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Research article

Identification of heterotic combination from indigenous lines for higher yields in multi-cut forage pearl millet

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Abstract

Variability and diversity analysis were performed for 16 different yield and yield-related traits on 81 forage pearl millet lines (75 inbred lines and 6 checks). The ANOVA revealed the presence of enough variability among all forage pearl millet lines. High GCV and PCV were recorded for characters such as leaf to stem ratio, green and dry fodder yield in the first and second cut, as well as total green and dry fodder yield. For other traits, moderate and low GCV and PCV were recorded. High heritability and high genetic advance as a percentage mean were obtained for plant height, number of leaves per tiller, leaf /stem ratio, green fodder yield in first and second cut, total green fodder yield, dry fodder yield in first and second cut, and total dry fodder yield. For other traits, high heritability and moderate genetic advance as a percentage mean were recorded. The dendrogram revealed four distinct clusters, indicating the presence of divergence. For the crossing programme, 10 parent lines were selected from these 81 inbred lines. 45 crosses were made with a half-diallel method by using the protogynous nature of forage pearl millet lines. These 45 crosses or hybrids were evaluated for their yield traits by analysis combining ability (GCA and SCA) and heterosis (average and heterobeltiosis heterosis). The GCA effect and mean performance of parents indicated that the genotypes viz., IIMR AVS95 and IIMR AVS98, were good combiners for total green fodder yield. Based on the SCA effect, the hybrids, *viz.*, IIMR AVS50 x IIMR AVS95, IIMR AVS77 x IIMR AVS98 and IIMR AVS95 x IIMR AVS11, recorded a positive effect. Considering mean performance, SCA effect and heterobeltiosis, the hybrids IIMR AVS50 x IIMR AVS95, IIMR AVS77 x IIMR AVS98 and IIMR AVS95 x IIMR AVS11 were identified as the superior performing hybrids for further utilization to improve fodder yield in pearl millet.

Keywords: Combining ability, Forage pearl millet, Genetic diversity, Genetic variability, Half-diallel, Heterosis, R software

Introduction

One of the main millet crops, pearl millet (*Pennisetum glaucum* (L) R.Br.), is used as both grain and feed. Pearl millet is resistant to various environmental pressures, adaptable in a variety of climate conditions with high biomass (Daduwal *et al*., 2024; Supriya *et al*., 2024). Crop is primarily grown in the dry and hot agro-ecologies of Africa and Asia, where recurrent droughts are common (Bhattarai *et al*., 2019; Kumawat *et al*., 2016). Pearl millet green fodder has properties of low prussic acid (commonly found in sorghum and Sudan grass), high in protein and minerals, and palatable to animals (Yadav and Singh, 2012). Farmers in India prefer to grow pearl millet as a fodder crop rather than a grain crop in the Punjab state, as the forage pearl millet market is growing well in India (Kapoor and Singh, 2017; Ashok *et al*., 2016). Pearl millet ensures the production of multi-cut hybrids due to high regeneration ability and broad tillering potential (Govintharaj *et al*., 2021). Forage of pearl millet can be fed to the animals at any stage of crop growth without any deleterious effect (Govindaraj *et al*., 2017, 2018; Chaudhary *et al*., 2019).

In the arid and semi-arid regions, a lack of sufficient quantity of fodder is the major problem for livestock/ cattle production. Forage pearl millet has been utilized as form of pasture, silage, hay and grazing in countries like USA (Burton, 1995; Davis *et al*., 2003), in New Mexico and West Texas (Marsalis *et al*., 2012), in summer season in Australia and South America (Hanna, 1996), in South Africa (Hammes, 1972) and Brazil (De Assis *et al*., 2018).

Overall, the demand has increased for pearl millet dry fodder and cultivation of forage pearl millet also increased in north-western India (Reddy *et al*., 2012). In recent years, feed shortage has remained a burning issue, so researchers need to make efforts to ensure regular feed supply for dairy cattle development and cattle welfare improvement (Meena *et al*., 2012, 2013).

