Range Management and Agroforestry 44 (2) : 255-262, 2023
ISSN 0971-2070 (Print); 2249-5231 (Online)
https://doi.org/10.59515/rma.2023.v44.i2.06

Research article

Studies on combining ability and heterosis in three-way hybrids in forage pearl millet

Ruchika Bhardwaj, Sarabjeet Singh, Rabinder Singh Sohu* and Harpreet Kaur Oberoi

Punjab Agricultural University, Ludhiana-141004, India
*Corresponding author e-mail: rssohu@rediffmail.com

Received: 6th October, 2022 Accepted: 16th September, 2023

Abstract

In the present study, two A_5 CMS lines, *viz.* ICMA 03333 and ICMA 01777 were crossed with 15 different maintainers having high biomass during *kharif* 2016. The thirty male sterile F_1s were crossed with two high biomass pollinators, *viz.* Giant Bajra and RBC-2 during *Kharif* 2017 to generate three-way hybrids. A total of sixty, three-way hybrids were evaluated in summer (Environment I) and *kharif* (Environment II) for agronomic traits, *viz.* plant height (cm), green fodder yield (kg/plot) and dry fodder yield (kg/plot) and quality traits, *viz.* dry matter (%), *In vitro* dry matter digestibility (%) and crude protein (%) during *kharif* 2018. Significant variability was present in parents and hybrids for a majority of the traits under both environments. The pooled analysis of variance over environments revealed that combining ability varies with the change in environments. The lines ICMA 01777 × PB 111B and the tester Giant Bajra were identified as good general combiners for green fodder yield and its component characters as well as for quality traits, under both environments. The three-way hybrids, *viz.* (ICMA01777 × PB220B) × GB, (ICMA01777 × ICMB97111) × GB, (ICMA01777 × PB111B) × GB, and (ICMA01777 × ICMB00444) × GB were found to be promising cross combinations for almost all the traits under study. The high SCA cross combinations also showed high heterotic effects. Additive gene action was predominant in the inheritance of yield traits, whereas for fodder quality traits non-additive gene action was predominant.

Keywords: Combining ability, Fodder yield, Heterosis, Pearl Millet, Quality traits, Three-way forage hybrids

Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is an important coarse grain cereal being recognized for its high levels of resilience to climate change as it has inherent adaptability to drought and high temperatures (Kumawat *et al.*, 2016). It is a highly cross-pollinated crop that occupies more than 30 mha area in more than 30 countries across Asia, Africa, the Americas and Australia. India is the largest producer of pearl millet, both in terms of area (7.5 million ha) and production (9.07 million tons), with an average productivity of 1305 kg/ha (Directorate of Millet Development, 2018) in the country. In India, it is grown in drier areas of central and western regions (Rajasthan, Maharashtra, Gujarat, Uttar Pradesh and Haryana) covering near about 90 % of the total area in these states. Pearl millet is used in many ways as food, forage, health, nutrition, livelihood and biological purposes. Pearl millet is an essential source of fodder and is a valuable feed for livestock (Meena and Nagar, 2018). In the summer season, pearl millet provides a viable option as a green forage crop in northwestern India. In Punjab state, pearl millet is the second major fodder crop after sorghum and is grown on about 1.5 lakh hectare area (Anonymous, 2018). It supplies green fodder in the lean period during the summer months of May to July and in combination with other fodder crops during the *kharif* season. In marginal to poor environments, the dry fodder and straw of pearl millet are also used to feed the livestock, particularly during the dry periods when green fodder is in limited availability. Hence the development of high fodder-yielding cultivars/ hybrids of pearl millet is of paramount importance to bridge the gap in fodder demand and supply (Kumar *et al.*, 2023). Since the crop is highly cross-pollinated, open-pollinated varieties (OPVs) and hybrids are two important cultivar options, but higher productivity is realized through hybrids (Jukanti *et al.*, 2016). However, the higher seed rate (approx. three times higher) of forage types than grain types limits the use of commercial single cross hybrids. Pearl millet is a short-duration crop with high regenerability. This crop has the ability to grow well with little rainfall, making it a viable option for summer forage in areas without irrigation. Since pearl millet fodder has no antinutritional components like HCN content, it can be grazed, cut and fed at any growth stage, unlike sorghum. Thus, there is a need to produce forage hybrids for the *kharif* and *summer* seasons.

