Received: 25 Aug 2025 | Revised: 13 Nov 2025 | Accepted: 13 Nov 2025

Electronic Journal of Plant Breeding

Research Article

Heterosis and combining ability analysis using landrace-based hybrids for yield and yield components in *rabi* sorghum

Basavaraj M Pattanashetti[1*], G. M. Sajjanar[2], M. S. Maralappanavar[3], K. O. Swaroop[1] and C. D. Soregaon[4]

[1]Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad 580005, Karnataka, India
[2]Department of Genetics and Plant Breeding, College of Agriculture Vijayapura, University of Agricultural Sciences, Dharwad, Karnataka, India
[3]Department of Genetics and Plant Breeding, College of Agriculture Dharwad, University of Agricultural Sciences, Dharwad 580005, Karnataka, India
[4]AICRP on Sorghum, Regional Agricultural Research Station, Vijayapur, University of Agricultural Sciences Dharwad, Karnataka, India
[*]**E-Mail:** basavarajpattanashetti1208@gmail.com

Abstract
Sorghum, called the “King of Millets,” is a staple cereal in the semi-arid tropics of Africa and Asia, and in India it is grown in both *kharif* and *rabi* seasons. Hybrid breeding mainly relies on heterosis and commonly uses the A_1 (*milo*) cytoplasm source, but rabi hybrids remain less popular due to poor adaptation. Landraces, with their genetic diversity and natural stress tolerance, offer strong potential for developing climate-resilient hybrids. Such landrace-based hybrids help maintain productivity under limited water conditions and support food security in climate-vulnerable regions, making them important for sustainable sorghum cultivation. With this idea, a trial was undertaken at the Regional Agricultural Research Station, Vijayapura, to evaluate 18 hybrids (2 lines and 9 testers including landraces) and five checks using Line × Tester design during *rabi* 2022 for ten yield related traits. Notable variations were identified among hybrids, with varying Line × Tester interactions. The two testers showed strong additive genetic effects for test weight, while the cross 104A×RLT-9 exhibited noteworthy non-additive genetic effects for panicle weight, grain yield, and other traits, indicating its potential in heterosis breeding programs. Likewise, the principal component analysis uncovered distinct trait variability, with grain yield and related traits (*viz*: grain yield, panicle weight, and harvest index) driving major variation. GCA and SCA biplots identified key parents and hybrids contributing to yield improvement. This information would be valuable for selecting parent plants to improve specific morphological traits towards development of increased potential genotypes in sorghum.

Keywords: Additive genetic effects, Heterosis, Line × Tester, Non-additive genetic effects, Sorghum

INTRODUCTION

Sorghum, often called as the “King of Millets” or “Great Millet” due to its notable grain size compared against other millets, is a vital staple food and fodder crop in developing countries, earning a reputation as a ‘failsafe’ crop. Sorghum is a highly diverse crop known for its resilience to heat, drought, and numerous biotic and abiotic constrains. It thrives in tropical and subtropical regions and has strong growth potential during both *kharif* and *rabi* seasons. Globally, India ranks fifth in sorghum production, with approximately 4.10 million hectares under cultivation, yielding 4.40 million tonnes annually and a productivity of 1100 kg/ha in 2022-2023

(Anonymous, 2023). Known locally as "Jowar," sorghum is primarily grown in peninsular and central India, with Maharashtra, Karnataka, Andhra Pradesh, Gujarat, Madhya Pradesh, Rajasthan, Uttar Pradesh, and Tamil Nadu being the major producing states.

