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Genetic diversity studies for grain quality and productivity traits in *Rabi* sorghum

Introduction

Sorghum originating in tropical Africa is a crop with extreme genetic diversity. The grain productivity of *Rabi* sorghum in India is lower (750kg/ha) than *Kharif* sorghum (1100kg/ha) even though *Rabi* sorghum is highly valued because of its excellent grain and fodder quality. The varieties and hybrids developed did not become popular because of poor grain quality and shoot fly susceptibility.

To enhance grain quality, productivity and shoot fly tolerance of *Rabi* sorghum, prior information on the nature and magnitude of genetic diversity present in germplasm collection is a pre-requisite. An attempt was made in the present investigation to study the nature and magnitude of genetic divergence and also to identify divergent parents from distantly related clusters for hybridization programme.

A total of 100 *Rabi* sorghum germplasm including 20 land races, 10 exotic lines, 21 indigenous IS lines, 11 released (*kharif* and R*abi*) varieties, 45 B and R lines and 3 speciality sorghum types were grown in a randomized block design with 3 replications during *Rabi* season of 2004-05 at Regional Agricultural Research Station, Bijapur. Five randomly selected plants from each line were utilized for recording of observations on fifteen. Genetic diversity was studied using Mahalanobis D^2 statistic[1] and clustering was done following Tocher's method.

The genotypes were grouped into 23 clusters (Table 1) indicating the presence of greater diversity among the genotypes under study.

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The maximum number of genotypes (46) were grouped in cluster I followed by cluster II (21), cluster IV (9), cluster VII (3) and cluster X (3). The rest of the clusters were of solitary types. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adoptive complexes. These genotypes may be very unique and useful in breeding point of view.

Intercluster distances presented in Table 2 reveal maximum divergence between clusters XXII and XXIII (125.27) followed by cluster XXIII and XXI (115.73). The intracluster distance varies from 26.64 (cluster VII) to maximum distance of 30.4 (cluster I). This reveals the presence of divergent genotypes within the clusters.

Table 1 Distribution of 100 *Rabi* sorghum germplasm lines into different clusters

Cluster No.	No. of genotypes	Genotypes
1	46	Jevargi-L, D-Maldandi, Yannigar, Dodd Mogra, SVD-9662, Yarnal-L, IS-3420, Hattarkihal-L-3, IS-36348, Ramkha, BRJ-357, GRC-17-1, Katizapur-L, B.K. Chandki, H1D, IS-37257, IS-19248, IS-40766, IS-32248, Pop-sorg-Shiggov, M.H.Jola, G.M., Harnidagadi, Kovlagi-L, RS-585, BRJ-362, IS-37232, IS-4882, SSV-74, E-36-1, IS-4657, SPV-1516, 9B, ICSB-37B, IS-22464, IS-37283, BJMS-2B, SFR-2, Ravasab, Sweet Sorg, IS-18579, 116B, IS-4587, IS-23490, M31-2B, RSLG-262
2	21	SPV-570, M-35-1, CSV-216R, SFR-7, IS-13771, RR-9817, M148-138, SPV-489, RRJ-359, RS-29, BRJ-356, BJMS-3B, CSV8R, RS-615, BRJ-67, BRJ-364, BRJ-204, Kouta Aurad, RR-9818, CSV14R, BRJ-62
3	1	Sel-3
4	9	104B, P2B, ICSB83B, 53B, 401B, BJMS-1B, 296B, 117B, Swati
5	1	DSV-5
6	1	IS-4946
7	3	5-4-1, Nilgal-L, N. Maldandi
8	1	Chittapur-L
9	1	JP-1-1-5
10	3	IS-2312, IS-18551, Basavanamoti
11	1	DSV-4

Table Continued

Cluster No.	No. of genotypes	Genotypes
12	1	Dadagi Solapur
13	1	IS-4703
14	1	SVD-9662
15	1	R-354
16	1	SPV-1546
17	1	Semiloose
18	1	Pop-Sorg-Shiggov
19	1	C-43
20	1	IS-33720
21	1	SPV-1588
22	1	BRJ-360
23	1	101B

