Plant Archives Vol. 26, Supplement 2, 2026 pp.2666-2670 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-2.335

COMBINING ABILITY ANALYSIS IN FORAGE SORGHUM (*Sorghum Bicolor* L. Moench)

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(Date of Receiving : 15-04-2026; Date of Revision : 14-06-2026; Date of Acceptance : 06-07-2026)

ABSTRACT

Present investigation was conducted at three locations *viz.*, Instructional Farm, RCA, Udaipur (E_1), Krishi Vigyan Kendra, Chittorgarh (E_2) and Agriculture Research Sub Station, Vallabhnagar (E_3), to estimate the combing ability for fourteen chracters in forage sorghum during *kharif* 2025. In this study, a half diallel mating design was used to generate 45 crosses using 10 parental genotypes during *kharif* 2024 at the Instructional Farm, RCA, Udaipur. The field performance of the hybrids, parents and standard checks were evaluated for green fodder yield per plant and important phenological, fodder quality traits. Significant GCA and SCA effects were observed for most of the traits evaluated, indicating the presence of additive and non additive gene action. The higher magnitude of SCA variance than GCA variance for green fodder yield per plant, days to 50 percent flowering and days to maturity indicated the predominance of non-additive gene action in the inheritance of these traits. The estimates of GCA effects for yield and yield contributing characters revealed that good general combiner parents for green fodder yield per plant were SSG-59-3, MP Chari and SPV-2979. Thirteen crosses exhibited significantly superior SCA effects on the pooled basis and three crosses *viz.*, SSG-59-3 x SU-1655, MP Chari x SU-1664 and SPV-2979 x SU-1674 in all the environments as well as on pooled basis for green fodder yield per plant. In addition to green fodder yield per plant the cross MP Chari x SU-1664 also exhibited significant SCA effects in desirable direction for plant height, leaf length, leaf breadth, leaves per plant, leaf stem ratio, stem girth and crude protein content. The main conclusion from this study is that both additive and non-additive gene effects are important for the studied traits.

***Keywords*:** Forage sorghum, General combining ability, Specific combining ability, Green fodder yield and diallel analysis**.**

Introduction

Sorghum (*Sorghum bicolor*), is a versatile and resilient cereal grain that has been cultivated for millennia. It belongs to the grass family, *Poaceae* and is classified under the genus *Sorghum*. Sorghum is a plant that usually reaches a height of 2 to 5 metres; however, dwarf varieties also exist. It has been originated in Africa and spread across the globe due to its adaptability to diverse climates. Sorghum has a robust root system, which aids in its ability to withstand drought and grow in regions with limited water availability. Sorghum is a diploid (2n=2x=20) species mostly grown in central and peninsular India in states like Maharashtra, Karnataka, Andhra Pradesh, Madhya Pradesh, Gujarat, Tamil Nadu, Rajasthan and Uttar Pradesh.

The success of the breeding procedure is determined by the useful gene combinations, organized in the form of good combining lines and isolation of valuable genotypes. Some lines produce outstanding progenies when crossed with other lines, while other lines may appear equally desirable but do not produce good progenies when crossed. The lines, which perform well in hybrid combination, are eventually of great importance to the plant breeders. Sorghum hybrids are widely adaptable, high-yielding, disease-resistant and they play an important role in enhancing sorghum productivity (Rakshit *et al.* 2014). Combining ability analysis is one of the most effective tools for identifying superior parents for hybridization programmes.

Materials and Methods

For this experiment, 10 parents obtained from AICRP on Sorghum, Udaipur were crossed in a half-diallel fashion during *Kharif* 2024 and developed 45 crosses (excluded reciprocals). These 45 crosses along with 10 parents and 2 checks *viz*., PC-1080 and CSV-35 F were evaluated in randomized block design with three replications during *kharif* 2025 at three different locations *viz.,* Instructional Farm, RCA, Udaipur (E_1), Krishi Vigyan Kendra, Chittorgarh (E_2) and Agriculture Research Sub Station, Vallabhnagar (E_3).

Observations were recorded on ten randomly selected competitive plants from each genotype in each replication across all the three locations for plant height, leaf length, leaf breadth, leaves per plant, leaf spot diseases, leaf stem ratio, stem girth, total soluble solids, green fodder yield per plant and dry fodder yield per plant. The selected plants were tagged and properly labeled for recording the observations. The phonological characters *viz*., days to 50 percent flowering and days to maturity were recorded on plot basis. Two quality traits *viz.*, crude protein content and hydrocyanic acid content were analyzed by taking two samples of forage sorghum per genotype and the average was taken. Crude protein content estimation was done by micro kjeldahl's method given by linder (1944) and HCN content was estimated by the alkaline picrate method given by Gilchrist *et al.*, (1967).

