



HETEROSIS AND COMBINING ABILITY IN FORAGE PEARL MILLET (*Pennisetum glaucum* L.) UNDER STRESS AND NON-STRESS ENVIRONMENTS

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ABSTRACT

The present investigation was undertaken for genetic analysis of forage yield and quality traits in pearl millet (*Pennisetum glaucum*). A set of 15 CMS lines and 4 populations as testers were crossed in all possible combinations to obtain 60 top cross hybrids. The hybrids were evaluated for general combining ability (gca), specific combining ability (sca), heterosis over two environments viz., water stress and irrigated. Analysis of variance for quality characters revealed significant differences due to genotypes, environments and significant genotype x environment interaction for all quality traits. The variance due to gca and sca were significant and varied with change in the environment for all quality traits. 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 line 05111A was found best general combiner for higher quality under both the environments. Among testers, Giant bajra was best combiner for quality under both environments. The top cross hybrids 91777A × RBC-2 and 01555A × RBC-2 were good specific combiners for high protein and fiber content. Hybrids 220A × Giant bajra, 01555A × NDFB-2 and 408A × GFB-1 exhibited high positive significant heterosis under both the environments. The existence of significant heterotic effect over commercial check also suggested the presence of non-additive gene action and dominance for quality traits.

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

INTRODUCTION

Forages are the mainstay of livestock and the genetic potential of high yielding animals can only be realized if they are fed quality fodder. At present, India faces a net deficit of 61.1% green fodder, 21.9% dry crop residues and 64% feeds (Anonymous, 2012). The available forages are poor in quality and deficient in energy, protein and minerals. 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 and occupies 28% area (1.42 lakh ha) under *kharif* fodders (Anonymous, 2012).

Among all the *kharif* fodders, pearl millet plays a vital role in meeting the demand and supply of fodders. Pearl millet is a highly cross-pollinated crop with protogynous flowering and wind borne pollination mechanism, which fulfils one of the essential biological requirements for hybrid development. Pearl millet has gained importance for its forage value, wide agro-ecological adaptations, wide germplasm with varying degrees of photoperiod sensitivity associated with forage yield and excellent

regenerability permitting multi-cut forage production. 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 as grain crop in Punjab state. It can be fed to animals at any stage of growth without deleterious effects.

A preliminary knowledge about breeding value of parents and inheritance of different characters is essential for successful breeding programme. Studies on combining ability of parents are crucial in choosing parents, as it gives an idea of general combining ability (gca) of parents and specific combining ability (sca) of their cross combinations. Line x tester analysis is widely used to study combining ability of parents to be chosen for heterosis breeding (Kempthorne, 1957). It also provides guideline to determine the value of source populations and appropriate procedures to use in crop improvement programme. Besides breeding value of parents, the heritability values of different characters are imperative in providing guidelines for handling breeding material for the improvement of various characters. Bidinger *et al.* (2003) derived top cross hybrids which had positive drought response index in pearl millet. Parent offspring correlations not only provide idea about heritability of different characters but can be employed to have an idea about the association of parent plant characters with quality components of their hybrids. This may help in establishing certain criteria in selection of superior lines that may combine well for yield and quality. This information, in fact, helps in exploiting heterosis for commercial purpose. For development of effective heterosis breeding programme in pearl millet, the information about genetic architecture and estimated prepotency of parents in hybrid combinations is essential.

The plant quality characters are controlled by polygenes and are often highly responsive to environmental forces (Pethani and Kapoor, 1995). Therefore, it is essential to evaluate the material under different environments/seasons to identify desirable plant types with high stable forage yield. Burton (1962) demonstrated the potential of heterosis for forage production in pearl millet with parent hybrid 'Gahi 1' which yielded 52% more than common and 35% more than starr. Gahi 3 replaced Gahi 1 and was the first single cross forage hybrid produced using cytoplasmic male sterility (Burton, 1983). Exploitation of heterosis through single crosses is well established for forage production in pearl millet (Hanna *et al.*, 1997). The availability of diverse sources of cytoplasmic-nuclear male sterility enhances the possibility of exploiting heterosis for forage production (Yadav, 1999). However, there are no 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. The present studies were undertaken to evaluate male sterile lines and their populations, and also to assess heterosis through top crosses over different environments along with gene action involved in inheritance of quality parameters.

