RESEARCH ARTICLE

STUDIES ON COMBINING ABILITY IN FORAGE SORGHUM FOR YIELD AND QUALITY PARAMETERS

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Abstract: Estimates of variance among line with respect to gca was found highly significant for all the attributes and variance among testers with respect to gca was recorded highly significant for all the traits except stem girth. The variances among crosses due to interaction between lines x testers genotypes with respect to sca were expressed highly significant for all the characters except stem girth and number of leaves per plant. Average degree of dominance $(\delta^2_s/\delta^2_g)^{0.5}$ exhibited partial dominance for plant height, leaf length, leaf breadth, internode length, leaf area, leaf stem ratio and green fodder yield and over dominance was observed for days to 50% flowering, number of leaves per plant, stem girth, total soluble solids and protein content. GCA effects and *per se* performance among the parents HC260, Pusa Chari23, SPV815, Pusa Chari6, HC260 and HC171 were found to be as good general combiner and the F_1's hybrids *i.e.* HC260 x HC308, HC260 x G48, SSG-59-3 x G48, HJ513 x HC308, HJ513 x HC171, ICSV700 x HC308, UP Chari2 x G48, UP Chari1 x Pant Chari6, Pusa Chari9 x HC171 and Rajasthan Chari1 x G48 were identified with significant and positive SCA for fodder yield which may be utilized for obtaining transgressive segment in the next generation and also could be exploited for development of hybrids.

Keywords: *Sorghum bicolor*, Gene action, Combining ability, Quality parameters

INTRODUCTION

Sorghum is known as poor man's crop and has the potentialities of being used solely either as food or feed or fodder. The major sorghum growing countries in the world are United States, India, Nigeria and Mexico. More than half of the world's sorghum is grown in semi-arid tropics (India and Africa), where it is staple food as chapatti or roti in India, injera in Ethiopia, tortillas in Latin America, etc., for millions of population. It is grown for four main purposes i.e. for grain, forage production, sugar/alcohol production and for fiber (including broomcorn, where stiff stems and panicles are used for brooms). The lower milk production in India is mainly attributed to production and feeding of poor quality forage and that too in inadequate amount (46.6 percent of requirement). To increase the milk production in the country, emphasis has to be given on bridging the gap between supply and demand of fodder. The area under forage crops in India is also very meager *i.e*. 4.4 percent of the total cultivated land. It is, therefore, essential to maximize forage production per unit area. The milk production mainly depends upon the breed of animals and health management apart from feeding practices which costs 70-75% of the total cost of milk production. Livestock play a crucial role in the development and progress of mankind. They contribute about 30 percent of the value of output in agriculture. India is the largest livestock holding country in the world. Its present livestock inventories exceed 453 million with growth rate of more than 1.5 percent per annum, maximum (5.43 crore) of which population is found in Rajasthan. White revaluation resulted in the fast development of dairy industry but on the other hand the production of forage did not raise, as a consequence there is a chronic shortage of green and dry fodder. If the requirement of green and dry fodder yield is estimated as per global standards for optimum productivity, the presently available quantity of green and dry fodder falls short by 33.5 and 23.0 percent, respectively. This has lowered the production capacity and fertility of Indian livestock (Kumar and Singh, 2012). The cultivated area under different forage crops is 4.4 per cent of the total area under cultivation, of which about 2.3 m ha is under forage sorghum. 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 through exploitation of heterosis. Hence it is necessary to understand the genetic nature of the parents. 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.

MATERIAL AND METHOD

In the present study, F_1's material was obtained from crossing fifteen females (HC260, Pusa Chari23, SPV815, Pusa Chari6, CSV15, Pant Chari3, SSG-59-3, HJ513, UP Chari4, ICSV700, UP Chari3, UP

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Chari2, UP Chari1, Pusa Chari9 and Rajasthan Chari 1) and four males (HC308, Pant Chari6, G48 and HC171) as per line x tester mating design in *Kharif* season 2016. The experiment was laid out with 60 F_1's progenies and their respective parents in randomized block design with three replications at Crop Research Center, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut during *Kharif* 2016. Each F_1's and parents were sown in two rows of 5.0 m length with inter row spacing of 30 cm and intra row spacing of 10 cm. All the recommended practices were followed to raise good crop of *kharif* sorghum. The observations on twelve yield and yield attributing characters *viz.*, days to 50% flowering, plant height, number of leaves per plant, stem girth, leaf length, leaf breadth, internode length, total soluable solids, leaf area, leaf stem ratio, protein content and green fodder yield per plant were recorded on five randomly selected plants per replication. Mean of five plants for each entry for each character was calculated and used for statistical analysis. Data was analyzed by the methods outlined by Panse and Sukhatme (1967) using mean values of five random plants in each replication from all treatments to find out the significance of treatment effect. The variation among the hybrids was further partitioned into genetic components attributable to general combining ability (GCA) and specific combining ability (SCA) following the method suggested by Kempthorne (1957). The total soluble sugars (%) *i.e.*, brix was directly scored with the help of hand refractometer. Crude protein content of selected genotypes was estimated by using Microkjeldhal method. Total nitrogen was estimated by using Kel-plus (digestion and distillation unit). Crude protein value was obtained by multiplying the total nitrogen by the conversion factor.

