International Journal of Plant & Soil Science

Volume 36, Issue 2, Page 110-120, 2024; Article no.IJPSS.112061
ISSN: 2320-7035

Field Insights into the Genetic Symphony: Decoding Gene Dynamics for Enhanced Sorghum Yield (*Sorghum bicolor* [L.] Moench)

Senthilkumar V. [a*], **Davda B. K.** [b], **Madhuri M.** [a], **Kaldate Supriya** [a], **Modha K. G.** [a] **and Joshi A. J.** [a]

[a] *Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari (Gujarat), India.*
[b] *Main Sorghum Research Station, Athwa Farm, Navsari Agricultural University, Surat (Gujarat), India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2024/v36i24370

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/112061

Original Research Article

Received: 22/11/2023
Accepted: 24/01/2024
Published: 27/01/2024

ABSTRACT

In this investigation using line × tester analysis, fifteen parents (3 Cytoplasmic Male Sterility females and 12 males) and 36 hybrids, including the standard check CSH-25, underwent evaluation in a randomized block design with three replications. Notably, significant general combining ability variances for 1000-seed weight and highly significant specific combining ability variances for all traits were observed. The research highlights the prevalence of additive genetic variance in 1000-seed weight and the combined influence of additive and nonadditive gene effects in panicle length ratio. Recognized good general combiners, such as SR 2991 , SR 2950 , SR 2872, SR 2984 and 691A, provide valuable insights for breeding strategies. Subsequent evaluations of promising hybrids, particularly 691 A × SR 2991, 691 A × SR 2872 and 691 A × SR

---

*Corresponding author: E-mail: senthilkumaranpbg12@gmail.com;

2950 hold potential for optimizing grain yield, panicle length, and dwarfness. These findings provide nuanced insights for future Sorghum breeding programs, enhancing understanding of gene dynamics for improved productivity and emphasizing the pivotal role of hybrid sorghum in contemporary agricultural contexts.

Keywords: Sorghum; general combining ability insights; additive-nonadditive gene effects; sustainable crop productivity.

1. INTRODUCTION

Sorghum (*Sorghum bicolor* [L.] Moench) is an important cereal crop in India that is used for dual purposes, i.e., feed and fodder. The word sorghum is derived from the Spanish word "*Sorgo*", which means "rising above" [1]. Sorghum belongs to the natural order Poales, tribe Andropogenae, and family Poaceae; it includes annual sorghum with ten pairs of chromosomes (2n = 20). The genome size of sorghum is 730 Mb [2]. Sorghum is normally a self-pollinated crop, but cross-pollination averages approximately 6 to 10 percent and may reach as high as 30 percent in Sudan grass. Cultivated sorghum is grouped into five races based on panicle morphology, *viz., bicolor, kafir, guinea, caudatum* and *durra* [3]. It originated in the Ethiopian region of East Africa and is now grown in more than 80 countries across the globe. India is the sixth-largest producer of sorghum in the world [4]. According to statistical data, the area under which this crop is cultivated in India is approximately 5.65 million hectares, with an annual production of 4.50 million tons and a productivity of 500 kg/ha. [5].

Line × tester analysis provides information about the role of the cytoplasm in the effects of GCA on A-lines and on the effects of SCA and heterosis of sorghum hybrids. The concept of combining ability is considered to be a landmark in the development of efficient and effective breeding methodologies for different crop plants. Analysis of combining ability provides guidelines for assessing the relative quality of the parental material. By utilizing this technique, breeders can choose the best combination of parents as well as specific cross combinations for further exploitation. The parental material may be used to develop hybrids or build up populations with desirable and fixable genes depending upon the nature of the gene action [6]. The assessment of the GCA effects of hybrid parents is important for determining their suitability for developing hybrids, as the mean performance of parental lines need not always be a good indicator of their GCA effects. Hybridization technology results in increased yield, profitability and adaptability to stressful environments. The success of the breeding procedure is determined by useful gene combinations organized in the form of good combining lines and the isolation of valuable germplasms [7]. Accordingly, good knowledge of the gene action involved in the inheritance of quantitative characters of economic importance is required to develop an efficient breeding plan leading to rapid improvement.

