

## TOP CROSS ANALYSIS FOR HETEROSIS AND COMBINING ABILITY IN FORAGE PEARL MILLET (*Pennisetum glaucum* L.)

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### SUMMARY

A set of 15 CMS lines was top crossed to four populations as testers to obtain 60 top cross hybrids. The hybrids were evaluated for general combining ability (gca), specific combining ability (sca) and heterosis. The mean squares due to parents differed significantly for all the characters, thus indicating the presence of variability in the parent material for all the 16 traits. The variances due to gca and sca were significant. The computed variance ratio ( $\sigma^2_{sca}/\sigma^2_{gca}$ ) revealed the predominance of non-additive gene action in the inheritance of quality traits. The perusal of the estimates of general and specific combining ability variances indicated the preponderance of non-additive gene action in the inheritance of all the traits. For GFY, five CMS lines 01777A (5.36), 543A (5.03), 92222A (4.70), 315A (3.03) and 111A (1.78) and two testers viz., RBC-2 (0.79) and Giant Bajra (0.64) were good general combiners with highly significant positive gca effects. The hybrids 315A × RBC-2, 543A × GFB-1, 01777A × Giant Bajra, 92222A × GFB-1 and 408A × Giant Bajra topped the list of crosses for forage yield. This high yielding ability was contributed by significant values of traits viz., plant height, number of tillers per plant and leaf area index.

**Key words :** Combining ability, environments, forage, heterosis, hybrids, pearl millet, quality

Pearl millet [*Pennisetum glaucum* (L.) R. Br.], commonly called cat tail millet and bulrush millet in different parts of the world, is a major **kharif** fodder crop of Punjab which occupies 28 per cent area (1.42 lakh ha) of **kharif** fodders (Anonymous, 2013). Among all the **kharif** fodders, pearl millet plays a vital role in meeting the demand and supply of fodders. Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is nutritious forage crop capable of providing good tonnage of green fodder even under the poorest of the growing conditions. Further, due to its properties of drought resistance, quick growth, low prussic acid, high in protein and minerals and palatable to animals, farmers prefer to grow pearl millet as fodder crop rather than grain crop in Punjab state. It can be fed to animals at any stage of growth without deleterious effects.

Many biometrical methods have been developed to obtain information on combining ability. Top cross mating design (Line × Tester) is widely used to study combining ability of parents to be chosen for heterosis breeding (Kempthorne, 1957). The estimation of heterosis for forage yield and its component characters would be useful to judge the best hybrid combination for exploitation of superior

hybrids. However, the selection of promising parents to obtain superior hybrids primarily depends on the predominance of the genes for the additive effect due to heterosis and heterobeltiosis (Beche *et al.*, 2013). However, there are scanty reports of exploitation of heterosis for forage production in pearl millet through top cross hybrids. The top cross hybrids have many advantages over single cross hybrids like the more variable pollinator and the top cross hybrid can be constantly selected to maintain disease resistance. Further, the open pollinated pollinators are more vigorous as they do not suffer from inbreeding depression, leading towards easier seed production of both hybrids and pollinators. At the same time, the nicking problems are less in producing top cross hybrid seed because of greater temporal spread of flowering in open-pollinated male parents and it requires lesser number of generations to breed an open pollinated population as pollinator than an inbred line as pollinator in a single cross. In view of this, the present studies were undertaken to evaluate male sterile lines and tester populations, and also to assess heterosis through top crosses with gene action involved in inheritance of various agro-morphological traits along with green and dry fodder yield and quality parameters.