MATERIALS AND METHODS

The experimental material comprised of 15 CMS lines and 4 populations of pearl millet. CMS lines 111A, 543A, 315A, 308A, 503A and 220A were procured from PAU, Ludhiana (India) and lines 408A, 01555A, 05111A, 92222A, 91777A, 04777A, 01777A, 92666A and 92333A from ICRISAT, Hyderabad (India). All belonged to A₁ cytoplasmic source, except 315A, 408A, 503A and 01777A which belonged to cytoplasmic source of A₂, A₃, A₅ and A₅, respectively. The four testers used were

'Giant Bajra' (very leafy, profuse tillering, 9-10% protein, moderately resistant to diseases, 50-75 t ha⁻¹ fodder yield) from MPKV, Rahuri, 'RBC-2' (resistant to foliar diseased insect pest, 30-45 t ha⁻¹ fodder yield) from RAU, Rajasthan, 'GFB-1' (plants tall with higher number of leaves and tillers plant⁻¹, 7-8% protein, 45-50 t ha⁻¹ fodder yield) from GAU, Anand and 'NDFB-2' (very good under salt effected soils, 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. CMS (A) lines crossed to populations to get top cross hybrids and hybrids valuated for heterosis. In *kharif* 2012, 15 CMS lines were crossed to 4 populations to produce 60y top crosses (Table 2). In *kharif* 2013, during the month of April, 60 top crosses and parents i.e. CMS lines and populations along with local checks FBC 16 and PHBF-1 were evaluated in a lattice design with 2 replications over 2 environments. The environments were created by applying normal 5 irrigations at regular interval of 15 days throughout the crop growth till the onset of monsoon in one environment (Env-1) and by skipping the 2nd and 4th irrigation in the other environment (Env-2). The maximum and minimum temperature ranged between 42.1 to 25.1°C with maximum in 2nd week of June (4-10th June) and minimum in 3rd week of August (13-19th August). The relative humidity ranged from 35 to 90% with minimum in 2nd week of June and maximum in 2nd week of August. The observations were recorded on green fodder yield and quality parameters viz., crude protein, crude fiber and *in vitro* dry matter digestibility (IVDMD) under both the environments. Green fodder yield was recorded on per plot basis after 1st cut was taken at 60 days after sowing in both the environments and subsequent cuts 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°C and separately ground to pass through 20 mesh sieves. Crude protein was estimated as per McKenzie and Wallace (1954). Crude fibre was analyzed as per Goering and Vansoest (1970). IVDMD was determined by the method of Tilley and Terry (1967). The data was statistically analyzed according to Hookstra *et al.* (1983) and combining ability analysis for different traits done as per the model suggested by Kempthorne (1957).

RESULTS AND DISCUSSION

The pooled analysis of variance revealed that the 2 environments differed significantly in expression of all the characters, except crude fiber (Table 1). The mean squares due to hybrids were significant for all the characters under both the environments. The significant interaction of parents with environments for quality characters, except crude fiber, indicated differential expression of characters in the two environments. The significant differences due to interaction of parents v/s hybrids with environments indicated that heterotic effects varied with change in environment for all the quality characters under both the environments. The analysis of variance for combining ability revealed that female x male interaction variance was highly significant for all the characters under both

Table 1: Pooled analysis of variance for experimental design for quality traits

Source	GFY (kg plot ⁻¹)	CP (%)	CF (%)	IVDMD (%)
Environments	1757.80**	6.17**	0.0003	1619**
Parents	99.04**	2.18**	0.0020**	53.09**
Parents x Env	9.57**	0.53**	0.0004	57.47**
Hybrids	83.29**	3.72**	0.0037**	92.70**
Hybrid x Env	17.95**	1.30**	0.0014**	38.66**
(P vs Hyb.) x Env	0.09**	0.11	0.0005	6.20
Error	4.33	0.19	0.0003	12.25

