



*Research Paper*

**GERMPLASM EVALUATION OF RABI SORGHUM, *Sorghum bicolor* (L.)  
MOENCH**

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**Abstract**

In order to assess the divergence among 80 elite rabi sorghum germplasm accessions which were procured from ICRISAT, Mahalanobis  $D^2$  statistics was applied. The analysis of variance revealed significant differences among the germplasm accessions for all the traits. The 80 accessions were grouped into 14 clusters, where cluster IV was the largest containing 13 germplasm accessions followed by cluster III with 12 accessions and cluster V with 10 accessions. The inter cluster distance was maximum between cluster II and cluster XI followed by cluster XI and XII and cluster II and VII. Based on their inter cluster distance and *per se* performance of genotypes, the entries *viz.*, IS 1053, IS 4959, IS 6440 and IS 2724 were selected which could be intercrossed to obtain high heterotic expression and also to recover desirable transgressive segregants.

Key words: Rabi sorghum, divergence, Mahalanobis  $D^2$ .

**INTRODUCTION**

Sorghum is a Rabi (winter) season crop in western and southern India. Among the sorghum growing countries India ranks first in acreage but second in production. In India it is grown over an area of 16 million hectare with total production of about 11.6 million tons. In spite of premier position occupied by India (717 kg per hectare) in the world millets scenario, per hectare yields are very low as compared to world average. This wide gap is an eye opener to intensify the breeding programme at national level. This may be due to limited geographical distribution of rabi sorghum confined to Indian sub continent and inadequate utilization of available genetic diversity. The present study were undertaken to analyze the variability among the quantitative traits in sorghum germplasm accessions received from ICRISAT. It also aimed to characterize the germplasm for certain useful agro-morphological traits. The identified accessions may prove to be an important gene pool for different traits.

**MATERIALS AND METHODS**

Seeds of 80 elite germplasm accessions were procured from ICRISAT, Patancheru which were grown in 5m row length at spacing of 45 x 15 cm under augmented design with two checks (M 35-1 and CSV 15R) at Agricultural Research Station, Tandur during 2011-12 rabi season. The germplasm accessions were evaluated for 8 phyto-morphological traits including days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of leaves per plant, 1000 - seed weight (g), seed yield (kg/ha) and fodder yield (t/ha). The observations were recorded on five randomly selected plants for different traits at appropriate growth stages. 1000- seed was counted by electronic seed counter (The Indosan Company, Haryana) and weighed by electronic balance. Range, mean, coefficient of variation and simple

correlation coefficients were computed using standard statistical methods (Kempthorne, 1957). The multivariate analysis of genetic divergence using  $D^2$  statistic (Mahalanobis, 1936) was carried out as described by Rao, 1952. The data were analyzed statistically using the software WINDOSTAT, developed by INDOSTAT services Ltd. Hyderabad, India. Regarding relative contribution of the traits towards total genetic divergence, rank 1 is given to the highest mean difference and  $p$  for the lowest mean difference, where  $p$  is the total number of characters. Finally, the percent contribution for each character was calculated by taking total number of ranks of all the characters to hundred.

## RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the traits studied. Based on  $D^2$  statistics, the 80 genotypes were grouped into 14 clusters with variable number of entries revealing the presence of considerable amount of genetic diversity in the material (Table 1). Cluster IV had maximum number of 13 genotypes and cluster III with 12 genotypes. Cluster V had 10 genotypes, cluster VII and IX had 8 genotypes each, cluster II with 6 genotypes and cluster VIII and XIV with 4 genotypes, clusters XII, XIII and I with two genotypes each and cluster X and XI were solitary clusters. However, lines derived from the same source of parentage/ origins were grouped in different clusters demonstrating the impact of selection pressure in increasing genetic diversity. Similar results were reported by Mahajan *et al.*, 2010 and Sameer Kumar *et al.*, 2010.

Average intra and inter cluster  $D^2$  values among the 80 genotypes revealed that cluster I showed minimum intra cluster value (5.77) indicating that the genotypes within this cluster were similar (Table 2) while cluster XIV showed maximum intra cluster  $D^2$  value (316.34) followed by cluster VII (126.76) revealing thereby the existence of diverse genotypes in these clusters. The inter cluster  $D^2$  values ranged from 120.64 (cluster X and XII) to 3703.9 (cluster II and XI) which indicated that the genotypes included in these clusters may give high heterotic response and thus better segregants.

The cluster means and contribution of each trait towards genetic divergence are presented in Table 3. The data revealed considerable differences among the clusters for most of the characters studied. The cluster XI (IS 3240 and IS 5051) recorded highest seed yield per plant and fodder yield, whereas cluster X (IS 13328) had more plant height, panicle length and more number of leaves per plant. Cluster II recorded earliness in flowering and maturity whereas cluster VIII recorded high test weight. Among the eight characters studied, seed yield contributed the most (97.22%) towards divergence of genotypes followed by plant height (1.96%), days to maturity (0.57%) and days to 50% flowering (0.25%).

Promising donors identified for various economic traits can be further used for future breeding programme. Genotype IS 8871 was found to be one of the useful donors for early initiation of flowering, days to 50% flowering, genotype IS 8315 for days to maturity, genotype IS 2914 was found superior for shorter plant height, genotype IS 2724 for lengthy panicle, genotypes IS 14541 and IS 21154 for more number of leaves per plant, genotype IS 4997 and IS 9997 for high test weight and genotypes IS 1053, IS 4959 and IS 6440 for high seed yield. 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 are deemed desirable. On this basis, the genotypes 1053, 4959 and 6440 were selected. Inter crossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden variability by breaking linkage (Thoday, 1960). Progenies derived from such diverse crosses are expected to show wide spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in the advanced generations. Hence, these genotypes might be used in a multiple crossing programme to recover transgressive segregants.

