Plant Archives Vol. 24, No. 2, 2024 pp. 1439-1444



Plant Archives

Journal homepage: http://www.plantarchives.org DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.2.201

EVALUATION OF COMBINING ABILITY EFFECTS OF RESTORER LINES FOR YIELD AND YIELD ATTRIBUTING TRAITS IN FORAGE PEARL MILLET

Pranathi Chinthakuntla^{1*}, D. Shivani¹, Avinash Singode² and Seva Nayak Dheeravathu³

¹Department of Genetics and Plant Breeding, P.J.T.S.A.U., Rajendranagar, Hyderabad - 500 030, Telangana, India.

²Department of Genetics and Plant Breeding, ICAR-IIMR, Hyderabad, Telangana, India.

³Department of Plant Physiology, ICAR-IIMR, Hyderabad, Telangana, India.

*Corresponding author E-mail : sonychinthakuntla123@gmail.com

(Date of Receiving-02-06-2024; Date of Acceptance-12-08-2024)

ABSTRACTThrough a line × tester analysis involving 35 hybrids generated by crossing 7 pearl millet restorer lines as
testers with five cytoplasmic male sterile (CMS) lines as females, combining ability estimates were determined.
The results revealed a predominance of non-additive gene effects, indicated by higher values of specific
combining ability (*sca*) compared to general combining ability (*gca*), along with less than unity variance
ratio of gca to sca across all traits studied. The *gca* estimates highlighted that the line IIMR AVS 11 and the
tester ICMV 08111 S1-1-2 exhibited strong general combining abilities across all traits among the lines and
testers, respectively. Notably, the cross combinations IIMR AVS 21 x IP 15535 S1-10-1-1 followed by IIMR
AVS 11 x IP 2761 S1-9-4-2-1-4 emerged as the most promising specific combinations for all traits examined.
Key words : Forage pearl millet, *GCA*, *SCA*, Gene action, Green fodder yield, Dry fodder yield.

Introduction

Pearl millet, [*Pennisetum glaucum* (L.) R.Br.] is an ethnobotanically important species in the genus Pennisetum L. (Rich), belonging to the family Poacea. It is a multipurpose cereal crop known as Bajri, Sajje, Kambu, Kamban, Sajjalu, etc. in various parts of India and bulrush, cattail or spiked millet in English. It is one of the few diploids (2n=14) in the genus which is well spread in the tropics and the subtropics. Pearl millet originated and was domesticated in the Sub-Saharan region of West and Central Africa and later migrated to eastern Africa, semi-arid regions of South Asia and other parts of the world. It is one of the major sources of food and feed in arid and semi-arid regions of the world. Pearl millet is inherently drought and heat tolerant crop.

Pearl millet accounts for more than half of the total worldwide production of all millets. Its flowering pattern is protogynous, which assures a high degree of crosspollination. It can be grown in a wide range of soils but does not prefer acidic and water logging soils. It is widely cultivated in the states of Rajasthan, Maharashtra, Gujarat, Uttar Pradesh, Haryana, Telangana, Karnataka and Tamilnadu (Anonymous, 2013). Around 90 million people in the Sahelian region of Africa and north western India consume pearl millet grain as a staple food (Srivastava *et al.*, 2020).

Green fodder of pearl millet is preferred over that of sorghum because its HCN content is low and can be fed to cattle without harm at any stage of growth (Yadav *et al.*, 2013). Testing the parents for their combining ability is very important because the high yielding parents may not combine well to give good hybrids. Line \times tester analysis helps in testing a large number of genotypes to assess the gene action and combining ability.

Combining ability provides useful information regarding the selection of suitable parents for effective

hybridization programme and at the same time elucidates the nature and magnitude of different types of gene action. To assess the combining ability for yield and contributing traits it is essential to determine the nature and magnitude of gene actions in a line \times tester mating design to identify good combiners including CMS lines and restorers. One of the most effective mating patterns for evaluating the combining ability impacts, which helps the breeder choose the best parents for hybridization, is the line x tester analysis approach (Kempthorne, 1957).

Materials and methods

The experiment was carried out at ICAR – Indian Institute of Millet Research, Rajendranagar, Hyderabad to develop 35 hybrids from five diverse male sterile lines and seven inbred males using line x tester mating during *kharif*, 2023. The experimental material comprising of 12 parents, 35 crosses and three standard checks (TSFB 15-8, Raftaar and Wonder leaf) were evaluated in a randomized block design with two replications at ICAR – Indian Institute of Millet Research, Rajendranagar, Hyderabad during *rabi* 2023- summer 2024. The trial was sown in the month of August, 2023. A two-row plot measuring 3.0 meters in length was designed to hold each entry, with a gap of 45 cm between rows and 15 cm between plants.