The combining ability analysis for the diallel mating design was performed according to Model-I (fixed effect) and Method-II (parents and one set of F_1's without reciprocals) proposed by Griffing (1956). This includes partitioning of variation among sources attributable to general combining ability (GCA) and specific combining ability (SCA) components. The combining ability analysis of data for each environment was carried out separately, using Griffing's method II, model I (1956). The combining ability analysis over the environments was carried out using the method suggested by Singh (1973 and 1979), which is an extension of Griffing's method II, model I (1956) to estimate the interactions of general and specific combining ability effects with environments.

Results and Discussion

The analysis of variance (ANOVA) for combining ability revealed highly significant mean squares due to general combining ability (GCA) and specific combining ability (SCA) for nearly all 14 evaluated traits in individual environments as well as on pooled basis. Significant GCA differences are attributed to additive gene effects and additive x additive interaction variances, whereas differences in SCA effects resulted from non-additive genetic variances (dominance and epistasis). The significance of GCA x E and SCA x E mean squares indicated that both additive and non-additive gene actions interacted substantially with environmental fluctuations. This highlights the necessity of multi-environmental testing to compute unbiased variance estimates (Tables 1 and 2). Similar results have also been reported in sorghum by Kumari *et al.* (2018), Parmar *et al.* (2019), Dev *et al.* (2019), Talaviya *et al.* (2023) and Begna *et al.* (2025).

The selection of parents for crossing and using them in the plant breeding program are determined by the nature and size of the impacts of combining abilities. Parents with desirable and significant GCA effects were considered good combiners while parents showing non-significant estimates but in a desirable direction were classified as average combiners. The estimates of GCA effects for yield and yield contributing characters revealed that good general combiner parents for green fodder yield per plant were SSG-59-3, MP Chari and SPV-2979 (Table 3). The significant GCA effects in the positive direction were exhibited by parent SSG-59-3 for plant height, leaves per plant and stem girth while MP Chari for plant height, leaf breadth, leaves per plant, leaf stem ratio and stem girth girth (Table 3). For quality traits, good general combiner parents were MP Chari and SU-1655 for crude protein content while parents MP Chari and SU-1664 for hydrocyanic acid content in desirable direction (Table 3).

Out of 45 crosses, 12 for days to 50 percent flowering and days to maturity, 11 for plant height and leaf length, 13 for leaf breadth, 14 for leaves per plant, 20 for leaf spot diseases, 7 for leaf stem ratio, 11 for stem girth, 13 for total soluble solids and green fodder yield per plant, 18 for dry fodder yield per plant, 15 for crude protein content and 19 for hydrocyanic acid content manifested significant desirable specific combining ability values on the pooled basis. None of the crosses were found good specific combiner for all the traits studied. A perusal of SCA effects among crosses revealed that the maximum magnitude of positive SCA effects for green fodder yield per plant was exhibited by cross MP Chari × SU-1664 in E_1, E_2, E_3 as well as over the environments. Thirteen crosses showed significantly superior SCA effects in pooled analysis. Among them crosses SSG-59-3 x SU-1655 and SPV-2979 x SU-1674 expressed positive and significant SCA effects in all the 3 environments as well as on pooled basis for green fodder yield per plant (Table 3). In addition to green fodder yield per plant, the cross MP Chari x SU-1664 also exhibited significant SCA effects in desirable direction for plant height, leaf breadth, leaves per plant, leaf stem ratio, stem girth and crude protein content (Tables 3) while crosses SSG-59-3 x SU-1655 and SPV-2979 x SU-1674 exhibited significant SCA effects in desirable direction for hydrocyanic acid content (Tables 3) These results are in accordance with the findings of Yadav and Pahuja (2014), Jain and Patel (2016), Kumar and Shrotria (2016), Dehinwal *et al.* (2017), Kumari *et al.* (2018), Parmar *et al.* (2019), Chapara *et al.* (2020), Veldandi *et al.* (2021), Talaviya *et al.* (2023), Ingle *et al.* (2023), Zhang *et al.* (2024) and Begna *et al.* (2025).

