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COMBINING ABILITY AND HETEROSIS STUDIES FOR YIELD AND WATER USE EFFICIENCY IN FORAGE SORGHUM [*SORGHUM BICOLOR* (L.) MOENCH] TOPCROSSES UNDER NORMAL AND WATER STRESS ENVIRONMENTS

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SUMMARY

Sorghum is an important fodder crop of Punjab during **kharif** season. There is deficiency of fodder during this season and increase in productivity through hybrid breeding is an effective solution. As water stress is one of the major causes for crop losses worldwide therefore there is a need to breed for more water use efficient genotypes. To achieve the objective 15 male sterile lines were crossed to four random mating populations to generate 60 topcrosses to study combining ability and heterosis for forage yield and physiological traits affecting water use efficiency (WUE) under two environments viz., normal (N) and water stress (S). Based on general combining ability (gca) effects, male sterile lines viz., 2077A, NSS1007A, NSS1008A and population RSSV-9 were good general combiner parents for green fodder yield and WUE under both the environments. Two topcross hybrids 94002A x RSSV-9 and NSS1007A x Ramkel had high sca effects and significant heterosis over commercial check Punjab Sudax Chari (PSC-1) for green fodder yield and WUE traits in both the environments. As the released interspecific hybrid PSC-1 faces seed production problems under Punjab conditions, these two high yielding and water use efficient, intraspecific hybrids will help to overcome the problem of hybrid seed production.

Key words : Forage sorghum, environments, combining ability, heterosis

Sorghum is an important **kharif** fodder crop of Punjab. The green fodder requirement in the state is more than the green fodder production. There is little scope of increasing area under fodder crops, thus, increasing the productivity is the only solution to overcome the fodder deficiency. After the discovery of cytoplasmic-genetic male sterility in sorghum (Stephens and Holland, 1954), exploitation of heterosis became practical breeding approach to increase productivity. The topcross between an inbred line and an open pollinated parent as suggested by Davis (1927) and Jenkins and Brunson (1932) offers some advantages over single cross hybrids and are easy to breed. The concepts of general combining ability (gca) and specific combining ability (sca) were defined in terms of topcross data (Sprague and Tatum, 1942). To initiate the hybrid breeding programme for the improvement of any character, it is important to know combining ability of parents, extent of heterosis and genetic control for that particular character.

Increasing crop drought tolerance is the core issue for modern agriculture under global climate change. To cope with such a situation the water use efficiency (WUE) of genotypes needs to be improved. Direct selection for fodder yield in dry environments is inefficient due to large seasonal variation in weather and generally a large genotype x environment interaction which results in low heritability for yield. The selection for an underlying physiological trait, that limits yield under stress environment, could be effective and can contribute substantially to yield improvements (Richards *et al.*, 2002). The accumulation of the amino acid proline in tissues of several plant species is regarded as a general response to water and other kinds of stresses (Chen *et al.*, 1964; Barnett and Naylor, 1966). Proline has been proposed to act as a compatible solute that adjusts the osmotic potential in the cytoplasm. Thus, proline can be used as a metabolic marker in relation to stress (Caballero *et al*., 2005). Scanty reports are available regarding use of top crosses and inheritance of physiological traits affecting water use efficiency (WUE) and selection of parents for high fodder yield under water stress conditions in forage sorghum hybrids. The purpose of present study was evaluation of sorghum A-lines and random mating populations for combining ability and to assess heterosis for yield and WUE traits through topcrosses under normal and water stress environments.

MATERIALS AND METHODS

Sixty topcrosses were obtained by crossing 15 cytoplasmic male sterile lines (A-lines) with four random mating populations. For the adequate production of top cross seed, staggered planting of both CMS lines and random mating populations was done. Twenty ears of each topcross from each CMS line were harvested. Sixty topcrosses and the parents were evaluated along with hybrid check Punjab Sudax Chari (PSC-1) in a randomized block design with three replications under two environments viz., normal (N) and water stress (S). The environments were created by applying normal five irrigations in normal environment and by skipping the second and fourth irrigations in the water stress environment. The topcrosses were planted at the experimental area of Forage Section, Department of Plant Breeding and Genetics, Punjab Agricultural University (PAU), Ludhiana on 16th April, 2012. All the entries were planted in a plot size of 3 x 1.25 m (3 meter row length and 0.25 meter distance between the rows) with five rows of each. The standard agronomic practices as per package of practices of the PAU were followed to raise the crop.

