

Evaluation of sorghum (*Sorghum bicolor*) germplasm lines for their yield components*

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Sorghum (*Sorghum bicolor* (L.) Moench), the fifth most important cereal crop worldwide, is best known for its adaptation to drought-prone semi-arid tropical regions in poor soils. To meet the increased demand for foodgrains and to make sorghum cultivation more profitable, productivity of sorghum needs to be improved. To increase the productivity of sorghum, there is a continuous demand for high-yielding sorghum cultivars with broad genetic base. Sorghum is endowed with high variability due to its wide range of adaptation in tropical and temperate climates, and free gene exchange among various races. Sorghum breeders in India have used germplasm lines belonging to different races (Audilakshmi *et al.* 2003), and its yield has been increased by more than 50%. Of late, in India and in the world, the potential yield levels of sorghum have reached a plateau, and there is an urgent need for diversification of the genetic base of the breeding material to break the yield plateau. Further improvement in yield can be brought out by component breeding where the genotypes will be improved for important yield components through pyramiding of the genes responsible for different yield components such as number of primary branches, number of secondary branches, number of grains/panicle, panicle length, width and weight etc (Aruna and Audilakshmi 2008). Identification of important agronomic traits in different germplasm lines and incorporating them in elite background is very important for yield improvement. Even more important is to ensure that the selected germplasm line passes on the trait of our interest to the next generation. The concept of general and specific combining ability is useful to characterize the genotypes for their ability to pass on the trait of interest. Hence, a field experiment was conducted to evaluate sorghum germplasm lines for their general combining ability for yield and important yield components to facilitate their use in sorghum

*Short note

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improvement. This study gives a picture on the utility of different germplasm lines in developing sorghum varieties and hybrids with improved yield.

The material encompassed 14 male parents (including 11 germplasm lines from world collection and 3 male parents of the promising sorghum hybrids); 3 male sterile lines and their 42 hybrids crossed in line × tester mating design. The germplasm lines used belong to different races and different places of origin (Table 1). The male parents included are ‘C43’, ‘CS 3541’ and ‘AKR 150’ which are the male parents of popular commercial hybrids ‘CSH 16’, ‘CSH 9’ and ‘CSH 14’ respectively. The female parents included ‘27A’, ‘296A’ and ‘AKMS 14A’ are the female parents of ‘CSH 16’, ‘CSH 9’ and ‘CSH 14’ respectively. The experiment was conducted at Directorate of Sorghum Research (DSR), Rajendranagar, Hyderabad during 2006 rainy season. The material was planted in a randomized block design with 3 replications under rainfed conditions. For every accession, data was recorded on 10 plants for the characters: primary branch length, number of primary branches, number of secondary branches, grains/primary branch, number of grains/unit length of primary branch, number of secondary branches/primary branch, panicle weight, grain yield and number of whorls. The data were subjected to analysis of

Table 1 Sorghum germplasm lines used

Germplasm lines (IS nos.)	Race	Origin
IS nos. 606, 1291	Bicolor (B)	USA, Tanzania
IS nos. 72	Caudatum (C)	Mexico
IS nos. 10466	Kafir (K)	Uganda
IS nos. 5725	Guinea-bicolor (GB)	India
IS nos. 472	Guinea-kafir (GK)	USA
IS nos. 2950	Guinea-durra (GD)	USA
IS nos. 399	Caudatum-bicolor (CB)	USA
IS nos. 900	Kafir-bicolor (KB)	USA
IS nos. 1357, 2300	Kafir-caudatum (KC)	India, Sudan

variance to test the significance of differences between the genotypes used in the study. Combining ability analysis was done by the method developed by Kempthorne (1957).