**Table. 1 Group constellations of rabi sorghum germplasm based on divergence analysis**

Cluster	Number of cultivars	Entry
I	2	IS 6422, IS 9718
II	6	IS 6286, IS 8827, IS 16104, IS 5664, IS 4913, IS 5275
III	12	IS 8755, IS 18417, IS 22145, IS 14541, IS 19516, IS 4897, IS 14567, IS 3109, IS 5195, IS 4936, IS 2931, IS 19361
IV	13	IS 2175, IS 11084, IS 5244, IS 18493, IS 8682, IS 19190, IS 5459, IS 15014, IS 4510, IS 8871, IS 2914, IS 21478, IS 21154
V	10	IS 880, IS 21461, IS 4625, IS 4886, IS 4425, IS 4852, IS 3365, IS 7556, IS 5279, IS 1069
VI	7	IS 8315, IS 22153, IS 1029, IS 3318, IS 17903, IS 1003, IS 18004
VII	8	IS 4234, IS 4687, IS 6440, IS 2472, IS 3742, IS 6415, IS 3609, IS 4959
VIII	4	IS 4997, IS 7053, IS 19066, IS 4603
IX	8	IS 3240, IS 5051, IS 4643, IS 9231, IS 5046, IS 9997, IS 4882, IS 1596
X	1	IS 13328
XI	1	IS 1053
XII	2	IS 2222, IS 22069
XIII	2	IS 4501, IS 10422
XIV	4	IS 2668, IS 4848, IS 2724, IS 3569

**Table. 2 Average intra and inter cluster distances ( $D^2$  values) for fourteen clusters of rabi sorghum germplasm**

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	5.77	2889.05	2453.63	1982.35	1405.86	2244.77	573.26	1168.23	695.50	2594.10	815.10	2705.29	1742.25	195.64
II		82.13	444.29	912.89	1488.32	648.37	3456.31	1722.61	2206.65	301.20	3703.90	198.37	1148.86	2895.35
III			98.03	483.39	1054.57	224.18	3021.01	1287.91	1772.25	157.67	3268.41	264.48	715.62	2461.14
IV				115.38	588.45	279.31	2549.57	818.77	1302.60	619.56	2796.79	730.07	254.92	1991.46
V					122.07	846.13	1973.36	254.10	731.82	1193.66	2219.96	1304.82	350.73	1419.05
VI						73.48	2812.23	1078.99	1563.69	354.36	3059.59	465.50	506.67	2252.91
VII							126.76	1736.64	1259.95	3161.77	263.21	3272.65	2309.84	604.58
VIII								70.46	498.08	1427.46	1982.92	1539.03	578.01	1184.45
IX									174.04	1912.36	1504.99	2023.25	1063.12	721.48
X										0.00	3409.16	120.64	854.37	2601.40
XI											0.00	3520.22	2556.97	838.11
XII												77.39	965.61	2712.05
XIII													80.05	1752.66
XIV														316.34

**Table . 3 Eigene values, proportion of the total variance represented by first three principal components, cumulative percent variance and component loading of different characters in rabi sorghum germplasm**

	PC1	PC2	PC3
<b>Eigene value (root)</b>	<b>92870100.0</b>	<b>65662.79</b>	<b>20208.23</b>
<b>Percent Var. Exp</b>	<b>99.90552</b>	<b>0.07064</b>	<b>0.02174</b>
<b>Cumulative variance explained</b>	<b>99.90552</b>	<b>99.97616</b>	<b>99.99790</b>
Days to 50% flowering	0.00329	0.04755	0.64875
Days to maturity	0.00379	0.07237	0.75387
Plant height (cm)	0.00814	0.99600	-0.08606
Panicle length (cm)	0.00008	-0.00779	0.04661
Number of leaves per plant	-0.00016	0.01857	0.03436
Test weight (g)	0.00006	-0.00014	0.00443
Seed yield (kg/ha)	0.99995	-0.00853	-0.00429
Fodder yield (t/ha)	0.00067	-0.00056	-0.00074

**Table 4: Cluster means of eighty germplasm accessions for eight quantitative traits in rabi sorghum**

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Number of leaves per plant	Test weight (g)	Seed yield (kg/ha)	Fodder yield (t/ha)
Cluster I	81.00	143.00	161.00	21.50	8.00	2.85	3112.00	4.95
Cluster II	57.83	116.33	154.33	15.67	5.50	2.52	223.67	3.10
Cluster III	71.33	129.58	156.92	17.58	7.67	2.63	659.33	2.62
Cluster IV	66.62	124.00	172.08	16.54	7.31	2.58	1131.39	3.02
Cluster V	73.80	132.60	161.20	16.30	6.20	2.69	1708.60	2.96
Cluster VI	67.29	129.29	162.29	15.29	6.57	2.43	867.86	2.37
Cluster VII	77.25	136.50	190.25	15.50	6.75	2.73	3678.25	4.61
Cluster VIII	74.75	132.00	146.00	15.75	6.50	2.93	1944.75	3.00
Cluster IX	70.13	129.50	175.38	15.38	6.13	2.73	2426.50	3.78
Cluster X	82.00	137.00	140.00	22.00	10.00	2.98	518.00	2.60
Cluster XI	82.00	138.00	172.00	19.00	6.00	2.15	3927.00	5.20
Cluster XII	83.50	141.50	166.00	17.50	6.00	2.62	407.00	2.05
Cluster XIII	61.50	119.50	169.00	18.50	7.00	2.46	1370.50	2.60
Cluster XIV	74.75	135.50	186.25	19.50	6.50	2.86	3111.75	4.58

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