Table 1. Analysis of variance for twelve characters in parents and F_1 generation of forage sorghum

Source of variations	**d.f.**	**Days to 50% flowering**	**Plant height (cm)**	**No. of leaves per plant**	**Stem girth (cm)**	**Leaf length (cm)**	**Leaf breadth (cm)**	**Internode length (cm)**	**Total soluble solids (%)**	**Leaf area (cm^2)**	**Leaf stem ratio (w/w)**	**Protein content (%)**	**Green fodder yield per plant (g)**
Replication	2	0.67	2.71	0.02	0.03	0.35	0.04	0.13	0.87	60.62	0.06	0.15	58.07
Treatment	78	51.12**	6162.37**	7.66**	0.16**	80.45**	3.33**	30.80**	5.20**	8863.80**	0.28**	2.08**	8789.45**
Parents	18	79.32**	4059.94**	15.01**	0.12**	42.66*	1.24**	29.35**	6.25**	3363.22**	0.36**	1.86**	2819.88**
Line	14	82.58**	4740.64**	13.77**	0.11**	50.09**	1.04**	32.78**	6.88**	3256.03**	0.22**	2.19**	2684.71**
Tester	3	39.11**	1903.35**	25.38**	0.20**	19.03**	1.25**	22.28**	2.40**	1911.45**	0.31**	0.99**	4384.02**
Parents (L *vs* T)	1	154.32**	999.95**	1.27	0.01	9.55**	4.00**	2.64**	9.04**	9219.14**	0.42**	1.48**	199.85**
Parents *vs* crosses	1	0.70	22023.53**	1.85**	0.14*	6.58**	7.57***	88.83**	3.05**	23275.96**	0.32**	4.89**	42572.09**
Crosses	59	43.37**	6534.96**	5.52**	0.17**	93.23**	3.89**	30.26**	4.91**	10305.60**	0.29**	2.10**	10038.09**
Error	156	4.94	22.88	0.36	0.04	1.44	0.14	0.43	0.31	411.45	0.02	0.29	23.62

*Significant at 5% probability level and ** Significant at 1% probability level

Table 2. Analysis of variance for combining ability12 characters in forage sorghum

Source of variation	**d.f.**	**Days to 50% flowering**	**Plant height (cm)**	**No. of leaves per plant**	**Stem girth (cm)**	**Leaf length (cm)**	**leaf breadth (cm)**	**Internode length (cm)**	**Total soluble solids (%)**	**Leaf area (cm^2)**	**Leaf stem ratio (w/w)**	**Protein content (%)**	**Green fodder yield per plant (g)**
Line (GCA)	14	100.52**	25929.34**	3.02**	0.40**	158.03**	10.61**	90.10**	6.92**	24478.47**	0.43**	3.58**	30895.97**
Tester (GCA)	3	135.62**	938.53**	28.60**	0.05	158.84**	3.52**	53.19**	4.89**	16388.96*	0.32**	1.95**	9089.19**
Line x Tester (SCA)	42	17.72**	469.90**	4.71**	0.10	66.95**	1.68**	8.68**	4.24**	5146.79**	0.02	1.62**	3153.24**
Error	118	5.60	24.78	0.42	0.02	1.48	0.17	0.36	0.37	471.13	0.06	0.37	24.34

Estimates of genetic components, its ratio (σ^2g/σ^2s) average degree of dominance $(\sigma^2s/\sigma^2g)^{0.5}$

Source of variation	**Days to 50% flowering**	**Plant height (cm)**	**No. of leaves per plant**	**Stem girth (cm)**	**Leaf length (cm)**	**leaf breadth (cm)**	**Internode length (cm)**	**Total soluble solids (%)**	**Leaf area (cm^2)**	**Leaf stem ratio (w/w)**	**Protein content (%)**	**Green fodder yield per plant (g)**
σ^2 A	12.94	929.81	3.99	0.06	97.59	4.83	4.02	2.08	903.00	1.99	0.34	1943.14
σ^2 D	26.76	360.47	4.77	0.08	37.27	1.03	3.01	2.82	546.75	1.09	0.58	1505.84
$\sigma^2 g / \sigma^2 s$	0.52	4.95	0.79	0.93	3.74	3.77	1.56	0.72	4.09	0.06	0.68	1.69
$(\sigma^2 s / \sigma^2 g)^{0.5}$	2.95	0.29	1.88	1.29	0.57	0.66	0.80	6.75	0.39	0.07	2.71	0.97
δ^2g (males)	5.11	3.02	0.57	1.95	2.02	1.03	0.08	0.19	1.05	5.02	6.03	3.01
δ^2g (females)	4.96	2.99	0.47	1.81	2.31	1.56	0.07	0.18	0.99	4.32	5.00	2.89
δ^2g (pooled)	0.62	0.57	0.69	0.49	0.35	0.22	0.32	0.59	0.41	0.72	0.50	0.82
δ^2s (females x males)	9.21	7.42	1.56	2.31	12.14	7.77	6.52	3.33	6.53	8.02	2.82	18.54

* Significant at 5 % probability level, and ** Significant at 1 % probability level.