In a hybrid combination, the effects of general combining abilities (GCA) and specific combining abilities (SCA) are important factors to determine the potential value of an inbred line (Falconer, 1981). Diallel crossings have been used in genetic studies to find superior progenitors for hybrid creation and to ascertain the inheritance pattern of essential traits.

Materials and Methods

Experimental site and design: This experiment was conducted at the Research Farm, ICAR-Indian Institute of Millet Research. Each plot size consisted of 2m x 0.45m with 2 rows. The study was carried out in three trials, each trial included 25 inbred lines with 6 checks in two replications, making a total of 81 forage pearl millet lines (75 inbred lines and 6 checks) in a randomized block design in *kharif* 2022. Based on the source, nutritional value, wild germplasm, and high-yielding ability, 10 superior inbred lines were selected for the crossing programme. About 45 crosses were made by the half diallel method in *Rabi*, 2022, by utilizing the protogynous nature. Sufficient seed for the next generation's sowing was obtained. In the *summer*, 2023, all 45 F_1 hybrids were evaluated by randomized block design (RBD) in two replications with plot size (2m x 0.45m with 2 rows) in the field of ICAR-IIMR.

Observations and analysis: The parameters used for genetic variability and diversity analysis were days to 50% flowering, plant height (cm), leaf length (cm), leaf width (cm), number of leaves per tiller, number of tillers, internodal length (cm), stem thickness (mm), leaf-to-stem ratio, green fodder yield in first cut and second cut (kg/plot), total green fodder yield (kg/plot), dry fodder yield in the first cut and second cut (kg/plot), total dry fodder yield (kg/plot), and regeneration ability. Green fodder yield in the first cut was taken 90 days after sowing and the second cut was taken 31 days after the first cut. Stem thickness was recorded by using a Vernier calliper. Regeneration ability was estimated based on the ratio of the number of tillers in the first cut and the total number of tillers (regenerated tillers from existing tillers and new tillers) in the second cut. The number of tillers in the second cut was recorded 20 days after the first cut.

F_1 hybrids were analyzed by general combining ability (GCA), specific combining ability (SCA) and heterosis based on yield parameters, *viz*., plant height (cm), green fodder yield in first cut and second cut (t ha^{-1}), total green fodder yield (t ha^{-1}), dry fodder yield in first cut and second cut (t ha^{-1}) and total dry fodder yield (t ha^{-1}). Combining ability was analyzed by following Method 2 and Model I of Griffing (1956). Average heterosis and heterobeltiosis were used to identify better heterotic crosses in forage-specific pearl millet lines. Based on high SCA and heterosis, the best hybrids were identified.

Statistical analysis: Genetic variability was analyzed by R software using the genetic variability package (Popat *et al*., 2020). The analysis of divergence using the dendrogram was done by Darwin 6.0.21, utilizing WARD (minimum variance) of Darwin (Perrier and Jacquemoud-Collet, 2006). The combining ability and heterosis were analysed by Windostate 9.2 (Indostat, 2023).

Results and Discussion

Analysis of variance: Significant differences were recorded among lines for all 16 yield and yield-related variables. Analysis of variance (ANOVA) indicated the presence of sufficient variability. In combining ability, ANOVA indicated that GCA was significant for all the traits and SCA was significant for four traits (green fodder yield in the first cut, total green fodder yield, dry fodder yield in the first cut and total dry fodder yield). This indicates additive and non-additive gene actions.

Genetic variability: PCV was recorded higher than GCV for all the traits in both cuts (First and second cut, respectively), revealing that reported variation is also influenced by environment (Table 1). Higher PCV and GCV was reported for leaf to stem ratio (57.44, 55.80), green fodder yield in first cut (28.02, 26.11), green fodder yield in second cut (33.71, 32.33), total green fodder yield (21.35, 20.27), dry fodder yield in first cut (29.10, 26.86), dry fodder yield in second cut (33.72, 32.29), total dry fodder yield (21.63, 20.14), respectively. The high genetic variability indicates the effectiveness of selection. Similar findings for leaf stem ratio were reported by Shanmuganathan *et al*. (2006), Satapute *et al*. (2014), Govintharaj *et al*. (2017), and for green fodder yield by Shanmuganathan *et al*. (2006), Satapute *et al*. (2014) and Subbulakshmi *et al*. (2022).