In the choice of parents, high mean value is the main criterion among the breeders. Further, the parents with high gca effects are desirable for obtaining useful segregants in early generations (Manonmani and Fazullah Khan 2005). The parents with high general combining ability which facilitate gains in the breeding programme and higher proportion of high-yielding derivatives need to be selected. Hence, the potentiality of parents, especially new germplasm lines to produce better offsprings with superior genes was evaluated based on their general combining ability effects. To get outstanding recombinants in segregating generations, the parents of the hybrids must be good general combiners for the characters to which improvement is sought (Gravois and McNew 1993). The estimates of general combining ability effects for germplasm lines revealed that none of the 14 lines showed desirable significant gca effects for all the traits together indicating that different parents should be used for genetic improvement of different yield components (Table 3). In the present study, different germplasm lines have been identified with good general combining ability for different yield components.

Considering both *per se* performance and gca effects, the germplasm line, 'IS 472' with moderate mean performance and significant general combining ability effects for panicle weight, number of grains/primary branch and yield/plant indicate that this line is a good general combiner for these important yield components. The germplasm lines with superior *per se* performance for yield and other important yield-attributing traits were 'IS 1291' and '2950', however both of them were found to be poor general combiners for most of the traits studied. The study showed that the lines with very good *per se* performance do not appear to transmit

desirable genes to their progeny. Such a behaviour could result from intra- and/or inter-allelic interaction of genes concerned with the characters. Different germplasm lines were identified to be good combiners for each of the yield component, viz 'IS 1291' for number of whorls, 'IS 399' for number of secondary branches, 'IS 1357' for primary branch length and grains/primary branch, 'IS 10466' for number of secondary branches/primary branch, 'IS 2300' for number of grains/unit length of primary branch, 'IS 72' for panicle weight and number of secondary branches, 'IS 900' for number of grains/primary branch. Previous studies (Aruna and Audilakshmi 2008) showed that the traits, like number of grains/unit length of primary branch and number of secondary branches/primary branch had strong positive correlation with grain yield. In the present study 'IS 2300' for grains/unit length of primary branch and 'IS 10466' for number of secondary branches/primary branch were found to be the best with good *per se* performance and combining ability.

The analysis of variance for combining ability (line \times tester mating design) indicated significant differences among the treatments for all the characters except length of primary branches indicating the existence of genetic diversity among the genotypes included in the study. Variations among the line \times tester interactions were significant for all the traits except panicle weight, primary branch length and number of secondary branches/primary branch which indicated the manifestation of parental genetic variability in their crosses. For most of the traits studied, viz panicle weight, seeds/primary branch, number of primary and secondary branches, yield/plant and seeds/unit length of primary branch, the variances due to both gca and specific combining ability were found to be significant showing the importance of both additive and non-additive components in the control of these traits (Table 2). The sca variance was significant and of higher

Table 2 Analysis of variance and combining ability ANOVA for various traits in sorghum

Source	DF	Mean sum of squares								
		Panicle weight	Primary branch length	No of seeds/primary branch	No of Primary branches	No of secondary branches	Yield/plant (g)	Seeds/unit length of primary branch	No of secondary branches/primary branch	No. of whorls
Replications	2	22.7	23.21	24.17	23.41	1007.8	32.08	0.08	0.78	476.5
Treatments	58	912.2**	48.19	482.7**	688.8**	22729**	711.0**	7.24**	2.47**	398.7**
Crosses	41	293.2**	14.24*	463.8**	724.0**	14341.9*	524.4**	6.51**	2.16**	440.2**
Line effect	2	359.30	16.19	2273.1**	3379.7**	44246.3**	372.3	42.3**	5.20*	535.7
Tester effect	13	983.61	21.63	707.86**	952.0**	29166.0**	778.5	7.84*	3.20*	407.2
L \times T effect	26	573.7	10.39	202.6**	405.7**	4629.5**	409.0**	3.09**	1.41	449.4**
Error	116	34.14	41.35	21.83	189.2	430.9	30.3	1.19	0.99	230.3
σ^2 gca		3.83*	0.33**	50.50**	69.02**	1257.9**	6.52*	0.86**	0.11**	0.86
σ^2 sca		178.5**	0.56	60.08**	53.91*	1425.3**	124.5**	0.68**	0.10	82.5**
σ^2 gca/ σ^2 sca		0.02	0.59	0.84	1.28	0.88	0.05	1.26	1.1	0.01