Although forage pearl millet varieties are an option for resource-poor farmers, the three-way hybrids developed using male sterile F_1 as productive female parents after crossing with distant maintainers as male parents would help in economic seed production owing to the higher seed yield capacity of F_1 sterile hybrids than a CMS line. The A_5 cytoplasmic male sterility system offers a greater chance for developing genetically diverse male-sterile hybrids using distantly related maintainer lines, as about 99 per cent of lines are maintainers of the A_5 CMS system (Rai *et al.,* 2000). The A_5 system is the consentient option for seed parent evolution because it simplifies the process of generating male sterile F1's and has a large number of maintainers as well as it is a stable male sterility system (Rai *et al*., 2009). Also, these hybrids would be able to fulfil the needs of the seed industry as well as farmers for forage pearl millet because of the high seed production potential of sterile F_1's used as a female parent. Thus, three-way forage hybrids would offer a favoured cultivar choice in the state where forage pearl millet is of greater importance. In the present study, efforts were made to develop three-way forage pearl millet hybrids utilizing A_5 CMS to cater the growing demand for fodder pearl millet.

To exploit heterosis for commercial purposes, it is important to understand the combining ability of parents, gene actions influencing yield and its components, and the extent of heterosis. Therefore, for choosing desirable parents, a study on the combining ability of parents is essential as it gives an idea of the general combining ability (GCA) of the parents and the specific combining ability (SCA) of their particular cross combinations. Many biometrical procedures have been developed to obtain information on combining ability; line × tester analysis (Kempthrone, 1957) is one of the most widely used methods to study the combining ability of the parents to be chosen for heterosis breeding. It also provides guidelines to determine the breeding values of source populations and appropriate procedures to be used in crop improvement programmes. Therefore, 30 single crosses (F_1) as females and two males as a tester were evaluated for combining ability for fodder yield and its contributing traits along with quality traits, *viz.* dry matter, *in-vitro* dry matter digestibility and crude protein in three-way hybrids in *summer* and *kharif* season 2018.

Materials and Methods

Experimental site and design: The experiment was carried out at Forage, Millets and Nutrition Research Farm, Punjab Agricultural University, Ludhiana located at 30° 91' N, 75° 85' E and 256 m above sea level in the Punjab state, India. The present study was conducted during *kharif* 2016, to develop three-way forage hybrids in pearl millet. To develop F_1 hybrids, two A_5 cytoplasm-based CMS lines, *viz.* ICMA 03333 and ICMA 01777 were crossed with 15 different maintainers from different cytoplasmic sources during *kharif* 2016. The thirty sterile F_{1S} generated were crossed with two high biomass pollinators during *kharif* 2017 to generate high green forage three-way hybrids. During *kharif* 2018, the 60 three-way hybrids and their parents along with three checks *i.e*. FBC-16, PCB-164 and PHBF-1 were evaluated in two replications in *summer* (Env 1) and *kharif* (Env II) seasons. The fertilization was done @ 50 kg of N (110 kg urea) per hectare in two equal doses, the first half as the basal dose and the second half, three weeks after sowing when the crop height was 10-15cm. The 60 three-way forage hybrids were planted in two rows of 4 m length with a row-to-row spacing of 22 cm in Alpha lattice design in both seasons. Three cuts were taken under both the seasons *i.e*. at 50 DAS, 80 DAS and 110 DAS.

***Observations and analysis*:** Three-way forage hybrids were evaluated for forage yield in the field in *kharif* 2018 and for quality traits at the Forage Evaluation Laboratory, Department of Plant Breeding and Genetics, PAU, Ludhiana. The observations were recorded on five random plants in both environments from each replication. The agronomic data was recorded for traits, *viz.* plant height (cm), green fodder yield (kg/plot) and dry fodder yield (kg/plot). The material was evaluated for quality traits, *viz*. dry matter (%), *in vitro* dry matter digestibility (%) and crude protein (%) for only the first cut in both seasons.

Statistical analysis: The data was analysed using SAS software version 9.3 for analysis of variance. The combining ability analysis was done by the standard method as given by Kempthome (1957). The standard heterosis was calculated as per the standard procedure.

Results and Discussion

The success of this study was based on the fact that all the maintainers of different cytoplasmic sources used in the present study when crossed with A_5 cms lines were able to maintain the sterility of A lines. This was confirmed by bagging the individual panicles of A x B cross and the seed setting of bagged panicles was recorded. Fortunately, all the thirty F_1s of A_5 x B crosses were sterile as there was no seed set in the bagged panicles confirming the male sterility. These thirty sterile F_{1s} were then crossed with two pollinators (Giant bajra and RBC-2) for the generation of three-way forage hybrids.

