MORPHOMETRIC DIVERSITY OF RABI SORGHUM GERMPLASM LINES

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SUMMARY

Hundred **rabi** sorghum genotypes grown at Agricultural Research Station, Tandur, ANGRAU, A. P. during **rabi** 2011-12 were observed for eight different morphological characters and the data were subjected to analysis of variance. Significant differences were recorded among the genotypes with regard to different morphological characters. Eighty genotypes of **rabi** sorghum were grouped into 14 clusters following the Tocher's method of clustering analysis utilizing data on a set of yield and its component characters. Clusters X and XI formed individual clusters and had the maximum genetic divergence. Maximum inter-cluster value was observed between clusters XI and VI followed by VI and IX which indicated that the genotypes included in these clusters may give heterotic response and thus better segregants. The lines derived from the same source of parentage were grouped into different clusters demonstrating the impact of selection pressure in increasing genetic diversity.

Key words: Rabi sorghum, morphological characters, clustering analysis, genetic divergence

The use of Mahalanobis D² statistics for estimating genetic divergence had been emphasized by many workers. Sorghum is one of the important cereal crops and it is main staple food for the world's poorest and most insecure people across the semi-arid tropics of the world. India contributes about 60 per cent of the sorghum production. The major challenge facing sorghum research in India is to evolve technologies that will enable the transformation of subsistence farming into commercial and profitable production. Improvement of rabi sorghum did not receive much emphasis and efforts as the kharif sorghum until 1990s. But in rabi sorghum, the fodder yield given is even more important than that in kharif sorghum. Higher levels of resistance against major pests and diseases, stringent maturity duration to suit different receding soil moisture regimes and certain levels of thermo insensitivity are essential in rabi cultivars for better adaptability. The information about the extent of genetic divergence is critical for the improvement programme of any crop. The present study was undertaken to estimate the genetic diversity among hundred germplasm accessions of rabi sorghum.

MATERIALS AND METHODS

Seeds of hundred elite germplasm accessions

received from Directorate of Sorghum Research, Hyderabad were grown in 5 m row length at spacing of 45 x 15 cm under augmented design at Agricultural Research Station, Tandur during 2011-12 rabi season. The germplasm accessions were evaluated for eight phyto-morphological traits including days to 50 per cent 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. Range, mean, coefficient of variation and simple correlation coefficients were computed using standard statistical methods (Kempthorne, 1957). The multivariate analysis of genetic divergence using D² 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 was given to the highest mean difference and ñ for the lowest mean difference, where ñ 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.

TABLE 1 Average intra and inter cluster distances (D² values) for 16 clusters of ${\bf rabi}$ sorghum germplasm

Clusters I	I	П	Ш	2	>	IV	IIA	ΝШ	XI	×	IX	IIX	XIII	XIX	XX	XVI
	524.09	1768.44	524.09 1768.44 3026.14 4278.26 5	4278.26	5597.19	1082.23	754.28	806.96	861.14	7483.42	1171.52	3532.82	5376.05	2740.11	10748.80	15505.12
П		626.68	1429.88	2649.75	3945.01		2349.55	2386.50	2487.00	5821.75	2819.38	1917.46	3731.29	1401.66	9078.85	13834.99
H			540.81	1391.86	2640.32		3619.90	3677.93	3776.66	4510.55	4103.58	892.04	3509.70	1346.69	7770.44	12523.79
\geq				719.74	1463.54	3421.20	4871.66	4939.37	5036.60	3283.28	5359.00	1196.01	1549.52	2249.74	6534.15	11278.21
>					529.02		6196.93	6261.43		1947.91	6685.98	2297.06	1119.04	3391.50	5190.34	9934.14
M						647.86	1642.66	1613.40	1729.96	6603.18	2079.70	2620.36	4457.77	1845.77	9854.38	14614.63
VII								517.46		8087.58	502.09	4162.46	6010.04	3373.11	11362.90	16115.54
VIII								0.00	223.37	8147.78	600.64	4137.36	5986.63	3244.86	11406.14	16169.00
XI									0.00	8250.95	393.55	4267.95	6118.87	3407.23	11516.90	16276.73
×										510.97	8576.88	4091.57	2417.02	5177.89	3302.07	8038.86
XI											0.00	4624.80	6475.27	3788.26	11849.63	16605.07
XII												0.00	1851.07	1127.53	7296.73	12062.85
XIII													0.00	2845.18	5493.41	10252.72
XIV														0.00	8337.48	13097.52
XV															0.00	4766.28
XVI																0.00

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the traits under study. Based on D² analysis, the 100 germplasm accessions were grouped into 16 clusters with a variable number of entries revealing the presence of considerable amount of genetic diversity in the material (Table 1). The cluster I comprised a maximum number of 33 genotypes, followed by cluster II with 26 genotypes and clusters III and IV with nine genotypes. The cluster V comprised six genotypes, VI comprised five genotypes and cluster X comprised three genotypes, while the rest of the clusters had one genotype each. The pattern of distribution of genotypes into various clusters was at random suggesting that the genetic diversity was not related to geographic diversity. This might be attributed to the forces other than geographical separation, which was responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation. Similar results were reported by Sameer Kumar et al. (2010) in genetic divergence studies in **rabi** sorghum.