## MATERIALS AND METHODS

The experimental material comprised 15 CMS lines and four populations of pearl millet. CMS lines 111A, 543A, 315A, 308A, 503A and 220A were procured from PAU, Ludhiana and lines 408A, 01555A, 05111A, 92222A, 91777A, 04777A, 01777A, 92666A and 92333A from ICRISAT, Hyderabad with all belonging to A<sub>1</sub> cytoplasmic source, except 315A, 408A, 503A and 01777A which belonged to cytoplasmic source of A<sub>2</sub>, A<sub>3</sub>, A<sub>4</sub>, and A<sub>5</sub>, respectively. The four testers used were 'Giant Bajra' (very leafy, profuse tillering, 9-10% protein, moderately resistant to diseases and 50-75 t/ha fodder yield) from MPKV, Rahuri; 'RBC-2' (resistant to foliar diseases insect-pests and 30-45 t/ha fodder yield) from RAU, Rajasthan; 'GFB-1' (plants tall with higher number of leaves and tillers/plant, 7-8% protein and 45-50 t/ha fodder yield) from GAU, Anand and 'NDFB-2' (very good under salt affected soils and higher in protein) from NDUA & T, Faizabad. The commercial released multi-cut varieties from PAU viz., FBC-16 and PHBF-1 were used as check. In **kharif** 2012, 15 CMS lines were crossed to four populations to produce 60 top crosses. The field experiment was conducted at Forage Research Farm, PAU, Ludhiana (Punjab, India) (30° 90' N of 75° 86' E, at an average elevation of 252.0 m above mean sea level). The site experiences semi-arid and sub-tropical climate with hot dry summer and severe cold winter. Average annual rainfall was about 650 mm, 67 per cent of which was received in three months (June to August) during the south-west monsoon.

During **kharif** 2013, 60 top crosses developed during previous year along with the parents i. e. CMS lines and populations along with two local checks viz., FBC 16 and PHBF-1 were evaluated in a lattice design with two replications. The experimental plot comprised four rows of 5 m length. Row to row spacing was maintained at 30 cm and no plant to plant spacing was maintained as material was to be analyzed for fodder related traits. Recommended package of practices to raise a good crop was followed. Observations were recorded on five random plants selected from each entry on 16 quantitative traits viz., EV–Early vigour, DEI–Days to ear initiation, NOT–No. of tillers/metre row length, PH–Plant height, LSR–Leaf : stem ratio, GFY–Green fodder yield, DFY–Dry fodder yield, RA–Regenerability, NOL–No. of leaves per plant, RLWC–Relative leaf water content, LAI–Leaf area index, CC–Chlorophyll content, SLW– Specific leaf weight, CP–Crude protein, CF–Crude fiber and IVDMD–*In vitro* dry matter digestibility.

GFY and DFY were recorded on per plot basis after first cut was taken at 60 days after sowing in both the environments and subsequent cut at 45 days interval. To perform estimation of quality parameters, replicated samples were collected from the representative sample drawn from the green fodder harvested. All the samples were dried to a constant weight in a hot air oven at 80 ° and separately ground to pass through 20 mesh sieves. Crude protein was estimated by following the method of McKenzie and Wallace (1954). Cell wall constituents (Crude fibre) were analyzed by the method of Goering and Van Soest (1970). *In vitro* dry matter digestibility was determined by the method of Tilley and Terry (1963). The statistical analysis was carried out according to Hookstra *et al.* (1983) and combining ability analysis for different traits was done as per the model suggested by Kempthorne (1957).

## RESULTS AND DISCUSSION

### Analysis of Variance

The analysis of variance for all the 16 characters under study is presented in Table 1. The mean squares due to parents differed significantly for all the characters, thus indicating the presence of variability in the parent material for all the 16 traits. The parent entries involving lines showed highly significant differences for all the 16 characters and the mean square due to testers was highly significant for all the characters except EV and IVDMD. Highly significant differences among all the characters were observed even for line vs. tester except for CC. The hybrids showed highly significant variation for all the characters but mean square due to interaction component (Parents vs. hybrids) which is a measure to overall heterosis was highly significant for 15 characters but could not express variability for IVDMD trait.

The analysis of variance for combining ability variance due to lines, testers and lines x testers interaction in respect to 16 quantitative traits is presented in Table 2. The variance due to females was highly significant for all the traits. The mean square due to males suggested that the variance due to general combining ability (gca) of the population was highly significant for all the characters except days to ear initiation, chlorophyll content and IVDMD. The female x male interaction variance was highly significant for all the characters, which indicated the importance of specific combining ability (sca) in the

