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Research Note

Genetic divergence for yield attributing traits in the Rabi sorghum germplasm

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Abstract

Mahalanobis D^2 statistics was used to assess the divergence among the 45 rabi sorghum landraces, 13 advanced breeding lines and 4 popular cultivars. The analysis of variance revealed significant differences among the genotypes for all the 7 traits studied. The 62 genotypes were grouped into 15 clusters where cluster I was the largest comprising of 41 genotypes followed by cluster III with 7 genotypes and cluster XI with 2 genotypes. The inter cluster distance was maximum between cluster XIII and XIV followed by cluster XIV and XV, cluster XII and XV, cluster XII and XIII and cluster V and XIV. Based on the inter cluster distance and per se performance, the elite variety Phule Anuradha, the landraces RSV 1426, SSRG 147, Pusegaon local and the advanced breeding line RSV 1420 can be utilized in breeding programmes as potential parents for crop improvement. Seed yield contributed maximum to divergence (31.84 %) followed by plant height (20.62 %) and days to 50% flowering (14.38 %).

Keywords

Rabi sorghum, Genetic Divergence, Multi variate analysis, Principal components

Sorghum is the third most important cereal crop cultivated extensively in India after wheat and rice. Rabi sorghum is highly valued as a food crop because of its excellent grain quality, nutritional status and low glycemic index. However the yields are lower (750 kg/ha) when compared to *kharif* sorghum (1100 kg/ha) as it is grown as a rainfed crop under the influence of various biotic and abiotic stresses (Anonymous, 2006). Crop improvement efforts in the past have not made much impact on improving the productivity as the genetic diversity and phenotypic variability among the breeding lines is limited. All the Rabi sorghum types belong to a single race i.e. *durra* type (Reddy *et al.*, 2003). However rabi landraces had considerable genetic diversity among them and hence deployed in the development of the many elite high yielding cultivars like CSV 216R and Phule Maulee. A need for making critical studies in identifying divergent and good combining parents was emphasized (Prabhakar and Raut 2010). The parents with greater genetic divergence are expected to yield heterotic hybrids in addition to generating broad spectrum of variability in the segregating generations. The D^2 analysis is a multivariate statistical tool for effective discrimination of various genotypes on the basis of genetic divergence (Murthy and Arunachalam 1966). In the present study D^2 analysis has been applied to assess the diversity among the 62 rabi sorghum genotypes and to identify divergent parents to effect hybridization for the purpose of yield improvement.

The material comprised of 45 rabi landraces, 13 advanced breeding lines obtained from Directorate of Sorghum Research, Hyderabad and 4 popular varieties viz., M-35-1, CSV-22R, Phule Chitra and Phule Anuradha. The present study was carried out in Rabi 2013-14 at Agricultural research Station, Tandur. Each Genotype was sown in 4 rows of 5m length with a spacing of 45 cm between the rows and 15 cm within the row. The experiment was laid out in a randomized block design with 3 replications. Recommended package of practices were followed to raise a normal crop. In each genotype, five plants were selected randomly and used for collecting data on seven characters namely days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), test weight (g) seed yield (Kg/ha) and fodder yield (Kg/ha). The multivariate analysis of genetic divergence using D2 statistic (Mahalanobis, 1936) was carried out as described by Rao (1952). The data was analysed by INDOSTAT services Ltd (version 8.5), Hyderabad, India. The percent contribution of each character to the total divergence was calculated by ranking each character on the basis of transformed uncorrelated values. Rank 1 was given to the highest mean difference and for the lowest mean difference where n 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.

The analysis of variance revealed significant differences among the genotypes studied. Based on D^2 statistics and Tochers method, the 62 accessions were grouped into 15 clusters with variable number of entries in each cluster revealing considerable amount of genetic diversity in the material (Table 1). It was observed that cluster I had maximum number of genotypes i.e. 41 followed by cluster III with 7 genotypes and cluster XI with 2 genotypes. The remaining 12 clusters were represented by single genotypes which independently diverged from the others. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. These genotypes may be very unique and useful in breeding point of view. The checks CSV-22R and Phule chitra were included in the same cluster i.e. cluster I with 30 Rabi landraces and 9 advanced rabi adapted breeding lines while M35-1 and Phule Anuradha grouped in to separate clusters. These results are in conformity with Narkhede *et al* (2000) Umakanth *et al* (2003) and Sameer Kumar *et al* (2010).

