Available online at www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.7618

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **7 (2):** 582-590 (2019)

Research Article

International Journal of Pure & Applied Bioscience

Study of Combining Ability for Quality Component in Forage Sorghum [*Sorghum bicolor* (L.) Moench]

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Received: 13.03.2019 | Revised: 19.04.2019 | Accepted: 25.04.2019

ABSTRACT

The study envisaged assessing the general combining ability of the parents and specific combining ability of the hybrids, using line x tester mating design. Twenty four hybrids (derived from mating four testers with six lines in L x T design) along with their parents and checks ((SSG 59-3 and MFSH 4)) were evaluated at two locations with two date of sowing (Early and late sowing) during the kharif season of 2015-16. Data on five randomly taken plants from each genotype in each replication were recorded on different quantitative characters at first cut (55 days after sowing) and second cut (45 days after first cut). The ratio of σ^2 GCA/σ^2 SCA was less than unity for all the characters indicating preponderance of non-additive gene action (dominance and epistasis). Female parents 9A and 56A were also better combiners for HCN content, IVDMD and DDM in more than two different environments. HJ 513 and G 46 were found to be good general combiner male parents for protein content, protein yield, IVDMD and DDM in more than two different environments. The Cross combination of 465A × HJ 513 and 9A × IS 2389 were better for protein yield, IVDMD and DDM in more than two different environments. This suggests the usefulness of heterosis breeding or any breeding plan which makes use of specific combining ability effects for improvement in these traits.

Key words: *Forage sorghum, Quality traits, Variance, Gene action and Combining ability.*

INTRODUCTION

Sorghum is one of the most important staple food and fodder crops in parts of the semi-arid tropics of the world and cultivated in areas considered to be too dry and hot for other cereals, because of its tolerance to drought and heat stress. It is highly palatable and digestible than maize and pearl millet as for as the nutritional quality is concerned. It produces a tonnage of dry matter having digestible nutrients (50%), crude protein (8%), fat (2.5%) and nitrogen free extracts (45%)[2]. The farmers have a preference for sorghum as it can be utilized for different purposes like fresh fodder, hay and silage and grows well in hot and dry climate[5].

Cite this article: Dehinwal, A.K., Pahuja, S.K., Kumar, R., Singh, H., Sharma, S. and Chauhan, P.K., Study of Combining Ability for Quality Component in Forage Sorghum [*Sorghum Bicolor* (L.) Moench], *Int. J. Pure App. Biosci.* **7(2):** 582-590 (2019). doi: http://dx.doi.org/10.18782/2320-7051.7618

It has quick growth habit, quick recovery or regeneration after cutting or grazing and its ability to provide highly palatable and nutritious fodder for cattle. Improvement of sorghum is much emphasized owing to its importance as food and fodder crop. It is necessary to improve the fodder sorghum yield with nutritionally superior qualities in order to obtain better animal performance. The fodder yield is the primary trait targeted for improvement of fodder sorghum productivity. Combining ability analysis helps in identifying the parents, which could be used for hybridization programme to produce superior hybrids. In the present study, an attempt has been made to estimate the general and specific combining ability effects of the parents and crosses in forage sorghum.

MATERIALS AND METHODS

The experimental material for the present study comprised of 24 forage sorghum hybrids, 10 parents (six female and four male) and two standard checks (SSG 59-3 and MFSH 4). Hybrids were developed in a Line x Tester mating fashion on six females (lines) using four males (testers). The crosses were made in research area of Forage section, Department of Genetics and Plant Breeding, CCS HAU, Hisar during the *kharif* season of 2014-15. Hybrids and parents were evaluated at two locations *i.e*. research area of Forage Section, Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar and Regional Research Station Uchani, Karnal with two date of sowing (Early and late sowing) during the *kharif* season of 2015-16. All the thirty six genotypes were grown in a randomized block design in three replications of a two-row plot of 4.0 m length. All the recommended cultural package of practices was followed from sowing to harvesting of the crop. Data on five randomly taken plants from each genotype in each replication were recorded on different quality characters *viz.* TSS content [total soluble sugars (%)], protein content (%), protein yield (g/plant), IVDMD [(*in vitro* dry matter digestibility (%)], dry matter digestibility (g/plant) and HCN content (mg/kg green weight) in all the four environments (Table 2 and 3) at first cut (55 days after sowing) and second cut (45 days after first cut).

RESULTS AND DISCUSSION

Estimates of variances due to general and specific combining ability for all the characters under study are presented in Table 1. General combining ability variances for female parents were highly significant for all the characters. The general combining ability variances of males were highly significant for all the traits. The SCA variances (σ^2 SCA) were higher than GCA variance (σ^2 GCA) for almost all the characters (Table 4). The ratio of σ^2 GCA/σ^2 SCA was less than unity for all the characters indicating preponderance of non-additive gene action (dominance and epistasis). Similar results have been reported by Agarwal and Shrotria[1], Pandey *et al.*[8], Prabhakar *et al.*[9] and Rani *et al.*[10].