Table 3. Estimates of general combining ability effect of line and testers with respect to twelve characters of forage sorghum

Line/Tester	**Days to 50% flowering**		**Plant height (cm)**		**No. of leaves per plant**		**Stem girth (cm)**		**Leaf length (cm)**		**Leaf breadth (cm)**	
Line	**Mean**	**GCA**	**Mean**	**GCA**	**Mean**	**GCA**	**Mean**	**GCA**	**Mean**	**GCA**	**Mean**	**GCA**
HC 260	75.12	2.25**	319.56	94.06**	18.00	0.59**	2.11	0.19**	69.86	2.43**	7.17	2.38**
Pusa Chari 23	80.33	2.84**	302.53	81.89**	16.66	0.56**	1.99	0.04	71.33	1.55*	6.52	0.04
SPV 815	78.31	4.59**	213.00	67.08**	12.46	-0.12	1.8	0.24**	71.60	3.30**	5.91	2.10**
Pusa Chari 6	87.00	2.46**	298.60	42.42**	14.40	0.39**	1.62	0.39**	76.16	4.42**	6.92	2.05**
CSV 15	84.02	0.06	198.63	-17.86**	10.90	-0.21	2.06	-0.29**	70.96	1.44**	6.24	-0.82**
Pant Chari 3	72.66	-6.52**	295.66	3.63	15.30	-0.48**	1.65	-0.47**	63.70	8.91**	7.35	-1.70**
SSG -59-3	85.33	2.99**	289.20	-25.77**	14.77	-0.27	1.64	-0.06	75.86	-6.72**	7.25	0.77**
HJ 513	90.66	4.29**	285.80	40.66**	14.06	0.80**	2.00	-0.07	71.93	3.31	8.12	0.92**
UP Chari 4	82.64	0.05	297.50	34.42**	13.30	0.16	2.17	0.18**	75.76	1.79**	6.64	0.29**
ICSV 700	83.65	1.04	190.46	-20.89**	9.96	-0.48**	1.75	-0.08	65.86	-1.06**	6.33	0.74**
UP Chari 3	79.66	-1.64*	266.30	23.53**	11.80	-1.01**	1.62	0.01	73.66	2.12**	7.05	-0.17
UP Chari 2	88.33	0.98	289.13	33.65**	15.73	0.42*	1.70	0.10	71.43	-2.22**	7.29	0.03
UP Chari 1	85.00	-0.29	287.79	23.89**	15.00	0.24	1.78	0.03	72.00	-0.32	7.33	0.32**
Pusa Chari 9	86.66	-0.43	292.70	31.17**	14.20	0.55**	1.77	1.13**	64.66	3.91**	7.44	1.18**
Rajasthan Chari 1	77.00	1.43*	268.30	29.99**	12.06	0.34*	1.72	0.23**	76.73	0.79	6.30	0.93**
Tester												
HC 308	85.33	-0.45	306.40	4.65**	17.83	0.63**	2.07	0.40**	74.03	2.49**	7.49	2.02**
Pant Chari 6	92.00	2.55**	297.03	3.16**	13.50	0.43**	1.52	-0.04	74.30	0.29	7.93	0.30**
G 48	85.33	-0.79*	249.03	-3.50**	10.83	-1.15**	2.06	0.01	72.60	-1.87**	6.70	-0.38**
HC 171	84.00	1.71**	280.66	4.32**	14.80	1.08**	1.80	0.34**	68.83	0.91	8.17	2.05**

Line/Tester	**Internode length (cm)**		**Total soluble solids (%)**		**Leaf area (cm^2)**		**Leaf stem ratio (w/w)**		**Protein content (%)**		**Green fodder yield per plant (g)**	
Line	**Mean**	**GCA**	**Mean**	**GCA**	**Mean**	**GCA**	**Mean**	**GCA**	**Mean**	**GCA**	**Mean**	**GCA**
HC 260	24.27	0.72**	10.93	0.21	354.11	17.27**	0.43	0.08**	6.54	0.77**	406.65	70.71**
Pusa Chari 23	20.66	6.74**	7.43	0.92**	330.75	44.94**	0.39	0.05**	6.91	0.73**	390.40	61.10**
SPV 815	21.54	5.20**	6.66	0.74**	301.43	31.65**	0.34	-0.06**	5.81	0.01	350.76	43.88**
Pusa Chari 6	17.21	9.03**	7.83	1.01**	374.23	17.65**	0.37	-0.06**	7.06	0.56**	354.20	80.07**
CSV 15	23.72	2.98**	7.00	0.43**	314.16	-34.72**	0.59	-0.01	6.05	-0.01	300.70	14.89**
Pant Chari 3	18.06	0.48*	7.43	-1.33**	332.3	-	0.42	-0.06**	7.44	0.04	369.66	-

					0	53.60**						19.58**
SSG -59-3	25.77	1.49**	9.06	-0.95**	390.66	5.52	0.42	0.05**	6.69	0.16	375.53	22.73**
HJ 513	17.58	-0.01	10.56	0.76**	415.09	62.13**	0.34	-0.06**	8.76	-0.07	363.03	-19.45**
UP Chari 4	18.69	-1.42**	9.93	-0.39*	357.38	23.84**	0.41	0.03**	7.22	-1.54**	342.03	-19.40**
ICSV 700	24.46	1.84**	6.96	0.03	296.28	31.74**	0.49	0.02	7.37	0.26	289.20	29.60**
UP Chari 3	18.67	0.54**	10.73	1.35**	368.73	1.33	0.34	0.05**	6.53	-0.07	336.30	-20.76**
UP Chari 2	16.27	0.25	6.86	-0.33*	370.11	-7.79	0.46	-0.02*	7.35	0.40*	351.40	-13.42**
UP Chari 1	21.74	-0.40*	8.53	1.17**	374.76	14.44*	0.56	0.02**	8.77	-0.15	356.80	-3.05
Pusa Chari 9	18.60	1.56**	8.06	1.36**	359.57	43.70**	0.43	0.10**	6.33	0.16	349.46	56.16**
Rajasthan Chari 1	14.95	0.51	7.36	0.55**	343.24	51.62**	0.39	0.01	6.54	0.39*	340.93	-12.12**
Tester												
HC 308	16.13	1.12**	7.76	0.43**	393.90	12.96**	0.50	0.35**	7.41	0.29**	388.33	24.17**
Pant Chari 6	18.96	-0.68**	8.46	-0.37**	394.29	15.42**	0.55	0.01	7.83	-0.15**	318.10	-8.93**
G 48	20.96	0.58**	6.63	0.09	345.72	-26.10**	0.3	-0.05**	7.52	-0.15	316.80	15.11**
HC 171	22.43	1.22**	6.66	-0.06	399.61	22.28**	0.47	0.44**	6.92	0.31**	378.20	19.86**