Ludhiana represents the Indo-Gangetic plains and is situated at $30^0$54´N latitude, $75^0$51´E longitude and at a mean height of 247 meters above sea level. The maximum and minimum air temperature ranged between 43.7°C to 17.6°C and the relative humidity ranged from 17.0 to 88.0 per cent during the crop season. Total rainfall received during the crop season was 124.6 mm.

Data were recorded for green fodder yield (kg/plot), dry fodder yield (kg/plot), relative leaf water content (%), leaf area index, photosynthetic capacity (SPAD reading), specific leaf weight (mg/cm^2) and proline content (nmol/g). Relative leaf water content (RWC) was calculated (Weatherley, 1950) as [(Fresh weight-Dry weight)/(Saturated weight-Dry weight)] x 100. Leaf area index (LAI) was measured using canopy analyzer (Sunscan-type SS1) in each row of all lines in a plot, under field conditions. Photosynthetic efficiency in terms of chlorophyll content was recorded by soil plant analytical development (SPAD) chlorophyll meter in five intact plants per plot (using third-fourth leaf from top of plant) in each replication of all genotypes. Specific leaf weight (SLW) was measured as the ratio of dry matter of leaves per plant (g) divided by leaf area per plant. Proline content was estimated according to method suggested by Bates *et al.* (1973).

The mean data were subjected to analysis of variance based on the line x tester as proposed by Kempthorne (1957). Heterosis values were calculated as the increase or decrease of F_1 over respective male parent and commercial check (PSC-1) and were expressed in percentage.

RESULTS AND DISCUSSION

The analysis of variance showed significant variation among the populations (male parents), CMS lines (female parents), hybrids and parent versus hybrids comparison for all the characters except for photosynthetic capacity (data not shown). The analysis of variance for combining ability in normal environment and water stress environments showed that the mean squares due to males and females were significant for all the characters except for photosynthetic capacity and green fodder yield in case of females under stress environment (Tables 1 and 2). The mean squares due to male x female were significant for all the characters in both the environments which indicated the importance of specific combining ability (sca) in the genetic expression of these characters among hybrids.

The differences in gca are mainly due to additive genetic effects and higher order additive interaction. In contrast, the differences in sca are attributed to non-additive dominance and other types of epistasis (Falconer, 1989). This analysis, therefore, allows broad inferences on the nature of the gene effects for a trait under study. The ratios of sca and gca variances (s^2sca/s^2gca) in both the environments indicated the preponderance of non-additive gene action in the interaction of all the traits (Tables 1 and 2). These findings are in agreement with those already reported by Iyanar and Khan (2004), Sumalini *et al.* (2005) and Mohammed (2009). The proportional contribution of lines, testers and line x tester revealed that contribution of line x tester was greater than that of either lines or testers for all the characters under both the environments which confirms

TABLE 1
Combining ability analysis for different traits under normal environment

Source	d. f.	Green fodder yield (kg/plot)	Dry fodder yield (kg/plot)	Relative water content (%)	Leaf area index	Photosynthetic cap (SPAD reading)	Specific leaf wt. (mg/cm^2)	Proline (nmol/g)
Rep	2	26.24	1.92	571.79	5.90	221.36	8.59	686.70
Males (T)	3	197.54**	24.52**	93.51**	9.23**	234.17**	8.90**	11805.00**
Female (L)	14	41.62**	4.94**	61.24**	8.03**	173.86**	9.27**	6519.30**
Male x female (T x L)	42	30.09**	2.92**	86.33**	3.73**	109.18**	7.85**	6333.60**
Error	118	5.84	0.41	10.87	0.14	18.23	0.64	222.30
Estimation of genetic components								
s^2_{gca}		3.14	0.41	†	0.17	3.33	0.04	99.25
s^2_{sca}		8.08	0.84	25.15	1.20	30.32	2.40	2037.10
s^2_{sca}/ s^2_{gca}		2.57	2.05	‡	7.06	9.11	60.00	20.52
Proportional contribution								
Contribution of lines		23.89	26.05	18.00	37.88	31.52	26.69	23.24
Contribution of testers		24.30	27.71	5.89	9.33	9.10	5.49	9.02
Contribution of lines x testers		51.81	46.19	76.12	52.79	59.38	67.82	67.74

*,**Significant at P=0.05 and P=0.01 levels, respectively.

† Negative component interpreted as zero.

‡ Genetic ratio not calculated because of negative genetic component.