General combining ability effects

The data obtained from the crosses and parental lines were subjected to line x tester analysis. The estimates of general combining ability (GCA) effects of all the parents comprising six female and four male parents for all the characters in all the four environments have been presented in Table 2. The brief description of different characters for general combining ability analysis is as follows:

Total soluble sugars (TSS)

Among lines14A (0.84) and 56A (-0.52) in E_1 and 31A (0.73) in E_4 were found to be good general combiners for this character. Among testers, IS 2389 (0.41 and 0.54) in E_1 and E_3, and HJ 541 (0.49) in E_4, respectively showed positive significant GCA effects for this character.

Protein content

Among female parent, 9A (0.66) exhibited high positive and significant GCA effects for protein content in E_1, 14A (0.46) in E_2, 467A (0.38 and 0.35) in E_3 and E_4, respectively. Other lines which recorded significant positive GCA effects were 465A (0.30) in E_2, 56A

(0.23) in E_3 and 9A (0.09) in E_4 indicated their suitability as good general combiner for protein content. In case of testers, genotype HJ 541 (0.42) exhibited positive significant GCA effects for protein content in E_1 while G 46 (0.21) in E_2. The male G 46 (0.50) recorded positive significant GCA effects in E_3 while IS 2389 (0.26) in E_4. The other good combining male parent was HJ 541 (0.27 and 0.25) in E_3 and E_4, respectively for protein content.

Protein yield per plant

In case of female parents, 9A (0.68) in E_1, 14A (1.31) in E_2, 467A (0.78 and 1.50) in E_3 and E_4, respectively showed high positive and significant GCA effects for this character. Other lines which recorded significant positive GCA effects were 14A (0.53) in E_1 and 9A (0.41) in E_4which indicated their suitability as good source material for this character. Among testers, genotypes G 46 (0.90, 0.44 and 0.83) in E_1, E_2, and E_3, and HJ 541 (0.86) in E_4 recorded high positive and significant GCA effects for this character. HJ 513 (0.54) in E_1 was also found to be good general combiner for this character.

***In vitro* dry matter digestibility (IVDMD)**

Among lines, 9A (4.01 and 2.15) in E_1 and E_2 respectively, 467A (3.08) in E_3 and 9A (5.86) in E_4 recorded high positive and significant GCA effects for this character. Other female parents which showed significant positive GCA effects were 467A (2.81) in E_1, 14A (2.09) and 56A (2.02) in E_2, 465A (2.93) in E_3 and 465A (3.71) in E_4 indicated their suitability as good general combiner for this character. As far as testers are concerned, G 46 (1.55) in E_1, HJ 513 (2.15) in E_2, HJ 513 (2.68) in E_3, HJ 513 (1.22) and HJ 541 (1.00) in E_4 recorded positive GCA effects for this character. The other good combining testers were IS 2389 (1.20) in E_1 and G 46 (1.03) in E_4 which indicated their suitability as source material for this character.

Table 1: Analysis of variance for combining ability for different quality characters in different environments in forage sorghum

SV	D.F	Env.	TSS	CP	PY	IVDMD	DDM	HCN
Replication	2	E_1	2.54	3.06	1.41	7.87	12.96	130.62
		E_2	1.19	5.61	9.34	8.25	48.33	99.94
		E_3	2.13	3.13	3.17	8.25	17.93	107.65
		E_4	1.14	2.82	0.88	7.87	30.00	122.36
Hybrids	23	E_1	1.60**	2.13**	10.72**	46.03**	343.46**	405.64**
		E_2	0.66	1.18**	7.19**	74.01**	245.54**	443.50**
		E_3	1.59**	2.50**	5.00**	66.37**	165.36**	389.73**
		E_4	1.90**	1.62**	7.07**	131.84**	226.08**	458.43**
Lines	5	E_1	1.27**	1.73**	2.85**	88.09**	154.69**	598.79**
		E_2	0.92*	2.03**	6.05**	83.77**	206.62**	424.43**
		E_3	0.10	1.07**	3.55**	110.20**	258.90**	538.48**
		E_4	2.16**	0.73**	8.25**	197.92**	239.91**	569.50**
Tester	3	E_1	2.59**	2.20**	12.96**	80.69**	855.76**	41.52**
		E_2	0.52	1.09**	2.19**	54.57**	110.31**	38.46**
		E_3	2.57**	3.95**	5.98**	74.83**	157.24**	156.46**
		E_4	2.74**	2.17**	8.51**	84.82**	183.12**	73.16**
Lines x Testers	15	E_1	1.52**	2.25**	12.90**	25.08**	303.93**	414.09**
		E_2	0.60	0.92**	8.57**	74.65**	285.56**	530.86**
		E_3	1.90**	2.69**	5.28**	50.07**	135.80**	386.81**
		E_4	1.65**	1.81**	6.38**	119.22**	230.06**	498.46**
Error	46	E_1	0.55	0.02	0.37	0.01	8.80	0.04
		E_2	0.46	0.07	0.30	0.01	9.12	0.05
		E_3	0.57	0.01	0.31	0.01	8.32	0.12
		E_4	0.60	0.01	0.19	0.01	5.48	0.06

D.F. = Degree of Freedom * Significant at 5% level **Significant at 1% level

S.V. = Source of variation Env. = Environments TSS = Total Soluble Sugar content

CP = Protein content PY = Protein yield IVDMD = *In vitro* dry matter digestibility