S. no.	Genotype	Pedigree				
	Lines					
1	IIMRAVS 10	ERP127-6-2-4-5				
2	IIMRAVS 21	ELB 124-10-3-4-2				
3	IIMRAVS 32	ELB 124-11-3-1-7				
4	IIMRAVS 11	ELS G66-3-1-3-3				
5	IIMRAVS 18	ELB 124-4-3-1-3				
	Testers					
1	IP 15564-3	IIMRAVS 80				
2	IP 15564-5	IIMRAVS 81				
3	IP 15535 S1-10-1-1	IIMRAVS 82				
4	IP 2761 S1-9-4-2-1-4	IIMRAVS 88				
5	IP 15564 S1-3-1	IIMRAVS 91				
6	ICMV 08111 S1-1-1	IIMRAVS 92				
7	ICMV 08111 S1-1-2	IIMRAVS 93				
Standard checks						
1	TSFB 15-8					
2	Raftaar					
3	Wonder leaf					

List of parents used for the study

Five randomly chosen plants were used for the observations and data on seven characters *viz.*, number of leaves per plant, number of tillers per plant, days to

50% flowering, plant height(cm), leaf length (cm), green fodder yield (t ha⁻¹) and dry fodder yield(t ha⁻¹) was recorded.

Results and Discussion

Analysis of variance showing mean sum of squares for 7 quantitative traits are presented in Table 1. The analysis of variance showed highly significant variations among the genotypes for all the traits except for the number of new tillers. Thus, the results quantified indicated that considerable amount of genetic variation exist among genotypes for the different traits. The mean squares due to crosses were significant for all the 7 characters indicating the presence of greater variation among the crosses under study.

In the present study, the results on the estimates of combining ability variance revealed that mean sca variance was relatively greater in magnitude than gca variance for all the traits. The ratio of 6^2 gca/ 6^2 sca less than unity indicated the preponderance of non-additive gene effects for all the characters under study (Aswini *et al.*, 2021; Bhardwaj *et al.*, 2015; Mungra *et al.*, 2014). Non-additive gene interactions also significantly influence the expression of yield and its related traits (Azhaguvel and Jayaraman, 1998; Yadav *et al.*, 2002; Parmar *et al.*, 2013; Patel *et al.*, 2008; Dhuppe *et al.*, 2006 and Karvar *et al.*, 2017).

Parental genetic contributions (gca) varied significantly across different traits. Table 2 presents a detailed analysis of general combining ability (gca) to identify superior parent lines for future hybrid breeding programs.

For days to 50% flowering, one line IIMR AVS 11 (-1.92) and one tester ICMV 08111 S1-1-2 (-1.90) displayed negative and significant general combining ability (*gca*) effects, indicating that they are both useful parents for producing offspring with early flowering traits.

None of the lines demonstrated a significant influence on leaf length. Consequently, all lines exhibited average combining ability for leaf length. In contrast, two testers IP 15564-5 and ICMV 08111 S1-1-2 found notably positive effects on leaf length, indicating their superior potential for improving this characteristic in offspring. Of all the parental lines, only oneline IIMR AVS 18 showed a significant positive effect for number of leaves per plant. This suggests its potential as a valuable parent for increasing leaf count. None of the testers found significant effects on leaf number.

One tester ICMV 08111 S1-1-2 (652) and two lines, IIMR AVS 21 (6.27), IIMR AVS 11 (9.04) showed positive

Source	d.f.	DFF	IL	NL	PH	NT	GFY (t ha ⁻¹)	DFY (t ha ⁻¹)		
Replications	1	2.80	203.66	2.92 *	7.82	3.65	0.000	0.12		
Genotypes	46	15.52*	127.16*	1.24**	320.30**	2.78*	73.27*	19.41*		
Lines	4	3.85	49.16	0.58	289.92*	1.85	80.12	22.35		
Testers	6	15.64	77.85	0.63	233.10*	2.95	100.63*	28.08*		
Lines vs Testers	1	15.20	112.93	0.00	1.54	3.21	9.47	17.98		
Crosses (C)	34	16.08*	130.20*	1.28 **	297.72 **	2.83 *	66.60 **	17.98 **		
Error	34	8.06	66.94	0.56	79.14	1.45	28.24	7.63		
Variance components for different characters in pearl millet										
ó²gca		1.53	6.82	0.04	32.03	0.02	2.18	0.03		
ó²sca		2.17	26.30	0.40	79.79	0.80	13.70	4.29		
ó²gca/ó²sca		0.70	0.25	0.11	0.40	0.02	0.15	0.008		

Table 1 : ANOVA of combining ability and variance components for different traits in forage pearl millet.