Table 3 Estimates of gca effects of lines and testers for different traits in sorghum

Trait	Panicle weight	Primary branch length	No of seeds/ primary branch	No of Primary branches	No of secondary branches	Yield/ plant (g)	Seeds/unit length of primaty branch	No of secondary branches/ primary branch	No. of whorls
'IS 606'	16.17** (28.2)	2.76** (15.5)	7.63** (51.8)	-10.9* (37.9)	-41.5** (269.9)	13.25** (19.67)	-0.69* (3.56)	0.56 (7.15)	1.15 (8.42)
'IS 472'	14.11** (50.0)	1.14 (12.4)	10.75** (55.3)	-7.07 (52.9)	-11.7** (348.1)	14.03** (27.7)	0.09 (4.45)	0.52 (6.68)	-4.35 (11.4)
'IS 5725'	-7.94** (49.0)	-1.17 (8.99)	-17.1** (52.9)	20.6** (72.7)	133.3** (536.9)	-12.7** (27.3)	-1.41** (4.17)	-0.32 (7.83)	-1.25 (12.5)
'IS 1291'	-6.61** (66.0)	-1.06 (9.37)	-12.4** (56.9)	-1.59 (46.6)	-92.3** (279.5)	-6.35** (35.7)	-0.76* (6.15)	-1.3** (6.01)	19.06** (8.93)
'IS 399'	-11.3** (25.5)	0.13 (13.9)	-0.33 (37.2)	1.65 (46.5)	40.37** (346.6)	-8.35** (13.7)	-0.2 (2.67)	0.63 (7.47)	-3.19 (7.95)
'IS 1357'	-7.25* (53.0)	2.08* (14.3)	6.82** (77.3)	-14.0** (47.8)	-67.8** (336.0)	-4.55* (31.5)	0.51 (6.18)	0.46 (7.16)	-3.38 (8.60)
'IS 10466'	-13.3** (29.0)	-0.69 (8.38)	-7.81** (40.4)	-6.13 (45.0)	10.17 (392.7)	-11.1** (12.0)	-0.66 (4.82)	0.71* (8.75)	-5.59 (5.27)
'IS 2300'	-0.39 (32.7)	-2.8** (6.02)	-0.24 (33.6)	-0.10 (43.7)	26.46** (313.7)	1.14 (22.0)	1.53** (5.74)	0.24 (7.18)	-2.85 (7.73)
'IS 2950'	-10.8** (36.3)	1.46 (13.0)	-6.89** (64.0)	-8.67 (55.5)	-73.4** (357.1)	-5.30** (36.0)	-1.48** (5.00)	-0.41 (6.72)	-2.75 (10.2)
'IS 72'	9.23** (56.0)	-0.76 (6.73)	-6.37** (41.2)	6.99 (73.6)	30.85** (362.7)	2.56 (34.0)	0.21 (6.12)	-0.38 (4.93)	-3.45 (8.33)
'IS 900'	-6.22** (56.6)	0.24 (13.6)	10.69** (48.8)	1.15 (71.2)	11.57 (557.4)	-7.85* (20.7)	0.46 (3.59)	-0.07 (7.83)	-4.05 (8.57)
'C 43'	5.95** (54.0)	-0.95 (6.71)	6.05** (51.6)	-2.47 (57.7)	15.00* (353.6)	7.48* (37.5)	0.89* (7.68)	0.32 (6.16)	-3.21 (10.0)
'CS 3541'	4.11* (45.7)	-1.53 (6.88)	7.18** (62.2)	0.25 (41.0)	3.27 (318.6)	5.52** (29.9)	1.39* (9.03)	-0.23 (7.74)	6.84 (9.68)
'AKR150'	14.25** (53.0)	1.13 (8.15)	2.03 (49.8)	20.3** (62.9)	15.74* (452.7)	12.28** (30.7)	0.11 (6.10)	-0.68 (7.21)	7.01 (9.00)
SE (gj) ±	2.06	0.98	1.58	5.21	6.27	1.99	0.34	0.35	4.73
SE (gj-gk) ±	2.91	1.39	2.23	7.36	8.86	2.81	0.48	0.49	6.70
27A	-3.18** (34.3)	0.56 (15.6)	-5.26** (33.7)	0.17 (62.1)	11.71** (373.5)	-2.96** (20.3)	-0.83** (8.47)	-0.03 (6.02)	-3.72 (8.47)
AKMS 14A	2.58** (41.3)	-0.67 (9.25)	8.41** (55.1)	-9.05** (49.5)	-36.7** (332.5)	2.99** (30.3)	1.11** (9.27)	0.37* (6.72)	0.33 (9.27)
296 A	0.60 (47.0)	0.11 (5.69)	-3.14** (42.7)	8.88** (52.3)	24.98* (317.7)	-0.03 (32.7)	-0.28 (7.4)	-0.34* (6.09)	3.39 (7.40)
SE (gi) ±	0.95	0.45	0.73	2.41	2.90	0.92	0.16	0.16	2.19
SE (gi-gk) ±	1.35	0.64	1.03	3.41	4.10	1.30	0.22	0.23	3.10