GFY = Green fodder yield, CP = Crude protein, CF = Crude fiber, IVDMD = *In vitro* dry matter digestibility

*Significance at 5% level, **significance at 1% level

Table 2: Pooled analysis of variance for combining ability for quality traits

Source	d.f.	GFY (kg plot ⁻¹)	CP (%)	CF (%)	IVDMD (%)
Lines	14	142.17**	2.88**	0.0058**	144.52**
Testers	3	55.50**	6.24**	0.0071**	5.62
Lines x Testers	42	65.65**	3.82**	0.0028**	81.64**
Env x Lines	14	21.30**	1.26**	0.0025**	25.50*
Env x Testers	3	13.42*	1.00**	0.0022**	25.22
F x M x Env	42	17.15**	1.33**	0.0009**	44.01**
Error	156	4.33	0.19	0.0003	12.25

GFY= Green fodder yield, CP = Crude protein, CF = Crude fiber, IVDMD = *In vitro* dry matter digestibility;

*Significance at 5% level, **significance at 1% level

the environments (Table 2), which indicated the importance of specific combining ability (sca) in genetic expression of these characters in hybrids. The analysis of variance over environments revealed significant differences for all traits, except IVDMD, among testers and environment x testers but gca of lines (female parents) interacted significantly with environments for all quality characters. The female x male x environment interactions for combining ability were significant for all the quality characters revealing that sca of crosses varied with change in environments. Similar results were reported by Mahmoud and Ahmed (2010), Makumbi *et al.* (2011) and Bibi *et al.* (2012).

Green fodder yield (GFY)

In Env-1, the gca effect varied from -6.22 to 5.36. Out of 15 parental, CMS lines 01777A, 543A, 92222A, 315A and 111A were good general combiners with highly significant positive gca effects (Table 3). In Env-2, CMS line 92222A closely followed by 01777A, 543A, and 315A was best general combiners for GFY. Among these lines, 92222A, 315A, 543A and 01777A showed significant positive gca effect under both the environments. Three CMS lines 220A, 05111A and 408A were average combiners in both environments. Line 01777A, with significant gca values, was best combiner under both environments. In male parents, RBC-2 and Giant Bajra were best general combiners in Env-1 but in Env-2 only Giant Bajra showed significantly positive gca effect for this trait.

A total of 14 cross combination exhibited significant positive sca effects in Env-1 and highest value was found in cross 220A × GFB-1, closely followed by 408A × Giant Bajra. In Env-2, 15 crosses had significant sca effect and crosses 408A × NDFB-2, 92333A × GFB-1, 315A × RBC-2 and 04777A × GFB-1 were most desirable based on their sca effect. Top crosses 408A × Giant Bajra, 408A × NDFB-2, 315A × RBC-2, 04777A × GFB-1 were identified as good specific combinations under both the environments for this character. In general, the crosses having high sca effects involved at least one parent with poor gca in both environments which indicated the prevalence of primarily non-additive gene action. This reveals the possibility of dispersion of genes in parents and their complementation when brought together in hybrid combinations. These results are consistent with those of Saraswathi *et al.* (1996), Kenga *et al.* (2005) and Amit and Joshi (2007).

In Env-1, six hybrids exhibited positive heterosis over check for GFY, ranging between 5.55 to 13.88% (Table 4). These crosses involved CMS lines 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 x RBC-2 and 503A x NDFB-2, respectively. NDFB-2 was poor yielding pollinator for all the CMS lines which resulted in negative heterosis for this trait.