*Significant at 5% level, ** Significant at 1% level

DFF-Days to 50% flowering, LL-Leaf length (cm), NL-Number of leaves per plant, PH-Plant height (cm), NT-Number of tillers per plant, GFY - Green fodder yield tonnes per hectare, DFY - Dry fodder yield tonnes per hectare.

Fable 2 : General combining ability of parents for different traits in forage pearl millet.								
S. no.	Parents	DFF	LL	NL	PH-1	NT	GFY (t ha ⁻¹)	DFY(t ha ⁻¹)
	Lines						•	•
1	IIMRAVS 10	1.50	-3.82	0.03	-6.40*	-0.25	-2.55	0.28
2	IIMRAVS 21	-0.78	0.25	-0.02	6.27 *	-0.04	2.91	0.87
3	IIMRAVS 32	1.35	0.56	-0.46*	-6.57*	0.38	-0.23	-0.36
4	IIMRAVS 11	-1.92*	1.77	-0.07	9.04 **	-0.11	0.50	0.40
5	IIMRAVS 18	-0.14	1.23	0.53 *	-2.34	0.02	-0.63	-1.19
	S.E.	0.74	2.14	0.20	2.50	0.33	1.66	0.91
	Testers							
1	IP 15564-3	-0.30	-4.73	-0.31	-1.82	0.84 *	1.69	-0.74
2	IP 15564-5	2.30*	7.04 **	0.36	-4.85	0.24	-2.39	0.61
3	IP 15535 S1-10-1-1	0.30	-0.11	0.18	5.37	-0.55	2.96	0.97
4	IP 2761 S1-9-4-2-1-4	-1.20	-0.98	-0.11	-2.80	-0.05	0.95	1.60
5	IP 15564 S1-3-1	-0.80	-3.27	0.02	1.47	0.44	1.24	0.25
6	ICMV 08111 S1-1-1	1.60	-3.87	0.06	-3.89	-0.55	-5.00*	-0.70
7	ICMV 08111 S1-1-2	-1.90*	5.95 *	-0.18	6.52 *	-0.35	0.56	-2.00
	S.E.	0.88	2.53	0.24	2.96	0.39	1.97	1.07

T

*Significant at 5% level, ** Significant at 1% level.

DFF-Days to 50% flowering, LL-Leaf length (cm), NL-Number of leaves per plant, PH-Plant height (cm), NT-Number of tillers per plant,

GFY – Green fodder yield tonnes per hectare, **DFY** – Dry fodder yield tonnes per hectare.

significant gca effects for plant height among the parents, suggesting good general combiners for plant height.

There were no significant positive or negative gca effects for the number of tillers per plant among the parents associated with any of the lines. All lines may thus be regarded as average combiners for the number of tillers. In contrast, tester line IP 15564-3 showed a positive and significant impact, indicating its potential as a superior parent for increasing tiller count. Neither the lines nor the testers among the parents showed significant positive general combining ability effects on green fodder yield, indicating a generally modest genetic contribution to this trait. The present study also revealed that there were no significant positive or negative gca impacts for dry fodder yield among the parents for either lines or testers.

Detailed estimates of specific combining ability (sca) effects for various cross combinations are presented in

Pranathi Chinthakuntla et al.

Table 3 : Specific combining ability of hybrids for different traits in forage pearl millet.