This research, with its nuanced insights into both additive and nonadditive genetic components, sheds light on the intricate dynamics of gene interactions in hybrid sorghum. The findings contribute to a deeper understanding of these dynamics, providing a foundation for tailored Sorghum breeding programs geared towards enhanced productivity. As hybrid sorghum gains importance in agricultural landscapes, the identified hybrids and their parental lines become pivotal in steering future breeding strategies for improved yield, agronomic traits, and overall crop performance.

2. MATERIALS AND METHODS

The present investigation was carried out at the College Farm, N.M. College of Agriculture, Navsari Agricultural University, Navsari during the summer and *Kharif*, 2018. The experimental material for the present investigation comprised three male sterile lines used as female parents and twelve testers used as male parents. All the experimental materials were collected from the Main Sorghum Research Station, Athwa Farm, Navsari Agricultural University, Surat (Gujarat). These females and males were crossed by hand pollination in a line × tester mating system during the summer of 2018. The seeds of individual parental lines and hybrid seeds obtained from female plants were harvested. All the hybrids, along with their 15 parents and one standard check, were grown in accordance with a randomized block design with three replications during *Kharif,* 2018. Parents and 36 F_1 plants were sown in a single row 3 meters in length. The row-to-row and plant-to-plant distances were

45 cm and 15 cm, respectively. For recording, five competitive plants were randomly selected from each plot for all three replications, and mean observations were taken. For observation on days to 50 percent flowering and days to maturity were recorded on a plot basis.

The replication wise mean values for all the characteristics were subjected to statistical analysis for computing the mean, variance, general combining ability (GCA) and specific combing ability (SCA). The variation among hybrids was further partitioned into sources attributed to general and specific combining ability components in accordance with the procedure of Kempthorne [8].

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

Analysis of variance for combining ability revealed that general combining ability (gca) variance was significant only for 1000 seed weight, indicating that GCA variance significantly contributed to these characteristics. On the other hand, the specific combining ability (sca) variance was highly significant for all the characters studied, revealing the significant contribution of hybrids to the variance in SCA components for almost all the characters (Table 1) and similar findings was also reported by Gite *et al.* [7].

3.2 Gene Action

A clear picture of the relative importance of additive and nonadditive gene effects in controlling a character can be obtained on the basis of the general predictability ratio [9]. In the present study, the general predictability ratio reached 0.50 for all the tested parameters except for panicle length and 1000-seed weight, which indicates that the majority of the genes affected by these traits are nonadditive and emphasize the use of a heterosis breeding approach to exploit available vigour. In the case of the 1000-seed weight, the general predictability ratio closed to unity, revealing the preponderance of the additive genetic system in the inheritance of that characteristic, which emphasized the effectiveness of the selection in future breeding programmes. However, when the ratio was between 0.51 and 0.70 for panicle length, this difference pinpointed the importance of both additive and nonadditive gene effects in the inheritance of this trait. Both additive and nonadditive genetic variances can be utilized at a time through reciprocal recurrent selection for population improvement in the present material. The preponderance of nonadditive types of gene action for grain yield and other traits was previously reported by Thakare *et al.* [10]. The preponderance of the additive type of gene action for determining 1000 seed weight was previously reported by Chikuta *et al.* [11].

3.3 Combined Ability Analysis

3.3.1 General combining ability

The gca effects of the parents revealed that none of them was found to be superior for all the characters. (Table 2 and Fig. 1.). An overall appraisal of the effects of gca revealed that four male parents, namely, SR 2991, SR 2950, SR 2872 and SR 2984, and one female parent, 691, were good general combiners for grain yield. Among these good general combiners for grain yield, the topper male parents SR 2991 and SR 2950 were found to be good general combiners for all the characters studied, except for SR 2950 for plant height. These can be used in future breeding programmes for the development of early-maturing and high-yielding hybrids or varieties that combine all these characteristics. While female 691 A was depicted as a good combiner for days to 50 percent flowering and 1000 seed weight and male SR 2872 was depicted for early flowering, both of these traits can be utilized for the development of genotypes suitable for terminal draught prone areas. By critical examination of the other traits of the parents, SR 2993, SR 2957 and SR 2997 were found to be good general combiners for determining the weight and panicle length of the 1000 seeds. These findings can be utilized in future breeding for the development of promising genotypes with bold grains and long panicle lengths. For days to 50 percent flowering, parents SR 2997 and SR 2993 exhibited good general combining ability. However, the parents of SR 2993 and SR 2997 were observed to be good general combiners for early maturity and can be utilized for the development of early hybrids or varieties. For plant height, the parents SR 2914, SR 2957, SR 2997 and SR 2999 were reported to be good combiners for dwarfness and can be utilized for a dwarf breeding programme. These findings are similar to those of Kalpande *et al.* [6] More *et al.* [12] and Chikuta *et al.* [11].