TABLE 2

Combining ability analysis for different traits under water stress environment

Source	d. f.	Green fodder yield (kg/plot)	Dry fodder yield (kg/plot)	Relative water content (%)	Leaf area index	Photosynthetic cap (SPAD reading)	Specific leaf wt. (mg/cm^2)	Proline (nmol/g)
Rep	2	271.80	19.13	325.22	6.02	790.30	15.21	4346.70
Males (T)	3	61.90**	6.30**	98.38**	2.57**	94.20**	10.90**	154898.00**
Female (L)	14	14.54	2.60**	50.06**	3.30**	33.49	11.76**	35426.40**
Male x female (T x L)	42	21.39**	1.42*	117.69**	1.86**	62.18*	14.13**	17448.30**
Error	118	3.58	0.25	3.87	0.17	29.65	0.85	550.10
Estimation of genetic components								
s^2_{gca}		0.59	0.11	†	0.04	0.06	†	2727.00
s^2_{sca}		5.94	0.39	37.94	0.56	10.84	4.43	5633.00
s^2_{sca}/ s^2_{gca}		10.07	3.55	‡	14.00	180.67	‡	2.07
Contribution of lines		0.59	0.11	†	0.04	0.06	†	2727.00
Contribution of testers		5.94	0.39	37.94	0.56	10.84	4.43	5633.00
Contribution of lines x testers		10.07	3.55	‡	14.00	180.67	‡	2.07

*, **Significant at P=0.05 and P=0.01 levels, respectively.

† Negative component interpreted as zero.

‡ Genetic ratio not calculated because of negative genetic component proportional contribution.

predominance of interaction of parents in the performance of topcross hybrids. The prevalence of non-additive gene action for all the characters suggested that development of hybrids would be beneficial in forage sorghum. The pooled analysis of variance over environments (data not given) revealed that gca of lines and testers interacted significantly with the environments for all the characters except for relative water content in case of testers. The female x male x environment interaction for combining ability were also significant for all the characters. This indicated that gca of parents and sca of crosses varied with change in environment as also reported earlier by Pathak and Sanghi (1992), Mahmoud and Ahmed (2010) and Bibi *et al.* (2012) in sorghum.

Combining ability analysis was performed to identify good combiner parents for yield and water use efficiency traits. Under normal (N) environment, A-lines, 2077A, AKMS-14A and NSS1007A were identified with significant gca effects for green and dry fodder yield (Table 3). The line, 2077A had highest gca effects for yield and significant gca effects for all the physiological traits affecting water use efficiency except specific leaf weight. Another line AKMS-14A had significant gca effects for photosynthetic capacity and specific leaf weight. The line NSS1007A was observed as a good general combiner for specific leaf weight, photosynthetic capacity and proline content, whereas NSS1008A was good general combiner for green fodder yield and specific leaf weight.

Three A-lines viz., 2077A, NSS1007A and NSS1008A also had significant gca effects for green and dry fodder yield under water stress environment and were stable across environments with respect to high gca effects for yield. In addition, the lines 940031A and NSS1005A were found to be good general combiners for yield. The lines 940031A, 2077A and NSS1005A were good general combiners for physiological traits affecting water use efficiency with significant gca effects for relative water content, leaf area index and proline content in stress environment. The female NSS1007A was good general combiner for leaf area index and proline content and NSS1008A had significant gca effects for proline content also.

Estimates of gca effects for the populations under environments showed that the population RSSV-9 was good general combiner male parent for green fodder yield and dry fodder yield in both the environments. In normal environment RSSV-9 had significant gca effects for proline content, however, under water stress environment, the same population was good combiner for relative water content, photosynthetic capacity and proline content. In general, the parents showing high mean performance did not show high gca effects for yield and other traits indicating the importance of combining ability analysis in selecting the parents to be used in hybrid breeding.

When interactions exist between male and female parents, as in this experiment, information on both gca and sca effects becomes imperative. Estimates of sca effects were calculated for all the 60 topcrosses. For green fodder yield, 12 topcrosses had significant values for sca effects under normal and 14 under water stress environment (Table 4). The cross combinations viz., 94002A x RSSV-9, 940031A x SSG59-3, AKMS-14A x HC308, NSS1002A x HC308 and NSS1007A x Ramkel appeared to be the promising with high sca effects for green fodder yield and WUE traits in both the environments. The worth of the topcross hybrids can be adjudged only if these show considerable heterosis over their respective male parents. The presence of considerable amount of heterosis over male parents for green fodder yield and high water use efficiency proved that the topcross hybrids were better than their respective male parents. The significant positive heterosis over check hybrid PSC-1 was exhibited by the hybrids for all the characters. A total of 47 topcross hybrids under Env-N and 13 topcross hybrids under Env-S exhibited significant heterosis over PSC-1 with respect to green fodder yield and WUE traits (Table 5). Maximum heterosis for green fodder yield was manifested by the cross AKMS-14A x HC308 (57.92%) under Env-N and for the cross 94002A x RSSV-9 (27.25%) under Env-S. Ten hybrids viz., 94002A x RSSV-9, AKMS-14A x RSSV-9, AKMS27-A x RSSV-9, 2077A x RSSV-9, NSS1007A x RAMKEL, NSS1002A x HC308, NSS1005A x HC308, NSS1006A x RSSV-9, NSS1005A x RAMKEL and NSS1008A x RSSV-9 for yield and WUE traits recorded significant positive heterosis across both the environments. These hybrids showing stable performance are more water use efficient and can prove to be high yielding under water stress environment. Prevalence of significant and positive standard heterosis for green fodder yield in sorghum has been reported by Aggarwal and Shrotria (2005), Bhatt (2008) and Hussain *et al.* (2012). As the released hybrid PSC-1 is an interspecific hybrid between sorghum and sudan-grass, its seed production is a problem under Punjab conditions. The production of topcross hybrids