In Env-2, 7 hybrids expressed positive heterosis over commercial check FBC-16. The highest heterosis was manifested by 408A x NDFB-1 followed by 543A x GFB-1, 315A x RBC-2 and 92222A x RBC-2. The lowest negative heterosis was seen in 503A x NDFB-2 under Env-1 and Env-2. Out of total only 4 crosses viz., 315A x RBC-2, 543A x GFB-1, 01777A x Giant Bajra and 408A x Giant Bajra expressed positive and significant heterosis under both the environments. Prevalence of significant and positive heterosis for green fodder yield in pearl millet has been reported by Devanand and Das (1997).

Table 3: Estimation of general combining ability effects of parents for different traits

Parents	ENV-1				ENV-2			
	GFY (kg plot ⁻¹)	CP (%)	CF (%)	IVDMD (%)	GFY (kg plot ⁻¹)	CP (%)	CF (%)	IVDMD (%)
<u>Lines</u>								
111A	1.78**	-0.66**	0	0.2	-0.05	0.85**	-0.01**	5.32**
92222A	4.70**	0.44**	0	-2.06	4.45**	0.12	0.00	-6.57**
315A	3.03**	-0.07	-0.02**	1.36	1.95*	-0.38**	-0.04**	3.60**
308A	-1.35*	-0.73**	0.02**	-0.69	-3.2**	-0.82**	-0.01**	-1.87*
503A	-3.22**	-0.82**	0	-0.61	-5.9**	-0.78**	0.01**	1.94**
220A	0.22	0.44*	0	-0.17	0.45	-0.40**	-0.01**	0.04
92333A	-3.40**	0.59**	0	3.09*	-3.8**	-0.01	0.02**	5.02**
543A	5.03**	-0.17	0	2.16	3.58**	0.05	0.02**	0.78
91777A	-0.10	-0.12	-0.01	0.54	-0.42	-0.40**	-0.03**	-0.75
92666A	-2.47**	-0.47**	0.01	0.60	-1.05	0.21	-0.02**	0.08
05111A	-6.22**	0.41*	0.02**	5.01**	0.58	0.44**	0.09*	2.27**
01555A	-1.91*	0.58**	0	-0.54	-0.17	0.41**	-0.01**	1.03
04777A	-0.97	-0.16	-0.02**	0.56	-2.05*	-0.43**	-0.02**	1.05
01777A	5.36**	0.1	0	-5.54**	4.33**	0.54**	0.01**	-4.57**
408A	-0.47	0.62**	0	-4.19**	1.33	0.59**	0.0	-7.40**
SE±	0.59	0.17	0.006	1.50	0.80	0.12	0.004	0.70
CD _{0.05}	1.19	0.34	0.013	2.99	1.60	0.24	0.008	1.53
CD _{0.01}	1.54	0.44	0.016	3.86	2.06	0.32	0.01	1.98
<u>Testers</u>								
RBC-2	0.79**	-0.18*	0.0	-0.68	-0.15	-0.09	0	0.37
Giant Bajra	0.64*	0.34**	0.0	1.23	1.74**	0.58**	-0.01**	-0.32
NDFB-2	-1.23**	-0.10	-0.01	-10.0**	-0.76*	-0.46**	-0.01**	-0.5
GFB-1	-0.20	-0.07	0.0	-0.65	-0.83*	-0.03	0.02**	0.45
SE±	0.27	0.08	0.003	0.69	0.37	0.05	0.001	0.35
CD _{0.05}	0.55	0.15	0.006	1.38	0.74	0.11	0.003	0.71
CD _{0.01}	0.72	0.20	0.007	1.80	0.95	0.14	0.004	0.91

GFY = Green fodder yield, CP = Crude protein, IVDMD = *In vitro* dry matter digestibility, CF = Crude fiber, Env 1= Water stress, Env 2= Normal irrigation; *significant at 5% level, **significant at 1% level