DDM = Dry matter digestibility HCN = HCN content

E_1 = Early sowing at Hisar E_2 = Early sowing at Karnal

E_3 = Late sowing at Hisar E_4 = Late sowing at Karnal

Table 2: General combining ability effects of parents in different characters in different environments in forage sorghum

Female parents	TSS content				Protein content				Protein yield per plant			
	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
9A	-0.10	-0.22	-0.08	0.10	0.66**	0.21**	0.14**	0.09*	0.68**	0.17	-0.06	0.41**
14A	0.84*	-0.18	0.05	-0.06	0.08	0.46**	-0.36**	-0.13**	0.53*	1.31**	-0.85**	-0.72**
31A	0.15	-0.31	-0.08	0.73*	0.10*	-0.38**	-0.31**	0.17**	-0.13	-0.33	-0.24	-0.25
56A	-0.52*	0.32	-0.08	0.06	-0.20**	0.01	0.23**	-0.16**	-0.24	-0.23	0.07	-0.45**
465A	0.15	0.07	0.05	-0.44	-0.19**	0.30**	-0.08*	-0.32**	-0.41	-0.16	0.30	-0.49**
467A	-0.10	0.32	0.13	-0.40	-0.45**	-0.60**	0.38**	0.35**	-0.43*	-0.76**	0.78**	1.50**
SE (d)	**0.30**	**0.28**	**0.39**	**0.31**	**0.06**	**0.10**	**0.04**	**0.04**	**0.25**	**0.22**	**0.23**	**0.17**
Male parents												
HJ 513	-0.09	-0.07	-0.02	-0.45*	-0.06	-0.36**	-0.51**	-0.48**	0.54**	-0.11	-0.41*	-0.69**
HJ 541	0.16	0.13	-0.19	0.49*	0.42**	0.06	0.27**	0.25**	-0.83**	-0.39*	-0.07	0.86**
IS 2389	0.41*	-0.21	0.54*	-0.09	-0.43**	0.09	-0.26**	0.26**	-0.61**	0.07	-0.36*	0.22
G 46	-0.48*	0.15	-0.33	0.05	0.07	0.21*	0.50**	-0.03	0.90**	0.44**	0.83**	-0.39**
SE (d)	**0.24**	**0.23**	**0.25**	**0.25**	**0.05**	**0.09**	**0.03**	**0.03**	**0.20**	**0.18**	**0.18**	**0.14**
Female parents	**In vitro dry matter digestibility**				**Dry matter digestibility per plant**				**HCN content**			
	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
9A	4.01**	2.15**	-0.45**	5.86**	5.12**	0.60	-1.54	6.92**	-10.84**	-9.75**	-9.20**	-9.42**
14A	-2.12**	2.09**	-4.31**	-1.67**	-0.17	6.68**	-6.76**	-4.90**	-0.88**	1.59**	-0.02	3.10**
31A	-1.22**	0.14**	-2.66**	-2.67**	-2.55*	0.68	-2.57*	-4.42**	-1.93**	-1.66**	-3.31**	-1.83**
56A	-1.13**	2.02**	1.42**	-0.28**	-1.82	0.92	0.60	-1.19	1.66**	1.97**	-2.06**	-3.39**
465A	-2.34**	-2.37**	2.93**	3.71**	-4.05**	-3.98**	5.27**	2.36**	11.13**	8.50**	10.32**	11.13**
467A	2.81**	-4.02**	3.08**	-4.94**	3.47**	-4.90**	5.00**	1.23	0.86**	-0.64**	4.27**	0.41**
SE (d)	**0.04**	**0.05**	**0.05**	**0.04**	**1.21**	**1.23**	**1.17**	**0.95**	**0.08**	**0.09**	**0.14**	**0.09**
Male parents												
HJ 513	0.33**	2.15**	2.68**	1.22**	3.39**	3.50**	3.29**	-0.44	0.46**	-1.18**	2.52**	-0.88**
HJ 541	-3.08**	0.68**	-0.12**	1.00**	-9.75**	-1.65	-1.97*	4.45**	-1.59**	-1.10**	0.91**	0.99**
IS 2389	1.20**	-1.48**	-2.28**	-3.25**	0.37	-1.85*	-2.96**	-3.12**	-0.76**	0.36**	-4.27**	-2.34**
G 46	1.55**	-1.35**	-0.29**	1.03**	5.99**	0.00	1.65	-0.90	1.89**	1.92**	0.84**	2.23**
SE (d)	**0.04**	**0.04**	**0.04**	**0.03**	**0.98**	**1.01**	**0.96**	**0.78**	**0.06**	**0.07**	**0.11**	**0.08**

E_1 = Early sowing at Hisar E_2 = Early sowing at Karnal E_3 = Late sowing at Hisar E_4 = Late sowing at Karnal

Dry matter digestibility per plant (DDM)

Lines 9A (5.12) in E_1 14A (6.68) in E_2, 465A (5.27) in E_3 and 9A (6.92) in E_4 were found to be the best general combiner for this character. Other female parents which showed significant positive GCA effects were 467A (3.47 and 5.00) in E_1 and E_3, and 465A (2.36) in E_4, respectively which indicated their suitability as good general combiner for this character. Among testers, genotypes G 46 (5.99) in E_1, HJ 513 (3.50 and 3.29) in E_2 and E_3, and HJ 541 (4.45) in E_4, respectively showed positive significant GCA effects for this character. Other male parent which recorded significant positive GCA effects was HJ 513 (3.39) in E_1 and hence was suitable as good general combiner for this character.