TABLE 3

Estimates of gca effects of parents for different traits under normal (N) and water stress (S) environments

S. No.	Hybrids	Green fodder yield (kg/plot)		Dry fodder yield (kg/plot)		Relative water content (%)		Leaf area index		Photosynthetic cap (SPAD reading)		Specific leaf wt. (mg/cm^2)		Proline (nmol/g)	
		N	S	N	S	N	S	N	S	N	S	N	S	N	S
Lines															
1	94001A	-1.54**	-1.50**	-0.39**	-0.77**	1.51**	0.65	0.11*	0.09	1.65**	-2.48	0.19*	1.80**	-37.67**	-100.70**
2	94002A	-0.34	-0.01	-0.24**	0.02	-2.85**	-0.84	1.16**	0.38**	1.43*	1.48	0.40**	-0.17	-22.67**	-25.70**
3	94003A	0.40	-0.96*	-0.19*	-0.38**	1.35**	2.85**	0.63**	0.51**	2.99**	0.92	-0.59**	-0.79**	-10.17**	-55.70**
4	940012A	0.06	0.17	0.41**	-0.16	-0.39	0.99*	1.48**	0.53**	2.79**	1.63	-1.39**	-0.05	-10.17**	16.80*
5	940031A	-2.86**	1.24*	-0.05	0.52**	3.44**	2.81**	0.64**	0.29**	-3.50**	1.59	0.05	-1.66**	17.33**	41.80**
6	940056A	-0.70*	-0.67	0.74**	-0.59**	2.88**	-0.75	-0.93**	-0.42**	0.69	0.11	-0.79**	0.91**	-20.17**	-68.20**
7	AKMS-14A	2.63**	-1.29*	0.79**	-0.19	-0.86**	-0.84	-0.64**	-0.58**	1.59**	0.59	0.21*	-0.01	-30.17**	-53.20**
8	AKMS27-A	-0.80*	-0.50	-0.34**	-0.10	1.56**	-0.80	-1.60**	-1.22**	1.70**	1.05	0.68**	0.41	-10.17**	-40.70**
9	2077A	4.10**	1.25*	1.11**	0.48**	2.39**	2.12**	0.35**	0.40**	5.68**	1.73	-0.79**	-1.46**	42.33**	54.30**
10	NSS1002A	-0.94**	-1.50**	-0.60**	-0.29*	0.06	0.87	-0.78**	-0.55**	-4.57**	-2.10	-0.22*	-0.24	17.33**	4.30
11	NSS1003A	-2.08**	-0.67	-0.63**	-0.26*	-3.01**	-2.25**	0.15**	0.04	-1.24*	-2.96*	-0.21*	1.36**	27.33**	19.30**
12	NSS1005A	0.23	1.37*	0.09	0.91**	1.24**	2.76**	0.32**	0.58**	1.10*	1.61	-1.02**	-0.42	22.33**	71.80**
13	NSS1006A	-1.33**	0.42	-1.20**	-0.08	-1.42**	-2.30**	-0.50**	-0.44**	-9.74**	-1.87	0.20*	-0.40	12.33**	44.30**
14	NSS1007A	2.25**	1.42**	0.74**	0.53**	-2.81**	-1.90**	-0.06	0.25*	2.20**	-0.38	1.75**	-0.50*	12.33**	74.30**
15	NSS1008A	0.91**	1.25*	-0.22**	0.33*	-3.09**	-3.39**	-0.32**	0.12	-2.76**	-0.93	1.53**	1.21**	-10.17**	16.80*
SE		0.31	0.53	0.08	0.14	0.43	0.55	0.05	0.11	0.55	1.52	0.10	0.26	1.93	6.54
Testers															
16	SSG59-3	-2.93*	-1.25**	-0.85**	-0.45**	1.79	1.41**	-0.61**	-0.32**	-0.43	0.14	0.30	-0.52*	-21.83**	-74.50**
17	HC308	1.04	-0.11	0.09	-0.07	-1.08	-0.97*	0.22	0.25**	0.53	-1.40	0.06	0.55**	10.17*	-0.50
18	RSSV-9	1.88*	1.58**	0.93**	0.45**	0.55	1.11**	0.44*	0.08	2.70	1.95*	0.29	-0.29*	14.17*	68.80**
19	Ramkel	0.01	-0.22	-0.17	0.08	-1.25	-1.55**	-0.05	0.00	-2.80*	-0.69	-0.65	0.26	-2.50	6.20
SE		0.67	0.24	0.18	0.06	0.92	0.25	0.10	0.05	1.19	0.70	0.22	0.12	4.16	3.03