Moderate PCV and GCV were reported for plant height (11.60, 11.34), leaf length (10.77, 9.59), number of leaves per tiller (12.19, 11.45), number of tillers (12.86, 11.02), stem thickness (11.00, 9.51) and regeneration ability (12.38, 10.44), respectively. It exhibits moderate variability in traits. It may be useful for selection. Similar findings for plant height were recorded by Shanmuganathan *et al*. (2006), Satapute *et al*. (2014) and Rani *et al*. (2022), for leaf length from Vidyadhar *et al*. (2007), for the number of leaves per tiller from Vidyadhar *et al*. (2007) and Meena

Table 1. Estimation of variability, heritability and genetic advance for yield and related parameters in forage pearl millet

S. N	Characters	Mean	Range		PV	GV	PCV (%)	GCV (%)	h^2	GAM
			Min	Max						
1	DFF	56.47	51.00	70.00	13.42	11.24	6.49	5.94	83.74	11.19
2	PH	152.29	103.20	198.60	312.02	298.10	11.60	11.34	95.54	22.83
3	LL	56.73	43.00	76.20	37.33	29.61	10.77	9.59	79.33	17.60
4	LW	3.00	2.20	3.90	0.08	0.05	9.31	7.72	68.80	13.20
5	NLT	6.80	4.80	9.00	0.69	0.61	12.19	11.45	88.21	22.15
6	NT	5.66	4.20	7.60	0.53	0.39	12.86	11.02	73.45	19.46
7	IL	19.20	14.20	22.40	2.81	2.58	8.73	8.37	91.87	16.53
8	ST	11.23	8.08	14.38	1.53	1.14	11.00	9.51	74.72	16.93
9	LSR	0.69	0.26	2.81	0.16	0.15	57.44	55.80	94.35	111.65
10	GFY-1	6.25	2.21	11.50	3.07	2.66	28.02	26.11	86.83	50.12
11	GFY-2	5.11	2.80	14.90	2.96	2.72	33.71	32.33	91.97	63.86
12	TGFY	11.36	6.66	24.20	5.88	5.30	21.35	20.27	90.14	39.65
13	DFY-1	3.03	1.08	5.75	0.78	0.66	29.10	26.86	85.20	51.08
14	DFY-2	2.48	1.21	7.14	0.70	0.64	33.72	32.29	91.65	63.67
15	TDFY-1	5.52	3.29	11.35	1.43	1.24	21.63	20.14	86.70	38.64
16	RGA	0.54	0.34	0.72	0.005	0.003	12.38	10.44	71.11	18.15

PV: Phenotypic variance; GV: Genotypic variance; PCV %: Phenotypic coefficient of variation; GCV%: Genotypic coefficient of variation; h2: Heritability in broad sense (%); GAM; Genetic advance as percent of mean; PH: Plant height (cm); LL: Leaf length (cm); LW: Leaf width (cm); NLT: Number of leaves per tiller; NT: Number of tillers; IL: Internodal length (cm); ST: Stem thickness (mm); LSR: Leaf stem ratio; GFY-1: Green fodder yield in first cut (kg/plot); GFY-2: Green fodder yield in second cut (kg/pot); TGFY: Total green fodder yield (first and second cut) (kg/plot); DFY-1: Dry fodder yield in first cut (kg/plot); DFY-2: Dry fodder yield in second cut (kg/plot); TDFY: Total dry fodder yield (first and second cut (kg/plot)); RGA: Regeneration ability; For combining ability, gene action and heterosis analysis yield data was taken in ton/hectare

et al. (2024). Characters such as days to 50% flowering, leaf width and internodal length recorded low PCV and GCV, exhibiting that the variance is low and the selection would not be effective for these traits.