Table 1. Analysis of variance in combining ability

Source of variation	**d. f**	**Mean square**					
		Days to 50 percent flowering	**Days to maturity**	**Plant height (cm)**	**Panicle length (cm)**	**Grain yield per plant (g)**	**1000 seed weight (g)**
Replication	2	24.56	20.02	76.576	8.29	10.57	2.82
Hybrids	35	47.95**	186.94**	1160.89**	21.55**	213.97**	49.47**
Line effect	2	90.81	63.58	1929.56	0.09	8.96	81.84**
Tester effect	11	57.54	313.98*	1577.41	32.52	299.76	118.80**
Line x Testers effects	22	39.26**	134.63**	882.75**	18.01**	189.71**	11.86**
Error	70	12.79	13.37	40.00	2.75	12.15	2.21
σ^2_f		1.81	1.65	38.57	0.14	1.53	1.61
σ^2_m		2.80	14.34	74.34	1.53	14.41	5.19*
σ^2_{GCA}		1.55	3.15	34.24	0.32	3.31	1.65*
σ^2_{SCA}		3.77*	12.95**	84.93**	1.733**	18.25**	1.14**
$\frac{2\sigma^2 g}{(2\sigma^2 g+\sigma^2 s)}$		0.27	0.08	0.01	0.58	0.05	0.88

** and ** are significant at the 5 percent and 1 percent levels, respectively*

Table 2. General combining ability effects in parents

Parents	Days to 50 percent flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Grain yield per plant (g)	1000 seed weight (g)
Lines						
691 A	-1.74**	0.88	-0.75	0.01	0.56	1.43**
27 A	0.37	0.63	-6.91**	0.04	-0.20	0.13
2219 A	1.37*	-1.52*	7.66**	-0.05	-0.36	-1.57**
S.E.(g_i)	0.57	0.69	1.01	0.26	0.51	0.24
S.E.(g_i-g_j)	0.80	0.98	1.44	0.37	0.72	0.34
Tester						
SR 2999	1.03	8.58**	-18.76**	-2.21**	-6.63**	-4.29**
SR 2950	-0.29	-7.63**	-0.91	2.14**	8.54**	4.16**
SR 2991	-1.18	-3.63*	15.25**	1.97**	9.93**	2.80**
SR 2993	-3.63**	-4.08**	3.37	-1.83**	-3.98**	2.51**
SR 2872	-3.07**	0.47	-2.13	0.77	5.61**	-3.00**
SR 2896	2.92*	3.58*	-5.22*	-1.73**	-3.65**	1.45**
SR 2914	2.25	8.13**	-18.87**	-3.40**	-3.32**	-8.52**
SR 2957	0.92	-2.75	-9.53**	0.54	-4.84**	2.63**
SR 2997	-1.96	-9.63**	-7.46**	2.56**	0.009	1.66**
SR 2990	-2.51*	0.13	7.16**	0.91	-6.45**	-0.75
SR 2984	4.37**	6.47**	23.82**	0.25	3.45**	1.06*
SR 2926	1.14	0.36	13.31**	0.02	1.34	0.27
S.E.(g_i)	1.14	1.39	2.03	0.52	1.02	0.48