*, **Significant at P=0.05 and P=0.01 levels, respectively.

TABLE 4

Estimation of sca effects of parents for different traits under normal (N) and water stress (S) environments

S. No.	Hybrids	Green fodder yield (kg/plot)		Dry fodder yield (kg/plot)		Relative water content (%)		Leaf area index		Photosynthetic cap (SPAD reading)		Specific leaf wt. (mg/cm^2)		Proline (nmol/g)	
		N	S	N	S	N	S	N	S	N	S	N	S	N	S
Lines															
1	94001A x SSG59-3	4.80**	1.34	1.12**	0.16	-1.74	-2.17*	0.74**	-0.52**	5.16**	-2.65	-3.92**	-4.58**	54.33**	82.00**
2	94002A x RSSV-9	4.76**	4.31**	1.35**	0.8**	2.22	-0.84	0.45**	0.69**	-3.37	-0.02	1.94**	1.96**	13.33*	113.67**
3	940012A x SSG59-3	0.93	3.00**	-0.16	0.92**	-6.68**	-4.53**	-1.19**	-0.23	-1.71	0.41	0.93**	1.89**	36.83**	94.50**
4	940012A x HC308	2.04*	0.19	-0.66*	0.24	5.63**	6.51**	0.41*	1.37**	4.67*	0.59	-1.73**	-3.78**	4.83	-9.50
5	940031A x SSG59-3	2.19*	3.56**	0.61*	0.20	-0.10	1.41	0.78**	-0.22	-7.15**	-3.02	-0.41	-0.99*	49.33**	29.50**
6	940056A x SSG59-3	-2.31*	2.17**	-0.88**	0.91**	4.76**	1.70*	-0.26	0.52**	2.50	2.03	-1.10**	-1.70**	16.83*	9.50
7	940056A x Ramkel	3.66**	-0.53	1.13**	-0.35	-2.54	-4.98**	0.55**	0.00	-3.06	-6.01*	-0.36	0.32	17.50**	48.83**
8	AKMS-14A x HC308	3.30**	1.98*	1.46**	0.56*	-3.33*	-3.63**	-0.97**	-0.08	8.27**	0.43	0.17	1.36**	54.83**	70.50**
9	AKMS-14A x RSSV-9	1.46	5.30**	-0.75**	0.94**	5.13**	3.42**	2.28**	1.05**	3.24	14.17**	-0.20	1.03*	-49.17**	21.17*
10	AKMS27-A x HC308	-1.06	2.19**	-0.70*	0.38	1.98	-1.50	-0.05	-0.38*	-1.95	2.10	1.69**	2.24**	64.83**	78.00**
11	AKMS27-A x RSSV-9	4.90**	1.50	0.68*	0.49*	-1.19	2.72**	-0.30*	0.12	-1.02	-0.49	-2.71**	-0.05	-19.17**	-11.33
12	2077A x Ramkel	0.20	1.55*	-0.07	0.28	6.24**	10.39**	0.14	0.79**	2.88	8.01**	0.17	0.10	-25.00**	26.33*
13	NSS1002A x HC308	3.37**	4.86**	1.39**	1.36**	3.61*	-0.04	1.67**	0.32	2.29	6.18*	-1.61**	-1.82**	67.33**	173.00**
14	NSS1003A x SSG59-3	8.18**	-2.83**	1.45**	-0.95**	4.84**	4.17**	-0.20	-0.60**	-0.75	2.10	0.08	0.62	-60.67**	-88.00**
15	NSS1003A x Ramkel	-1.03	3.47**	-0.23	1.03**	-14.92**	-18.84**	-0.42*	0.64**	-6.27**	0.20	1.05**	2.17**	70.00**	71.33**
16	NSS1005A x HC308	0.74	2.32**	0.66*	0.70**	-1.61	-0.93	-0.07	-0.01	0.42	-0.63	-0.10	-0.47	82.33**	105.50**
17	NSS1005A x RSSV-9	3.86**	-3.36**	0.92**	-0.59**	-2.94*	-4.94**	0.19	0.05	-3.67*	-2.05	-0.10	-0.46	-21.67**	-63.83**
18	NSS1005A x Ramkel	-0.53	4.07**	-0.75**	1.05**	8.56**	9.38**	0.24	0.04	7.00**	-1.58	0.07	-0.91*	5.00	88.83**
19	NSS1007A x SSG59-3	1.35	1.75*	0.05	0.23	-4.99**	-6.05**	-0.29	-0.01	-8.09**	0.85	-1.85**	-1.79**	14.33*	47.00**
20	NSS1007A x Ramkel	3.05**	1.72*	-0.80**	0.37	-7.15**	-4.86**	0.35*	0.70**	-1.15	-1.78	-0.17	-0.47	25.00**	76.33**
21	NSS1008A x Ramkel	4.72**	-0.11	0.89**	0.00	0.69	1.13	-0.69**	-0.96**	1.15	1.37	-0.15	-0.60	17.50**	-26.17
	SE	1.17	0.91	0.31	0.24	1.59	0.95	0.18	0.20	2.06	2.63	0.39	0.45	7.20	11.33