Table 4. Estimates of specific combining ability effect with respect 12 characters in forage sorghum

Crosses	**Days to 50% flowering**		**Plant height (cm)**		**No. of leaves per plant**		**Stem girth (cm)**		**Leaf length (cm)**		**Leaf breadth (cm)**	
	Mean	**SCA**	**Mean**	**SCA**	**Mean**	**SCA**	**Mean**	**SCA**	**Mean**	**SCA**	**Mean**	**SCA**
HC 260 X HC 308	91.16	5.76**	163.32	20.11**	11.80	2.99**	1.80	-0.17	75.89	2.57**	6.38	1.09**
HC 260 X Pant Chari 6	85.16	-3.24**	148.61	-13.12**	13.45	-0.14	1.93	0.01	81.38	10.27**	7.14	0.58**
HC 260 X G 48	85.93	2.87**	152.21	16.85**	13.63	1.62**	1.93	0.64**	65.48	3.48**	5.72	-0.16
HC 260 X HC 171	81.15	-3.39**	170.10	15.86**	13.74	0.50	2.20	0.20	60.56	-9.36**	5.80	-0.51
Pusa Chari 23 X HC 308	88.86	2.86**	170.23	-5.14	14.81	-0.13	2.04	0.22**	69.87	-2.32**	6.80	0.10
Pusa Chari 23 X Pant Chari 6	89.40	0.41	171.06	-2.88	16.00	1.26**	1.66	-0.12	70.08	0.10	6.22	-0.75**
Pusa Chari 23 X G 48	85.15	-0.50	171.16	3.93	11.98	-1.18**	1.88	0.05	69.62	1.79	6.39	0.09
Pusa Chari 23 X HC 171	82.38	-2.76**	170.49	4.09	14.44	0.05	1.71	-0.15	69.23	0.44	7.30	0.56**
SPV 815 X HC 308	78.36	-0.21	188.69	-1.50	14.62	0.37	1.95	0.12	74.10	-0.97	6.90	0.33
SPV 815 X Pant Chari 6	78.86	-2.70**	179.49	-9.21**	12.49	-1.56**	1.52	-0.25**	72.63	-0.21	5.77	-1.08**
SPV 815 X G 48	78.13	-0.09	187.65	5.61	12.39	-0.09	1.89	0.07	71.09	0.41	7.87	1.70**
SPV 815 X HC 171	80.70	2.99**	186.31	5.10	14.99	1.28**	1.92	0.06	72.38	0.74	5.65	-0.95**
Pusa Chari 6 x HC 308	80.97	0.28	201.28	-13.57**	13.82	-0.95**	1.85	0.06	67.72	-1.60	4.34	-0.27
Pusa Chari 6 x Pant Chari 6	82.30	-1.39	219.65	6.29	13.25	-1.31**	1.56	-0.18	67.54	0.42	5.19	0.30
Pusa Chari 6 x G 48	80.01	-0.34	219.36	12.66**	14.50	1.51**	1.90	0.10	68.62	3.65**	4.10	-0.11
Pusa Chari 6 x HC 171	81.28	1.45	200.49	-5.38	14.95	0.74	1.85	0.02	63.45	-2.47**	4.74	0.09
CSV 15 x HC 308	82.56	-0.65	277.43	2.30	13.86	-0.30	1.25	-0.24**	78.70	3.51**	5.92	0.07
CSV 15 x Pant Chari 6	87.43	1.22	269.34	-4.30	14.60	0.63	2.01	0.56**	69.44	-3.55**	7.11	0.99**
CSV 15 x G 48	81.75	-1.12	267.78	0.81	12.93	0.54	1.413	-0.09	67.14	-3.69**	8.87	-0.58**