Performance of promising top cross hybrids for fodder yield

Based on the performance, top 5 hybrids are selected for forage yield in individual environment (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 environment. The hybrids 315A × RBC-2, 543A × GFB-1, 01777A × Giant Bajra, 92222A × GFB-1 and 408A × Giant Bajra in Env-1 and 408A × NDFB-2, 543A × GFB-1, 315A × RBC-2, 408A × Giant Bajra and 92666A × Giant Bajra in Env-2, 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 for GFY under both the environments. All 5 promising hybrids exhibited high positive and significant standard heterosis for GFY. This high yielding ability may be due to possession of significant plant height, number of tillers m⁻¹ row length, number of leaves plant⁻¹, 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 major role in determining heterosis. These promising hybrids exhibited positive 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 crop. These hybrids had combination of parents with high × low, low × high and high × high gca effects. These also had considerably high sca effects through non-significant. Thus, these can be directly used as hybrids or apply standard selection procedure in segregating

Table 4: Standard heterosis (%) for different traits over best check under individual environments

Hybrids	GFY (kg plot ⁻¹)		CP (%)		CF (%)		IVDMD (%)	
	Env 1	Env 2	Env-1	Env- 2	Env -1	Env- 2	Env- 1	Env- 2
111A × RBC-2	-19.4**	-24.3**	-30.9**	30.12**	2.97**	-3.70**	-7.70*	17.87**
111A × Giant Bajra	-2.70	-9.7**	-28.9**	-7.83**	0.50	-8.20**	0.0	9.68**
111A × NDFB-2	-30.5**	-39.0**	-28.7**	-30.7**	15.61**	16.97**	-5.94	2.23**
111A × GFB-1	-61.1**	-19.5**	-17.9**	-23.7**	1.67**	4.66**	8.21**	13.78**
92222A × RBC-2	-13.8**	17.0**	-36.5**	-33.4**	7.80**	2.23**	-16**	-10.4**
92222A × G B	-19.4**	-9.7**	5.0**	-6.6**	3.71**	0.0	3.16	-26.0**
92222A × NDFB-2	-22.2**	-9.7**	-4.3**	-10.9**	-1.67**	5.41**	0.99	-6.9**
92222A × GFB-1	8.33**	-2.4	-15.6**	-16.3**	11.33**	14.0**	-12.2**	-1.86
315A × RBC-2	13.8**	19.5**	-33.2**	-15.7**	9.85**	14.0**	-4.75	11.91**
315A × Giant Bajra	-30.5**	-34.1**	-7.8**	-15.6**	4.08**	-17.9**	1.18	-2.04
315A × NDFB-2	-22.2**	-4.8*	-17.9**	-36.7**	-9.29**	-22.0**	11.48**	5.21**
315A × GFB-1	-47.2**	-34.1**	-17.9**	-22.8**	-10.0**	-7.46**	-4.95	15.45**
308A × RBC-2	-41.6**	-37.8**	-17.8**	24.7**	22.67**	-10.0**	-4.35	-7.26**
308A × Giant Bajra	-47.2**	-24.3**	-29.2**	-29.8**	3.53**	11.94**	-8.31*	-26.6**
308A × NDFB-2	-38.8**	-39.0**	-24.8**	-21.8*	9.29**	2.98**	4.95	0.37
308A × GFB-1	-55.5**	-53.6**	-38.1**	-36.0**	5.76**	7.27**	-5.54	23.27**
503A × RBC-2	-36.1**	-39.0**	-13.1**	-33.1**	-3.71**	-5.41**	0.39	13.00**
503A × Giant Bajra	-25.0**	-21.9**	-25.0**	-20.0**	3.9**	3.91**	0.39	-1.40
503A × NDFB-2	-88.8**	-87.8**	-41.5**	-39.3**	6.87**	29.47**	-11.3**	9.58**
503A × GFB-1	-75.0**	-58.5**	-16.2**	-17.5**	12.00**	10.44**	-2.17	-2.97
220A × RBC-2	-33.3**	-34.1**	-26.2**	-38.1**	11.15**	10.44**	-10.1**	-5.95**
220A × Giant Bajra	-68.0**	-12.1**	13.1**	5.87**	-3.71**	-3.73**	9.50**	0.93