*, **Significant at P=0.05 and P=0.01 levels, respectively.

TABLE 5

Per cent heterosis for different crosses over standard check (PSC-1) under normal (N) and water stress (S) environments

S. No.	Hybrids	Green fodder yield (kg/plot)		Dry fodder yield (kg/plot)		Relative water content (%)		Leaf area index		Photosynthetic cap (SPAD reading)		Specific leaf wt. (mg/cm^2)		Proline (nmol/g)	
		N	S	N	S	N	S	N	S	N	S	N	S	N	S
Lines															
1	94001A x SSG59-3	20.38**	-20.88	-24.06	-45.26	-0.45	-2.52	-18.83	-20.00	-8.77	-22.17	-72.78	-79.31	-10.00	-52.00
2	94001A x RSSV-9	7.55**	-16.48	-19.34	-29.93	1.67**	4.62**	-46.10	-23.08	-10.08	-20.43	-15.19	23.45	-70.00	-68.00
3	94001A x Ramkel	13.02**	-18.68	-29.25	-38.69	5.04**	1.63**	-22.73	6.15	-25.39	-0.33	22.78*	11.72	-30.00	-44.00
4	94002A x HC308	7.55**	-47.25	-31.60	-51.09	-1.79	0.98**	0.00	-9.23	-2.49	-8.59	-55.70	-20.00	-60.00	-60.00
5	94002A x RSSV-9	54.15**	27.25**	6.60	5.84	-2.44	-3.12	16.23*	67.69**	-19.83	5.22**	42.41**	20.00	0.00	48.00**
6	94002A x Ramkel	4.53**	-14.29	-34.43	-21.90	-13.57	-10.48	11.69*	69.23**	-42.80	-9.78	0.00	-47.59	-20.00	-44.00
7	94003A x SSG59-3	1.89*	-20.88	-42.45	-34.31	6.26**	7.01**	-24.68	16.92	2.88**	13.7**	-15.19	-64.83	-30.00	-60.00
8	94003A x HC308	34.34**	-14.29	-23.58	-28.47	-11.13	-12.53	5.84	103.08**	-24.02	-17.93	-15.82	-37.24	-70.00	-64.00
9	94003A x RSSV-9	37.17**	-7.69	3.30	-23.36	-0.69	2.95**	-33.12	12.31	-29.25	-7.17	-17.72	-13.79	100.00**	28.00**
10	94003A x Ramkel	9.43**	-28.57	-37.26	-35.04	2.80**	7.66**	6.49	20.00	-11.39	-0.22	-26.58	6.90	-60.00	-52.00
11	940012A x SSG59-3	7.55**	1.10	-30.66	-15.33	-8.77	-5.13	-29.87	13.85	-20.03	1.20	-10.76	16.55	0.00	0.00
12	940012A x HC308	36.23**	-9.89	-24.53	-21.90	2.72**	5.99**	17.53**	113.85**	-5.63	-3.26	-65.82	-78.62	0.00	-12.00
13	940012A x RSSV-9	20.38**	-7.69	6.13	-45.99	-3.05	-4.96	18.83**	15.38	-22.12	-1.30	-34.81	-75.86	0.00	16.00**
14	940012A x Ramkel	11.13**	-25.27	-16.51	-18.98	-2.15	-0.38	14.29*	13.85	-15.58	0.98	-24.68	90.34**	-60.00	-36.00
15	940031A x SSG59-3	-1.89	11.87**	-26.42	-16.06	3.90**	4.83**	-7.79	3.08	-43.06	-10.11	-8.86	-76.55	40.00**	-16.00