Analysis of variance: The pooled analysis of variance for different fodder characters in parents and hybrids was conducted (Table 1). The mean sum of squares for parents was significantly different for all the traits indicating the presence of variability for all the traits over the environment *i.e.* summer and *kharif*. The parent entries involving male lines showed significant differences for all the traits except plant height and crude protein (%) and the mean square due to female lines was highly significant for all the traits. The hybrids showed highly significant variation for all traits and the mean square due to interaction component (parents vs. hybrids) also showed significant difference for all the traits (Table 1). This indicated that heterotic effects were significantly influenced by environmental changes. The results were in accordance with the findings of Bibi *et al.* (2012) and Singh *et al.* (2014) who also reported the effect of changing environments on the performance of different traits.

The pooled analysis of variance for combining ability for different characters was also conducted (Table 2). The variance due to females was highly significant for all the characters. The mean squares due to males suggested that the variance due to the GCA of the hybrids was highly significant for all the characters. The female vs male interaction was also highly significant for all the characters. A perusal of the data (Table 1) further revealed that the females showed comparatively less influence of environment on green fodder yield, dry fodder yield, dry matter (%), in vitro dry matter digestibility and crude protein but more on plant height, whereas the males were comparatively less affected by the environment for fodder quality characters *viz.*, in vitro dry matter digestibility and crude protein, and more for plant height, green fodder yield, dry fodder yield and dry matter (%) across the environments.

The detailed combining ability analysis revealed that GCA was highly significant for all the characters under study which indicated that the additive variance was important for these traits. These results were in conformity with the earlier findings (Badurkar *et al.*, 2018; Gavali *et al.,* 2018). The data on GCA effects also indicated that the effects varied significantly for different characters in different parents and also in different environments. The $\sigma^2_{GCA}/\sigma^2_{SCA}$ value was more than one *i.e.*, the magnitude of GCA variance was greater than the SCA variance, for plant height, green fodder yield and dry fodder yield which

Table 1. Pooled analysis of variance for different traits in pearl millet

Sources of variation	df	PH (cm)	GFY (kg/plot)	DFY (kg/plot)	DM (%)	IVDMD (%)	CP (%)
Envs	1	7104.28**	118.81**	43.70*	450.52**	10.90**	1692.86**
Parents	31	50.47**	3.94**	0.73**	33.05**	13.87**	0.20**
Envs x Lines	29	53.88**	3.91**	0.78**	34.10**	14.25**	0.22**
Envs x Testers	1	1.24	4.16**	0.65**	10.37**	0.25**	0.05
Parents vs Hybrids x Envs	59	1625.53**	4.13**	0.71**	20.83**	31.10**	0.64**
Hybrids x Envs	1	111181.8**	210.33**	3.76**	139.16**	418.43**	48.12**
Error	91	9.19	0.07	0.04	2.12	0.02	0.03

PH: Plant height; GFY: Green fodder yield; DFY: Dry fodder yield; DM: Dry matter; IVDMD: *In vitro* dry matter digestibility; CP: Crude protein; *(P<0.05); **(P<0.01)

indicated the predominance of additive gene action in the inheritance of these traits. But contrary to this study Kumar *et al.* (2017) reported the predominance of non-additive gene action as they observed a greater magnitude of SCA variance than the GCA variance for dry fodder yield and plant height. SCA variances were highly significant for all the traits under study indicating epistatic gene action which was also reported by Patel *et al.* (2008) and Gavali *et al.* (2018). A higher magnitude of mean squares of SCA for dry matter (%), in vitro dry matter digestibility and crude protein, indicated the predominance of non-additive gene action to control these characters, therefore, heterosis breeding will be rewarding to achieve the objective of getting good cross combinations for higher fodder quality. The predominance of non-additive gene action in the inheritance of fodder quality traits was also reported earlier (Singh *et al.*, 2014; Karvar *et al.*, 2017; Gavali *et al.,* 2018). The significant magnitude of both GCA and SCA effects indicated the importance of both additive and non-additive components in the inheritance of the majority of the characters studied (Kumawat *et al.*, 2019).