HCN content

In forage sorghum, low HCN is desirable trait. The highest negative GCA effects were recorded for 9A in all the four environments which indicated its suitability as source material for low HCN content. Other female parents which showed significant negative GCA effects were 31A in E_1 and 56A in E_3 and in E_4 and identified as good general combiner for HCN content. Among the testers, HJ 541 (-1.59) in E_1, HJ 513 (-1.18) in E_2, IS 2389 (-4.27 and -2.34) in E_3 and E_4, respectively exhibited negative significant GCA effects for HCN content. Other male parents which showed significant negative GCA effects were IS 2389 (-0.76) in E_1, HJ 541 (-1.10 and -0.88) in E_2 and E_4, respectively indicated their suitability as source material for HCN content. Similar results have been reported by Bello *et al.*[3], Singh *et al.*[12], Tariq *et al.*[13] and Pandey *et al.*[8].

Specific combining ability effects

Specific combining ability is the average performance of a specific cross combination expressed as deviation from the population mean. SCA effect is the main cause for superiority of a cross. It is inferred that superiority of a cross cannot be fixed through selection. The estimates of specific combining ability effects are provided in Table 3 and the description of different characters is as under:

Total soluble sugars (TSS)

The high SCA effects were observed by the crosses 31A × IS 2389 (1.63) (poor x good GCA) and 14A × HJ 513 (1.49) (good x poor) for total soluble sugars in E_1; crosses 9A × HJ 541 (1.50) (poor x poor) and 14A × IS 2389 (1.49) (poor x poor) in E_2; crosses 9A × G 46 (1.16) (poor x poor) and 31A × G 46 (1.16) (poor x poor) in E_3; and crosses 9A × is 2389 (1.67) (poor x poor) and 467A × HJ 513 (1.67) (poor x good) in E_4. Hybrids 14A × G 46 (1.06) in E_1 and 31A × G 46 (1.24) in E_4 had also significant SCA effects for this character.

Protein content

The highest SCA effects were shown by the crosses 56A × HJ 541 (1.51) (good x good GCA) followed by 465A × IS 2389 (1.23) (good x good) and 465A × HJ 513 (1.07) (good x poor) for protein content in E_1 and crosses 14A × HJ 541 (0.79) (good x poor) and 31A × G 46 (0.74) (good x good) had high SCA effects in E_2. On the other hand, high SCA effects were shown by crosses 467A × IS 2389 (1.31) (good x good) and 465A × HJ 541 (1.23) (good x good) for this character in E_3 while crosses 14A × G 46 (0.97) (good x poor) followed by 465A × IS 2389 (0.87) (good x good) and 467A × IS 2389 (0.71) (good x good) in E_4 recorded high SCA effects. Crosses 14A × G 46 (0.77) in E_1; 465A × HJ 513 (0.66) in E_2; 9A × HJ 513 (1.12 and 0.66) in E_3 and E_4, respectively had also significant SCA effects for this character.

Table 3: Specific combining ability effects of hybrids in different characters in different environments in forage sorghum