CSV 15 x HC 171	82.90	0.55	267.34	1.19	12.75	-0.87	1.29	-0.24**	5.52	3.73**	5.39	-0.49
Pant Chari 3 x HC 308	71.83	4.80**	247.51	-13.38**	12.83	-1.06**	1.11	-0.20	83.82	1.16	4.96	0.09
Pant Chari 3 x Pant Chari 6	80.86	1.23	245.08	-14.33**	12.82	-0.87	1.30	0.03	86.22	5.77**	5.01	-0.23
Pant Chari 3 x G 48	76.62	5.33**	283.60	30.85**	13.65	1.54**	1.34	0.03	70.38	7.92**	4.84	1.27**
Pant Chari 3 x HC 171	79.16	3.24**	248.78	-3.14	13.74	0.40	1.49	0.14	80.25	1.00	4.96	-0.04
SSG-59-3 x HC 308	88.08	1.93	257.76	-25.28**	14.95	0.85	1.71	-0.01	61.14	-5.89**	7.59	0.15
SSG-59-3 x Pant Chari 6	97.23	2.68**	289.07	7.53	14.62	0.71	1.56	0.22**	64.32	-0.50	7.55	-0.17
SSG-59-3 x G 48	83.46	2.85**	299.03	24.12**	11.03	1.29**	1.57	0.75**	61.69	8.98**	6.53	1.51**
SSG-59-3 x HC 171	83.02	-2.27**	267.69	-6.37	13.28	-0.27	1.70	-0.06	71.06	7.38**	8.03	0.53**
HJ 513 x HC 308	89.48	5.93**	299.58	11.65**	15.37	1.79**	1.70	0.81**	84.21	7.16**	7.53	1.06**
HJ 513 x Pant Chari 6	94.03	3.58**	290.26	-6.18	15.51	0.53	1.99	0.32**	64.32	-10.52**	8.98	1.12**
HJ 513 x G 48	84.61	-2.49**	301.61	11.83**	14.11	0.71	1.57	-0.14	71.70	-1.00	6.97	-0.22
HJ 513 x HC 171	83.46	3.12**	281.64	17.31**	13.20	1.43**	1.52	0.67**	78.02	4.37**	6.77	1.84**
UP Chari 4 x HC 308	82.21	-0.99	299.59	7.90	14.60	0.07	2.13	0.18	75.44	-0.09	6.87	-0.08
UP Chari 4 x Pant Chari 6	85.02	-1.18	296.79	6.59	13.88	-0.45	1.70	-0.21	74.08	0.75	7.10	-0.13
UP Chari 4 x G 48	83.85	0.99	259.38	-24.16**	11.94	-0.82	1.93	-0.03	71.82	0.65	6.52	-0.03
UP Chari 4 x HC 171	83.52	1.18	292.38	9.67**	15.19	1.20**	2.06	0.07	70.82	-1.31	7.22	0.24
ICSV 700 x HC 308	83.58	4.61**	291.07	12.91**	15.89	1.99**	1.74	0.04	74.95	2.27**	7.75	1.35**
ICSV 700 x Pant Chari 6	89.31	2.12	280.83	4.16	13.65	-0.04	1.51	-0.14	65.02	-5.46**	8.07	0.39
ICSV 700 x G 48	83.45	-0.40	255.78	-14.23**	10.58	-1.54**	1.77	0.07	72.63	4.30**	6.54	-0.46
ICSV 700 x HC 171	82.23	-1.10	266.34	-2.84	12.94	-0.41	1.76	0.03	68.17	-1.11	7.16	-0.27
UP Chari 3 x HC 308	81.06	-0.46	281.31	0.51	12.94	-0.42	1.74	0.05	74.24	-1.63	5.98	-0.51
UP Chari 3 x Pant Chari 6	82.49	-2.03**	287.33	8.02	12.93	-0.23	1.67	-0.08	75.39	1.73	7.04	0.26
UP Chari 3 x G 48	82.24	1.06	257.60	-15.05**	11.11	-0.48	1.96	0.17	74.42	2.91**	5.83	-0.27
UP Chari 3 x HC 171	82.08	1.42	278.33	6.51	13.94	1.13	1.79	-0.04	69.45	-3.02**	7.04	0.51
UP Chari 2 x HC 308	83.54	-0.60	294.63	3.71	15.76	0.96	1.72	-0.16	73.12	1.60	8.46	1.77**
UP Chari 2 x Pant Chari 6	89.31	0.17	295.35	5.92	15.12	0.53	1.96	0.12	65.20	-4.12**	6.43	-0.54*
UP Chari 2 x G 48	82.99	5.81**	278.81	15.96**	13.15	1.84**	2.02	0.93**	62.46	6.70**	6.39	1.09**
UP Chari 2 x HC 171	82.51	-0.79	276.28	-5.66*	12.61	-1.64**	1.82	-0.09	75.35	7.23**	5.41	-1.32**
UP Chari 1 x HC 308	82.62	-0.25	286.08	4.92	16.60	1.98**	1.94	0.13	72.07	-1.35	6.06	-0.93**
UP Chari 1 x Pant Chari 6	85.53	-0.34	284.57	17.90**	14.44	1.03**	1.52	0.25**	73.09	5.87**	7.71	1.45**
UP Chari 1 x G 48	84.32	1.79	263.82	-9.19**	13.64	0.81	1.74	-0.08	71.58	2.52**	6.09	-0.49
UP Chari 1 x HC 171	80.80	-1.21	271.56	-0.63	11.25	-2.82**	2.04	0.19	66.99	-3.03**	7.99	0.98**
Pusa Chari 9 x HC 308	81.74	-0.98	292.51	4.07	14.20	-0.42	2.05	0.09	65.55	-5.28**	7.20	-0.65**
Pusa Chari 9 x Pant Chari 6	85.15	-0.57	293.87	6.92	13.90	-0.53	1.98	0.12	72.89	4.26**	7.92	-0.21
Pusa Chari 9 x G 48	83.55	1.17	268.28	-12.01**	12.29	-0.56	1.69	-0.23*	69.97	3.49**	7.23	-0.21
Pusa Chari 9 x HC 171	82.25	3.38**	280.47	13.13**	15.58	1.59**	1.97	0.52**	64.96	2.47**	8.94	1.07**
Rajasthan Chari 1 x HC 308	81.28	-3.31**	308.03	20.78**	13.5	-1.15**	2.00	0.05	75.36	0.83	7.23	-0.36
Rajasthan Chari1xPantChari6	85.62	-1.97	285.45	-0.32	15.96	1.44**	1.81	-0.15	71.53	-0.80	6.89	-0.98**
Rajasthan Chari 1 x G 48	86.12	3.87**	270.75	18.36**	12.02	1.92**	2.15	0.64**	72.23	2.06**	8.10	0.90**
Rajasthan Chari 1 x HC 171	87.14	3.41**	266.19	-12.10**	14.80	0.63	2.05	0.01	69.04	-2.09**	8.07	0.44
Crosses	**Internode length (cm)**		**Total soluble solids (%)**		**Leaf area (cm^2)**		**Leaf stem ratio (w/w)**		**Protein content (%)**		**Green fodder yield per plant (g)**	