Eigene values proportion of the total variance represented by first three principal components, cumulative per cent variance and component loading of different characters presented in Table 2.

Average intra and inter-cluster D² values among the hundred genotypes revealed that the solitary clusters

TABLE 2
Eigene values, proportion of the total variance represented by first three principal components, cumulative per cent variance and component loading of different characters in **rabi** sorghum germplasm

	PC1	PC2	PC3
Eigene value (root)	672058600	9454973	35521.13
Per cent Var. Exp.	98.6069	1.38727	0.00521
Cumulative variance explained	98.6069	99.9941	99.999
Days to 50% flowering	0.00030	0.00035	0.07983
Days to maturity	0.00010	0.00202	0.05585
Plant height (cm)	-0.0014	0.01053	0.99450
Number of leaves/plant	0.00000	0.00086	0.03672
Test weight (g)	0.00000	0.00010	0.00404
Seed yield (kg/ha)	-0.41151	0.911	-0.01027
Fodder yield (t/ha)	-0.9114	-0.4115	0.00314

showed intra-cluster value of 0.00, while cluster IV (719.74) showed maximum intra-cluster distance followed by cluster VI (647.86) and cluster II (626.68) revealing the existence of diverse genotypes in these clusters. The inter-cluster D² values ranged from 393.55 to 16605.07. Minimum inter-cluster D² values were observed between clusters XI and IX indicating the close relationship among the genotypes included in these clusters. Maximum inter-cluster value was observed between clusters XI and VI followed by VI and IX which indicated that the genotypes included in these clusters may give heterotic response and thus better segregants. The lines derived from the same source of parentage

 $TABLE \ 3$ Cluster means of hundred germplasm accessions for seven quantitative traits in ${\bf rabi}$ sorghum

Cluster No.	Days to 50% flowering	Days to maturity	Plant height	No. of leaves/ plant	Test weight (g)	Seed yield (kg/ha)	Fodder yield (t/ha)
Cluster I	70.94	125.45	173.70	7.70	2.70	807.06	1542.79
Cluster II	70.88	126.50	177.69	7.69	2.63	1579.35	3029.04
Cluster III	68.33	124.56	173.89	7.44	2.70	2028.44	4263.56
Cluster IV	69.11	124.11	180.33	7.67	2.64	2454.11	5445.00
Cluster V	67.17	122.67	185.17	7.50	2.86	3015.17	6661.67
Cluster VI	70.60	128.00	183.60	8.00	2.78	1420.80	2245.20
Cluster VII	55.00	106.00	132.00	4.00	2.45	333.00	1086.00
Cluster VIII	78.00	135.00	156.00	10.00	2.99	777.00	824.00
Cluster IX	70.00	123.00	151.00	6.00	2.38	555.00	805.00
Cluster X	71.67	128.67	168.33	6.33	2.44	3829.33	8372.67
Cluster XI	71.00	124.00	124.00	6.00	2.97	222.00	597.00
Cluster XII	72.00	123.00	172.00	8.00	2.69	2830.00	4416.00
Cluster XIII	71.00	126.00	205.00	9.00	2.64	3829.00	5974.00
Cluster XIV	78.00	137.00	163.00	9.00	3.06	2886.00	3290.00
Cluster XV	65.00	126.00	195.00	8.00	2.68	5494.00	11209.00
Cluster XVI	66.00	122.00	178.00	8.00	2.87	7270.00	15632.00

were grouped into different clusters demonstrating the impact of selection pressure in increasing genetic diversity.

The cluster means and contribution of each trait towards divergence are presented in Table 3. The data revealed considerable differences among the clusters for most of the characters studied. The cluster XVI recorded the highest seed yield and fodder yield. The knowledge on characters influencing divergence is an important aspect to a breeder which can be estimated by D² analysis. Cluster VII recorded lowest mean for days to 50 per cent flowering, days to maturity and number of leaves per plant. Cluster VIII recorded highest mean for number of leaves per plant, whereas cluster XIV recorded highest mean for test weight and cluster XIII recorded high mean for plant height. The character fodder yield (85.52%) contributed maximum towards total divergence followed by seed yield (14.32%) indicating that the divergence of genotypes was due to these two traits (Table 4). Sameer Kumar et al. (2011) reported the maximum contribution of fodder yield towards genetic divergence in rabi sorghum which is in

TABLE 4
Per cent contribution of different characters towards genetic divergence

Days to 50% flowering	0.02
Days to maturity	0.00
Plant height (cm)	0.14
No. of leaves/plant	0.00
Test weight (g)	0.00
Seed yield (kg/ha)	14.32
Fodder yield (t/ha)	85.52

consonance with the findings of the present study.

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 one or more characters were seemed to be desirable. On this basis, IS 3963, IS 4507, IS 4529, IS 4531 and IS 4654 were selected. Inter-crossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden potential variability by disrupting the undesirable linkages (Thoday, 1960). The progeny derived from such diverse crosses are expected to have wide spectrum of genetic variability, providing a greater scope for isolating transgressive segregants in the advanced generations. Hence, these genotypes could be utilized in a multiple crossing programme to recover desirable transgressive segregants.

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