Hybrids	TSS content				Protein content				Protein yield per plant				*In vitro* dry matter digestibility			
	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
9A × HJ 513	-0.29	0.03	-0.31	0.04	0.40**	-0.14	1.12**	0.66**	-2.14**	-1.82**	1.19**	1.00**	-2.14**	5.21**	4.27**	3.48**
9A × HJ 541	-0.04	1.50**	-0.15	0.26	-0.34**	0.29	-0.88**	-0.41**	-1.48**	-1.86**	-0.86*	1.16**	-2.26**	3.19**	-0.41**	-6.65**
9A × IS 2389	0.22	0.00	0.30	1.67**	-0.61**	-0.49*	-0.34**	0.34**	1.37**	2.58**	-0.26	-0.35	1.50**	-7.01**	-0.61**	0.05**
9A × G 46	0.10	-1.03*	1.16*	-0.97	0.56**	0.34	0.10	-0.59**	2.25**	1.09**	-0.06	-1.82**	2.90**	-1.39**	-3.26**	3.12**
14A × HJ 513	1.49**	-0.01	0.90	-0.63	-0.67**	-0.14	-0.58**	0.09	-1.90**	-1.48**	-0.71	-0.69*	4.24**	1.16**	0.03	5.26**
14A × HJ 541	-0.74	-0.21	-0.60	0.26	-0.31**	0.79**	-0.17*	0.57**	0.35	2.79**	0.57	0.67*	0.01	4.93**	-2.47**	-0.58**
14A × IS 2389	0.17	1.49**	0.34	-0.33	0.21*	-0.10	0.15*	-1.63**	0.22	-0.99*	0.07	-2.31**	-2.95**	-3.21**	0.99**	-4.60**
14A × G 46	1.06*	-0.07	-0.63	0.70	0.77**	-0.55**	0.60**	0.97**	1.34**	-0.32	0.07	2.34**	-1.30**	-2.89**	1.45**	-0.09**
31A × HJ 513	0.97	-0.06	-0.48	-0.59	-0.39**	-0.67**	-0.62**	0.03	-0.16	0.71	-0.30	0.35	-2.65**	-7.66**	0.41**	1.07**
31A × HJ 541	-0.29	-0.08	0.85	-0.37	0.10	0.15	0.91**	-0.16*	1.42**	0.15	1.64**	-1.83**	-2.28**	2.36**	-3.84**	-5.76**
31A × IS 2389	1.63**	0.08	-1.54**	0.72	-0.15	-0.22	-0.96**	-0.50**	0.54	-0.31	-2.25**	1.66**	1.84**	6.05**	1.85**	-1.51**
31A × G 46	-1.31*	0.06	1.16*	1.24*	0.44**	0.74**	0.67**	0.66**	-1.81**	-0.56	0.91*	-0.18	3.08**	-0.75**	1.59**	6.20**
56A × HJ 513	-0.37	0.15	-0.31	-0.09	-0.34**	-0.18	0.03	-0.95**	0.64	-0.29	-0.31	-0.20	-2.52**	-2.93**	-7.06**	0.50**
56A × HJ 541	0.22	-0.21	-0.15	0.13	1.51**	-0.33	-0.18*	0.37**	1.95**	1.12**	-1.63**	0.86**	4.13**	-0.62**	-0.62**	5.15**
56A × IS 2389	-0.37	-0.21	0.30	-0.79	-0.85**	0.34	0.02	0.71**	-2.40**	-0.88*	2.01**	0.29	0.55**	3.80**	0.60**	6.90**
56A × G 46	0.52	0.26	0.16	0.74	-0.32**	0.17	0.13*	-0.13*	-0.19	0.05	-0.08	-0.94**	-2.17**	-0.25**	7.08**	-12.5**
465A × HJ 513	0.30	0.07	0.90	-0.09	1.07**	0.66**	-0.94**	-0.37**	3.98**	2.95**	0.05	-1.40**	0.96**	6.13**	3.70**	-9.23**
465A × HJ 541	0.88	-0.46	-0.60	0.63	-0.83**	-0.58**	1.23**	-0.22**	-0.71	-1.34**	1.47**	-0.43	0.83**	-6.30**	4.20**	8.65**
465A × IS 2389	-0.87	0.04	0.34	-0.29	1.23**	-0.06	-0.18*	0.87**	-0.36	-1.39**	-1.17**	1.53**	1.33**	-0.63**	-1.33**	0.48**
465A × G 46	-0.31	0.35	-0.63	-0.26	-1.47**	-0.03	-0.10	-0.28**	-2.91**	-0.22	-0.31	0.30	-3.11**	0.80**	-6.56**	0.10
467A × HJ 513	-0.12	-0.18	-0.69	1.67**	-0.07	0.47*	1.00**	0.58**	-0.42	-0.07	0.13	0.95**	2.10**	-1.92**	-1.35**	-1.08**
467A × HJ 541	-0.04	-0.04	0.65	-0.91	-0.12	-0.32	-0.90**	-0.14*	-1.53**	-0.87*	-1.19**	-0.43	-0.43**	-3.56**	3.14**	-0.82**
467A × IS 2389	0.22	-0.21	0.26	0.01	0.17	0.53**	1.31**	0.20**	0.62	0.98*	1.60**	-0.81*	-2.26**	1.00**	-1.50**	-1.31**
467A × G 46	-0.06	0.43	-0.22	-0.47	0.02	-0.68**	-1.40**	-0.63**	1.33**	-0.04	-0.54	0.29	0.60**	4.48**	-0.29**	3.21**
SE (d)	**0.60**	**0.56**	**0.62**	**0.63**	**0.11**	**0.21**	**0.08**	**0.08**	**0.49**	**0.45**	**0.45**	**0.35**	**0.08**	**0.10**	**0.09**	**0.08**
5% significant value	1.00	0.94	1.04	1.05	0.18	0.35	0.13	0.13	0.82	0.75	0.75	0.58	0.13	0.17	0.15	0.13
1% significant value	1.45	1.35	1.49	1.52	0.27	0.51	0.19	0.19	1.18	1.08	1.08	0.84	0.19	0.24	0.22	0.19

Table 3 contd…..