The goal of sorghum breeding is to develop high-yielding varieties and hybrids with enhanced quality, disease and pest resistance, drought tolerance, and other beneficial agronomic traits (Klein *et al*., 2008). In order to produce huge amounts of hybrid seed economically, this approach solely relies on cytoplasmic nuclear male sterility (CMS). Sorghum CMS was first identified when the "*kafir*" nuclear genome was combined with an unsuitable "*milo*" cytoplasmic background. This led to the discovery of A_1 CMS, which has been employed thereafter to develop hybrids. These F_1 hybrids significantly improved sorghum cultivation, offering a 50-60% increase in grain yield compared to traditional landraces. Hybrids have become popular in *kharif* due to their high yield. Although, a plethora of hybrids have been developed in Indian national programme for cultivation during *rabi*, most of these were not accepted by farmers due to lack of terminal drought tolerance, resistance to shoot fly, grain quality traits comparable to M 35-1, the most popular variety. (Reddy *et al*., 2006; Sajjanar *et al*., 2011). The *milo* source of male sterility is particularly sensitive to cold temperatures and shoot flies. To enhance the frequency of hybrids with gratifying grain quality, tolerance to low temperature and resistance to diseases and pest in post-rainy seasons, it is crucial to ensure that at least one or both seed parents possess *rabi* adapted traits.

Sorghum landraces grown during the *rabi* season are known for their high-quality grains, which are typically bold, white and tastier, and possess traits well-suited to *rabi* conditions. Landraces are the varieties that farmers have developed and cultivated over decades through traditional selection methods (Biodiversity Act, 2004). Of late, developments in sorghum breeding emphasize the significance of utilizing hybrid vigour to increase yields while preserving the high grain quality critical for *rabi* sorghum. However, progress in *rabi* sorghum remains limited, highlighting the need for research on combining ability and heterosis using diverse germplasm sources and landraces (Sandeep and Biradar, 2020). Considering this, the current study was intended to evaluate combining ability effects, gene action, and heterosis by employing a Line × Tester (L×T) analysis with *rabi* landraces as pollen parents, focusing on yield and its related traits.

MATERIALS AND METHODS

The investigation was carried out during *rabi* 2022 at Regional Agricultural Research Station, Vijayapura. The location is positioned at 16° 49' N latitude and 75° 43' E longitude, at an altitude of 593 meters above mean sea level. It falls within the Northern Dry Zone of Karnataka (Zone 3) and receives mean annual rainfall of 590 mm.

Eighteen hybrids developed by crossing two *milo* cytoplasm based male sterile lines (104 A and BJMS 1A), with nine testers (including landraces and elite genotypes) were evaluated along with five checks (M 35-1, BJV 44, CSV 29R, SPV 2217 and CSH 19R) in randomized block design with two replications. Each entry was planted in two rows of 2 m length with intra and inter-row spacing of 15 cm and 45 cm respectively. Optimal crop management practices were implemented to establish a healthy crop stand. Observation on yield and yield-contributing traits namely, plant height (cm), panicle length (cm), panicle breadth (cm), panicle weight (g), grain yield per plant (g), 1000 seed weight (g), grain number per panicle, fodder yield per plant (g) and harvest index (%), were recorded on five randomly selected competitive plants from each genotype, while days to 50 per cent flowering was recorded on a per-plot basis. Mean of the five tagged plants from each experimental unit was used for analysing line × tester method in R studio (v: 2024.04.1+748).

The combining ability effects, including general (*gca*) and specific (*sca*) combining abilities, were estimated as per Kempthorene (1957**)**, and Arunachalam (2001), (σ^2gca/σ^2sca) and (σ^2D/σ^2A)$^{-1/2}$ ratios, which were used to rate the relative weight of additive *versus* the non-additive type of gene actions. Heterosis was measured as a percentage change, either an increase or decrease, in the values of various traits relative to the mid-parent (relative heterosis), the better parent (heterobeltiosis) and the hybrid/check (standard heterosis) for all the hybrids as per Falconer (1996). The mid-parent values were calculated using the corresponding female and male plants of a given cross, while the mean values of the better parent were determined using the better parent, which could be either the B line of CMS parents or the male line of a specific cross for a particular trait. principal component analysis (PCA) was employed to efficiently capture and interpret the multidimensional variation contributed by genetically diverse local landraces, enabling identification of trait clusters and distinct hybrid groups useful for strategic parent selection.