	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
HC 260 X HC 308	20.55	3.79**	10.97	2.44**	343.89	72.63**	0.69	0.83**	7.88	1.59**	434.67	98.35**
HC 260 X Pant Chari 6	17.50	0.29	7.36	-0.36	413.06	79.34**	0.45	-0.07	5.88	0.04	282.26	-20.96**
HC 260 X G 48	16.38	2.09**	7.06	1.04**	266.57	65.62**	0.31	0.90**	4.93	1.89**	213.90	83.14**
HC 260 X HC 171	17.12	-1.99**	7.00	-1.04**	249.67	-66.35**	0.54	0.04	5.27	-0.74	317.76	-4.24
Pusa Chari 23 X HC 308	16.37	-2.85**	7.63	-0.26	337.71	-5.88	0.39	-0.01	7.74	-0.05	298.96	-36.96**
Pusa Chari 23 X Pant Chari 6	20.02	0.35	8.00	0.91	309.72	-36.33**	0.39	-0.05	6.44	-0.90	299.29	-3.54
Pusa Chari 23 X G 48	22.23	1.31**	7.13	-0.34	316.02	1.50	0.48	0.04	7.07	-0.28	310.17	3.52
Pusa Chari 23 X HC 171	22.75	1.19**	7.10	-0.30	359.05	30.71**	0.45	-0.52**	8.75	-1.23**	378.60	46.98**
SPV 815 X HC 308	18.71	1.03**	7.30	-0.27	363.15	2.97	0.27	-0.09	7.140	0.06	358.99	5.84
SPV 815 X Pant Chari 6	17.80	-0.33	6.94	0.16	297.75	-54.89**	0.41	0.02	7.106	0.47	355.84	25.79**
SPV 815 X G 48	19.03	-0.36	7.65	0.50	397.32	86.22**	0.47	0.07	6.350	-0.29	321.39	-2.48
SPV 815 X HC 171	19.68	-0.34	6.69	-0.39	290.63	-44.30**	0.42	0.02	6.563	-0.24	379.69	-29.15**
Pusa Chari 6 x HC 308	9.340	0.89	7.72	-0.59	209.01	-21.86**	0.44	0.07	7.656	0.14	509.23	-7.87
Pusa Chari 6 x Pant Chari 6	11.33	2.44**	6.72	-0.79	249.03	5.70	0.43	0.01	7.586	0.51	500.82	-3.19
Pusa Chari 6 x G 48	9.21	-0.95	6.05	-1.84**	199.97	8.16	0.39	-0.02	6.633	-0.45	515.41	7.58
Pusa Chari 6 x HC 171	8.41	-2.38**	11.05	3.23**	213.63	-2.00	0.34	-0.06	7.050	-0.20	526.27	3.48
CSV 15 x HC 308	18.37	-2.09**	8.11	-0.64	330.81	7.00	0.37	-0.05	6.736	-0.32	434.17	-7.75
CSV 15 x Pant Chari 6	20.31	-0.59	7.90	-0.05	350.97	34.71**	0.59	0.12	6.773	0.16	443.34	24.52**
CSV 15 x G 48	22.20	0.04	8.70	0.38	232.34	-42.40**	0.42	-0.04	7.693	1.07**	425.30	2.66
CSV 15 x HC 171	25.45	2.65**	8.56	0.31	289.25	-9.31	0.42	-0.03	5.86	-0.91	408.17	-2.43
Pant Chari 3 x HC 308	21.16	3.06**	6.87	-0.12	295.87	0.95	0.34	-0.03	7.03	-0.07	349.53	-7.92
Pant Chari 3 x Pant Chari 6	19.51	1.11**	7.44	1.25**	307.22	9.84	0.41	-0.01	6.80	0.14	324.13	-27.23**
Pant Chari 3 x G 48	18.02	1.64**	6.25	1.31**	242.05	43.80**	0.49	0.19	6.913	0.95	400.66	72.49**
Pant Chari 3 x HC 171	17.78	-2.52**	5.68	-0.82	282.70	3.02	0.34	-0.05	6.51	-0.32	375.80	2.66
SSG-59-3 x HC 308	16.40	-2.56**	7.81	0.44	329.79	-24.26**	0.46	-0.01	6.88	-0.34	399.61	-20.15**
SSG-59-3 x Pant Chari 6	19.50	0.09	6.93	0.36	344.79	-1.72	0.63	0.11	6.01	-0.68	414.01	27.33**
SSG-59-3 x G 48	22.11	1.44**	5.94	1.00**	284.98	29.01**	0.46	0.55**	6.77	-0.01	441.35	80.87**
SSG-59-3 x HC 171	22.34	1.04**	7.08	0.20	403.79	64.98**	0.47	-0.04	7.98	1.03**	367.39	-48.05**
HJ 513 x HC 308	17.46	2.01**	8.01	1.07**	450.24	39.59**	0.37	0.65**	7.27	1.28**	398.38	90.80**
HJ 513 x Pant Chari 6	17.07	-0.84	8.22	-0.25	410.50	-2.61	0.25	-0.16	6.05	-0.50	341.18	-3.30
HJ 513 x G 48	18.13	-1.04**	10.26	1.57**	354.88	-6.70	0.59	0.18	6.51	-0.04	319.50	-28.80**
HJ 513 x HC 171	21.70	1.89**	8.14	1.45**	375.14	20.27**	0.38	-0.02	6.99	0.27	394.56	91.30**
UP Chari 4 x HC 308	15.39	-0.67	6.82	-1.11**	368.05	-4.32	0.40	-0.06	6.49	0.97	394.43	16.80**
UP Chari 4 x Pant Chari 6	17.43	0.93	7.76	0.63	373.70	-1.12	0.51	0.07	5.55	0.47	359.36	4.83
UP Chari 4 x G 48	18.78	1.02**	8.72	1.22**	332.73	-0.57	0.58	0.09	4.44	-0.65	324.52	-3.84
UP Chari 4 x HC 171	17.11	-1.29**	6.70	-0.79	363.13	6.01	0.47	-0.02	4.45	-0.79	375.53	2.21
ICSV 700 x HC 308	20.78	1.47**	7.98	1.36**	412.56	32.29**	0.43	-0.01	7.87	1.55**	415.78	90.84**
ICSV 700 x Pant Chari 6	18.75	-1.02**	7.39	-0.15	372.59	-0.14	0.50	0.03	7.40	0.52	395.85	-7.68
ICSV 700 x G 48	20.67	-0.36	8.86	0.94	337.39	-3.82	0.42	-0.06	6.25	-0.63	413.51	6.16
ICSV 700 x HC 171	21.57	-0.09	7.42	-0.43	346.69	-8.33	0.55	0.07	6.61	-0.44	424.67	2.36
UP Chari 3 x HC 308	18.85	0.83	9.29	-0.37	315.40	-34.46**	0.42	-0.06	6.90	-0.10	379.84	3.56
UP Chari 3 x Pant Chari 6	16.74	-1.73**	10.16	1.30**	376.84	24.52**	0.56	0.03	6.83	0.28	356.97	3.80
UP Chari 3 x G 48	21.24	1.51**	9.33	0.09	308.15	-2.64	0.51	-0.01	6.50	-0.06	330.23	-6.76
UP Chari 3 x HC 171	19.76	-0.61	8.16	-1.01**	347.18	1.57	0.55	0.04	6.60	-0.12	381.36	9.40