220A × NDFB-2	-58.3**	-36.5**	-15.4**	-30.1**	-1.11**	-4.03**	-8.11*	10.1**
220A × GFB-1	11.1**	0.0	-22.8**	-30.8**	7.80**	7.00**	0.00	-1.17
92333A × RBC-2	-69.4**	-58.5**	7.81**	-18.8**	11.15**	16.23**	-11.9**	5.21**
92333A × Giant bajra	-47.2**	-46.3**	-10.8**	-21.0**	-1.11**	5.41**	-11.8**	8.47**
92333A × NDFB-2	-52.7**	-53.6**	-21.2**	-21.4**	2.78**	-2.61**	15.44**	11.45**
92333A × GFB-1	-61.1**	-7.3**	-20.0**	-11.3**	5.39**	29.66**	14.25**	15.92**
543A × RBC-2	-8.3**	-7.3**	-3.7**	-14.8**	-2.00**	3.35**	-6.33	-10.8**
543A × Giant Bajra	-41.6**	-31.7**	-17.9**	-19.1**	18.58**	11.00**	8.91*	14.71**
543A × NDFB-2	-2.7	-4.8*	-40.3**	-33.1**	-4.00**	11.94**	3.36	-13.0**
543A × GFB-1	11.1**	19.5**	-20.1**	-2.2**	1.48**	33.58**	3.36	18.62**
91777A × RBC-2	-8.3**	-7.3**	-15.9**	-12.7**	5.94**	13*	0.0	7.26**
91777A × Giant Bajra	-27.7**	-2.4	-19.0**	-32.3**	7.24**	5.00**	1.18	18.24**
91777A × NDFB-2	-55.5**	-58.5**	-17.6**	-29.8**	-15.2**	-52.0**	0.39	-10.9**
91777A × GFB-1	-63.8**	-31.7**	-26.8**	-29.7**	1.11**	6.90**	-4.95	-16.4**
92666A × RBC-2	-36.1**	-29.2**	-16.7**	-21.7**	1.48**	-1.11**	14.45**	2.60
92666A × Giant Bajra	-61.1**	4.8*	-23.7**	10.9**	10.78**	-7.27**	-10.5**	14.33**
92666A × NDFB-2	-47.2**	-39**	-18.7**	-36.6**	8.55**	2.79**	-12.0**	-8.75**
92666A × GFB-1	-63.8**	-48.7**	-38.8**	-15.6**	17.65**	6.71**	7.12**	-3.91*
05111A × RBC-2	-69.4**	-41.4**	-37.5**	-34.6**	12**	61.94**	-2.57	-5.30**
05111A × Giant Bajra	-77.7**	4.87**	-5.30**	1.56**	1.48**	16.00**	14.85**	1.86
05111A × NDFB-2	-80.5**	-2.4	-8.75**	-15.3**	2.97**	7.64**	8.71*	5.77**
05111A × GFB-1	-63.8**	-41.4**	-1.80**	-3.4**	29.92**	72.57**	10.89**	18.24**
01555A × RBC-2	-33.3**	-2.4	-15.8**	0.0	7.06**	9.88**	11.88**	23.64**
01555A × Giant Bajra	-47.2**	-12.1**	-24.8**	-42.4**	7.06**	1.30**	6.53	3.35
01555A × NDFB-2	-69.4**	-34.1**	4.38**	2.86**	-2.04**	-5.41	-17.4**	-8.56**
01555A × GFB-1	-45.8**	-46.3**	-8.2**	-13.2**	5.94**	5.22**	-13.2**	-7.0**
04777A × RBC-2	-69.4**	-63.4**	-27.9**	-34.3**	6.87**	11.38**	1.78	6.70**
04777A × Giant Bajra	-41.6**	-36.5**	-13.6**	-13.6**	-7.43**	-12.3**	8.51*	-1.11
04777A × NDFB-2	-61.1**	-24.3**	-15.9**	-15.4**	-8.17**	-5.59**	-2.37	12.84**
04777A × GFB-1	-2.70	-7.3**	-24.2**	-30.2**	-10.2**	0.0	-11.2**	-6.90**
01777A × RBC-2	-19.4**	-2.4	-12.6**	-23.1**	-4.0**	0.0	-11.2**	-10.2**
01777A × Giant Bajra	10.2**	-7.3**	-6.2**	27.0**	12.08**	7.83**	-7.92**	-1.30
01777A × NDFB-2	-16.6**	-7.3**	-25.6**	-20.4**	2.60**	14.36**	-5.54	9.31**
01777A × GFB-1	-8.3**	-4.8*	-24.2**	-30.1**	2.97**	13.00**	-26.9**	-28.0**
408A × RBC-2	-65.2**	-43.9**	-11.0**	-14.2**	-2.04**	-6.15**	-13.7**	-13.9**
408A × Giant Bajra	5.5**	7.31**	-17.7**	-19.2**	11.52**	13.80**	-7.72*	-8.0**
408A × NDFB-2	-30.5**	41.4**	-17.5**	-15.6**	1.67**	7.46**	-9.10*	-18.8**
408A × GFB-1	-73.6**	-70.7**	3.59**	4.81**	6.31**	3.17**	-10.5**	-10.6**
SE±	1.73	2.36	0.50	0.36	0.017	0.011	4.40	2.25
CD _{0.05}	2.87	3.92	0.83	0.60	0.028	0.019	7.30	3.74
CD _{0.01}	3.59	4.90	1.04	0.74	0.035	0.022	9.15	4.68