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences across all the traits studied (**Table 1**). The line × tester interactions showed significant variation across traits, except for plant height, panicle length, and breadth, indicating that hybrid performance was influenced by the specific combination of parental line and tester. The most crucial step in hybridization programs is selecting superior parental genotypes to develop new hybrids with desirable traits. However, a high-performing genotype may not always yield better hybrids. Breeding designs like diallel and L × T are used to evaluate the *gca* and *sca* of parental lines and assess hybrid performance. Combining ability analysis is valuable for selecting parent lines that can be utilized in hybridization programs to develop superior hybrids. Typically, *gca* is associated with additive gene

Table 1. Analysis of variance among lines, testers and hybrids for yield and yield components in *rabi* sorghum

Source of variation	df	Days to 50% flowering	Plant height	Panicle length	Panicle breadth	Panicle weight	Grain yield/ plant	Test weight	Grain number/ panicle	Fodder yield/ plant	Harvest index
Replicates	1	7.11**	228.32	19.26*	9.33**	287.11	180.45	21.26 **	22.00	1406.25*	37.84
Crosses	17	9.93***	801.26**	10.12*	0.79	478.37**	409.93**	13.69***	5409.438***	1353.20***	307.11***
Line Effect	1	40.11*	102.23	3.36	2.96	802.15	767.29	22.17	11337.09	4203.36	1192.40
Tester Effect	8	11.42	1485.45**	14.18	0.63	269.17	283.28	13.53	3385.69	1301.40	174.96
Line×Tester Effect	8	4.67 **	204.45	6.91	0.68	647.09***	491.92**	12.79***	6692.22***	1048.736***	328.59***
Error	17	0.81	221.97	3.60	0.76	102.72	85.03	1.99	981.60	168.13	21.83
Total	35	5.42	503.52	7.22	1.02	290.45	245.57	8.23	3104.85	779.11	160.85

***, **, *- significance at .1%, 1% and 5% respectively

effects, while *sca* expresses from non-allelic interactions (Jinks, 1954). Estimating combining ability aids in predicting the performance of different lines in hybrid combinations. The combining ability analysis showed that among the female parents, 104 A demonstrated significant *gca* effects for days to fifty percent flowering and harvest index in the desirable direction. Among the male parents, RLT-9 displayed significant positive *gca* effects for plant height, panicle length, test weight, and fodder yield per plant. IC345188 and *Local bidar* exhibited significant *gca* effects for days to 50 per cent flowering in the desired direction (**Table 2**). Out of the eighteen hybrids, 104 A × RLT-9 exhibited significant positive *sca* effects for panicle weight, grain number panicle^{-1}, grain yield plant^{-1}, and harvest index. The hybrids104 A x C-43 and BJMS 1A x RLT-9 recorded significant *sca* effects for days to fifty percent flowering and test weight, respectively in the desired direction (**Table 3**). Therefore, out of the 18 hybrids, 104 A × RLT-9 is anticipated to be promising in terms of grain yield and other related yield components, making it suitable for use in heterosis breeding programs.

Understanding the nature and extent of gene action is crucial for assessing genetic potential of a population and determining the most suitable breeding methods for that population (Prabhakar *et al*., 2010). For all the traits studied, the predictability ratio (*gca/sca*) was less than one, indicating the pre-dominance of non-additive gene action in the inheritance of these traits. This suggested that *sca* alone offered greater predictability for improving those traits. These findings were in accordance with

Table 2. General combining ability effects of lines and testers for different characters in *rabi* sorghum