High heritability and high genetic advance percent of mean was reported for plant height (95.54, 22.83), number of leaves per tiller (88.21, 22.15), leaf to stem ratio (94.33, 111.65), green fodder yield in first cut (86.83, 50.12), green fodder yield in second cut (91.97, 63.86), total green fodder yield (90.14, 39.65), dry fodder yield in first cut (85.20, 51.08), dry fodder yield in first cut (91.65, 63.67) and total dry fodder yield (86.70, 38.64), respectively. This exhibited that selection would be effective for improving these traits in future generations. These results are in agreement with the findings of Satapude *et al*. (2014) and Shanmuganathan *et al*. (2006) for plant height, while Satapude *et al*. (2014), Subbulakshmi *et al*. (2022) and Meena *et al*. (2024) for leaf stem ratio and green fodder yield.

High heritability and moderate genetic advance percent of mean were reported for days to 50% flowering (83.74, 11.19), leaf length (79.33, 17.60), leaf width (68.80, 13.20), number of tillers (73.45, 19.46), internodal length (91.87, 16.53), stem thickness (74.72, 16.93), regeneration ability (71.11, 18.15), respectively. Selection may be effective for improving these characters; these shows less environmental effect. Similar results have been obtained for Days to 50% flowering by Bind *et al*. (2015) and for leaf length by Vidyadhar *et al*. (2007) and Satapude *et al*. (2014).

Genetic diversity: All lines can be divided into four different clusters by using WARD (minimum variance). The largest cluster contained 39 lines, followed by clusters III and IV, both with 17 lines each, while cluster II consisted of 8 lines (Table 2).

Combining ability: The analysis of general combining ability or *GCA* effects of 10 parents for seven yield traits was recorded (Table 3). The lines, IIMR AVS71, IIMR AVS73, IIMR AVS77 and IIMR AVS41 exhibited positive and significant *GCA* effects for plant height. The highest positive significant *GCA* effects for green fodder yield in the first cut were observed in the lines *viz*., IIMR AVS50 and IIMR AVS77. For green fodder yield in the second cut, only one line, *viz*., IIMR AVS95, showed highly significant positive *GCA* effects. Genotypes IIMR AVS98 and IIMR AVS95 recorded positive and significant *GCA* effects for

Table 2. Clustering pattern of forage pearl millet lines by ward (minimum variance)

S.N.	Cluster	Genotype
1	Cluster I	IIMR AVS36, IIMR AVS34, IIMR AVS41, IIMR AVS52, IIMR AVS43, IIMR AVS26, IIMR AVS22, IIMR AVS32, IIMR AVS51, IIMR AVS95, Bulk-1, IIMR AVS6, IIMR AVS60, IIMR AVS5, IIMR AVS1, Bulk-4, Bulk-2, IIMR AVS29, IIMR AVS28, IIMR AVS39, IIMR AVS37, IIMR AVS55, IIMR AVS53, IIMR AVS94, IIMR AVS71, IIMR AVS77, IIMR AVS56, IIMR AVS75, IIMR AVS72, IIMR AVS63, IIMR AVS35, IIMR AVS49, IIMR AVS40, IIMR AVS58, IIMR AVS57, IIMR AVS62, IIMR AVS59, IIMR AVS64, IIMR AVS73,
2	Cluster II	IIMR AVS50, IIMR AVS44, IIMR AVS65, IIMR AVS61, IIMR AVS48, IIMR AVS47, IIMR AVS46, IIMR AVS45
3	Cluster III	IIMR AVS11, IIMR AVS8, IIMR AVS54, IIMR AVS38, IIMR AVS33, IIMR AVS23, IIMR AVS7, IIMR AVS74, IIMR AVS98, IIMR AVS19, IIMR AVS13, IIMR AVS99, TSFB15-8, IIMR AVS42, IIMR AVS24, Foragen-raftar, Wonderleaf
4	Cluster IV	IIMR AVS31, IIMR AVS30, IIMR AVS3, IIMR AVS25, IIMR AVS12, IIMR AVS10, IIMR AVS18, IIMR AVS2, IIMR AVS14, IIMR AVS15, IIMR AVS16, IIMR AVS4, IIMR AVS21, IIMR AVS27, IIMR AVS20, IIMR AVS17, IIMR AVS9