TABLE 1  
Analysis of variance for experimental design for different characters

Source of variation	d. f.	EV	DEI	NOT	PH	LSR	GFY	DFY	RA	NOL	RLWC	LAI	CC	SLW	CP	CF	IIVDMD
Parents	18	1.08**	102.44**	125.58**	1840.5**	0.89**	42.44**	2.32**	1.33**	157.79**	102.70**	0.31**	70.95**	0.008**	1.13**	0.0013**	57.52**
Lines	14	0.90**	70.03**	149.33**	1191.1**	1.04**	22.50**	1.43**	0.78**	183.91**	121.70**	0.29**	78.02**	0.005**	0.93**	0.0007**	61.96**
Testers	3	0.11	34.66**	25.66**	429.3**	0.13**	64.12**	3.22**	2.86**	43.12*	48.00**	0.15*	61.57**	0.024**	0.32	0.002**	47.98
Lines x Testers	1	6.58**	759.58**	92.80**	15081.8**	1.03**	256.67**	12.11**	4.42**	136.07**	0.71	1.15**	0.01	0.009**	9.89**	0.006**	23.96
Parents vs. Hybrids	1	4.95**	90.88**	230.54**	19167.0**	9.35**	407.02**	16.04**	26.43**	2544.4**	38.96**	6.06**	771.86**	0.003**	2.31**	0.0002	20.28
Hybrids	59	1.66**	55.88**	74.07**	1540.7**	0.12**	47.72**	1.89**	2.93**	233.57**	70.57**	0.34**	43.77**	0.005**	1.80**	0.0009**	43.39**
Error	78	0.38	4.57	4.70	58.96**	0.007	3.07	0.06	0.13	13.36	3.15	0.04	8.41	0.0003	0.25	0.0003	19.39

EV-Early vigour, DEI-Days to ear initiation, NOT-No. of tillers/meter row length, PH-Plant height, LSR-Leaf stem ratio, GFY-Green fodder yield, DFY-Dry Fodder yield, RA= Regenerability; NOL= No. of leaves per plant; RLWC=Relative leaf water content; LAI= Leaf area index; CC= Chlorophyll content; SLW= Specific leaf weight; CP= Crude protein; CF= Crude fiber; IIVDMD= *In vitro* dry matter digestibility.

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

TABLE 2  
Combining ability analysis of variance of parents and hybrids for different traits

Source of variation	d. f.	EV	DEI	NOT	PH	LSR	GFY	DFY	RA	NOL	RLWC	LAI	CC	SLW	CP	CF	IIVDMD
Replication	1	0.001	2.28	17.11	223.7	0.0028	24.8*	0.27	1.10	65.80	60.14	0.15	12.62	0.00007	0.34	0.0013	21.17
Lines	14	3.40**	147.13**	100.00**	4374.7**	0.17**	93.24**	3.35**	3.37**	345.53**	76.24**	0.56**	47.06**	0.0053**	2.03**	0.001**	54.96**
Testers	3	1.84**	7.65	29.57**	1364.6**	0.07**	25.84**	1.18**	9.27**	257.79**	76.3**	1.42**	5.65	0.0015**	1.64**	0.0013*	23.92
Lines x Testers	42	1.07**	28.91**	68.60**	615.39**	0.10**	34.10**	1.46**	2.33**	194.52**	68.27**	0.19**	45.39**	0.0058**	1.84**	0.001**	40.93**
Error	78	0.38	4.57	4.70	58.96	0.008	3.07	0.05	0.13	13.36	3.15	0.04	8.41	0.0003	0.25	0.0004	19.39
$\sigma^2$ sca	0.34	12.16	31.94	278.2	278.2	0.049	15.51	0.7	1.1	90.57	32.56	0.076	18.49	0.02	0.79	0.0002	10.76
$\sigma^2$ gca	0.08	2.55	↓	↓	118.12	0.0008	1.33	0.04	0.21	5.63	0.42	0.042	↓	↓	↓	0.00001	↓
$\sigma^2$ sca/ $\sigma^2$ gca	4.25	4.77	↔	↔	2.36	61.25	11.66	17.50	5.24	16.09	77.52	1.81	↔	↔	↔	20.00	↔
V <sub>A</sub>	0.32	10.2	-0.8	-0.8	472.48	0.0032	5.32	0.16	0.84	22.52	1.68	0.168	-4	-0.0004	-0.008	0.00004	-0.28
V <sub>D</sub>	1.36	48.64	127.76	1112.8	1112.8	0.196	62.04	2.8	4.4	362.28	130.24	0.304	73.96	0.08	3.16	0.0008	43.04

↓ Negative component interpreted as zero, ↔ Genetic ratio not calculated because of negative genetic component.

