clusters to secure yield improvement in sorghum.

Material and methods

The material for the present study comprised of 50 stabilized local collections and 4 popular genotypes *viz.*, M-35-1, CSV-22R, Phule maule and Phule chitra. The present study was carried out at Agricultural Research Station, Tandur during rabi 2008-09. Each accession was sown in 4 rows of 5m length with a spacing of 45 cm between the rows and 15 cm with in the row. The experiment was laid out in a randomized block design with 3 replications. Recommended package of practices were followed for raising a normal crop. In each accession, five plants were selected randomly and used for collecting data on days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), test weight (g) and seed yield (kg/ha). The data was subjected to statistical analysis using (Mahalanobis, 1936) D2 statistics and Tochers method as described by Rao (1952) for determining group constellation. Average inter and intra cluster distances were estimated as per the procedure outlined by Singh and Choudhary (1977).

Results and discussion

The analysis of variance revealed significant differences among the genotypes studied. Based on D^2 statistics and Tochers method, the 50 accessions along with 4 popular cultivars were grouped into 8 clusters however, with variable number of entries in each cluster revealing considerable amount of genetic diversity in the material (Table 1). It was observed that cluster 1 had maximum number of genotypes followed by cluster V with 10 genotypes and cluster IV with 9 genotypes. The three clusters II, VI and VII had 5 genotypes each and cluster III had 4 genotypes. Cluster I, IV and V together included 34 genotypes reflecting narrow genetic diversity among them. The narrow genetic diversity may be attributed to similarity in the base material

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from which they have been evolved. Further the cluster VIII was found to be the solitary cluster. However, lines derived from the same source of parentage were grouped into different clusters demonstrating the impact of selection pressure in increasing the genetic diversity. The checks, M-35-1, CSV-22R, Phule maule and Phule chitra were included in the cluster V, IV and III respectively indicating their distinctness or similarity from the germplasm accessions with respect to traits studied. Theses results were in agreement with the earlier reports of Narkhede et al. (2000) in rabi sorghum and Vishnuvardhan Reddy *et al.* (2005) in Sunflower.

Average intra and inter cluster D^2 values among 54 genotypes (Table 2) revealed that, cluster VI has the maximum intra cluster value (33.81) indicating that genotypes with in the cluster were similar. While cluster V showed the maximum intra cluster D^2 value (67.64), followed by cluster IV (66.05) and cluster VII (56.51) revealing the existence of diverse genotypes that fell in these clusters. The inter cluster D^2 values ranged from 87.59 to 834.91. Minimum inter cluster D^2 values were observed between the clusters III and VIII indicating the close relationship among the genotypes included in these clusters. Maximum inter cluster value (834.91) was observed between cluster VII and cluster VIII followed by (754.21), cluster III and VII and (702) cluster V and VIII which indicates that, genotypes included in these clusters are genetically diverse and may give rise to high heterotic response.

The cluster means and contribution towards each trait towards genetic divergence are presented in Table 2. The data revealed considerable differences among the clusters for most of the characters studied. The cluster VIII recorded highest seed yield and highest mean test weight (RSV 1037) whereas, cluster III (Yermala local, Kumbhari local, RSV 744 and Chungi maldandi) recorded highest mean for panicle length, The cluster II (RSV 1126, Hadaspar dagdi, RSV 821, PVR 657 and RSV 1080) recorded highest mean for plant height (184.20) and lowest mean for days to 50% flowering (58 days) and maturity (108 days) duration.

The data on inter cluster distances and *per se* performance of genotypes were used to select genetically diverse and agronomically superior genotypes. The genotypes, exceptionally good with respect to one or more characters were desirable. On the basis, the local genotype RSV 1037 was distinct and diverse can be selected as a promising line. Intercrossing of divergent groups would lead to wide genetic base in the base population and greater opportunities for crossing over to occur, which inturn may release hidden variability by breaking close linkage (Thody, 1960). The progenies derived from such crosses are expected to show wide variability, providing greater scope for isolating transgressive segregants in the advanced generations. Hence, these genotypes may be used repeatedly in the crossing programmes to recover transgressive segregants, which can be either released as a variety or can be utilized in the genetic enhancement of Sorghum crop.

Among the 6 characters studied seed yield contributed the most (94.20%) to the genetic divergence of the genotypes followed by plant height (6.49%) and days to 50% flowering (2.10%). However panicle length and test weight indicated a narrow range of diversity among the genotypes under study.

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Table 1: Average Inter and Intra cluster distances (D2 values) for 12 clusters in Rabi Sorghum genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	43.53	103.76	203.73	124.94	423.94	302.24	555.57	282.26
II		51.45	116.99	213.32	515.65	394.67	648.14	190.92
III			49.71	316.67	621.96	500.56	754.24	87.59
IV				66.05	314.19	193.45	444.37	396.04
V					67.64	131.05	146.51	702.09
VI						33.81	257.05	580.91
VII							56.51	834.91
VIII								0.00

Table 2: Cluster means for seed yield and related quantitative traits in Rabi Sorghum

Cluster	Days to 50% flowering	Days to maturity	Plant heigh (cm)t	Panicle length (cm)	Test weight (g)	Seed yield (kg/ha)
I	63.73	113.73	170.13	10.82	29.37	1279.60
II	57.80	107.80	184.20	12.82	32.94	1372.00
III	62.50	112.50	168.25	15.48	32.10	1478.75
IV	61.11	111.11	166.33	12.74	30.52	1166.67
V	60.90	109.80	183.60	12.42	32.59	859.40
VI	63.60	113.60	170.00	10.96	32.40	979.60
VII	66.40	116.40	167.60	11.92	30.86	726.00
VIII	60.00	110.00	179.00	14.40	35.90	1560.00
% CTD	2.10	0.00	3.49	0.21	0.00	94.20

% CTD: Percent contribution towards divergence