Table 3. General combining ability (GCA) effect for yield traits in forage pearl millet

S.N.	Parent lines	PH	GFY-1	GFY-2	TGFY	DFY-1	DFY-2	TDFY
1	IIMR AVS50	-7.20**	6.07**	-0.69	5.38	3.43**	-0.70	2.73
2	IIMR AVS71	11.31**	-0.79	-4.84*	-5.63	-0.15	-0.60	-0.75
3	IIMR AVS73	9.94**	-6.06**	-7.60**	-13.66**	-2.50*	-3.82**	-6.32**
4	IIMR AVS77	8.65**	8.03**	-4.51*	3.53	4.47**	-2.47*	2.01
5	IIMR AVS98	-5.74*	2.95	5.77*	8.72*	0.28	2.98*	3.25
6	IIMR AVS94	-7.67**	-2.60	-4.43	-7.04*	-0.74	-2.67*	-3.39*
7	IIMR AVS95	-2.36	2.18	16.46**	18.64**	1.41	8.43**	9.84**
8	IIMR AVS18	0.73	-8.32**	0.68	-7.64*	-4.94**	-0.15	-5.09**
9	IIMR AVS11	-13.27**	-5.21*	3.33	-1.87	-3.00**	1.38	-1.62
10	IIMR AVS41	5.60*	3.74	-4.17	-0.43	1.74	-2.39*	-0.65
	SEM	3.71	3.16	3.33	5.18	1.53	1.69	2.48
	CD (P<0.05)	7.45	6.33	6.67	10.38	3.06	3.38	4.98

*(P <0.05); **(P <0.01)

the trait total green fodder yield. For dry fodder yield in the first cut, the lines IIMR AVS50 and IIMR AVS77 showed positive values of *GCA* effects. While for dry fodder yield in the second cut the lines IIMR AVS98 and IIMR AVS95 observed positive significant GCA effects. For total dry fodder yield, single line IIMR AVS95 reported a significantly positive GCA effect. IIMR AVS95 was identified as the best parent for total green fodder yield and total dry fodder yield, whereas IIMR AVS71 was the best parent for plant height.

Among 45 F_1 hybrids evaluated, only three hybrids exhibited a highly significant *sca* effect for total green fodder yield (Table 4). The hybrids IIMR AVS71 x IIMR AVS98 and IIMR AVS73 x IIMR AVS41 exhibited significant *sca* effect for plant height, even though the performance of these crosses is less in contribution to yield. Same results have been obtained by Aswini *et al.* (2021) and Eldie (2021) in forage pearl millet for plant height. The hybrid IIMR AVS50 x IIMR AVS95, IIMR AVS73 x IIMR AVS41 and IIMR AVS77 x IIMR AVS98 showed highly significant *sca* effects for trait green fodder yield in the first cut. In contrast, IIMR AVS95 x IIMR AVS11 revealed a significant sca effect for green fodder yield in the second cut. For total green fodder yield, three F_1 hybrids showed significant sca effect *viz*., IIMR AVS50 x IIMR AVS95, IIMR AVS77 x IIMR AVS98 and IIMR AVS95 x IIMR AVS11. High sca effect indicates the presence of non-additive gene action. Same findings were obtained by Chawla and Gupta (1982), Singh *et al.* (2014) for negative significance, Aswini *et al.* (2021) for positive significance of gca and sca and Eldie (2021) for negative significance in forage pearl millet.