Details of characters are given in Table 1.

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

genetic expression of these characters among hybrids. The mean squares due to hybrids were also significant for all the characters. Similar results were reported by Bibi *et al.* (2012). The perusal of the estimate of general and specific combining ability variances (Table 2) indicated the preponderance of non-additive gene action in the inheritance of all the traits. The non-additive gene action is a manifestation of dominant gene action. The analysis of variance revealed highest magnitude of dominance than additive for all the characters. The findings are in agreement with the reports by and Indhubala *et al.* (2010). For the traits where the general combining ability variance was found to be negative, it was considered that there was no variation and hence the ratio of  $\sigma^2_{sca}/\sigma^2_{gca}$  could not be computed.

### Combining Ability Analysis

For EV, analysis of general combining ability (Table 3) revealed that the CMS lines 543A, 01777A and 315A with gca value of 0.52, 0.89 and 0.89, respectively, were found to be good general combiners. The CMS lines 111A, 92222A, 220A, 308A and 91777A were found to be average combiner; however, remained lines were poor combiners. Sca analysis (Table 4) revealed that out of 60 crosses, only five crosses viz., 04777A x GFB-1 (1.8), 408A x NDFB-2 (1.4), 05111A x RBC-2 (1.2), 308A x Giant Bajra (0.9) and 92333A x GFB-1 (0.78) were found to be good specific combiners. For DEI, the lines with delayed flowering were desirable for fodder yield, hence good combining ability was desirable for this trait. Among the CMS lines, 220A (3.99), 92333A (3.12), 408A (2.99) and 01555A (2.87) had highest positive significant gca effects and a total of 11 cross combinations had high positive significant sca effects. Most of the crosses with high sca effect involved at least one parent with high gca effects. Therefore, the inheritance of this character was under the control of both additive and non-additive gene action. Likewise for NOT, a total of six CMS lines and one tester showed significant gca effect and 19 crosses showed significant positive sca effect with 111A x Giant Bajra (11.1) exhibiting highest sca effect. Pearl millet needed to have high PH for the production of maximum forage yield. Study of gca (Table 3) revealed that four CMS lines viz., 111A, 315A, 543A and 01777A and one tester RBC-2 were found to be good general combiners for increased PH. Three cross combinations viz., 308A x Giant bajra, 92333A x NDFB-2 and 543A x GFB-1 were the best specific combiners for this trait. The

magnitude of gca for LSR varied from -9.0 to 0.25 and seven lines showed positive gca effects in desirable direction and in case of testers, GFB-1 and Giant Bajra were found to be good combiners. The magnitude of sca effects for leaf : stem ratio ranged from -0.48 (220A x GFB-1) to 0.62 (220A x NDFB-2). Seventeen and 22 cross combinations showed significant positive and negative sca effects, respectively. Highest positive sca effect was exhibited by 04777A x GFB-1 (0.35) followed by 220A x RBC-2 (0.28) and 05111A x Giant Bajra (0.23). Most of the hybrids with high sca effects did not involve good or average combiners. This indicated that the gca of parents was not reflected in sca of its cross combination, therefore, this character was controlled by the non-additive gene action. Similar results were reported by Mohammed (2009). For GFY, the gca effect varied from -6.22 to 5.36. Out of 15 parental CMS lines, five lines 01777A (5.36), 543A (5.03), 92222A (4.70), 315A (3.03) and 111A (1.78) were good general combiners with highly significant positive gca effects. In case of male parents, RBC-2 (0.79) and Giant Bajra (0.64) were best general combiners. A total of 14 cross combinations were found to have significant positive sca effects. Highest value was determined in the cross 220A x GFB-1 (8.88) closely followed by 408A x Giant Bajra (7.73). In general, the crosses having high sca effects involved at least one parent with poor general combining ability indicated the prevalence of primarily non-additive gene action. This reveals the possibility of dispersion of genes in the parents and their complementation when brought together in the hybrid combinations. These results are consistent with those of Kenga *et al.* (2005). For DFY, four CMS lines 01777A (1.24) followed by 92222A (0.86), 543A (0.86), 315A (0.62) and tester RBC-2 (0.23) showed highly significant gca effects. Among all top crosses, only 15 crosses had significant positive sca effect. As similar as in other traits it was evident that the inheritance of the character was also controlled by non-additive gene action as most of the crosses with high sca effect didn't involve the parents with good combining ability.