Line/Tester	Days to 50% flowering	Plant height	Panicle length	Panicle breadth	Panicle weight	Grain yield/ plant	Test weight	Grain number/ panicle	Fodder yield/ plant	Harvest index
104 A	-1.05**	-1.68	0.30	0.28	4.72	4.61	-0.78	17.74	-10.80**	5.75**
BJMS 1A	1.05**	1.68	-0.30	-0.28	-4.72	-4.61	0.78	-17.74	10.80**	-5.75**
IC286804	-0.19	7.75	-0.41	-0.31	-0.54	0.16	-2.21*	17.01	-9.47	2.73
IC289068	2.05*	12.67	-3.08**	0.23	-0.59	-1.73	2.28*	-27.83	9.02	-4.72
IC345188	-2.19**	-8.82	-1.25	-0.51	3.25	4.66	-0.94	20.60	-15.97*	7.57*
IC345195	0.30	9.59	-0.66	0.27	10.05	8.16	-1.42	35.83	4.27	1.43
IC345198	0.80	6.92	-0.50	-0.51	-2.69	-4.63	-1.45	-4.59	-12.47	1.71
Local Bidar	-3.19***	-0.65	-0.33	0.14	2.85	5.26	-0.93	21.51	-10.97	6.29
C43	0.05	-47.40***	3.16**	-0.14	-17.45*	-18.63**	0.41	-54.311*	-4.97	-8.52*
RLT-9	1.30	16.50*	2.41*	0.19	-4.25	-1.88	3.05**	-20.40	43.02***	-11.14**
SbABM	1.05	3.42	0.66	0.64	9.35	8.66	1.22	12.18	-2.47	4.63
CD 5% (Line)	0.72	6.33	0.91	0.40	7.07	5.55	0.80	18.96	6.18	3.36
CD 5% (Tester)	1.54	13.44	1.94	0.85	15.00	11.79	1.71	40.22	13.12	7.14

***, **, *- significance at 0.1%, 1% and 5% respectively

Table 3. Specific combining ability effects of hybrids for different characters in *rabi* sorghum

Crosses	Days to 50% flowering	Plant height	Panicle length	Panicle breadth	Panicle weight	Grain yield/ plant	Test weight	Grain number/ panicle	Fodder yield/ plant	Harvest index
104 A x IC286804	0.80	-7.64	0.02	-0.57	-2.37	0.58	2.24	-16.77	8.306	-1.78
104 A x IC289068	0.05	2.43	0.36	0.54	-4.12	-3.31	0.98	-15.53	6.306	-3.68
104 A x IC345188	1.30	6.43	0.69	-0.03	2.33	1.18	-0.08	11.25	10.80	-3.37
104 A x IC345195	0.80	-12.98	-1.22	-0.49	-9.57	-10.91	0.34	-34.09	1.05	-5.10
104 A x IC345198	0.30	-4.14	-0.72	-0.03	-11.52	-8.71	1.90	-42.91	11.30	-8.28
104 A x *Local Bidar*	-0.19	4.76	0.77	-0.20	-5.37	-4.21	1.01	-18.82	7.30	-3.90
104 A x C-43	-2.44*	9.18	2.44	0.58	10.74	8.88	-2.23	39.82	-11.19	12.20*
104 A x RLT-9	-0.19	-1.06	-2.13	-0.07	28.64*	24.73**	-2.82*	87.62**	-39.19***	18.65**
104 A x SbABM	-0.44	3.01	-0.22	0.29	-8.77	-8.21	-1.34	-10.55	5.30	-4.72
BJMS 1A x IC286804	-0.80	7.64	-0.02	0.57	2.37	-0.58	-2.24	16.77	-8.30	1.78
BJMS 1A x IC289068	-0.05	-2.43	-0.36	-0.54	4.12	3.31	-0.98	15.53	-6.30	3.68
BJMS 1A x IC345188	-1.30	-6.43	-0.69	0.03	-2.33	-1.18	0.08	-11.25	-10.80	3.37
BJMS 1A x IC345195	-0.80	12.98	1.22	0.49	9.57	10.91	-0.34	34.09	-1.05	5.10
BJMS 1A x IC345198	-0.30	4.14	0.72	0.03	11.52	8.71	-1.90	42.91	-11.30	8.28
BJMS 1A x *Local Bidar*	0.19	-4.76	-0.77	0.20	5.37	4.21	-1.00	18.82	-7.30	3.90
BJMS 1A x C-43	2.44*	-9.18	-2.44	-0.58	-10.74	-8.88	2.23	-39.82	11.19	-12.20*
BJMS 1A x RLT-9	0.19	1.06	2.13	0.07	-28.64*	-24.73**	2.82*	-87.62**	39.19***	-18.65**
BJMS 1A x SbABM	0.44	-3.01	0.22	-0.29	8.77	8.21	1.34	10.55	-5.30	4.72
CD 5%	2.18	19.01	2.74	1.20	21.22	16.67	2.42	56.88	18.56	10.10