In case of dry fodder yield, four hybrids IIMR AVS50 x IIMR AVS95, IIMR AVS73 x IIMR AVS41, IIMR AVS77 x IIMR AVS98 and IIMR AVS77 x IIMR AVS41 revealed significant sca effect in the first cut, whereas IIMR

Table 4. Specific combining ability effect of F_1 crosses for yield traits

S. N.	Crosses	PH	GFY-1	GFY-2	TGFY	DFY-1	DFY-2	TDFY
1	IIMR AVS50 × IIMR AVS71	12.94	-11.13	-7.22	-18.34	-5.39	-3.84	-9.23
2	IIMR AVS50 × IIMR AVS73	-1.27	-8.78	-5.12	-13.90	-4.35	-2.49	-6.84
3	IIMR AVS50 × IIMR AVS77	-1.50	9.99	2.76	12.76	5.09	1.29	6.38
4	IIMR AVS50 × IIMR AVS98	-7.55	12.92	8.49	21.40	6.07	4.20	10.27
5	IIMR AVS50 × IIMR AVS94	2.92	1.88	1.04	2.92	0.94	0.55	1.48
6	IIMR AVS50 × IIMR AVS95	9.38	14.30*	12.72	27.02*	7.15*	6.40	13.54*
7	IIMR AVS50 × IIMR AVS18	2.37	10.29	7.56	17.85	4.85	3.58	8.43
8	IIMR AVS50 × IIMR AVS11	1.24	7.27	4.19	11.46	3.61	2.01	5.62
9	IIMR AVS50 × IIMR AVS41	2.07	-3.52	-3.57	-7.09	-1.63	-1.69	-3.33
10	IIMR AVS71 × IIMR AVS73	-4.26	11.97	6.51	18.49	5.96	3.84	9.80
11	IIMR AVS71 × IIMR AVS77	-4.78	9.85	2.88	12.72	4.99	1.88	6.87
12	IIMR AVS71 × IIMR AVS98	20.04*	13.08	9.57	22.65	5.93	5.48	11.40*
13	IIMR AVS71 × IIMR AVS94	2.90	0.52	0.68	1.20	0.26	0.19	0.45
14	IIMR AVS71 × IIMR AVS95	-6.75	5.75	6.05	11.80	2.89	3.27	6.15
15	IIMR AVS71 × IIMR AVS18	8.39	7.24	5.94	13.17	3.29	3.25	6.54
16	IIMR AVS71 × IIMR AVS11	1.83	-4.56	-4.00	-8.56	-2.13	-1.89	-4.02
17	IIMR AVS71 × IIMR AVS41	-10.49	-2.79	-2.79	-5.58	-1.28	-1.45	-2.73
18	IIMR AVS73 × IIMR AVS77	-4.99	5.44	2.37	7.82	2.73	1.10	3.83
19	IIMR AVS73 × IIMR AVS98	-7.56	-13.56	-9.05	-22.61	-6.31	-4.61	-10.92
20	IIMR AVS73 × IIMR AVS94	16.47	13.08	9.22	22.30	6.44	4.45	10.89
21	IIMR AVS73 × IIMR AVS95	2.61	-5.84	-4.69	-10.54	-2.94	-2.41	-5.35
22	IIMR AVS73 × IIMR AVS18	-7.43	0.01	0.84	0.84	-0.04	0.35	0.31
23	IIMR AVS73 × IIMR AVS11	8.91	0.41	0.61	1.01	0.21	0.27	0.48
24	IIMR AVS73 × IIMR AVS41	18.29*	14.48*	6.95	21.42	7.06*	3.38	10.44
25	IIMR AVS77 × IIMR AVS98	1.79	15.93*	9.52	25.45*	7.41*	4.66	12.07*
26	IIMR AVS77 × IIMR AVS94	4.12	10.27	5.79	16.06	5.11	2.73	7.84
27	IIMR AVS77 × IIMR AVS95	-2.44	2.33	2.82	5.15	1.19	1.39	2.58
28	IIMR AVS77 × IIMR AVS18	-0.14	-3.99	-2.40	-6.38	-1.94	-1.24	-3.17
29	IIMR AVS77 × IIMR AVS11	14.07	6.85	2.95	9.81	3.38	1.35	4.72
30	IIMR AVS77 × IIMR AVS41	7.83	-16.63*	-8.32	-24.95*	8.09*	-4.07	-12.16*
31	IIMR AVS98 × IIMR AVS94	-6.57	-3.50	-1.79	-5.30	-1.59	-0.93	-2.52
32	IIMR AVS98 × IIMR AVS95	4.84	-2.97	-1.54	-4.51	-1.41	-0.81	-2.23
33	IIMR AVS98 × IIMR AVS18	4.07	-3.31	-1.74	-5.05	-1.57	-0.92	-2.49
34	IIMR AVS98 × IIMR AVS11	4.55	6.50	7.71	14.21	2.59	3.81	6.40
35	IIMR AVS98 × IIMR AVS41	-1.97	8.42	4.96	13.38	3.85	2.42	6.28
36	IIMR AVS94 × IIMR AVS95	7.34	-6.59	-6.45	-13.04	-3.33	-3.21	-6.55
37	IIMR AVS94 × IIMR AVS18	7.38	-4.88	-3.71	-8.59	-2.26	-1.73	-3.99
38	IIMR AVS94 × IIMR AVS11	-5.62	-3.81	-3.38	-7.19	-1.77	-1.64	-3.42
39	IIMR AVS94 × IIMR AVS41	-5.20	2.66	1.72	4.39	1.31	0.86	2.17
40	IIMR AVS95 × IIMR AVS18	6.06	-2.73	-2.49	-5.22	-1.28	-1.24	-2.52