For pearl millet, maximum number of leaves per plant is desirable character which contributes more production of forage yield. Estimation for general combining ability effects of lines, in case of number of leaves per plant was positive and significant for 543A (14.65), 91777A (6.28), 503A (5.53), 051111A (5.53) and 408A (3.65). Among four testers, only GFB-1 was found to be good general combiner with high gca value of 3.63. Out of 60 cross combinations, 15 crosses showed significant positive sca effects. The

TABLE 3  
Estimation of general combining ability effects of parents for different traits

S.No.	Parents	EV	DEI	NOT	PH	LSR	GFY	DFY	RA	NOL	RLWC	LAI	CC	SLW	CP	CF	IVDMD
<b>Lines</b>																	
1.	111A	0.39	-2.76**	6.05**	12.68**	0.07**	1.78**	0.14	-0.30*	1.40	-2.04**	-0.33**	4.12**	0.02**	-0.66**	0	0.2
2.	92222A	0.70**	-1.38	2.55**	-3.69	0.01	4.70**	0.86**	0.89**	0.03	-7.25**	0.30**	1.28	-0.03**	0.44**	0	-2.06
3.	315A	0.52*	0.24	2.92**	22.93**	-0.12**	3.03**	0.62**	0.70**	2.03	1.43*	0.30**	1.85	0	-0.07	-0.02**	1.36
4.	308A	0.27	-3.26**	-3.45**	10.93**	0.02	-1.35*	-0.35**	0.20	-8.85**	1.99**	-0.22**	0.77	0.01	-0.73**	0.02**	-0.69
5.	503A	-0.55**	1.87*	-1.83*	-7.69**	0.05	-3.22**	-0.70	-0.92**	5.53**	1.67**	0.09	-2.07**	0	-0.82**	0	-0.61
6.	220A	0.27	3.99**	-0.95	-7.44**	0.25**	0.22	-0.19*	0.89**	-6.35**	-0.48	0.25**	0.27	0.01	0.44*	0	-0.17
7.	92333A	-0.92**	3.12**	-4.08**	-35.94**	0.22**	-3.40**	-0.58**	-0.3*	-6.35**	-3.78**	0.25**	-5.63**	0	0.59**	0	3.09*
8.	543A	0.89*	-7.51**	5.30**	41.56**	-0.13**	5.03**	0.86**	0.45**	14.65**	3.49**	0.28**	1.93	-0.01	-0.17	0	2.16
9.	91777A	0.39	2.37**	2.92**	-18.70**	-0.10**	-0.10	-0.07	-0.23*	6.28**	1.48*	0.12	1.07	0.02**	-0.12	-0.01	0.54
10.	92666A	-0.55**	2.74**	-0.08	-18.00**	-0.23**	-2.47**	-0.30	-0.61**	-0.60	5.90**	-0.07	-0.87	-0.04**	-0.47**	0.01	0.60
11.	05111A	-1.11**	1.99**	-5.45**	-16.40**	0.20**	-6.22**	-1.16**	-0.23*	5.53**	-0.52	-0.41**	-0.16	-0.3**	0.41*	0.02**	5.01**
12.	01555A	-0.36	2.87**	-3.83**	-15.80**	-1.70**	-1.91*	-0.23**	-0.42**	-8.85**	-1.68**	0.12	2.70**	-0.04**	0.58**	0	-0.54
13.	04777A	-0.42*	3.12**	-2.33**	-11.07**	-9.00**	-0.97	-0.11	-0.11	-3.97**	-0.58	-0.31**	-0.90	-0.05**	-0.16	-0.02**	0.56
14.	01777A	0.89*	-10.30**	2.05**	48.40**	-0.10**	5.36**	1.24**	-0.98**	-4.10**	0.78	-0.01	1.85	0	0.1	0	-5.54**
15.	408A	-0.42*	2.99**	0.17	-1.69	-0.50**	-0.47	-0.02	0.95**	3.65**	-0.39	-0.37**	-2.46*	-0.02**	0.62**	0	-4.19**
SE		0.21	0.73	0.74	2.62	0.03	0.59	0.081	0.12	1.24	0.6	0.07	0.99	0.006	0.17	0.006	1.50
C. D. (P=0.05)		0.42	1.45	1.47	5.21	0.05	1.19	0.16	0.24	2.48	1.2	0.13	1.97	0.012	0.34	0.013	2.99
C. D. (P=0.01)		0.54	1.88	1.90	6.75	0.07	1.54	0.22	0.31	3.21	1.56	0.18	2.55	0.015	0.44	0.016	3.86
<b>Testers</b>																	
16.	RBC-2	0.12	-0.05	0.03	7.84**	-0.05**	0.79**	0.23**	-0.80	-2.97**	1.67**	-0.15	-0.39	0.0	-0.18*	0.0	-0.68
17.	Giant Bajra	0.29**	-0.58	-0.93**	1.97	0.05**	0.64*	0.02	0.07	-1.67**	-2.08**	0.07*	-0.19	0.0	0.34**	0.0	1.23
18.	NDFB-2	-0.25	-0.02	1.30**	-8.29**	-0.03*	-1.23**	-0.25**	0.28**	1.00	0.67*	-0.19	-0.03	-0.01	-0.10	-0.01	-10.0**
19.	GFB-1	-0.16	0.65	-0.47	-1.53	0.04**	-0.20	0.00	0.45**	3.63**	-0.26	0.28**	0.61	0.01	-0.07	0.0	-0.65
SE		0.01	0.33	0.34	1.21	0.01	0.27	0.037	0.06	0.57	0.28	0.03	0.45	0.002	0.08	0.003	0.69
C. D. (P=0.05)		0.19	0.67	0.68	2.41	0.03	0.55	0.075	0.11	1.15	0.55	0.06	0.91	0.005	0.15	0.006	1.38
C. D. (P=0.01)		0.25	0.87	0.88	3.12	0.04	0.72	0.090	0.14	1.48	0.72	0.08	1.18	0.070	0.20	0.007	1.80