GFY = Green fodder yield, CP = crude protein, CF = crude fiber, IVDMD = *In vitro* dry matter digestibility, Env 1= water stress, Env 2= normal irrigation; *significance at 5% Level, **significance at 1% Level

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 indicated that even though the individual lines had less gca effects, the line when crossed the gene contributing for forage yield from female and male combine 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.

Crude protein

Analysis of gca in Env-1 (Table 4) revealed that 6 CMS lines viz., 408A, 92333A, 01555A, 92222A, 220A and 05111A had positive significant gca effects and were good general combiners for crude protein. In Env-2, 5 lines namely, 111A, 408A, 01777A, 05111A and 01555A were good general combiners with positive and significant gca effects. Two CMS lines 92666A and 92222A were average general combiners and rest lines were poor general combiners. Two lines 05111A and 408A were best combiners for crude protein character with high gca value. In case of populations used as testers, only Giant Bajra showed significant positive gca effect in both the environments.

Ten crosses in Env-1 and 17 crosses in Env-2 showed positive and significant sca effects. Four crosses (92222A × NDFB-2, 503A × GFB-1, 220A × Giant Bajra and 408A × GFB-1) were good combiners. In Env-1, 5 cross hybrids 220A x Giant Bajra, 92333A x RBC-2, 92222A x Giant Bajra, 01555A x NDFB-2 and 408A x GFB-1 expressed significant positive heterosis over best check PHBF-1 (Table 5). In Env-2, 6 top cross hybrids expressed significant positive heterosis over check. Maximum positive heterosis was manifested by 111A x RBC-2 followed by 01777A x Giant Bajra. Among these hybrids, 220A x Giant Bajra, 01555A x NDFB-2 and 408A x GFB-1 manifested positive heterosis in both the environments.

Crude fiber

Only 2 female lines 308A and 05111A were good general combiners in Env-1 (Table 4). The rest lines, except 315A, 91777A and 04777A, were average combiners. In Env-2, 5 CMS lines 05111A, 92333A, 543A, 503A and 01777A were good general combiners with significant positive gca effects. CMS line 05111A was best general combiner for this trait as it was for crude protein too. These lines can be used in future breeding programs for the improvement of quality traits in water stress and normal environments. None of tester was found to be good general combiner in Env-1, whereas in Env-2 GFB-1 had significant positive gca effect.