***, **, *- significance at 0.1%, 1% and 5% respectively

Solanki *et al*. (2023), Srivastava *et al*. (2023), Kale (2011), Kenga *et al*. (2004) and Borikar *et al*. (2000). Promising parents with favourable *gca* effects and hybrids with high *sca* effects identified in the current study are presented in **Table 4** and these could be incorporated into hybrid breeding programs.

Heterosis is typically observed as an index to increase in yield, which is influenced by the contribution of various component traits. To evaluate the value of a cross, all yield-related component traits were analysed for heterosis manifestation. Grain yield is a complex quantitative trait that is influenced either directly or indirectly by many contributing factors. In this study, all the traits exhibited significant mid-parent heterosis in majority of the hybrids. The cross 104 A x IC345191 showed the highest standard heterosis for days to fifty per cent flowering in the desired direction. Early flowering and early maturing genotypes are generally preferred in *rabi* sorghum as they escape terminal drought, thereby avoiding yield loss and reduced grain size due to terminal drought stress. For test weight (1000 grain weight), BJMS 1A x RLT-9 cross exhibited standard heterosis over four checks except SPV 2217. Regarding fodder yield per plant, all the hybrids were significantly heterotic over the standard check. Though none of the hybrids displayed standard heterosis for grain yield per plant in the present investigation, the cross BJMS 1A x SbABM displayed better parent heterosis for grain yield plant^{-1}. Negative association between grain yield and fodder yield might have affected the performance of these hybrids. Similar findings were reported by Somegowda *et al*. (2021), Chavhan *et al*. (2022) and Nagesh Kumar *et al*. (2022). Enhancing sorghum grain yield is a significant challenge due to the involvement of numerous interconnected factors. Traits like panicle weight, grain number per panicle, and grain weight are controlled multiple genes (quantitative trait loci, QTLs) (Takanashi, 2023). Furthermore, these genes might have interacted with each other and the environment in complex ways, making breeding for high yield a nonlinear process. While traditional methods remain important, breeders now increasingly use graphical tools like PCA biplot analysis to visually represent crop breeding outcomes. PCA is a statistical technique that simplifies data by identifying key traits contributing to variation among genotypes. It reduces complexity and groups genotypes by maximizing variation. The mean values (1a), gca values of parents (1b) and sca values (1c) of hybrids by PCA biplot is presented in **Fig. 1**. As illustrated in PCA biplots, the top-performing parents with strong general combining ability were *Local Bidar* for days to fifty percent flowering, RLT 9 for plant height, test weight and fodder yield plant^{-1}, C 43 for panicle length, SbABM

Table 4. Promising parental lines based on *gca* effect and hybrids based on *sca* effect and their mean performance in *rabi* sorghum