Details of characters are given in Table 1.  
\*, \*\*Significant at P=0.05 and P=0.01 levels, respectively.

top five hybrids with high sca effects were 408A × GFB-1 (24.11) followed by 05111A × RBC-2, 91777A × Giant Bajra, 308A × NDFB-2 and 111A × Giant Bajra. The magnitude of gca for leaf area index varied from -0.41 to 0. Out of 15 female lines, five lines showed significant positive gca effects. In case of populations/testers, Giant Bajra and GFB-1 were good combiners. Only 11 top cross hybrids showed significant positive sca effects. The cross combinations having high sca effects involved the parents with good × poor, poor × average and average × average combining parents. Therefore, it is presumed that both additive and non-additive gene effects are important to the inheritance of this character. Crude protein is considered as the most important forage quality trait. Analysis of gca (Table 3) revealed that six CMS lines viz., 408A (0.62), 92333A (0.59), 01555A (0.58), 92222A (0.44), 220A (0.44) and 05111A (0.41) had positively significant gca effects and were good general combiners for crude protein and amongst testers only Giant Bajra had significant positive gca effect. A total of 10 crosses showed the positive and significant sca effects. For crude fibre, perusal of the data revealed that only two female lines 308A (0.02) and 05111A (0.02) were good general combiners and rest of all the lines except 315A, 91777A and 04777A were average combiners. CMS 05111A was the best general combiner for this trait as it was for crude protein too. None of testers was found to be good general combiner. Only five crosses viz., 543A × Giant Bajra (0.04), 05111A × GFB-1 (0.04), 111A × NDFB-2 (0.03), 308A × RBC-2 (0.02) and 04777A × RBC-2 (0.02) were found to be good specific combiners with significantly positive sca effects. The estimates for general combining ability effects for IVDMD revealed that two CMS lines viz., 05111A (5.01) and 92333A (3.09) had positive and significant gca effects. Giant Bajra (1.23) and RBC-2 (0.37) were recorded average general combiners as none was the good combiner. Highest sca values were exhibited by cross 01555A × RBC-2 (8.3) followed by 92666A × RBC-2 (8.1). The inheritance of quality traits (crude protein, crude fiber and IVDMD) was also controlled by non-additive gene action as most of the crosses with high sca effects did not involve good combiner parents. The results are consistent with the findings of Iyanar and Khan (2004) in sorghum crop.