Combining ability: The results pertaining to combining ability effects for different traits were recorded (Table 3-4). The critical examination of the GCA effect of lines revealed that line ICMA 01777 × PB 111B was proved to be the best combiner for all the traits studied in both environments. Environmentwise it was observed that in addition to line ICMA 01777 × PB 111B, line ICMA 01777 × ICMB 00444 was also proved to be a good general combiner for all the traits *viz*., plant height, green fodder yield, dry fodder yield, dry matter (%), in vitro dry matter digestibility and crude protein followed by line ICMA 01777 × PB 220B in Env 1 whereas in Env II, line ICMA 01777 × ICMB 00444 was a good general combiner for plant height, green fodder yield, dry matter (%), in vitro dry matter digestibility and crude protein; and line ICMA 01777 × PB 220B was good for plant height, dry matter (%), in vitro dry matter digestibility and crude protein. In addition to the above-mentioned good general combiners, line ICMA 01777 × ICMB 97111 was also a good general combiner for plant height, green fodder yield and crude protein in both environments, whereas in Env II this line was also a good general combiner for in vitro dry matter digestibility. Line ICMA 03333 × ICMB 02999 was observed to be a good combiner for dry matter (%), in vitro dry matter digestibility and crude protein but an average combiner for dry fodder yield in both environments. The tester Giant Bajra (GB) turned out to be a good general combiner for plant height, green fodder yield, dry fodder yield, dry matter (%) and crude protein under both environments, whereas for in vitro dry matter digestibility, the tester

Table 2. Pooled combining ability analysis of variance of parents and hybrids for different traits

Sources of variation	**df**	**PH (cm)**	**GFY (kg/plot)**	**DFY (kg/plot)**	**DM (%)**	**IVDMD (%)**	**CP (%)**
Env.	1	321758.93**	959.03**	534.21**	221.51**	107.91**	113.29*
Rep. x Env.	2	104751.12**	51.32**	44.09**	57.53**	9.72**	8.87**
Males(T)	1	126413.11**	103.81**	51.31**	405.18**	11.08**	11.86**
Female(L)	29	570.55**	3.57**	5.53**	15.36**	56.91**	1.50**
Males x Females	29	94.56	1.72**	6.84**	15.63**	67.17**	0.89
Males x Env.	1	64301.29**	50.27**	31.35**	189.77**	7.23*	5.49*
Female x Env.	29	231.41**	1.86*	2.47*	6.81*	21.37*	0.97*
Males x females x Env.	29	54.39**	0.83**	3.24**	8.64**	29.86**	0.43**
Pooled error	59	21.57	0.14	0.94	2.46	0.02	0.04
σ^2gca		1838.11**	2.01**	0.73**	6.07**	0.83**	0.17**
σ^2sca		67.47**	0.69**	0.45**	6.37**	33.67**	0.43**
σ^2gca/ σ^2sca		27.24	2.91	1.62	0.95	0.02	0.39

PH: Plant height; GFY: Green fodder yield; DFY: Dry fodder yield; DM: Dry matter; IVDMD: *In vitro* dry matter digestibility; CP: Crude protein; *(P<0.05); **(P<0.01)

Table 3. Estimation of general combining ability effects of promising parents for different traits under both environments