S.	Hybrids	DFF	LL	NL	PH-1	NT-1	GFY-1 (t ha ⁻¹)	DFY-1 (t ha ⁻¹)
no.								
1	IIMR AVS 10 x IP 15564-3	0.80	-4.41	0.49	-7.68	0.65	7.03	0.67
2	IIMR AVS 10 x IP 15564-5	0.70	12.70*	-0.49	5.24	-0.74	3.57	-0.73
3	IIMR AVS 10 x IP 15535 S1-10-1-1	-0.80	-3.63	0.59	2.21	0.05	-1.09	2.80
4	IIMR AVS 10 x IP 2761 S1-9-4-2-1-4	-3.80	6.13	-0.51	19.74**	0.55	-3.73	-1.32
5	IIMRAVS 10 x IP 15564 S1-3-1	4.30*	-15.37*	0.65	-15.08*	-0.94	-6.22	-5.47*
6	IIMR AVS 10 x ICMV 08111 S1-1-1	-1.10	-1.37	0.21	-11.21	-0.44	-2.37	5.33*
7	IIMR AVS 10 x ICMV 08111 S1-1-2	-0.10	5.94	-0.94	6.76	0.85	2.81	-1.26
8	IIMR AVS 21 x IP 15564-3	1.08	8.90	0.14	8.38	-0.55	2.46	2.28
9	IIMR AVS 21 x IP 15564-5	0.48	5.72	0.06	0.96	-1.45	-1.39	-1.07
10	IIMR AVS 21 x IP 15535 S1-10-1-1	-4.51*	0.68	0.04	-1.36	2.34 *	9.34 *	0.71
11	IIMR AVS 21 x IP 2761 S1-9-4-2-1-4	0.48	-6.24	-0.75	9.81	-0.65	7.10	0.98
12	IIMR AVS 21 x IP 15564 S1-3-1	-1.91	-4.65	-0.09	-6.06	1.34	-2.23	-2.36
13	IIMR AVS 21 x ICMV 08111 S1-1-1	2.68	0.14	-0.03	-4.89	-0.15	-5.58	0.54
14	IIMR AVS 21 x ICMV 08111 S1-1-2	1.68	-4.58	0.61	-6.81	-0.85	-9.70*	-1.10
15	IIMR AVS 32 x IP 15564-3	1.44	-1.90	1.08	-4.21	0.01	-6.38	-2.77
16	IIMR AVS 32 x IP 15564-5	0.84	-0.48	0.80	-3.58	1.11	0.95	3.46
17	IIMR AVS 32 x IP 15535 S1-10-1-1	1.84	6.27	-0.11	-4.31	-0.08	-3.95	-1.79
18	IIMR AVS 32 x IP 2761 S1-9-4-2-1-4	2.84	-5.75	-0.01	-2.03	-1.58	-1.59	-1.02
19	IIMR AVS 32 x IP 15564 S1-3-1	-3.55	8.53	-0.65	8.68	1.41	5.51	2.12
20	IIMR AVS 32 x ICMV 08111 S1-1-1	-1.95	0.23	0.003	10.95	-0.58	8.61	-3.36
21	IIMR AVS 32 x ICMV 08111 S1-1-2	-1.45	-6.89	-1.09	-5.46	-0.28	-3.15	3.38
22	IIMR AVS 11 x IP 15564-3	0.22	-0.31	-0.41	0.36	-1.48	3.42	1.10
23	IIMR AVS 11 x IP 15564-5	-0.37	-10.09	0.51	-7.80	0.11	-6.38	-1.20
24	IIMR AVS 11 x IP 15535 S1-10-1-1	3.12	-8.53	-1.31*	3.81	-1.58	-5.69	-3.06
25	IIMR AVS 11 x IP 2761 S1-9-4-2-1-4	-2.37	0.08	0.19	1.04	2.41 **	0.86	5.15 *
26	IIMR AVS 11 x IP 15564 S1-3-1	0.22	8.82	0.05	14.21 *	-1.08	1.82	3.60
27	IIMR AVS 11 x ICMV 08111 S1-1-1	-0.17	0.02	0.81	-10.36	0.91	1.97	-4.98 *
28	IIMR AVS 11 x ICMV 08111 S1-1-2	-0.67	9.99	0.16	-1.28	0.71	4.00	-0.63
29	IIMR AVS 18 x IP 15564-3	-3.55	-2.27	-1.31*	3.15	1.37	-6.53	-1.29
30	IIMR AVS 18 x IP 15564-5	-1.65	-7.85	-0.89	5.18	0.97	3.25	-0.45
31	IIMR AVS 18 x IP 15535 S1-10-1-1	0.34	5.20	0.79	-0.34	-0.72	1.39	1.33
32	IIMR AVS 18 x IP 2761 S1-9-4-2-1-4	2.84	5.77	1.09	-28.56**	-0.72	-2.64	-3.79
33	IIMR AVS 18 x IP 15564 S1-3-1	0.94	2.66	0.05	-1.74	-0.72	1.11	2.10
34	IIMR AVS 18 x ICMV 08111 S1-1-1	0.54	0.96	-0.99	15.52*	0.27	-2.63	2.46
35	IIMR AVS 18 x ICMV 08111 S1-1-2	0.54	-4.46	1.26*	6.80	-0.42	6.04	-0.38
	S.E.	1.97	5.67	0.54	6.62	0.88	4.41	2.41
	No. of crosses showing significant and positive <i>sca</i> effects	1	1	1	3	2	1	2
	No. of crosses showing significant and negative <i>sca</i> effects	1	1	2	2	0	1	2