### Magnitude of Heterosis

To initiate the hybrid breeding programme for the improvement of any characters, it is important to

know the extent of heterosis present for the particular character. The worth of the top cross hybrids can be adjudged only if these show considerable heterosis over their respective male and female parents. Now-a-days, lot of emphasis is being laid on the commercial exploitation of heterosis in various crops. In pearl millet, sufficient hybrid vigour is exhibited for various forage yield and its component characters (Bhadalia *et al.*, 2011). The released commercial hybrid PHBF-1 and composite FBC-16 were used as standard checks in the present investigation to obtain the standard heterosis.

For EV, only one cross 308A × Giant Bajra (6.2%) manifested positive heterosis over best check (PHBF-1). Few hybrids, namely, 315A × RBC-2, 543A × NDFB-2 and 04777A × GFB-1 had similar *per se* performance as of commercial checks. All top crosses except 01777A × RBC-2 and 01777A × NDFB-2 exhibited positive heterosis for late flowering. Highest heterosis for this trait was recorded in crosses 92333A × RBC-2 (45.55%) followed by 92333A × Giant Bajra (42.20%), 220A × NDFB-2 (42.1%) and 01555A × GFB-1 (41.11%). Among parents, 92333A line did not flower until harvested. Presterl and Weltzein (2003) reported significant and positive heterosis for this trait. For NOT, only two crosses, namely, 111A × Giant Bajra and 543A × NDFB-2 exhibited heterosis over best check viz., FBC 16. Lakshmana *et al.* (2010) reported significant and positive heterosis for this trait in pearl millet. Four crosses recorded significantly positive heterosis over FBC-16 for increased plant height and the tallest hybrid was 543A × GFB-1 (134 cm) closely followed by 01777A × GFB-1 (132.5 cm) and 01777A × Giant Bajra (108.5 cm) with heterotic value ranging between 5.74 to 33.4 per cent. Positive heterosis for this trait in pearl millet was reported earlier by Vetriventhan *et al.* (2008). For LSR, the extent of heterosis exhibited by  $F_1$  over their corresponding check ranged between 63.4 (220A × NDFB-2) to -82 per cent (91777A × RBC-2). Out of 60 hybrids, only six hybrids exhibited positive and significant heterosis over best check (FBC-16). For GFY, six hybrids exhibited positive heterosis over check for green fodder yield, ranging between 5.55 to 13.88 per cent. These crosses involved the CMS lines viz., 92222A, 315A, 220A, 543A with GFB-1 as pollinator and 01777A, 408A with Giant Bajra as pollinator. The maximum positive and negative heterosis was shown by 315A × RBC-2 (13.88%) and 503A × NDFB-2 (-88.88%), respectively. Prevalence of significant and positive heterosis for green fodder yield in pearl millet was reported by Nagaraju (2000).

TABLE 4  
Performance of promising top cross hybrids for green and dry fodder yield along with other traits with significant sca effects

Promising top cross hybrids	Mean fodder yield (kg/plot)		Standard heterosis		Gca effects (Lines x Testers)		Sca effects		Other characters with significant sca effects
	GFY	DFY	GFY	DFY	GFY	DFY	GFY	DFY	
315A × RBC-2	20.5	4.49	13.8**	21.3**	High × High	High × High	5.58**	1.50**	SLW
543A × GFB-1	20.0	4.00	11.1**	8.11**	High × Low	High × Low	4.07**	1.01**	NOT, PH, LSR, NOL, RLWC, SLW
01777A × Giant Bajra	19.8	3.76	10.2**	1.62**	High × High	High × Low	2.74**	0.13**	DEI
92222A × GFB-1	19.5	3.89	8.33**	7.43**	High × Low	High × Low	3.82**	0.98**	--
408A × Giant Bajra	19.0	3.74	5.55**	7.01**	Low × High	Low × Low	7.73**	1.43**	DEI, LSR, RA

Details of characters are given in Table 1.