41	IIMR AVS95 × IIMR AVS11	-9.09	10.85	15.67*	26.52*	5.23	7.88*	13.12*
42	IIMR AVS95 × IIMR AVS41	13.25	8.76	7.33	16.09	4.30	3.67	7.97
43	IIMR AVS18 × IIMR AVS11	10.42	4.90	7.42	12.32	1.90	3.50	5.40
44	IIMR AVS18 × IIMR AVS41	6.99	9.98	6.57	16.55	4.58	3.08	7.66
45	IIMR AVS11 × IIMR AVS41	-2.57	6.11	2.44	8.55	2.91	1.15	4.06
	SEM	12.32	10.48	11.04	17.17	5.06	5.60	8.23
	CD (P <0.05)	24.69	21.01	22.13	34.43	10.14	11.22	16.51

*(P <0.05); **(P <0.01)

AVS95 x IIMR AVS11 showed a significant sca effect in the second cut. For total dry fodder yield, four hybrids IIMR AVS50 x IIMR AVS95, IIMR AVS71 x IIMR AVS98, IIMR AVS77 x IIMR AVS98 and IIMR AVS95 x IIMR AVS11 showed significant sca effect. Crosses like IIMR AVS50 x IIMR AVS95, IIMR AVS77 x IIMR AVS98 and IIMR AVS95 x IIMR AVS11 exhibited high sca effect for yield traits, indicating better combinations from segregating generations of these crosses.

Gene action and heterosis: The results pertaining to the estimate of combining ability revealed that mean SCA variance (σ^2 SCA) was relatively greater in magnitude than GCA variance (σ^2 GCA) for the traits like green fodder yield in first cut, total green fodder yield and total dry fodder yield, indicating that these traits were predominantly under the control of non-additive gene action. Whereas, the results about the estimate of combining ability revealed that mean σ^2 GCA was relatively greater in magnitude than σ^2 SCA for traits like plant height, green fodder yield in second cut, dry fodder yield in first cut and dry fodder yield in second cut, indicating that these traits were predominantly under the control of additive gene action (Table 5).

The result of heterosis of seven (7) yield characters for mid-parent and better-parent heterosis is explained. For plant height, the mid-parent heterosis ranged from 0.28 to 15.12%. Ten (10) crosses recorded significant and positive heterosis in the desired direction. The cross IIMR AVS18 X IIMR AVS11 (15.12) recorded the highest mid-parent heterosis. For plant height, not a single cross had recorded either positive or negative significant heterosis, whereas the heterobeltiosis ranged from -6.16 to 11.96%.