** and ** are significant at 5 percent and 1 percent levels of significance, respectively*

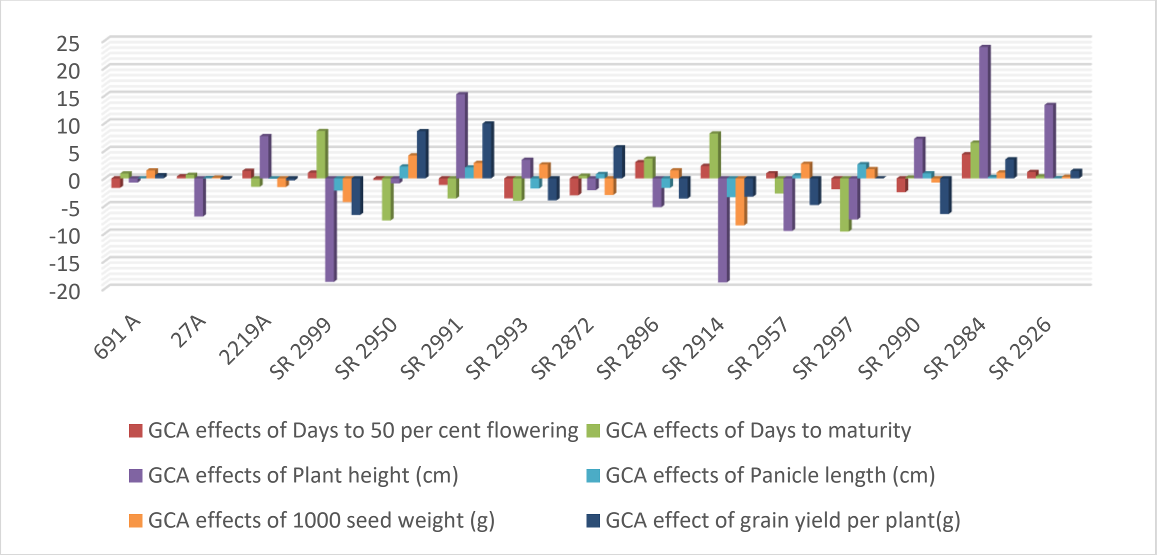

Fig. 1. General combining ability effects of various characters in parents

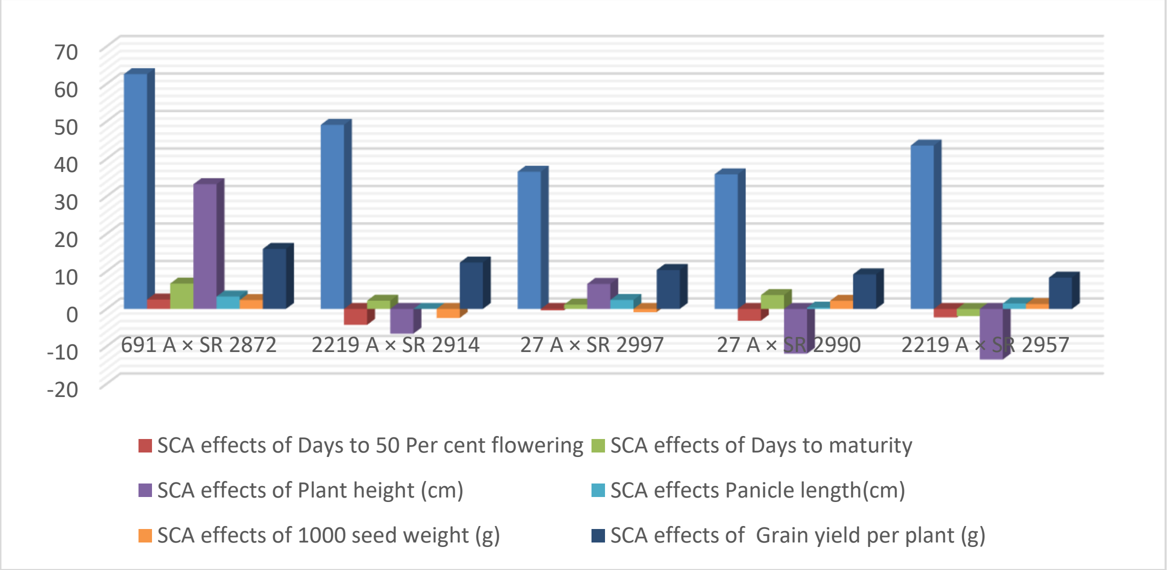

Fig. 2. SCA effects of various characters in selected crosses

3.3.2 Specific combining ability

The cross combinations with high SCA effects differed from character to character and displayed differences in their ranking. None of the cross combinations reported consistently high SCA effects for any of the characteristics. (Table 3)