For DFY, seven hybrids expressed positive heterosis over best check ranging between 1.15 (01777A x GFB-1) to 21.28 per cent (315A x RBC-2) and 315A x RBC-2 (21.28%) exhibited maximum heterosis followed by 543A x GFB-1 (8.11%), 92222A x GFB-1 (7.43%) and 01777A x Giant Bajra (1.62%). Remaining all hybrids showed negative heterosis over commercial check. Similar results were obtained by Manga and Dubey (2004) in pearl millet crop. For NOL, a total of 25 top crosses showed positive heterosis over commercial best check i. e. PHBF-1 and out of these, about 20 crosses had positive and significant heterosis. The magnitude of heterosis ranged between -49.36 to 88.6 per cent. Only three crosses viz., 315A x GFB-1 (22.5%), 92333A x Giant Bajra (15.0%) and 04777A x GFB-1 (12.5%) manifested positive heterosis over best check for LAI. For CP, a total of five top cross hybrids viz., 220A x Giant Bajra (13.13%), 92333A x RBC-2 (7.8%), 92222A x Giant Bajra (5%), 01555A x NDFB-2 (4.38%) and 408A x GFB-1 (3.6%) expressed significant positive heterosis over best check PHBF-1. Whereas for CF, as many as 45 hybrids expressed positive heterosis over both the commercial checks. maximum positive and significant heterosis was manifested by 05111A x GFB-1 (29.9%) closely followed by 308A x RBC-2 (22.67%) and maximum negative heterosis was expressed by 315A x GFB-1 (-10%). For IVDMD, the positive heterosis was manifested by 25 hybrids and maximum positive heterosis was expressed by 92333A x NDFB-2 (15.44%) closely followed by 92666A x RBC-2 (14.45%). The existence of significant heterotic effect over commercial checks suggested the presence of non-additive gene action and dominance for all morpho-physiological, yield and quality traits. Further supporting this conclusion was the fact that the ratio of  $\sigma^2_{sca}/\sigma^2_{gca}$  for all the traits was above unity. The presence of considerable amount of heterosis over two commercial checks for green and dry fodder yield, its contributing traits and other quality parameters, proved

that top cross hybrids were better than their respective male parents and had some advantages over single cross hybrids.

### Performance of Promising Top Cross Hybrids for Green and Dry Fodder Yield

Based on the performance, top five hybrids were selected for forage yield (Table 4). The promising hybrids were identified on the basis of *per se* performance, significant heterosis over best check and their sca effects under both the environments. The hybrids 315A × RBC-2, 543A × GFB-1, 01777A × Giant Bajra, 92222A × GFB-1 and 408A × Giant Bajra topped the list of crosses for forage yield. Three hybrids 315A × RBC-2, 543A × GFB-1 and 408A × Giant Bajra showed very good *per se* performance. All five promising hybrids exhibited high positive and significant standard heterosis for GFY. This high yielding ability was due to possession of significant plant height, number of tillers/m row length, number of leaves/plant, leaf area index, leaf : stem ratio, etc. (data not given). High percentage of heterosis was generally found in those hybrids in which at least one parent had high gca. Specific combining ability also played a major role in determining heterosis. These promising hybrids exhibited positively significant heterosis as they had significant high sca effects, along a line with high gca as one of its parents. Similar findings were reported by Bhadalia *et al.* (2011) in pearl millet.

These hybrids had combination of parents with high x low, low x high and high x high gca effects. These also had considerably high sca effects though they were not significant. Thus, these can be directly used as hybrids or apply standard selection procedure in segregating populations. This holds true for the crosses, which were obtained from high x high gca effect parent combinations. But these high yielding crosses obtained from high x low gca effects and also

low x high gca effects which indicate that even though the individual lines have less gca effects, but when they are crossed the gene contributing for forage yield from female and male combines well with each other without any negative effects. Thus, low x low gca effect crosses show higher yield when compared to high x high crosses.

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