Parents	PH (cm)		GFY (kg/plot)		DFY (kg/plot)		DM (%)		IVDMD (%)		CP (%)	
	Env 1	Env II	Env 1	Env II	Env 1	Env II	Env 1	Env II	Env 1	Env II	Env 1	Env II
ICMA03333×ICMB02999	-7.41**	-14.64**	0.97**	0.05	0.21*	0.22*	2.58**	2.18**	4.92**	5.54**	0.99**	0.82**
ICMA01777×ICMB92777	3.19	14.79**	1.41**	0.42**	0.14	0.45**	-1.13	-1.90**	1.57**	1.33**	0.22**	0.20
ICMA01777×PB111B	12.67**	25.35**	2.24**	0.92**	1.35**	0.93**	5.61**	5.09**	6.97**	8.24**	1.67**	1.18**
ICMA01777×ICMB02999	6.32*	15.42**	-0.23	-0.05	0.11	-0.12	1.36	1.08**	0.84**	-1.12**	0.80**	-0.25**
ICMA01777×ICMB04777	6.35*	16.97**	1.01**	0.25*	0.23*	-0.30**	0.17	-0.60	4.72**	5.06**	0.08**	-0.38**
ICMA01777×ICMB91777	2.69	16.69**	1.57**	0.35**	0.33**	-0.18	0.05	0.03	-5.26**	-2.54**	-0.13	0.40**
ICMA01777×PB220B	13.10**	21.85**	1.41**	0.42**	0.30**	-0.13	3.58**	3.31**	5.97**	6.53**	1.24**	1.11**
ICMA01777×ICMB00444	20.20**	42.17**	2.38**	1.42**	0.94**	0.46**	3.32**	2.05**	6.27**	5.52**	1.45**	1.14**
ICMA01777×ICMB97111	11.45**	21.67**	1.81**	1.05**	0.23*	0.41**	3.24**	2.04**	4.94**	8.78**	1.62**	1.26**
ICMA01777×PB543B	-2.85	7.15**	-0.51*	0.32**	-0.13	-0.31**	-0.15	-0.92**	1.67**	-1.82**	0.37**	-0.28*
SE (gi)	2.66	0.58	0.21	0.10	0.11	0.10	0.88	0.39	0.07	0.08	0.08	0.10
CD (P<0.05)	5.31	1.15	0.42	0.20	0.22	0.20	1.76	0.78	0.14	0.16	0.16	0.20
GB	9.09**	41.45**	0.79**	1.23**	0.40**	0.79**	1.93**	1.75**	-0.14**	-0.41*	0.25**	0.38**
RBC-2	-7.02**	-32.50**	-0.43**	-1.42**	-0.26**	-0.42**	-2.93**	-2.35**	0.34**	0.62**	-0.16**	-0.18**
SE (gi)	0.49	0.11	0.04	0.02	0.02	0.02	0.16	0.07	0.01	0.01	0.02	0.02
CD (P<0.05)	1.35	0.30	0.11	0.05	0.05	0.05	0.44	0.19	0.03	0.03	0.05	0.05

PH: Plant height; GFY: Green fodder yield; DFY: Dry fodder yield; DM: Dry matter; IVDMD: *In vitro* dry matter digestibility; CP: Crude protein; *(P<0.05); **(P<0.01)

Table 4. Estimation of specific combining ability effects of promising three way forage hybrids for different traits under both environments

Crosses	PH (cm)		GFY (kg/plot)		DFY (kg/plot)		DM (%)		IVDMD (%)		CP (%)	
	Env 1	Env II	Env 1	Env II	Env 1	Env II	Env 1	Env II	Env 1	Env II	Env 1	Env II
(ICMA01777×ICMB92777)×GB	4.32*	4.33**	1.63**	0.90**	0.14	-0.41**	-1.54	-1.60**	-10.98**	1.31**	-0.17*	0.18
(ICMA01777×PB111B)×GB	-2.06	2.07*	1.21**	0.60**	0.86**	0.70**	3.25**	3.44**	7.98**	7.94**	1.22**	1.57**
(ICMA03333×ICMB02999)×GB	-2.28	-4.29**	-0.07	0.55**	0.60**	0.55**	3.15**	3.04**	5.64**	7.64**	1.02**	1.06**
(ICMA01777×ICMB04777)×GB	8.31**	13.40**	0.59**	0.35**	0.05	-0.38**	-0.77	-1.33**	1.27**	-4.99**	-0.14	0.81**
(ICMA01777×ICMB1777)×GB	0.97	5.13**	0.68**	0.65**	0.01	-0.19	-1.22	-0.54	1.04**	-2.77**	0.89**	-0.21*
(ICMA01777×PB220B)×GB	7.46**	9.87**	1.40**	0.94**	0.68**	0.65**	2.83**	4.12**	7.64**	7.31**	1.16**	1.08**
(ICMA01777×ICMB00444)×GB	4.36*	9.05**	1.27**	1.13**	0.46**	0.63**	3.74**	3.91**	6.98**	6.94**	1.73**	1.37**
(ICMA01777×ICMB97111)×GB	-6.34**	-0.25	1.78**	0.96**	0.48**	0.55**	2.63**	2.42**	5.21**	6.69**	1.76**	1.70**
(ICMA03333×ICMB06999)×RBC-2	5.22**	9.74**	0.42*	0.53**	0.27*	0.42**	1.47	1.08**	-2.97**	2.14**	0.69**	0.41**
(ICMA03333×ICMB06555)×RBC-2	1.96	4.50**	0.65**	0.48**	0.01	0.25*	-2.42**	-1.86**	5.23**	0.04	-0.10	0.27**
SE (sij)	2.06	0.58	0.21	0.10	0.11	0.10	0.82	0.39	0.07	0.08	0.08	0.10
CD (P<0.05)	4.17	1.15	0.42	0.20	0.22	0.20	1.65	0.78	0.14	0.16	0.16	0.20