Based on a critical examination of sca effects, nine hybrids, *viz.,* 691 A × SR 2872, 2219 A × SR 2914, 27 A × SR 2997, 27 A × SR 2997, 2219 A × SR 2957, 27 A × SR 2993, 691 A × SR 2926, 2219 A × SR 2984 and 2219 A × SR 2999, exhibited positive significant sca effects in desirable directions and emerged as the best specific cross combination for grain yield (Fig. 3). Among these, the best specific cross combination for grain yield, 691A × SR 2926, was also found to be a good specific combination for early flowering, early maturity and panicle length; this combination can be utilized in future breeding programmes for the development of high-yielding genotypes or directly exploited as early-maturing and high-yielding hybrids. 691 A × SR 2872 and 27 A × SR 2990 were used for determining the 1000 seed weight, and 2219 A × SR 2914 was used for early flowering. 27A × SR

Table 3. Specific combining ability (SCA) effects of crosses for grain yield and yield traits sorghum

Sr. No.	Crosses	Days to 50 percent flowering		Days to maturity		Plant height (cm)		Panicle length (cm)		1000 seed weight (g)		Grain yield per plant (g)	
1	691 A × SR 2999	0.74		2.33		-1.94		-0.70		0.16		1.88	
2	691 A × SR 2950	3.40		7.55	**	19.25	**	0.44		0.48		2.92	
3	691 A × SR 2991	-4.03	*	7.55	**	-13.20	**	-0.82		-1.35		-1.89	
4	691 A × SR 2993	0.07		2.66		5.24		-0.84		-0.24		-2.62	
5	691 A × SR 2872	2.51		6.77	**	33.25	**	3.31	**	2.35	**	16.01	**
6	691 A × SR 2896	0.85		-6.66	**	-5.25		-0.27		-0.28		-0.72	
7	691 A × SR 2914	5.18	*	-2.22		-6.85		4.77	**	-0.23		-1.75	
8	691 A × SR 2957	3.18		-5.33	*	7.724	*	-0.72		-1.45		-5.03	**
9	691 A × SR 2997	-2.92		0.88		-17.29	**	-2.20	*	-0.94		-5.25	**
10	691 A × SR 2990	-2.03		4.11		-18.17	**	-2.73	**	0.24		-3.67	*
11	691 A × SR 2984	-0.93		-1.79		40.65	**	-3.54	**	0.84		-5.28	**
12	691 A × SR 2926	-6.03	**	-11.78	**	4.875		3.31	**	0.44		5.42	**
13	27 A × SR 2999	-2.37		-1.08		5.3		-1.06		0.42		-5.73	**
14	27 A × SR 2950	-3.70		-7.19	**	-7.82	*	-0.10		-2.20	*	3.51	
15	27 A × SR 2991	2.51		-1.19		0.96		0.01		-0.32		1.14	
16	27 A × SR 2993	2.29		0.58		15.70	**	1.27		-1.40		7.54	**
17	27 A × SR 2872	1.07		-12.31	**	-9.71	**	-2.99	**	1.47		-12.40	**
18	27 A × SR 2876	2.07		2.25		3.04		1.55		1.51		1.16	
19	27 A × SR 2914	-0.92		0.02		13.44	**	-1.67		2.64	**	-10.61	**
20	27 A × SR 2957	-0.92		7.25	**	5.75		-0.75		0.13		-3.32	
21	27 A × SR 2997	-0.37		1.13		6.66		2.40	*	-0.85		10.38	**
22	27 A × SR 2990	-3.14		3.69		-11.93	**	0.35		2.17	*	9.23	**
23	27 A × SR 2984	1.63		2.02		-6.02		1.88	*	-2.25	**	1.05	
24	27 A × SR 2926	1.85		4.80	*	-15.38	**	-0.89		-1.32		-1.95	
25	2219 A × SR 2999	1.63		-1.25		-3.35		1.76		-0.58		3.85	*
26	2219 A × SR 2950	0.29		-0.36		-11.43	**	-0.33		1.72	*	-6.43	**
27	2219 A × SR 2991	1.51		-6.36	*	12.24	**	0.81		1.67	*	0.74	
28	2219 A × SR 2993	-2.37		-3.25		-20.96	**	-0.42		1.64		-4.91	**
29	2219 A × SR 2872	-3.59		5.52	*	-23.55	**	-0.31		-3.82	**	-3.61	*
30	2219 A × SR 2876	-2.92		4.41		2.21		-1.28		-1.22		-0.44	
31	2219 A × SR 2914	-4.25	*	2.19		-6.58		-3.10	**	-2.40	**	12.37	**
32	2219 A × SR 2957	-2.25		-1.91		-13.48	**	1.47		1.32		8.35	**