Hybrids	Dry matter digestibility per plant				HCN content			
	E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
9A × HJ 513	-16.17**	-4.80	4.38*	6.34**	6.53**	6.19**	0.25	6.43**
9A × HJ 541	-8.53**	-8.27**	-0.53	2.31	-1.19**	-6.15**	-2.64**	-7.86**
9A × IS 2389	13.11**	9.74**	-0.04	-2.99	8.32**	9.38**	9.76**	7.25**
9A × G 46	11.59**	3.33	-3.82	-5.67**	-13.65**	-9.41**	-7.37**	-5.82**
14A × HJ 513	-1.61	-6.03**	-1.86	-0.12	-2.31**	-3.23**	-5.08**	-8.17**
14A × HJ 541	3.73	15.93**	1.69	0.29	-0.57**	-1.39**	-3.16**	1.82**
14A × IS 2389	-2.70	-7.87**	0.96	-7.93**	-6.29**	-5.49**	1.54**	-3.51**
14A × G 46	0.59	-2.03	-0.79	7.77**	9.17**	10.10**	6.70**	9.87**
31A × HJ 513	-1.29	0.38	2.21	2.97	-11.12**	-8.16**	-8.05**	-3.81**
31A × HJ 541	4.70*	1.98	0.57	-13.5**	1.91**	0.10	5.58**	3.86**
31A × IS 2389	5.77*	5.54*	-5.70**	8.61**	-12.38**	-16.90**	-13.92**	-17.98**
31A × G 46	-9.17**	-7.90**	2.93	1.48	21.58**	24.96**	16.39**	17.92**
56A × HJ 513	3.14	-3.58	-8.83**	3.94*	6.29**	5.45**	6.42**	5.21**
56A × HJ 541	7.16**	7.68**	-7.85**	6.92**	-3.27**	-5.37**	-3.04**	3.58**
56A × IS 2389	-9.29**	-3.19	11.17**	4.02*	-7.47**	-4.02**	-11.32**	-11.93**
56A × G 46	-1.01	-0.91	5.51*	-14.8**	4.46**	3.95**	7.94**	3.14**
465A × HJ 513	15.5**	19.19**	9.95**	-14.6**	3.62**	4.12**	8.62**	8.63**
465A × HJ 541	1.92	-10.65**	5.19*	6.67**	-6.58**	-5.57**	-8.85**	-12.71**
465A × IS 2389	-6.58**	-7.54**	-6.91**	4.29*	18.31**	18.37**	16.37**	21.07**
465A × G 46	-10.8**	-1.01	-8.23**	3.10	-15.35**	-16.92**	-16.14**	17.00**
467A × HJ 513	0.41	-5.17*	-5.84**	0.94	-3.01**	-4.37**	-2.16**	-8.29**
467A × HJ 541	-8.97**	-6.67**	0.92	-3.14	9.71**	18.39**	12.11**	11.31**
467A × IS 2389	-0.31	3.32	0.51	-6.00**	-0.50**	-1.34**	-2.42**	5.10**
467A × G 46	8.87**	8.52**	4.41*	8.20**	-6.20**	-12.68**	-7.53**	-8.12**
SE (d)	**2.42**	**2.47**	**2.35**	**1.91**	**0.16**	**0.17**	**0.28**	**0.19**
5% significant value	4.04	4.12	3.92	3.19	0.27	0.28	0.47	0.32
1% significant value	5.83	5.95	5.66	4.60	0.39	0.41	0.67	0.46

Protein yield per plant

The cross 465A × HJ 513 (3.98) (poor x good GCA) followed by 9A × G 46 (2.25) (good x good) and 56A × HJ 541 (1.95) (poor x good) for protein yield in E_1 while crosses 465A × HJ 513 (2.95) (poor x poor) followed by 14A × HJ 541 (2.79) (good x good) and 9A × IS 2389 (2.58) (poor x poor) in E_2 showed high SCA effects. On the other hand, maximum SCA effects were shown by cross 56A × IS 2389 (2.01) (poor x good) followed by 31A × HJ 541 (1.64) (poor x poor) and 467A × IS 2389 (1.60) (good x good) for this character in E_3 while cross 14A × G 46 (2.34) (good x good) followed by 31A × IS 2389 (1.66) (poor x poor) and 465A × IS 2389 (1.53) (good x poor) in E_4 recorded high SCA effects.

***In vitro* dry matter digestibility (IVDMD)**

The highest SCA effects were recorded by crosses 14A × HJ 513(4.24) (good x good GCA) followed by 56A × HJ 541 (4.13) (good x good) and 31A × G 46 (3.08) (good x good) in E_1 and crosses 465A × HJ 513 (6.13) (good x good) followed by 31A × IS 2389 (6.05) (good x good) and 9A × HJ 513 (5.21) (good x good) in E_2 for *in vitro* dry matter digestibility. On the other hand, maximum SCA effects were shown by crosses 56A × G 46 (7.08) (good x good) followed by 9A × HJ 513 (4.27) (good x good) and 465A × HJ 541

(4.20) (good x good) in E_3 while cross 465A × HJ 541 (8.65) (good x good) recorded highest SCA effects followed by 56A × IS 2389 (6.90) (good x good) and 31A × G 46 (6.20) (good x good) in E_4. Hybrids 9A × G 46 (2.90) in E_1; 14A × HJ 541 (4.93) in E_2; 465A × HJ 513 (3.70) in E_3 and 14A × HJ 513 (5.26) in E_4 also showed significant SCA effects for this character.

Table 4: Genetic variance for different characters under different environments in forage sorghum

Environment	E_1			E_2			E_3			E_4		
Characters	σ^2 GCA	σ^2 SCA	σ^2 GCA / σ^2 SCA	σ^2 GCA	σ^2 SCA	σ^2 GCA / σ^2 SCA	σ^2 GCA	σ^2 SCA	σ^2 GCA / σ^2 SCA	σ^2 GCA	σ^2 SCA	σ^2 GCA / σ^2 SCA
TSS	-4.66	2666.40	-0.002	-46.97	2356.16	-0.020	-8.57	789.02	-0.011	-1.32	1470.99	-0.001
CP	-0.02	6.51	-0.003	0.04	3.00	0.014	-0.01	7.92	-0.002	-0.02	5.16	-0.005
PY	-0.33	34.26	-0.010	-0.30	21.86	-0.014	-0.04	14.57	-0.002	0.13	19.91	0.007
IVDMD	3.95	114.75	0.034	-0.37	220.25	-0.002	2.83	178.47	0.016	1.48	372.40	0.004
DDM	13.42	1019.58	0.013	-8.47	744.60	-0.011	4.82	430.64	0.011	-1.24	661.38	-0.002
HCN	-6.26	1179.51	-0.005	-19.96	1392.84	-0.014	-2.62	1133.84	-0.002	-11.81	1377.11	-0.009