PH: Plant height; GFY: Green fodder yield; DFY: Dry fodder yield; DM: Dry matter; IVDMD: *In vitro* dry matter digestibility; CP: Crude protein; *(P<0.05); **(P<0.01)

Table 5. Standard heterosis (%) of promising three-way hybrids for different traits over best check FBC-16 under both environments

Crosses	PH (cm)		GFY (kg/plot)		DFY (kg/plot)		DM (%)		IVDMD (%)		CP (%)	
	Env 1	**Env II**	**Env 1**	**Env II**	**Env 1**	**Env II**	**Env 1**	**Env II**	**Env 1**	**Env II**	**Env 1**	**Env II**
(ICMA03333×PB274B)×GB	5.00	24.59*	18.44*	-7.12*	20.61*	-18.58*	2.05	-12.40	-8.90*	9.48	14.95*	-6.24
(ICMA03333× ICMB02999)×GB	-3.90	17.52*	22.48*	-2.59*	56.94*	21.97*	34.96*	39.01*	36.77*	31.16	19.96*	16.22*
(ICMA 03333× ICMB 04777)×GB	5.51	19.49*	27.41*	-4.53*	26.98*	-12.60*	0.00	-8.50	-18.61	12.02	7.96*	2.43*
(ICMA 03333× ICMB 91777)×GB	10.04*	23.12*	20.23*	-7.12*	43.48*	-3.57*	19.61*	3.77*	-21.02	16.18*	0.01	-0.22*
(ICMA 03333× ICMB 97111)×GB	5.00	15.55*	14.40*	-7.12*	53.59*	10.93*	34.27*	19.46*	-8.55*	-0.92	6.48*	2.12*
(ICMA 01777× ICMB 92777)×GB	10.68*	35.58*	41.77*	-0.65*	48.16*	-12.78*	4.55	-12.26	-30.45	16.82*	2.16*	1.58*
(ICMA 01777×PB111B)×GB	13.31*	39.52*	45.36*	2.27*	138.05*	147.26*	64.22*	37.06*	24.49*	39.77*	28.88*	22.66*
(ICMA 01777×PB274B)×GB	6.53	33.75*	13.06*	-6.47*	24.87*	-11.35*	10.77	-5.22	-6.59*	16.38*	18.47*	-5.35
(ICMA 01777× ICMB 02999)×GB	14.11*	38.69*	10.36*	-5.18*	40.38*	4.07*	27.16*	9.73*	-6.95*	15.26*	16.15*	2.05*
(ICMA 01777× ICMB 04777)×GB	16.74*	40.92*	28.76*	-2.59*	47.98*	-8.28*	15.27*	-5.82	6.32*	2.31	16.11*	2.05*
(ICMA 01777× ICMB 91777)×GB	7.42	36.86*	32.35*	0.05	50.65*	0.00*	12.28*	0.02	-21.19	0.35	13.36*	-0.11*
(ICMA 01777×PB220B)×GB	21.74*	41.56*	34.59*	-4.53*	63.20*	25.66*	43.10*	40.65*	17.81*	18.73*	21.02*	22.26
(ICMA 01777× ICMB 00444)×GB	25.13*	50.82*	43.11*	4.21*	66.07*	22.90*	46.16*	45.11*	17.84*	28.79*	20.00*	22.68*
(ICMA 01777× ICMB 97111)×GB	8.64*	36.67*	46.70*	6.15*	59.80*	24.98*	39.27*	34.43	23.15*	24.62*	20.24*	22.12*
(ICMA 01777×PB543B)×GB	3.69	27.72*	6.77*	-0.65*	17.48*	-8.43*	10.07	-7.89	3.65*	6.82	10.61*	-7.47
Range of standard heterosis	-16.53 to 25.13	-23.26 to 50.82	-13.68 to 46.70	-26.54 to 6.15	-28.80 to138.05	-51.46 to 147.26	-31.03 to 64.22	-35.67 to 45.11	-37.04 to 36.77	-27.28 to 28.88	-27.11 to 39.77	-19.18 to 22.68
SE	5.71	1.23	0.55	0.28	0.31	0.22	2.51	1.02	0.20	0.20	0.22	0.24
CD (P<0.05)	11.41	2.46	1.10	0.56	0.63	0.43	5.01	2.04	0.39	0.40	0.43	0.48

RBC 2 was found to be good general combiner in both the environments.