Conclusion

The main conclusion from this study is that both additive and non-additive gene effects are important for the studied traits. Parental lines exhibiting high general combining ability (GCA) effects are considered valuable in hybrid breeding programmes because their superior performance is largely governed by additive gene effects and additive × additive gene interactions, which are heritable, fixable and widely adaptable. Based on the results of the GCA analysis, three parental lines were identified as the best general combiners for green fodder yield per plant. The present study also identified crosses exhibiting significant high SCA effects for various traits derived from combinations involving either poor or good (or both) general combiner parents. Three superior crosses *viz.*, SSG-59-3 X SU-1655, MP Chari x SU-1664 and SPV-2979 X SU-1674 exhibited positive SCA effects for green fodder yield per plant and also for yield contributing traits, obtained by the cross combination of good x poor GCA values. Therefore, both GCA and SCA analysis are useful tools for characterizing parental lines and cross combinations based on genetic variances and the types of gene action involved in the inheritance of economically important traits.

Table 1: Analysis of variance for combining ability in individual environment for different characters in forage sorghum.

SN	Characters	Env	Source			Var Model I	
			GCA [9]	SCA [45]	Error [108]	GCA	SCA
1	Days to 50 per cent flowering	1	2.81	4.16**	1.61	0.30	38.32
		2	3.13	5.69**	1.82	0.33	58.06
		3	6.88**	5.14**	1.25	1.41	58.43
2	Days to maturity	1	6.86	7.65**	4.00	0.71	54.78
		2	5.77**	5.90**	2.22	0.89	55.21
		3	2.34	5.55**	1.60	0.18	59.26
3	Plant height (cm)	1	2590.42**	428.33**	76.61	628.45	5275.83
		2	1450.15**	476.13**	86.87	340.82	5839.04
		3	1782.71**	325.78**	93.85	422.22	3478.94
4	Leaf length (cm)	1	62.73**	13.87*	8.62	13.53	78.84
		2	20.86*	12.99*	8.49	3.09	67.43
		3	39.92**	31.00**	12.28	6.91	280.73
5	Leaf breadth (cm)	1	2.42**	0.22**	0.05	0.59	2.50
		2	1.98**	0.42**	0.05	0.48	5.44
		3	2.32**	0.34**	0.05	0.57	4.36
6	Leaves per plant	1	4.09**	0.69**	0.06	1.01	9.51
		2	3.03**	0.65**	0.03	0.75	9.16
		3	3.53**	0.69**	0.04	0.87	9.75
7	Leaf spot diseases (score 1-5)	1	0.57**	0.07**	0.01	0.14	1.00
		2	0.56**	0.09**	0.01	0.14	1.20
		3	0.60**	0.07**	0.01	0.15	0.95
8	Leaf stem ratio	1	0.00**	0.00*	0.00	0.00	0.00
		2	0.00**	0.00**	0.00	0.00	0.00
		3	0.00**	0.00**	0.00	0.00	0.01
9	Stem girth (cm)	1	0.08**	0.01**	0.00	0.02	0.15

		2	0.07**	0.02**	0.00	0.02	0.28
		3	0.09**	0.01**	0.00	0.02	0.10
10	Total soluble solids (%)	1	5.20**	0.58**	0.12	1.27	7.01
		2	5.97**	0.99**	0.13	1.46	12.95
		3	5.27**	0.61**	0.12	1.29	7.38
11	Green fodder yield per plant (g)	1	10288.66**	1486.23**	109.39	2544.82	20652.63
		2	6990.36**	1048.69**	115.07	1718.82	14004.23
		3	8884.70**	1092.40**	118.64	2191.51	14606.36
12	Dry fodder yield per plant (g)	1	2706.92**	393.29**	13.27	673.41	5700.24
		2	2626.11**	337.11**	11.83	653.57	4879.23
		3	2569.61**	347.83**	13.50	639.03	5015.00
13	Crude protein content (%)	1	1.66**	0.26**	0.02	0.41	3.66
		2	1.58**	0.27**	0.02	0.39	3.74
		3	1.73**	0.24**	0.01	0.43	3.33
14	Hydrocyanic acid content (ppm)	1	512.06**	216.04**	8.48	125.90	3113.38
		2	423.21**	274.75**	7.90	103.83	4002.83
		3	571.58**	238.11**	7.22	141.09	3463.40

*,** Significant at 5 and 1 percent respectively (Model I)