*Significant at 5% level, ** Significant at 1% level. **DFF**–Days to 50% flowering, **LL**–Leaf length (cm), **NL**–Number of leaves per plant, **PH**–Plant height (cm), **NT**–Number of tillers per plant, **GFY** – Green fodder yield tonnes per hectare, **DFY**– Dry fodder yield tonnes per hectare.

Table 3.

In a set of 35 crosses evaluated, only one combination IIMR AVS 21 x IP 15535 S1-10-1-1 (-4.51) recorded significant negative specific combining ability effects for days to 50% flowering. This underscores its potential as a noteworthy specific combiner in breeding programs. Both the parents were found to have negative and positive general combining ability (*gca*) effects, respectively, for days to 50% flowering, suggesting non additive gene action is primarily responsible for controlling this trait. Eldie *et al.* (2021) reported fewer significant positive specific combining ability (*sca*) effects for this trait.

Only one out of 35 cross combinations, IIMR AVS 10 x IP 15564-5 (12.70) demonstrated a positive and significant specific combining ability (*sca*) effect for leaf length, suggesting its potential as an exceptional combination for enhancing this trait. IP 15564-5 exhibited the most pronounced positive *gca* effects for leaf length, while IIMR AVS 10 displayed a less significant positive gca, suggesting a potential role for non-additive gene action.

Of the 35 crosses examined, only one IIMR AVS 18 x ICMV 08111 S1-1-2 (1.26) exhibited significant positive specific combining ability effects in the desired direction for the number of leaves. The pronounced positive gca effects of IIMR AVS 18 for leaf number contrasted with the insignificant negative gca of ICMV 08111 S1-1-2, indicating a likely predominance of non-additive gene action in the latter.

Among the 35 crosses, three crosses *viz.*, IIMR AVS 10 x IP 2761 S1-9-4-2-1-4 (19.74) followed by IIMR AVS 18 x ICMV 08111 S1-1-1 (15.52) and IIMR AVS 11 x IP 15564 S1-3-1 (14.21) showed positive significant sca effects and can be regarded as best specific combiners for plant height. The negligible contributions of both parents indicatenon-additive gene action as the primary mode of inheritance for plant height.

Out of all the crosses, two recorded significant positive specific combining ability effects in the desired direction. The cross IIMR AVS 11 x IP 2761 S1-9-4-2-1-4 (2.41) showed the highest positive significant effects, followed by IIMR AVS 21 x IP 15535 S1-10-1-1 (2.34), which were identified as the best specific combiners for number of tillers per plant. The low and statistically non-significant average performance of both parents in hybrid combinations for tiller count indicates that non-additive genetic effects are likely more important than additive ones for this trait.

Of the total crosses examined, only the combination of IIMR AVS 21 x IP 15535 S1-10-1-1 (9.34) exhibited a significantly positive specific combining ability (*sca*) effect for green fodder yield, distinguishing it as the optimal cross for enhancing this trait. For dry fodder yield, two crosses viz., IIMR AVS 10 x ICMV 08111 S1-1-1 (5.33) and IIMR AVS 11 x IP 2761 S1-9-4-2-1-4 (5.15) had significant positive specific combining ability effects in the desired direction.

Neither parent demonstrated significant positive general combining ability for green or dry fodder yield, indicating the likely importance of non-additive genetic factors in determining these traits. Bottom of Form

Eldie *et al.* (2021) and Keerthana *et al.* (2022) both reported significant positive specific combining ability (*sca*) effects for fodder yield and associated traits. Conversely, Yadav *et al.* (2022) found significant negative *sca* effects for the same traits.

Conclusion

Based on the results, it is concluded that among the 12 parent lines, one line IIMR AVS 11 and the tester ICMV 08111 S1-1-2 are identified as good general combiners. None of the parents showed significant effects on green and dry fodder yield individually, indicating a predominant non-additive gene action. However, several crosses exhibit significance, highlighting their potential for use in hybrid breeding programmes.