Sr. No.	Crosses	Days to 50 percent flowering		Days to maturity		Plant height (cm)		Panicle length (cm)		1000 seed weight (g)		Grain yield per plant (g)	
33	2219 A × SR 2997	3.29		-2.02		10.62	**	-0.19		1.79	*	-5.12	**
34	2219 A × SR 2990	5.18	*	-7.80	**	30.10	**	2.38	*	-2.42	**	-5.56	**
35	2219 A × SR 2984	-0.70		3.86		13.66	**	1.65		1.42		4.22	*
36	2219 A × SR 2926	4.18	*	6.97	**	10.50	**	-2.42	**	0.87		-3.46	
	S.E. (S_{ij})	1.98		2.40		3.52		0.91		0.83		1.78	

** and ** are significant at the 5 percent and 1 percent levels, respectively*

2990 and 2219A × SR 2957 also exhibited superior dwarfness in addition to grain yield and can be utilized in breeding programs for improvements in these traits in conjunction with grain yield. Critical examination of crosses for other traits revealed that, in the case of earliness, the cross combinations 691A × SR 2991, 27A × SR 2872, 2219A × SR 2990 and 27A × SR 2950 exhibited significant negative sca effects and could be best suited for breeding for earliness. These findings is supported by similar results reported by Chaudhari *et al.* [13]. Considering panicle length, the crosses 691 A × SR 2914, 27 A × SR 2872 and 27 A × SR 2990 had registered high sca effects in a positive direction. Similar results were observed by Ghorade *et al.* [14].

Among the most important yield-attributing traits for 1000 seed weight, the 27A × SR 2914, 691A × SR 2872 and 27A × SR 2990 crosses exhibited strong positive sca effects. Similar results are reported by Chikuta *et al.* [11]. From the observations made in the present study, the following relevant points emerged. The inspection of SCA effects and the mean performance of individual crosses indicated that the crosses having high SCA effects did not always possess a high mean.

The crosses identified as having a high SCA effect on grain yield per plant had a high 1000-seed weight. Thus, the 1000 seed weight was the most important yield-related trait. The crosses exhibiting high SCA effects were not always good × good combinations with respect to mean performance. These devices can be further evaluated for their pre-eminence in terms of performance. A total of 691 A × SR 2872 exhibited greater grain yield and high SCA. These top performing crosses involved all the types of parental combinations: Good × Good, Average × Good, Poor × Good and Average × Average. Only two crosses involved good parental combination, and at least one of the parents was either a poor or an average parent in the rest of the crosses. The SCA variance markedly surpassed the GCA variance, thereby resulting in a very low sca/gca ratio, which pinpointed the prominent prevalence of nonadditive gene action ruling the inheritance of grain yield. Notably, the most promising standard heterotic hybrids for grain yield did not exhibit high heterosis for all yield attributing traits, and there was mutual complementation of various yield-attributing characteristics [15].

Pertaining to the evaluation of combining ability performance, it can be concluded that the hybrids 691A × SR 2991,691A × SR 2872, 691A × SR 2950, 27A × SR 2950 and 2219A × SR 2997 appeared to be more promising for grain yield, panicle length and dwarfness; hence, the stability performance of these crosses could be checked and offer a scope for the improvement of grain yield in future breeding programs. The parents 691A, SR 2950, SR 2997, SR 2872 and SR 2991 were identified as good general combiners in the material under study, offering scope for further improvement in sorghum. Both additive and nonadditive genetic variants can be exploited simultaneously through population improvement programs, and heterosis breeding may be adopted to exploit nonadditive gene action and the development of hybrids at the commercial scale [16].

The present study needs to be further tested in observational/multilocation trials to determine the heterotic potential of these materials at the commercial level. Moreover, the cross combinations that show the least importance for SCA effects but originate from parental lines with high GCA effects can be used for recombination breeding with the easy selection of desirable segregants, particularly for developing better performing pure lines.