16	940031A x RSSV-9	18.49**	-5.49	4.25	-5.84	-1.22	0.34	4.55	30.77*	-14.99	-7.83	24.05*	-68.97	10.00**	24.00**
17	940056A x HC308	16.60**	-18.68	-19.34	-38.69	-1.14	-1.71	-44.16	-41.54	-20.09	-21.52	-28.48	35.86*	-60.00	-64.00
18	940056A x RSSV-9	21.32**	-14.29	6.60	-35.04	0.12	-0.60	-31.82	23.08	-12.37	25.22**	17.72	13.79	0.00	-16.00
19	940056A x Ramkel	35.28**	-20.88	1.89	-40.88	-3.45	-11.72	-31.82	-4.62	-31.48	-27.39	-41.77	20.00	-10.00	-20.00
20	AKMS-14A x SSG59-3	7.55**	-51.65	-19.34	-47.45	2.92**	6.29**	-56.49	-33.85	-36.39	-25.33	27.22*	-51.03	-50.00	-72.00
21	AKMS-14A x HC308	57.92**	-7.69	10.85	-15.33	-8.77	-9.37	-50.65	-4.62	-0.92	-7.17	0.63	28.28*	30.00**	-8.00
22	AKMS-14A x RSSV-9	52.26**	25.27**	-8.49	4.38	3.53**	2.35**	16.88**	40.00**	-6.54	48.59**	-1.90	4.14	-70.00	0.00
23	AKMS-14A x Ramkel	15.66**	-46.15	-27.36	-45.99	-11.25	-13.13	-53.90	-50.77	-28.93	-32.07	-40.51	-26.21	-50.00	-64.00
24	AKMS27-A x HC308	13.77**	-1.10	-35.85	-17.52	0.65*	-6.59	-51.30	-47.69	-20.75	-0.22	38.61**	55.17**	60.00**	0.00
25	AKMS27-A x RSSV-9	52.26**	5.49**	-4.25	-3.65	-1.22	1.50**	-51.95	-32.31	-14.66	2.28	-40.51	-9.66	-20.00	-8.00
26	AKMS27-A x Ramkel	3.77**	-36.26	-22.17	-36.50	-2.92	-0.43	-50.00	-44.62	-16.75	-8.70	-41.14	-56.55	-70.00	-68.00
27	2077A x SSG59-3	33.40**	-12.09	-7.55	-18.98	-2.97	-8.81	13.64*	67.69**	12.83**	8.37**	-2.53	-24.14	30.00**	-4.00
28	2077A x HC308	41.89**	-18.68	-1.89	-26.28	-0.41	-0.77	-14.29	-3.08	-22.91	-24.35	2.53	-28.28	0.00	-20.00
29	2077A x RSSV-9	48.49**	12.09**	-6.60	2.92	-0.97	-0.77	-51.30	-1.54	-20.55	-8.70	-58.86	-78.62	110.00**	32.00**
30	2077A x Ramkel	42.83**	5.49	-9.91	-3.65	6.66**	11.68**	-14.94	69.23**	-10.01	23.59**	-31.65	-33.79	10.00**	20.00**
31	NSS1002A x HC308	38.11**	9.89**	-9.91	0.00	0.81**	-2.57	-1.95	15.38	-24.74	2.83*	-41.14	-42.07	90.00**	56.00**
32	NSS1002A x RSSV-9	14.91**	-16.48	-27.83	-24.09	-9.50	-7.66	-24.68	35.38**	-25.39	-14.89	-18.35	7.59	20.00**	-4.00
33	NSS1002A x Ramkel	14.72**	-34.07	-27.83	-39.42	-2.92	-1.03	-70.78	-56.92	-38.15	-10.11	-25.32	-38.62	0.00	-32.00
34	NSS1003A x SSG59-3	36.42**	-42.86	-22.64	-58.39	2.07**	1.88**	-36.36	-26.15	-26.05	-8.26	-4.43	19.31	-60.00	-72.00

Contd.

TABLE 5 contd.