Table 3 Practical utility of divergent pairs

S No.	Traits	Genotypic pairs			D^2 values
I. Highly Divergent Pairs					
1		401-B	Vs	SPV570	
	PW	34.63		60.8	1208.22
	GY	22.84		39.64	
2		SPV570	Vs	Pop-sorghum shiggov	
	PW	60.8		33.5	1141.81
	GY	39.64		21.41	
3		R354	Vs	CS3541	
	PW	59.47		38.87	1138.61
	GY	53.4		21.53	
4		SPV570	Vs	R354	
	PW	60.8		59.47	1117.26
	GY	39.64		53.4	
5		BJMS-1B	Vs	R354	
	PW	45.8		59.47	1090.19
	GY	30.53		53.4	
II. Medium divergent pairs					
1		Yannigar	Vs	BRJ67	
	PW	25.87		56.4	585.75
	GY	16.38		49.3	
2		Ramkhe	Vs	ICSB 83B	
	PW	33.73		48	594.52
	GY	27.53		36.78	

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Table Continued

S No.	Traits	Genotypic pairs			D^2 values
3		Ramkhe	Vs	M31-2B	
	PW	33.73		36.77	597.9
	GY	27.53		35.65	
4		Ramkhe	Vs	BJMS-1B	
	PW	33.73		45.8	598.48
	GY	27.53		30.53	
5		Harni dagdi	Vs	Pop sorghum shiggov	
	PW	35		29.13	607.46
	GY	47.07		21.41	
III. Low divergent pairs					
1		E36-1	Vs	RS585	
	PW	43.07		42.4	12.39
	GY	40.79		38.6	
2		E36-1	Vs	SFR-2	
	PW	43.07		43.27	14.85
	GY	40.79		38.17	
3		E36-1	Vs	IS4882	
	PW	43.07		35.67	20.78
	GY	40.79		40.23	
4		DSV-4	Vs	BRJ357	
	PW	71.57		27.73	20.52
	GY	40.67		33.53	
5		ICSB37B	Vs	96B	
	PW	44.2		44.83	19.7
	GY	37.26		26.91	

Among the 15 quantitative traits studied, the highest contribution towards the divergence was by plant height. Similar results were reported by Kukadia et al.,[2] Dabholkar et al.[3] Days to flowering, panicle weight, panicle length, number of primaries per panicle, dead heart percentage and grain yield were also contributed towards diversity. These results are similar to results of Arunachalam et al.,[4] Biradar et al.[5]

Cluster XXII exhibited the highest mean for plant height, cluster XI showed highest panicle weight, cluster XX exhibited highest for number of primaries per panicle and seed bulk density. Cluster XX had highest seed reflectance, highest protein content in cluster 14 and cluster XV had recorded the highest grain yield per plant. It could be suggested that genotypes present in respective cluster with high mean performance for particular quantitative traits can be utilized in breeding programme to improve those traits (Table 3).

In the present study based on D2 values the genotypes were classified as highly divergent, medium divergent and less divergent pairs as indicated in Table 4. Among these maximum diversity was observed between the genotypes 401B vs SPV 570 followed by SPV 570 vs POP sorghum cv shiggav, medium diversity was observed between the Yannigar vs BRJ 67 and Ramkhe vs ICSB 83B, while very low diversity was observed between the genotypes E 36-1 vs SFR-2. Highly divergent pairs can be utilized for future hybridization programme for developing potential hybrids with high panicle weight and grain yield.

Clustering pattern obtained in the present study indicates that no relationship was observed between the geographical diversity and genetic diversity. In order to select genetically diverse genotypes the material should be screened for the important traits *viz.*, plant height, grain yield, days to flowering, panicle weight, panicle length and dead heart percentage.

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Conflict of interest

The author declares no conflict of interest.

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