UP Chari 2 x HC 308	16.64	-1.10**	8.63	0.64	439.53	98.79**	0.38	-0.02	7.26	-0.020	389.37	5.76
UP Chari 2 x Pant Chari 6	18.46	0.28	6.60	-0.59	298.01	-45.20**	0.44	-0.02	6.84	-0.18	335.16	-25.35**
UP Chari 2 x G 48	20.19	2.75**	7.11	1.46**	283.84	77.83**	0.44	0.89**	6.65	1.37**	375.80	81.47**
UP Chari 2 x HC 171	20.10	0.07	7.90	0.41	289.72	-35.77**	0.49	0.05	7.94	0.75	377.42	-1.87
UP Chari 1 x HC 308	18.08	1.00**	10.74	1.25**	309.94	-53.02**	0.50	0.74**	5.34	-1.57**	380.51	-3.46
UP Chari 1 x Pant Chari 6	15.99	1.53**	7.05	1.63**	400.25	34.83**	0.52	0.01	6.08	-0.39	379.81	88.93**
UP Chari 1 x G 48	18.27	-0.52	10.03	0.97**	309.75	-4.15	0.41	-0.09	8.32	1.95**	370.24	5.54
UP Chari 1 x HC 171	20.47	1.05**	8.40	-0.59	380.06	32.34**	0.51	0.03	6.74	0.10	388.65	-1.01
Pusa Chari 9 x HC 308	18.08	-0.97	6.08	-1.88**	334.90	-57.33**	0.57	0.05	6.66	-0.56	423.33	-29.86**
Pusa Chari 9 x Pant Chari 6	19.47	-0.02	7.12	-0.03	410.06	5.37	0.58	0.00	6.91	0.14	441.71	1.62
Pusa Chari 9 x G 48	20.94	0.19	7.53	0.06	359.33	6.17	0.56	-0.01	6.84	0.06	412.93	-0.98
Pusa Chari 9 x HC 171	22.18	1.80**	9.38	1.91**	412.77	35.79**	0.51	-0.04	7.30	1.36**	478.11	99.23**
Rajasthan Chari 1 x HC 308	16.17	-1.82**	10.77	1.90**	387.05	-3.09	0.38	-0.05	7.08	-0.37	388.63	3.72
RajasthanChari1xPantChari 6	19.06	0.57	7.12	-0.95**	350.32	-52.29**	0.5	0.02	6.92	-0.08	376.24	4.43
Rajasthan Chari 1 x G 48	20.40	1.71**	7.77	1.67**	415.57	54.49**	0.49	0.68**	7.46	1.44**	341.35	94.29**
Rajasthan Chari 1 x HC 171	20.86	0.53	8.090	-0.28	395.79	1.89	0.47	0.01	7.19	0.01	376.74	-3.86