The hybrid IIMR AVS 21 x IP 15535 S1-10-1-1 emerges as the top specific combiner for overall performance, followed closely by IIMR AVS 11 x IP 2761 S1-9-4-2-1-4. Specifically for green and dry fodder yield, the crosses IIMR AVS 21 x IP 15535 S1-10-1-1 and IIMR AVS 10 x ICMV 08111 S1-1-1 are identified as the most promising combinations, underscoring their importance in breeding efforts.

Acknowledgement

I am deeply grateful to my guides for their valuable assistance and guidance throughout this research. Their support and expert guidance were crucial in enabling the completion of this work.

References

Anonymous (2013). http://www.indiastat.com

- Aswini, M.S. Ganesan K.N. Ezhilarasi T. and Sivakumar S.D. (2021). Combining ability and heterosis studies in fodder pearl millet [*Pennisetum glaucum* (L.) R. Br.]. *Electron. J. Plant Breed.*, **12(3)**, 1011-1021.
- Azhaguvel, P. and Jayaraman N. (1998). Combining ability and heterosis of some productivity traits in pearl millet. *Trop. Agric. Res.*, **10**, 425-432.
- Bhardwaj, R., Kaur M., Sohu R.S. and Singh D.P. (2015). Combining ability studies in pearl millet [*Pennisetum*

glaucum (L.) R. Br.]. Forage Res., 41(2), 78-84.

- Dhuppe, M.V., Chavan A.A., Phad D.S. and Chandankar G.D. (2006). Combining ability studies in pearl millet. J. Maharashtra Agric. Univ., 31, 146-148.
- Eldie, Y.D. (2021). Combining ability studies for forage yield and its components in a diallel cross of pearl millet. *J. Bio. Agri and Healthcare*, **11(6)**, 38-41.
- INDIASTAT (2024). [online] Available of site of indiastat.com, citation at: <u>https://www.indiastat.com/table/agriculture/</u> area-production-productivity-bajraindia-1949-1950/7267.
- Karvar, S.H., Pawar V.Y. and Patil H.T. (2017). Heterosis and Combining Ability in Pearl Millet (*Pennisetum glaucum* (L.) R. Br.). *Electron. J. Plant Breed.*, 8(4), 1197-1215.
- Keerthana, K., Ganesan K.N., Iyanar K., Sivakumar S.D., Jeyakumar P. and Ezhilarasi T. (2022). Identification of superior pearl millet napier hybrids with enhanced green fodder yield and quality through genetic variability studies. *YMER*, **21(08)**, 1144-1154.
- Kempthorne, O. (1957) An Introduction to Genetic Statistics. John Wiley and Sons Inc. New York:545
- Mungra, K.S., Dobariya K.L., Sapovadiya M.H. and Vavdiya P.A. (2015). Combining ability and gene action for grain yield and its component traits in pearl millet (*Pennisetum*)

glaucum (L.) R. Br.). *Electron. J. Plant Breed.*, **6**(1), 66-73.

- Parmar, R.S.,, Patel N.B., Leua H.N. and Singh S.P. (2013). Combining ability and heterosis for grain yield and its traits in pearl millet (*Pennisetum glaucum* (L.) R. Br.). *Prog. Res.*, 8, 19-23.
- Patel, M.A., Yadavendra J.P., Patel D.H., Upahyaya N.V. and Shaikh J.A. (2008). Studies on heterosis for green fodder yield its contributing traits in pearl millet (*Pennisetum* glaucum (L.) R. Br.). Forage Res., 34 (3), 149-155.
- Srivastava, K.R., Bollam S., Pujarula V., Pusuluri M., Singh R.B., Potupureddi G and Gupta R. (2020). Exploitation of heterosis in pearl millet: a review. *Plants*, 9(7), 807.
- Yadav, O.P. and Rai K.N. (2013). Genetic improvement of pearl millet in India. *Agric Res.*, **2**, 275-292.
- Yadav, O.P., Sabharwal P.S., Beniwal C.R. and Hanuman (2002). Combining ability study or some newly developed male sterile lines for forage attributes in pearl millet. *Forage Res.*, 27, 277-280.
- Yadav, M.K., Gupta P.C., Sanadya S.K. and Chandel D. (2022). Heterosis and combining ability in diverse A and R lines of pearl millet tested in Western Rajasthan. *Electron. J. Plant Breed.*, **13**(2), 440-446.