CP = Protein content (%) TSS = Total soluble sugars (%) PY = Protein yield per plant (g)
IVDMD = *In vitro* dry matter digestibility (%)
DDM = Dry matter digestibility per plant (g) HCN = HCN content (mg/kg green weight) σ^2 GCA = GCA variance
σ^2 SCA = SCA variance
E_1 = Early sowing at Hisar E_2 = Early sowing at Karnal E_3 = Late sowing at Hisar
E_4 = Late sowing at Karnal

Table 5a: Promising general combining female parents for different characters in forage sorghum

Characters \ Environments	Female parents							
	Early sowing (Hisar) (E_1)		Early sowing (Karnal) (E_2)		Late sowing (Hisar) (E_3)		Late sowing (Karnal) (E_4)	
TSS content (%)	14A (0.84*)	-	-	-	-	-	31A (0.73*)	-
Protein content (%)	9A (0.66**)	31A (0.10*)	14A (0.46**)	465A (0.30**)	467A (0.38**)	9A (0.14**)	467A (0.35**)	31A (0.17**)
Protein yield (g/plant)	9A (0.68**)	14A (0.53*)	14A (1.31**)	-	467A (0.78**)	-	467A (1.50**)	9A (0.41**)
IVDMD (%)	9A (4.01**)	467A (2.81**)	9A (2.15**)	14A (2.09**)	467A (3.08**)	465A (2.93**)	9A (5.86**)	465A (3.71**)
Dry matter digestibility (g/plant)	9A (5.12**)	467A (3.47**)	14A (6.68**)	-	465A (5.27**)	467A (5.00**)	9A (6.92**)	465A (2.36**)
HCN content (mg/kg green weight)	9A (-10.84**)	-	9A (-9.75**)	-	9A (-9.20**)	56A (-2.06**)	9A (-9.42**)	56A (-3.39**)

Table 5b: Promising general combining male parents for different characters in forage sorghum

Ch. \ Env.	Male parents							
	Early sowing (Hisar) (E_1)		Early sowing (Karnal) (E_2)		Late sowing (Hisar) (E_3)		Late sowing (Karnal) (E_4)	
TSS	IS 2389 (0.41*)	-	-	-	IS 2389 (0.54*)	-	HJ 541 (0.49*)	-
CP	HJ 541 (0.42**)	-	G 46 (0.21*)	-	G 46 (0.50**)	HJ 541 (0.27**)	IS 2389 (0.26**)	HJ 541 (0.25**)
PY	G 46 (0.90**)	HJ 513 (0.54**)	G 46 (0.44**)	-	G 46 (0.83**)	-	HJ 541 (0.86**)	-
IVDMD	G 46 (1.55**)	IS 2389 (1.20**)	HJ 513 (2.15**)	HJ 541 (0.68**)	HJ 513 (2.68**)	-	HJ 513 (1.22**)	G 46 (1.03**)
DDM	G 46 (5.999**)	HJ 513 (3.39**)	HJ 513 (3.50**)	-	HJ 513 (3.29**)	-	HJ 541 (4.45**)	-
HCN	HJ 541 (-1.59**)	IS 2389 (-0.76**)	HJ 513 (-1.18**)	HJ 541 (-1.10**)	IS 2389 (-4.27**)	-	IS 2389 (-2.34**)	HJ 513 (-0.88**)

Table 6: Promising specific combining hybrids for different characters in forage sorghum

Ch. \ Env.	Hybrids							
	Early sowing (Hisar) (E_1)		Early sowing (Karnal) (E_2)		Late sowing (Hisar) (E_3)		Late sowing (Karnal) (E_4)	
TSS	31A × IS 2389 (1.63**)	14A × HJ 513 (1.49**)	9A × HJ 541 (1.50**)	14A × IS 2389 (1.49**)	9A × G 46 (1.16*)	31A × G 46 (1.16*)	9A × IS 2389 (1.67**)	467A × HJ 513 (1.67**)
CP	56A × HJ 541 (1.51**)	465A × IS 2389 (1.23**)	14A × HJ 541 (0.79**)	31A × G 46 (0.74**)	467A × IS 2389 (1.31**)	465A × HJ 541 (1.23**)	14A × G 46 (0.97**)	465A × IS 2389 (0.87**)
PY	465A × HJ 513 (3.98**)	9A × G 46 (2.25**)	465A × HJ 513 (2.95**)	14A × HJ 541 (2.79**)	56A × IS 2389 (2.01**)	31A × HJ 541 (1.64**)	14A × G 46 (2.34**)	31A × IS 2389 (1.66**)
IVDMD	14A × HJ513 (4.24**)	56A × HJ 541 (4.13**)	465A × HJ 513 (6.13**)	31A × IS 2389 (6.05**)	56A × G 46 (7.08**)	9A × HJ 513 (4.27**)	465A × HJ 541 (8.65**)	56A × IS 2389 (6.90**)
DDM	465A × HJ 513 (15.50**)	9A × IS 2389 (13.11**)	465A × HJ 513 (19.19**)	14A × HJ 541 (15.93**)	56A × IS 2389 (11.17**)	465A × HJ513 (9.95**)	31A × 2389 (8.61**)	467A × G 46 (8.20**)
HCN	465A × G 46 (-15.35**)	9A × G 46 (-13.65**)	465A × G 46 (-16.92**)	31A × IS 2389 (-16.90**)	465A × G 46 (-16.14**)	31A × IS 2389 (-13.92**)	31A × IS 2389 (-17.98**)	465A × HJ 541 (-12.71**)