Table 2: Pooled analysis of variance for combining ability for different characters in forage sorghum

SN	Characters	Source						Bartlet	Variance Model I			
		Env [2]	GCA [9]	SCA [45]	GCA x E [18]	SCA x E [90]	Pool Error [324]	[2]	GCA	SCA	GCA x E	SCA x E
1	Days to 50 per cent flowering	55.39**	9.63**	9.91**	1.59	2.54**	1.56	3.91	1.96	2.02	125.32	0.05
2	Days to maturity	110.38**	9.93**	10.55**	2.52	4.28**	2.61	23.69**	3.92	1.83	119.14	-0.14
3	Plant height (cm)	2630.73**	5575.21**	971.81**	124.04	129.21**	85.77	1.12	92.54	1372.36	13290.59	57.39
4	Leaf length (cm)	671.82**	97.93**	25.70**	12.79	16.08**	9.80	4.88	24.07	22.03	238.46	4.49
5	Leaf breadth (cm)	2.73**	6.62**	0.80**	0.05	0.09**	0.05	0.13	0.10	1.64	11.30	-0.01
6	Leaves per plant	1.54**	10.52**	1.89**	0.06	0.07**	0.04	9.71**	0.05	2.62	27.70	0.03
7	Leaf spot diseases (score 1-5)	0.19**	1.69**	0.21**	0.02**	0.01**	0.01	2.60	0.01	0.42	3.03	0.01
8	Leaf stem ratio	0.00**	0.00**	0.00**	0.00	0.00**	0.00	3.50	0.00	0.00	0.01	0.00
9	Stem girth (cm)	0.06**	0.23**	0.03**	0.00	0.01**	0.00	0.07	0.00	0.06	0.38	0.00
10	Total soluble solids (%)	0.69**	15.97**	1.84**	0.24*	0.17*	0.12	0.13	0.02	3.96	25.77	0.17
11	Green fodder yield per plant (g)	1327.26**	25703.43**	3333.07**	230.14**	147.12**	114.37	0.18	44.11	6397.27	48280.49	173.66
12	Dry fodder yield per plant (g)	255.76**	7836.51**	1026.42**	33.07**	25.90**	12.87	0.55	8.83	1955.91	15203.36	30.31
13	Crude protein content (%)	0.44**	4.91**	0.71**	0.03**	0.02**	0.02	2.21	0.02	1.22	10.48	0.02
14	Hydrocyanic acid content (ppm)	265.59**	1453.50**	694.94**	26.68**	16.98**	7.87	0.70	9.37	361.41	10306.18	28.22

*,** Significant at 5 and 1 percent respectively (Model I)

Table 3 : Magnitude of SCA effect of promising crosses and GCA effect of their parents in forage sorghum

S. N.	**Genotypes**	**SCA/GCA effects for green fodder yield per plant (g)**	**SCA/GCA effects for plant height (cm)**	**SCA/GCA effects for leaf breadth (cm)**	**SCA/GCA effects for leaves per plant**	**SCA/GCA effects for leaf stem ratio**	**SCA/GCA effects for stem girth (cm)**	**SCA/GCA effects for crude protein content (%)**	**SCA/GCA effects for HCN (ppm)**
1	SSG-59-3 X SU-1655	25.98**	13.84**	0.50**	1.16**	0.01*	0.15**	0.09*	-9.96**

2	MP Chari X SU-1664	67.59**	22.23**	0.39**	0.79**	0.02**	0.16**	0.57**	3.82*
3	SPV-2979 X SU-1674	35.13**	33.73**	0.11	0.48**	0.02**	0.03	0.70**	-20.75**
4	SSG-59-3	4.52**	12.50**	0.06	0.35**	0.00	0.07**	-0.00	2.42**
5	MP Chari	28.54**	13.21**	0.41**	0.23**	0.01**	0.07**	0.50**	-8.80*
6	SU-1655	-22.59*	-14.30*	-0.36*	-0.34*	-0.01*	-0.12*	0.10**	-3.52*
7	SU-1664	-13.68*	-13.27*	-0.07	-0.11*	-0.00	-0.07*	-0.54*	5.84*
8	SPV-2979	12.55**	-3.23*	0.12**	-0.10*	0.01*	0.01	-0.04*	-0.14
9	SU-1674	0.76	4.14**	0.33**	-0.06	-0.00	-0.02*	-0.33*	5.94**

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