4. CONCLUSION AND FUTURE PROSPECTS

In conclusion, the analysis of combining ability in this study provided valuable insights into the genetic architecture governing various agronomic traits in sorghum. The significant contribution of general combining ability (GCA) variance for 1000 seed weight highlighted the importance of certain parental lines in influencing this trait. On the other hand, the substantial specific combining ability (SCA) variance across all studied characteristics emphasized the crucial role of hybridization in generating desirable combinations for improved traits. Gene action analysis revealed a predominant role of nonadditive gene effects, especially for traits such as grain yield, highlighting the potential benefits of a heterosis breeding approach. The identification of specific cross combinations with positive and significant SCA effects for grain yield, early flowering, panicle length, and other traits provides valuable information for future breeding programs. The findings from this study pave the way for targeted breeding efforts aimed at developing high-yielding sorghum varieties with desirable agronomic traits. The promising parental lines identified as good general combiners, such as SR 2991, SR 2950, SR 2872, and 691A, offer potential candidates for the development of superior hybrids or varieties. The study also underscores the importance of considering both additive and nonadditive genetic components in breeding programs, allowing for a comprehensive approach to population improvement.

To further validate the outcomes of this study, observational and multilocation trials are recommended. Evaluating the identified cross combinations in diverse environmental conditions will provide a more robust understanding of their performance and heterotic potential at the commercial level. Additionally, the crosses showing less importance for SCA effects but originating from parental lines with high GCA effects present opportunities for recombination breeding. Harnessing such combinations may facilitate the development of better-performing pure lines through easy selection of desirable segregants. In summary, the comprehensive analysis of combining ability in this study contributes valuable knowledge to sorghum breeding strategies. The identified promising crosses and parental lines offer a solid foundation for ongoing efforts to enhance sorghum varieties, addressing the challenges of yield, early maturity, and other key agronomic traits in the context of sustainable agriculture.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Vavilov NI. The origin of variation, immunity of cultivated plants translated in 1950. Walthan, Mass USA; 1935.
2. Paterson AH, Bowers JE, Bruggmann R, Dubchak I, Grimwood J, Gundlach H, and Schmutz, J. The Sorghum bicolor genome and the diversification of grasses. Nature. 2009;457(7229):551.
3. Harlan JR, De Wet JMJ. A Simplified Classification of Cultivated Sorghum 1. Crop science. 1972;12(2):172-176.
4. Anonymous World Agricultural Production. (n.d.). Sorghum. World Agricultural Production; 2023a.
   Available:http://www.worldagriculturalproduction.com/crops/sorghum.aspx
5. Anonymous Area, production and yield report, Directorate of Agriculture, Government of India; 2019b.
6. Kalpande VV, Ghorade RB, Lad AP. Potential parents for yield its components in rabi sorghum. The Bioscan. 2015;10 (2):837-839.
7. Gite AG, NS. Kute VR. Patil, Heterosis studies for yield and its components traits in rabi sorghum (*Sorghum bicolor* (L.) Moench). J of Global Biosciences. 2015; 4(8):32.
8. Kempthorne O. An introduction to genetic statistics. New York, USA; 1957.
9. Baker RJ. Issues in diallel analysis. Crop Sci. 1978;18:533-536.
10. Thakare DP, Ghorade RB, Bagade AB. Combining Ability Studies in Grain Sorghum Using Line × Tester Analysis. International Journal of Current Microbiology and Applied Sciences. 2014; 3(10):594-603.
11. Chikuta S, Odong TL, Kabi F, Rubaihayo P, BomBom A, Okori P, Karuma AN. Combining ability and heterosis of selected grain and forage dual purpose sorghum genotypes. Journal of Agricultural Science. 2017;9(2).
12. More AV, Kalpande HV. Heterosis studies for grain yield and their parameters in rabi sorghum hybrids [*Sorghum bicolor* (L.) Moench]. Electronic Journal of Plant Breeding. 2016;7(3):730-736.
13. Chaudhari DR, Solanki BG, and Narwade AV. Heterosis for grain yield and its component traits in sorghum [*Sorghum bicolor* (L.) Moench]. An International e-journal. 2016;5(2):121-126.
14. Ghorade RB, Kalpande VV, Bhongle SB. SPH-1635-A dual-purpose high yielding kharif sorghum hybrid. International Journal of Agricultural sci. 2014;10(1):134-137.
15. Kale BH, Desai RT. Gene action studies over the different environment in sorghum [*Sorghum bicolor* (L.) Moench].Advance research journal of crop improvement. 2016;7(1):116-120.

16. Bohra A, Jha UC, Adhimoolam P, Bisht D, Singh NP. Cytoplasmic male sterility (CMS) in hybrid breeding in field crops. Plant cell reports. 2016;35(5):967-993.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/112061