Average inter cluster D^2 values among 62 genotypes (Table 2) revealed maximum inter cluster distance values between cluster XIII and cluster XIV (D=77) followed by cluster XIV and cluster XV (D=66.6), cluster XII and cluster XV (D=65), cluster XII and cluster XIII (D=63.3), cluster V and cluster XIV (D=62.9) while minimum genetic distance was observed between cluster II and cluster IV (D=13.4). The data on cluster means (Table 3) revealed considerable differences among the clusters for all the 7 characters studied. The cluster XIV (Phule Anuradha) recorded the least value for days to 50% flowering and days to maturity. The cluster VII (BJV 83) recorded the highest panicle length, Cluster IX (Gondavale local) showed the highest plant height, cluster X showed the highest test weight (CRS19) and the cluster XII recorded highest grain yield and fodder yield (Pusegaon local). The data on inter cluster distances and *per se* performance of genotypes can be used to select genetically diverse and agronomically superior genotypes. Thus in the breeding programmes, the elite variety Phule Anuradha can be used as a donor for reducing the crop duration in developing early maturing rabi varieties which surpass terminal drought stress more effectively. The advanced breeding lines CRS 19 and BJV 83 can be deployed in enhancing the test weight and panicle lengths respectively, as bolder grains and larger panicles are more preferred by farmers. The landraces Gondavale local 1 and Pusegaon local can be used for development of tall dual purpose lines and for improvement of grain and fodder yields respectively.

Based on per se performance and genetic divergence analyses, crosses between Phule Anuradha, the landraces RSV 1426, SSRG 147, Pusegaon local and the breeding line RSV 1420 may be attempted to combine the corresponding desirable traits, to obtain higher heterotic response and recover good transgressive segregants. Intercrossing of divergent groups leads to wide genetic base in the base population and greater opportunities for crossing over to occur, which releases hidden variability by breaking the close linkages (Thoday, 1960). Alternatively the donors identified can be utilized as elite genetic stocks/pre breeding lines for imparting the corresponding traits.

The characters contributing the most to the divergence should be given importance for the purpose of effective selection and in choosing the parents for hybridization. Among the 7 characters studied, seed yield contributed the most (31.84 %) to the total genetic divergence followed by plant height (20.62 %) and days to 50% flowering (14.38 %) while days to maturity recorded the least contribution (0.63 %). Panicle length (12.59 %), fodder yield (10.15 %) and test weight (9.78 %) indicated a narrow range of diversity among the genotypes (Table 4). Principal component analysis divided the variance exhibited by these seven traits in to four components which cumulatively explained 82 % of the total variance (Table 5). These results are in conformity with the findings of Sameer Kumar *et al* (2010) and Seetharam and Ganesamurthy (2013).

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Table 1. Clustering pattern of Rabi sorghum germplasm based on D^2 statistics

Cluster No.	No. of Genotypes	Genotypes
I	41	RSV 1425, RSV 1449, RSV 1460, RSV 1461, RSV 1462, RSV 1463, RSV1479, Tansolihalli local, Yadgir local, Dharampur local, Jamkhed local, Mundewadi local, Khadkhat local, Patoda local, Nimbodi local, Jamkhed local, Bidar local, Pathari local, Katarkhatav local, Aurad local, Mangalwedha local, Honsal local, Pusegaon local, Kavalagadda mungaru, Tikota, Bairadogi, Honawad-2, SSRG 201, SSRG 204, SSRG 206, SSRG 203, CSV22R, Phule chitra, RSV 1098, RSV 1415, RSV 1455, CRS 15, CRS 20, BJV 103, BJV 114, BJV 116, BJ 204
II	1	Halyal local
III	7	Honawad, SSRG 236, Tillehal local, RSV 1478, SSRG 164, SSRG 200, Mardi local
IV	1	RSV 1458
V	1	RSV 1420
VI	1	MSV 71
VII	1	BJV 83
VIII	1	SSRG 202
IX	1	Gondavale local
X	1	CRS 19
XI	2	SSRG 170, M35-1
XII	1	Pusegaon local
XIII	1	RSV 1426
XIV	1	Phule Anuradha
XV	1	SSRG 147

Table 2. Average Intra and Inter cluster distances for 15 clusters of rabi sorghum germplasm