From the present investigations it was observed that for plant height, green fodder yield and dry fodder yield, the cross combination (ICMA 01777 × PB 220B) × GB proved to be the best specific combiner in both environments. For green fodder yield and dry fodder yield, other good specific combiners were (ICMA 01777 × ICMB 97111) × GB and (ICMA 01777 × PB 111B) × GB, which showed that Giant Bajra proved to be the best general combiner to get good yield. For fodder quality traits, again (ICMA 01777 × ICMB 97111) × GB and (ICMA 01777 × PB 111B) x GB along with cross combination (ICMA 03333 x ICMB 02999) x GB and (ICMA 01777 × ICMB 00444) × GB were found to be promising for in vitro dry matter digestibility and crude protein. But on the whole, it was observed that (ICMA 01777 × PB 220B) x GB cross combination was found to be best as it was good for all the fodder yield and quality component traits in both the environments except for in vitro dry matter digestibility in Env II. Therefore, the cross combinations (ICMA 01777 × ICMB 97111) × GB and (ICMA 01777 × PB 111B) × GB were good for green fodder yield, dry fodder yield, dry matter (%), in vitro dry matter digestibility and crude protein in both the environments, whereas (ICMA 03333 × ICMB 02999) × GB was found productive for dry fodder yield, dry matter (%), in vitro dry matter digestibility and crude protein in both the environments. In Env 1, (ICMA 01777 × ICMB 00444) × GB cross combination was also proved to be good for green fodder yield, dry fodder yield, dry matter (%), in vitro dry matter digestibility and crude protein. It was further noted that the three-way cross combinations with tester RBC 2 were not found promising for any of the fodder yield and quality characters except for plant height in Env 1.

Heterosis: Significant and positive heterosis was observed for all the traits under study, *viz.* plant height, green fodder yield, dry fodder yield, dry matter, in vitro dry matter digestibility and crude protein under both environments (Table 5). The results were in accordance with the findings of Singh *et al.* (2014) who reported positive and significant heterosis for plant height, green fodder yield, dry fodder yield, dry matter, in vitro dry matter digestibility and crude protein. Based on heterosis, (ICMA 01777 × PB 111B) × GB cross combination was found to be best for simultaneous improvement in green fodder yield, dry fodder yield, in vitro dry matter digestibility and crude protein *i.e.* both for fodder yield and fodder quality characters in both the environments. The cross (ICMA 01777 × ICMB 00444) × GB was also proved to be good as it exhibited good heterosis for green fodder yield, dry fodder yield, dry matter (%), in vitro dry matter digestibility and crude protein in Env II, and in Env 1 this cross also showed good heterosis for plant height, green fodder yield, dry matter (%) and in vitro dry matter digestibility. The cross (ICMA 01777 × PB 220B) × GB was also found promising for plant height, dry fodder yield, dry matter (%) and crude protein in both environments; but in Env 1 this cross showed very good heterosis for in vitro dry matter digestibility. For green fodder yield, the maximum heterosis was shown by (ICMA 01777 × ICMB 97111) × GB in both environments, but for other yield and quality characters like dry fodder yield, dry matter (%), in vitro dry matter digestibility and crude protein, this cross combination showed good heterosis. Similarly, Ashok *et al.* (2016) also reported cross combinations which gave high SCA coupled with heterosis and per se performance for yield and quality traits.

Conclusion

From the present investigations, it could be concluded that the line ICMA 01777 × PB 111B proved to be a good general combiner and in combination with the Giant Bajra tester, it showed a very good cross combination with very good heterosis for green fodder yield, dry fodder yield, in vitro dry matter digestibility and crude protein in both the environments. Similarly, the ICMA 01777 × PB 220B in combination with Giant Bajra was promising for improving yield and quality characters. The (ICMA 01777 × PB 220B) × GB cross combination was the best specific combiner for all the fodder yield and quality component traits in both environments except for in vitro dry matter digestibility in Env I *i.e. kharif* season. Therefore, four cross combinations, *viz.* (ICMA 01777 × PB 220B) × GB, (ICMA 01777 × ICMB 97111) × GB, (ICMA 01777 × PB 111B) × GB and (ICMA 01777 × ICMB 00444) × GB, produced significant and desirable SCA effects and heterosis for most of the traits studied indicating the potential for exploiting hybrid vigour in breeding program.