For green fodder yield in the first cut, out of 45 crosses, 22 crosses exhibited significant positive heterosis over mid-parent, which varied from -2.63 to 81.80%. The greater mid-parent heterosis was recorded for IIMR AVS77 X IIMR AVS98 (81.80%) and IIMR AVS 71 X IIMR AVS98 (81.17%). These crosses are most desirable for this trait. Better parent heterosis for this trait ranged from -15.10 to 69.91%. Five crosses exhibited positive significant heterosis. While cross IIMR AVS77 X IIMR AVS98 was recorded highly significant with 67.98%, followed by IIMR AVS71 X IIMR AVS98 (67.77%), IIMR AVS50 X IIMR AVS77 (61.77%), IIMR AVS50 X IIMR AVS95 (60.20%) and IIMR AVS50 X IIMR AVS98 (58.84 %). These five crosses were identified as the most desirable hybrids for this trait. For green fodder yield in the second cut, relative heterosis ranged from -2.48 to 81.62 *percent*. Out of 45 crosses, 7 crosses manifested significant positive heterosis. The highest positive mid-parent heterosis was recorded for IIMR AVS77 X IIMR AVS98 (81.62). These crosses are useful for the development or selection of hybrids and desirable for high forage yield in multicut. In contrast, the better parent heterosis ranged from -27.83 to 75.24 *percent*. No crosses exhibited a significantly positive heterobeltiosis.

Table 5. Estimation of gene action nature for various traits in forage pearl millet hybrids

Characters	Nature of gene action	
	Additive	Non-additive
PH	✓	
GFY-1		✓
GFY-2	✓	
TGFY		✓
DFY-1	✓	
DFY-2	✓	
TDFY		✓

A total of 23 crosses were reported with significant positive relative heterosis for total green fodder yield, with a range from -2.56 to 81.74 *percent*. In those crosses, the highest relative heterosis was reported for IIMR AVS77 X IIMR AVS98 (81.74 %). This is the most desirable hybrid from Average heterosis, while significant positive heterobeltiosis was exhibited in five crosses. IIMR AVS77 X IIMR AVS98 recorded a highly significant positive heterosis with 69.41 *percent*. This cross was identified as the best and desirable. For this trait, IIMR AVS50 X IIMR AVS95 was reported as the best cross in heterosis.

For dry fodder yield in the first cut, average heterosis ranged from -2.43 to 81.70 *percent* and twenty-one (21) crosses manifested significant positive relative heterosis. The cross IIMR AVS77 X IIMR AVS98 (81.70) reported the highest relative heterosis, whereas for heterobeltiosis, six crosses exhibited positive significant heterosis. IIMR AVS71 X IIMR AVS98 recorded a highly significant positive better parent heterosis with 77.49 *percent*. The trait dry fodder yield in the second cut exhibited significant positive heterosis over mid-parent for five crosses, which varied from -2.50 to 81.82 percent. The cross IIMR AVS71 X IIMR AVS98 reported a highly significant relative heterosis of 81.82 *percent*. Heterobeltiosis ranged from -28.07 to 71.65 *percent*. No cross exhibited positive heterosis.

A total of 23 crosses recorded significant positive relative heterosis over mid-parent for total dry fodder yield, with a range from -2.46 to 81.65 *percent*. In these crosses, the highest average heterosis was reported for IIMR AVS77 X IIMR AVS98 with 81.65 *percent*. At the same time, the significant positive heterobeltiosis was exhibited in six crosses. IIMR AVS77 X IIMR AVS98 recorded the highest significant positive heterosis with 74.01 *percent*. This is identified as the best and desirable cross for this trait. This varied from -18.85 to 74.01 *percent*. For Total green fodder yield, cross IIMR AVS50 X IIMR AVS95 was identified as the positive best parent heterosis.

Conclusion

The hybrids *viz*., IIMR AVS50 X IIMR AVS95, IIMR AVS77 X IIMR AVS98, and IIMR AVS95 X IIMR AVS11 were identified with the desirable sca effects, high heterosis, and high per se performance for fodder yields. These hybrids can be considered useful for multi-location trials and future hybrid development programmes.

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