35	NSS1003A x HC308	2.64**	-9.89	-41.04	-32.12	-1.75	2.14**	-39.61	15.38	-30.82	-31.74	-43.04	-10.34	50.00**	0.00
36	NSS1003A x Ramkel	0.94	5.49**	-36.79	-3.65	-25.71	-31.44	-29.87	46.15**	-41.56	-17.17	-3.80	67.59**	90.00**	24.00**
37	NSS1005A x HC308	29.81**	12.09**	-10.38	11.68	-4.10	-1.28	-14.29	52.31**	-17.28	-7.28	-27.85	-17.93	110.00**	56.00**
38	NSS1005A x RSSV-9	52.26**	-14.29	5.19	-5.11	-3.74	-3.76	-5.19	47.69**	-21.07	-0.98	-23.42	-35.17	10.00**	16.00**
39	NSS1005A x Ramkel	16.79**	22.86**	-33.96	22.63**	8.08**	11.21**	-13.64	43.08**	-10.93	-8.04	-37.97	-33.10	20.00**	52.00**
40	NSS1006A x HC308	15.66**	-14.29	-27.36	-35.77	-13.97	-14.71	-44.16	-4.62	-37.83	-12.72	10.13	-65.52	20.00**	-4.00
41	NSS1006A x RSSV-9	29.62**	9.89**	-61.32	0.73	-0.20	1.41**	-35.06	-20.00	-28.60	-7.17	17.09	-0.69	40.00**	48.00**
42	NSS1006A x Ramkel	18.30**	-1.10	-19.34	-24.09	-3.13	-9.50	-27.92	32.31*	-45.03	-10.00	-39.87	-13.10	40.00**	32.00**
43	NSS1007A x SSG59-3	22.26**	1.10	-23.11	-15.33	-9.67	-10.78	-42.21	10.77	-33.70	-3.91	-3.80	-68.97	0.00	4.00**
44	NSS1007A x HC308	42.83**	-9.89	-9.91	-17.52	1.75**	3.72**	-46.75	-3.08	-11.98	-9.46	50.63**	56.55**	-10.00	-16.00
45	NSS1007A x RSSV-9	11.13**	-7.69	11.32	-8.03	0.85**	0.81**	9.09	38.46**	2.49**	0.00	45.57**	-46.90	10.00**	24.00**
46	NSS1007A x Ramkel	48.49**	7.69**	-25.47	-0.73	-16.00	-13.05	-18.83	58.46**	-24.74	-15.22	10.13	-25.52	30.00**	48.00**
47	NSS1008A x HC308	29.62**	-9.89	-18.40	-24.82	-6.86	-6.97	12.99*	52.31**	-31.28	-19.13	46.20**	4.83	-20.00	-16.00
48	NSS1008A x RSSV-9	29.62**	9.89**	-26.89	1.46	-9.55	-13.90	-35.06	9.23	-20.68	-0.87	27.85*	13.10	-10.00	32.00**
49	NSS1008A x Ramkel	50.38**	-5.49	-15.09	-13.14	-6.78	-7.27	-44.16	-24.62	-29.97	-6.74	6.33	6.90	0.00	-16.00
SE		0.18	0.15	0.50	0.39	0.27	0.16	0.36	0.32	0.32	0.44	0.68	0.75	0.12	0.20
C. D. (P=0.05)		0.30	0.25	0.84	0.65	0.45	0.27	0.60	0.53	0.53	0.73	1.14	1.25	0.20	0.33
C. D. (P=0.01)		0.43	0.36	1.20	0.93	0.65	0.38	0.86	0.76	0.76	1.05	1.63	1.79	0.29	0.48
Min.		-19.81	-51.65	-61.32	-58.39	-25.71	-31.44	-70.78	-56.92	-50.26	-32.07	-72.78	-79.31	-70.00	-72.00
Max.		57.92	27.25	11.32	22.63	9.14	11.68	23.38	113.85	12.83	48.59	64.56	148.97	110.00	56.00
PSC-1 (Mean)		17.70	15.20	7.10	4.60	82.10	77.90	5.10	2.20	50.90	30.70	5.30	4.80	100.00	250.00

*,**Significant at P=0.05 and P=0.01 levels, respectively.

is easier than single cross hybrids, therefore, these can be considered for further evaluation in the future breeding programmes.

The preponderance of non-additive gene action found in this investigation for fodder yield and the realization of high degree of heterosis suggest that exploitation of commercial heterosis would be the best method for utilization of such gene action. However, to exploit both types of gene action (additive and non-additive) parents showing good gca for forage yield may be intermated to develop a base population with new recombinants using male sterility which could be improved upon by following an appropriate method of recurrent selection. The elite population thus could be used as a source material for producing superior parents for hybrid combinations. The crosses, which showed very high level of heterosis, and high sca effects can be exploited further in future breeding programme to develop high yielding and water use efficient genotypes in forage sorghum.

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