CP = Protein content (%) TSS = Total soluble sugars (%) PY = Protein yield per plant (g)
IVDMD = *In vitro* dry matter digestibility (%)
DDM = Dry matter digestibility per plant (g) HCN = HCN content (mg/kg green weight) Env. = Environments
Ch. = Characters E_1 = Early sowing at Hisar E_2 = Early sowing at Karnal
E_3 = Late sowing at Hisar E_4 = Late sowing at Karnal
GCA and SCA value in parenthesis **Significant at 1% level of significance *Significant at 5% level of significance

Dry matter digestibility per plant (DDM)

The maximum SCA effects were observed by cross 465A × HJ 513 (15.50) (good x good GCA) followed by 9A × IS 2389 (13.11) (good x poor) and 9A × G 46 (11.59) (good x good) for this character in E_1 while by cross 465A × HJ 513 (19.19) (good x good) followed by 14A × HJ 541 (15.93) (good x poor) and 9A × IS 2389 (9.74) (poor x good) in E_2. On the other hand, maximum SCA effects were observed in the cross 56A × IS 2389 (11.17) (poor x good) followed by 465A × HJ 513 (9.95) (good x good) and 56A × G 46 (5.51) (poor x poor) for this character in E_3 and cross 31A × IS 2389 (8.61) (good x good) followed by 467A × G 46 (8.20) (poor x poor) and 14A × G 46 (7.77) (good x poor) in E_4. Hybrids 467A × G 46 (8.87) and 56A × HJ 541 (7.16) in E_1; crosses 467A × G 46 (8.52) and 56A × HJ 541 (7.68) in E_2; crosses 467A × G 46 (4.41) and 9A × HJ 513 (4.38) in E_3 and cross 56A × HJ 541 (6.92) and 465A × HJ 541 (6.67) in E_4 had also significant SCA effects which indicated that these crosses were good specific combiners for this character.

HCN content

The high SCA effects were shown by the crosses 465A × G 46 (-15.35) (good x good GCA) and 9A × G 46 (-13.65) (good x good) in E_1; 465A × G 46 (-16.92) (good x good GCA) and 31A × IS 2389 (-16.90) (good x good) in E_2; 465A × G 46 (-16.14) (good x good GCA and 31A × IS 2389 (-13.92) (good x good) in E_3 and 31A × IS 2389 (-17.98) (good x good GCA) and 465A × HJ 541 (-12.71) (good x good) in E_4, respectively. Other crosses which had significant SCA effects were 14A × G 46 (9.17) and 9A × IS 2389 (8.32) in E_1; 14A × G 46 (10.10) and 9A × IS 2389 (9.38) in E_2 ; 9A × IS 2389 (9.76) in E_3 and 14A × G 46 (9.87) and 465A × HJ 513 (8.63) in E_4. This indicated that these crosses were found to be good specific combiners for this character. Similar results have been reported by Reddy *et al.*[11], Bello *et al.*[3], Joshi *et al.*[6], Singh *et al.*[12] and Pandey *et al.*[8].

Two good combining female and male parents in all the four environments for various traits have been presented in Table 5a and Table 5b, respectively. Lines 9A, 31A and 467A were good general combiner female parents for protein content while 9A, 14A and 467A were good combiner female parents for protein yield in two environments. Female parents 9A and 56A were also better combiners for HCN content, IVDMD and DDM in more than two different environments. HJ 513 and G 46 were found to be good general combiner male parents for protein content, protein yield, IVDMD and DDM in more than two different environments. Similar results have been reported by Agarwal and Shrotria[1], Pandey *et al.*[8] and Rani *et al.*[10].

Best specific cross combinations for different characters have been presented in Table 6. Read-through of this table revealed that the cross combination of 465A × HJ 513 and 9A × IS 2389 were better for protein yield, IVDMD and DDM in more than two different environments. The cross combination of 465A × IS 2389 was better for protein content (crude protein) and 465A × HJ 513 was good specific combiner for IVDMD and DDM. The cross combination of 31A × IS 2389 and 465A × G 46 exhibited high and negative SCA effects for HCN content. Similar results have been reported by Kamdi *et al.*[7] and Bibi *et al.*[4]. Thus, the study reveals that there is lot of scope for the use of these lines in future breeding programmes in the development of either base populations or hybrids. The lines with lower hydrocyanic acid contents can be exploited for the improvement of quality of fodder sorghum thereby enhancing the nutritive value of the crop.

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