In Env-1, among 60, only 5 crosses 543A × Giant Bajra, 05111A × GFB-1, 111A × NDFB-2, 308A × RBC-2 and 04777A × RBC-2 were good specific combiners with significant positive sca effects. In Env-2, 20 cross combination had significant and positive sca effects. Two crosses 05111A × GFB-1 and 04777A × RBC-2 were good specific combiners under both environments. In Env-1, 5 cross hybrids 220A x Giant Bajra, 92333A x RBC-2, 92222A x Giant Bajra, 01555A x NDFB-2 and 408A x GFB-1 expressed significant positive heterosis over best check PHBF-1. In Env-2, 6 cross hybrids expressed significant positive heterosis over check. Maximum positive heterosis was manifested by 111A x RBC-2 closely followed by 01777A x Giant Bajra. Among these hybrids, 220A x Giant Bajra, 01555A x NDFB-2 and 408A x GFB-1 manifested positive heterosis under both the environments.

In vitro dry matter digestibility (IVDMD)

The estimates for gca effects in Env-1 revealed that two cms lines viz., 05111A and 92333A had positive and significant gca effects. In Env-2, five cms lines viz., 111A, 92333A, 315A, 05111A and 503A, with gca value of 5.32, 5.02, 3.60, 2.29 and 1.9, respectively were good general combiners. None of population, showed significant positive gca effect under both environments. Giant bajra and RBC-2 were recorded average general combiners in Env-1 and Env-2, respectively.

Table 5: Performance of promising top cross hybrids for green fodder yield

Top cross hybrids	Mean fodder yield (kg plot ⁻¹)	Commercial heterosis	gca effects (female × male)	sca effects
<u>Env-1</u>				
315A × RBC-2	20.5	13.8**	High × High	5.58**
543A × GFB-1	20.0	11.1**	High × Low	4.07**
01777A × Giant Bajra	19.8	10.2**	High × High	2.74**
92222A × GFB-1	19.5	8.33**	High × Low	3.82**
408A × Giant Bajra	19.0	5.55**	Low × High	7.73**
<u>Env-2</u>				
408A × NDFB-2	29.0	41.4**	High × Low	12.63**
543A × GFB-1	24.5	19.5**	High × Low	6.45**
315A × RBC-2	24.5	19.5**	High × Low	6.89**
408A × Giant Bajra	22.0	7.31**	High × High	3.13**
92666A × Giant Bajra	21.5	4.87**	Low × High	5.01**

** - significance at 1% level

The positive and significant sca effects were shown by 6 crosses in Env-1 and 21 crosses in Env-2. Highest sca value were exhibited by cross 01555A × RBC-2 followed by 92666A × RBC-2 in Env-1 and by 308A × GFB-1 followed by 01555A × RBC-2 in Env-2. Only 2 crosses namely, 92333A × GFB-1 and 01555A × RBC-2 were observed as very good specific combiners with significant sca effects under both environments. The positive heterosis was manifested by 25 hybrids under Env-1 and 31 hybrids under Env-2. Maximum positive heterosis was expressed by 92333A × NDFB-2 closely followed by 92666A × RBC-2 under Env-1. Maximum positive heterosis was manifested by hybrid 01555A × RBC-2 closely followed by 308A × GFB-1.

With respect to all three quality parameters three hybrids viz., 220A × Giant bajra, 01555A × NDFB-2 and 408A × GFB-1 exhibited high positive significant heterosis under both the environments (Table 5). In general, the crosses having high sca effects involved at least one parent with poor general combining ability in both environments 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. The results were consistent with the findings of Indhubala *et al.* (2010) and Iyanar and Khan (2004) in sorghum.

The type of gene action involved in the inheritance of all the traits were studied by comparing the gca effects of the parents involved in the crosses exhibiting high sca effects. The prevalence of non-additive gene action for quality characters indicated the family selection and heterosis breeding in the improvement of these characters which was evident from the analysis of variance for combining ability for the two environments.

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