References

Anonymous. 2018. Package of practices for *kharif* crops. Punjab Agricultural University, Ludhiana, India. pp. 35-38.

Ashok, A., P. Sumathi, P. Veerabadhiran, J. Revathi and S. Poornimajency. 2016. Development of heteroitic hybrids for quality, yield and its architectural traits in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Range Management and Agroforestry* 37: 181-184.

Badurkar, S. B., S. P. Pole, V. N. Toprope and N. P. Ingle. 2018. Combining ability for grain yield and its related traits in pearl millet [(*Pennisetum glaucum*) (L.) R. Br.]. *International Journal of Current Microbiology and Applied Sciences* 6: 956-961.

Bibi, A., H. A. Sadaqat, T. M. Khan, B. Fatima and Q. M. Ali. 2012. Combining ability analysis for green forage associated traits in sorghum-sudan grass hybrids under water stress. *Journal of Animal and Plant Sciences* 6: 115-137.

Directorate of Millet Development. 2018. http://Direcrorate of millet development (accessed on Dec. 10, 2022).

Gavali, R. K., N. S. Kute, V. Y. Pawar and H. T. Patil. 2018. Combining ability analysis and gene action studies in pearl millet [*Pennisetum glaucum* (L.) R Br.]. *Electronic Journal of Plant Breeding* 9: 908-915.

Jukanti, A. K., C. L. L. Gowda, K. N. Rai, V. K. Mangat and R. K. Bhatt. 2016. Crops that feed the world 11. Pearl Millet (*Pennisetum glaucum* L.): an important source of food security, nutrition and health in the arid and semi-arid tropics. *Food Science* 8: 307-329.

Karvar, S. H., V. Y. Pawar and H. T. Patil. 2017. Heterosis and combining ability in pearl millet (*Pennisetum glaucum* (L.) R. Br.). *Electronic Journal of Plant Breeding* 8: 1197-1215.

Kempthorne, O. 1957. *An Introduction to Genetic Statistics.* John Wiley and Sons Inc, New York. pp. 456-471.

Kumar Anil, R. Kumar Devvart and A. K. Dehinwal. 2017. Combining ability for grain yield and its components involving alloplasmic iso-nuclear lines of pearl millet. *International Journal of Current Microbiology and Applied Sciences* 6: 554-561.

Kumar, S., P. Singh, U. Devi, K.R. Yathish, P. L. Saujanya, R. Kumar and S.K. Mahanta. 2023. An overview of the current fodder scenario and the potential for improving fodder productivity through genetic interventions in India. *Animal Nutrition and Feed Technology* 23: 631-644.

Kumawat, K.R., P. C. Gupta and N. K. Sharma. 2019. Combining ability and gene action studies in pearl millet using line x tester analysis under arid conditions. *International Journal of Current Microbiology and Applied Sciences* 8: 976-984.

Kumawat, S.M., Mohd. Arif, S. S. Shekhawat and S. R. Kantwa. 2016. Effect of nitrogen and cutting management on growth, yield and quality of fodder pearl millet (Pennisetum glaucum L.) cultivars. *Range Management and Agroforestry* 37: 207-213

Meena, S. S. and R. P. Nagar. 2018. Evaluation of neem strains and productivity of pearl millet and cluster bean under agroforestry system in semi-arid climate. *Range Management and Agroforestry* 39: 121-125.

Patel, M. A., J. P. Yadavendra, D. H. Patel, N.V. Upahyaya and J. A. Shaikh. 2008. Studies on heterosis for green fodder yield its contributing traits in pearl millet (*Pennisetum glaucum* (L.) R. Br.). *Forage Research* 34: 149-155.

Rai, K. N., D. J. Andrews and A. S. Rao. 2000. Feasibility of breeding male sterile populations for use in developing inter-population hybrids in pearl millet. *Plant Breeding* 119: 335-339.

Rai, K. N., S. K. Gupta, R. Bhattacharjee, V. N. Kulkarni, A. K. Singh and A. S. Rao. 2009. Morphological characteristics of ICRISAT-bred pearl millet hybrid seed parents. Patancheru, Andhra Pradesh, India. pp. 1-176.

Singh, P., R. Kapoor and C. Batra. 2014. Heterosis and combining ability in forage pearl millet (*Pennisetum glaucum* L.) under stress and non-stress environments. *Applied Biological Research* 16: 214-222.