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV
Cluster I	22.1	27.0	29.2	27.2	28.8	28.2	33.1	33.5	29.1	32.8	35.6	39.6	39.5	46.5	43.6
Cluster II		0.00	38.8	13.4	40.1	30.6	33.9	25.8	37.4	38.4	25.4	32.1	46.9	36.0	51.0
Cluster III			20.9	39.7	32.4	41.6	45.2	47.4	39.6	43.4	34.8	57.8	34.5	61.0	43.7
Cluster IV				0.00	40.6	28.5	26.5	21.1	38.8	36.0	28.6	33.3	45.2	36.4	42.6
Cluster V					0.00	21.7	49.0	39.4	27.0	45.2	47.3	46.9	35.0	62.9	39.8
Cluster VI						0.00	38.7	26.7	23.9	41.3	45.2	31.0	38.4	52.9	42.3
Cluster VII							0.00	34.9	39.6	26.6	45.5	37.5	53.9	34.1	48.3
Cluster VIII								0.00	35.3	47.4	43.7	27.2	54.7	40.4	44.8
Cluster IX									0.00	42.7	51.8	31.2	44.0	54.8	55.8
Cluster X										0.00	48.2	44.4	54.1	38.1	52.1
Cluster XI											2.09	55.6	41.7	53.1	50.0
Cluster XII												0.00	63.3	36.9	65.0
Cluster XIII													0.00	77.0	46.0
Cluster XIV														0.00	66.6
Cluster XV															0.00

Table 3. Cluster means for seven yield and yield attributing traits in rabi sorghum germplasm

Cluster means	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Test wt (g)	Grain yield (Kg/ha)	Fodder yield (Kg/ha)
Cluster I	75.15	114.07	194.35	13.14	3.24	1721.89	5048.49
Cluster II	73.33	112.33	166.67	11.67	3.10	2332.43	6880.70
Cluster III	75.86	114.86	181.95	12.24	2.79	1054.52	3085.41
Cluster IV	73.67	112.67	175.00	16.67	3.10	2203.23	6830.10
Cluster V	80.33	119.00	210.33	7.67	3.23	1527.30	4536.00
Cluster VI	79.67	118.33	204.33	13.33	3.47	2169.00	6442.00
Cluster VII	70.67	109.33	205.00	26.67	3.40	1963.63	5832.00
Cluster VIII	75.33	114.33	201.33	15.00	2.43	2453.33	7605.33
Cluster IX	79.33	118.33	221.33	14.33	3.17	2068.53	5523.03
Cluster X	70.00	108.67	208.67	16.67	4.57	1705.07	5064.00
Cluster XI	73.33	112.33	137.00	12.50	2.78	1698.77	5176.08
Cluster XII	75.00	114.00	214.67	14.00	3.47	3018.30	8571.87
Cluster XIII	83.33	122.33	164.67	17.00	3.43	1167.40	3443.83
Cluster XIV	64.33	103.00	199.67	15.33	3.43	2671.70	7935.00
Cluster XV	76.33	114.67	200.00	18.67	2.70	987.73	4095.37

Table 4. Percent contribution of different traits to total genetic divergence

Source of variation	Times ranked first	% contribution
Days to 50% flowering	272	14.38
Days to maturity	12	0.63
Plant height (cm)	390	20.62
Panicle length (cm)	238	12.59
Test wt (g)	185	9.78
Grain yield (Kg/ha)	602	31.84
Fodder yield (Kg/ha)	192	10.15

Table 5. Principal component analysis depicting the variance explained by the first four principal components

Particulars	1 vector	2 vector	3 vector	4 vector
Eigen value (Root)	98.68707	52.70132	40.19572	34.02596
% variance explained	35.93264	19.18891	14.63554	12.38908
Cum. variance explained	35.93264	55.12155	69.75708	82.14618
Days to 50% flowering	0.35332	0.57494	0.52536	0.13376
Days to maturity	-0.03549	-0.25826	-0.03240	0.13974
Plant height (cm)	-0.26361	0.75803	-0.49209	0.12225
Panicle length (cm)	-0.18584	-0.02536	-0.36207	-0.34180
Test wt (g)	-0.15257	-0.08895	-0.31162	0.30480
Grain yield (Kg/ha)	-0.84079	0.00344	0.47225	0.22840
Fodder yield (Kg/ha)	-0.19919	0.13987	0.17198	-0.82809