Figures in the parentheses indicate *per se* performance, * $P=0.05$; ** $P=0.01$

magnitude compared to gca variance for panicle weight, yield/plant and number of whorls, indicating the predominant role of non-additive gene effects in the control of these traits. For number of seeds/primary branch, number of primary branches and number of secondary branches and seeds/unit length of primary branch, both general combining ability and specific combining ability variances were found to be equally important, indicating the importance of both additive and non-additive gene effects (Narain *et al.* 2007).

Consideration of different genetic parameters showed the presence of the higher proportion of specific combining ability variances for grain yield showing that it is a genetically complex character. Hence, direct selection for yield is not possible and it is suggested to go for component breeding since many of the yield components showed good correlation with yield along with high heritability value (Aruna and Audilakshmi 2008). Genetic improvement of grain yield/plant would be easier through indirect selection for those component traits having significant positive correlation with

yield, than through direct selection for yield. The germplasm identified in the present study can be used for genetic improvement of individual yield components in the parental lines of sorghum.

Thus, it can be stated that using germplasm lines, viz 'IS 472', 'IS 5725', 'IS 1357' and 'IS 10466' in breeding programme will result in production of high-yielding derivatives. These lines not only showed good *per se* performance for the yield-attributing traits, but also showed high gca effects for important yield components. Of these, 'IS 472' and 'IS 5725' belong to guinea-kafir and guinea-bicolor races which are not much utilized in sorghum breeding programmes (Aruna and Audilakshmi 2008). Hence, utilization of these germplasm lines in sorghum improvement programme will help in breaking the yield plateau.

SUMMARY

Before utilizing elite germplasm lines in breeding programme it is important to ascertain whether the line is passing on the desirable genes to next generation. Eleven diverse sorghum (*Sorghum bicolor* (L.) Moench) germplasm lines and 3 elite restorers were evaluated during 2006 for their general combining ability for yield components, using 3 male sterile lines. Fortytwo hybrids and 17 parents were raised in completely randomized block design with 3 replications during 2006 rainy (*kharif*) season. Both additive and non-additive gene effects were found to be important for number of seeds/primary branch, number of primary branches, number of secondary branches, and seeds/unit length of primary branch, whereas for panicle weight, yield/

plant and number of whorls non-additive gene effects were predominant. The germplasm lines, 'IS 606' and 'IS 472' were found to be good combiners for important yield components, like panicle weight, number of seeds/primary branch and yield/plant. Besides 'IS 606' was a good combiner for primary branch length also. Similarly, best combiners for each of the yield components were identified, and their utilization in the sorghum breeding programme is discussed.

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