RESULT AND DISCUSSION

The results of analysis of variance revealed that significant variability existed among the parents with regard to all the characters under investigation. Such divergences of parents lead to development of F_{1s} that differed significantly among themselves for all characters. The estimates of combining ability variances are translated in to genetic variance to understand the nature and magnitude of gene action and develop guidelines for selecting parents for hybridization. It is an established fact that additive genetic variance results mostly from additive gene action while non additive genetic variance is comprised of dominant and epistasis. Estimates of variance due to line x tester showed highly significant for all the characters except number of leaves per plant and stem girth. Further partitioning of treatment variance into parents and crosses were revealed highly significant differences for all the characters and variance due to parent *vs* crosses was observed significant for all the traits except days to 50% flowering (Table-1). These results are in general agreement with the findings Aaref *et al.* (2016), Rini *et al.* (2016) and Chikuta *et al.* (2017). The variance among line with respect to gca was found highly significant for all the attributes. The variance among testers with respect to gca was recorded highly significant for all the characters except stem girth while variances among crosses due to interaction between lines x testers genotypes with respect to sca were expressed highly significant for all the traits except stem girth and leaf stem ratio which indicate that both additive and dominance genetic variance were involved in the determination of these attributes and the parents and their progenies differed for their combining ability effects (Table 2). Aaref *et al.* (2016), Jain and Patel (2016) and Chikuta *et al.* (2017) reported that same of the morphological and quality traits were determined by additive and other by non additive effects for yield. The ratio δ^2g/δ^2s being more than unity for the traits *viz.*, plant height, leaf breadth, internode length, leaf area and green fodder yield per plant which indicated that the involvement of additive gene action. To exploit the additive genetic variance in the improvement of such attributes, pedigree method of breeding can be used. Similar findings were also observed by Jain and Patel (2016) and Chikuta *et al.* (2017). Average degree of dominance $(\delta^2_s/\delta^2_g)^{0.5}$ exhibited partial dominance for plant height, leaf length, leaf breadth, internode length, leaf area, leaf stem ratio and green fodder yield, suggesting there by the preponderance of additive type of gene action with partial dominance in the expression of these characters in this crop. Over dominance was observed for days to 50% flowering, number of leaves per plant, stem girth, total soluble solids and protein content which indicated that gene action is fixable and these attributes played an important role for population improvement in this crop. Magnitude of δ^2_s was higher than δ^2_g for all the traits except stem girth and protein content, indicating role of dominance gene action and interaction were involved in the expression of these traits (Table 2). These findings are in close conformity with Aaref *et al.* (2016), Jain and Patel (2016) and Chikuta *et al.* (2017). Parents among lines, HC260 were identified as a good general combiner for all the attributes except total soluable solids and protein content. Parent Pusa Chari23 appeared as a good general combiner for all the characters except stem girth and leaf breadth. Genotype SPV815 was found to be good general combiner for all the traits except number of leaves per plant, leaf stem ratio and protein content. Line Pusa Chari6 emerged as a good general combiner for all the characters except leaf stem ratio. Parent CSV15 expressed as a good general combiner for leaf length, internode length total soluble solids and green fodder yield per plant. Genotype SSG-59-3 was proved to be good general combiner for days to 50% flowering, leaf breadth, internode length, leaf stem ratio and green fodder yield per plant and line ICSV700 was considered as desirable good general combiner for leaf breadth, internode length, leaf area and green fodder yield per plant and parent Pusa Chari9 was identified as good general combiner for all the attributes except days to 50% flowering and protein content. Among the testers HC308 was appeared good general combiner for all the traits except days to 50% flowering. Male G48 possessed as a good general combiner for internode length and green fodder yield per plant and tester HC171 proved as a good general combiner for all the characters except total soluble solids (Table 3). Similar results have been reported by Kumar and Shrotria (2016), Rini *et al.* (2016) and Chikuta *et al.* (2017). These parents may be handled in suitable breeding programme *visa-vis* selection breeding for improvement productivity of green fodder yield and per unit area in this crop. 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 increased brix and protein contents can be exploited for the improvement of quality of fodder sorghum thereby enhancing the nutritive value of the crop. Out of the sixty F_1's hybrids, only sixteen cross combinations *viz.*, HC260 x HC308, HC260 x G48, Pusa Chari23 x HC171, SPV815 x Pant Chari6, CSV15 x Pant Chari6, Pant Chari3 x G48, SSG-59-3 x Pant Chari6, SSG-59-3 x G48, HJ513 x HC308, HJ513 x HC171, UP Chari4 x HC308, ICSV700 x HC308, UP Chari2 x G48, UP Chari1 x Pant Chari6, Pusa Chari9 x HC171 and Rajasthan Chari1 x G48 noted significant and positive specific combining ability effects for maximum attributes including green fodder yield per plant for 8 to 11 other contributing traits, which proved as best specific combiners for *per se* performance and also may be utilized for obtaining transgressive segment in the next generation (Table 4). These findings were supported by Aaref *et al.* (2016), Jain and Patel (2016), Kumar and Shrotria (2016), Rini *et al.* (2016), Chikuta *et al.* (2017). These identified specific cross combinations should be exploited through heterosis breeding may be used in recombination programme for tapping desirable transgrassive segregants in segregating generations. The inter mating between selected segregants in advanced generations would help to accumulate favorable, desirable alleles for further improvement in yield and its component traits. The crosses which exhibited high specific combining ability, involving good combiner and moderate combiner, such a combination may throw up desirable transgressive segregates, if the additive genetic system is present in the good combiner and complementary effect in present in the crosses, act in the same direction so as to maximize the desirable plant attributes. Breeding for homozygous line by routine pedigree method could mean only partial exploitation of additive genetic variance in order to exploit different type of gene action in a population. It is suggested that a breeding procedure which may accumulate the fixable type of gene effect and at the same time maintains considerable heterozygosity for exploiting the dominance gene effect, might prove most beneficial in improving the population under study.

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