S. No.	Characters	Best general combiner in desired direction	Best specific combiners in desired direction	*sca* effects of best specific combiners	Mean performance of best specific combiners
1	Days to 50% flowering	*Local bidar*	104 A × C-43	-2.44*	64.50
		IC345188	104 A × SbABM	-0.44	67.50
2	Plant height (cm)	RLT-9	BJMS 1A × IC345195	12.98	219.33
		IC289068	BJMS 1A × IC286804	07.64	212.66
3	Panicle length (cm)	C 43	104 A × C-43	2.44	25.17
		RLT 9	BJMS 1A × RLT 9	2.13	23.50
4	Panicle breadth (cm)	SbABM	104 A × C-43	0.58	6.25
		104 A	BJMS 1A × IC286804	0.57	5.50
5	Panicle weight (g)	IC345195	104 A × RLT 9	28.64*	85.00
		SbABM	BJMS 1A × IC345198	11.52	60.00
6	Grain yield per plant (g)	SbABM	104 A × RLT 9	24.73**	74.70
		IC345195	104 A × C-43	8.88	42.10
7	Test weight (g)	RLT 9	BJMS 1A × RLT 9	2.82	23.03
		IC289068	104 A × IC286804	2.24	15.60
8	Number of grains per panicle	IC345195	104 A × RLT 9	87.62	234.80
		Local bidar	BJMS 1A × IC345198	42.91	170.41
9	Fodder yield per plant (g)	RLT 9	BJMS 1A × RLT 9	39.19***	160.00
		BJMS 1A	BJMS 1A × C-43	11.19	84.00
10	Harvest index (%)	IC345188	104 A × RLT 9	18.65**	55.57
		104 A	104 A × C-43	12.20*	51.74

***, **, *- significance at 0.1%, 1% and 5% respectively

for panicle breadth and grain yield plant^{-1}, IC 345195 for panicle weight and number of grains panicle^{-1} (**Fig. 1b**).

Hybrids portraying high *sca* values for days to fifty per cent flowering were 104 A × C-43 and 104 A × SbABM. Further 104 A × RLT 9 exhibited significant positive *sca* effects for panicle weight, number of grains panicle^{-1}, grain yield plant^{-1}, and harvest index. The significance of a trait in relation to the principal components can be determined by the associated eigen values. The PCA results indicated that out of the 10 PCs, the first three components, each with eigen values greater than one, explained 80 per cent of the total variability (**Fig. 2a**), suggesting that the traits identified along these axes had a significant impact on the phenotype. The PC1 recorded 41 percent of the total variation and panicle weight, number of grains panicle^{-1}, and grain yield plant^{-1} contributed positively and significantly to PC1. Whereas test weight, fodder yield plant^{-1}, and days to fifty percent flowering contributed significantly to PC2 accounting for a total variability of 24 percent (**Fig. 2b**). These results were in line with the previous findings of Kashyap and Yadav (2020), Kavithamani *et al*. (2019), Abraha *et al*. (2016) and Nachimuthu *et al*. (2014). PCA had highlighted several key traits that played a significant role in classifying variation. These traits included panicle weight, number of grains panicle^{-1}, grain yield plant^{1}, test weight, fodder yield plant^{1}, and days to fifty percent flowering. The PCA results demonstrated a high level of genetic variation within the current study and identified the traits responsible for this diversity. Consequently, these findings were valuable for selecting parents to enhance various morphological traits analysed in the study.

Several factors continue to limit profitability of *rabi* sorghum including photoperiod sensitivity (Mukri *et al*., 2010), inadequate restorers, and low heterosis (Elangovan and Bahadure, 2013) in low-yielding hybrids during the *rabi* season. Continuous efforts are essential for making substantial progress in improving *rabi* sorghum.

In this study, the identified effective parents and hybrids could serve as a foundation for advancing *rabi* sorghum improvement. By exploiting both additive and non-additive genetic effects, it is possible to enhance traits more effectively. Analysis of variance showed significant differences across all studied traits. Specifically, line 104 A and tester RLT 9 were identified as best combiners, as well as the hybrids 104 A × RLT-9 and BJMS 1A × RLT-9, were identified as the best specific combiners for grain yield

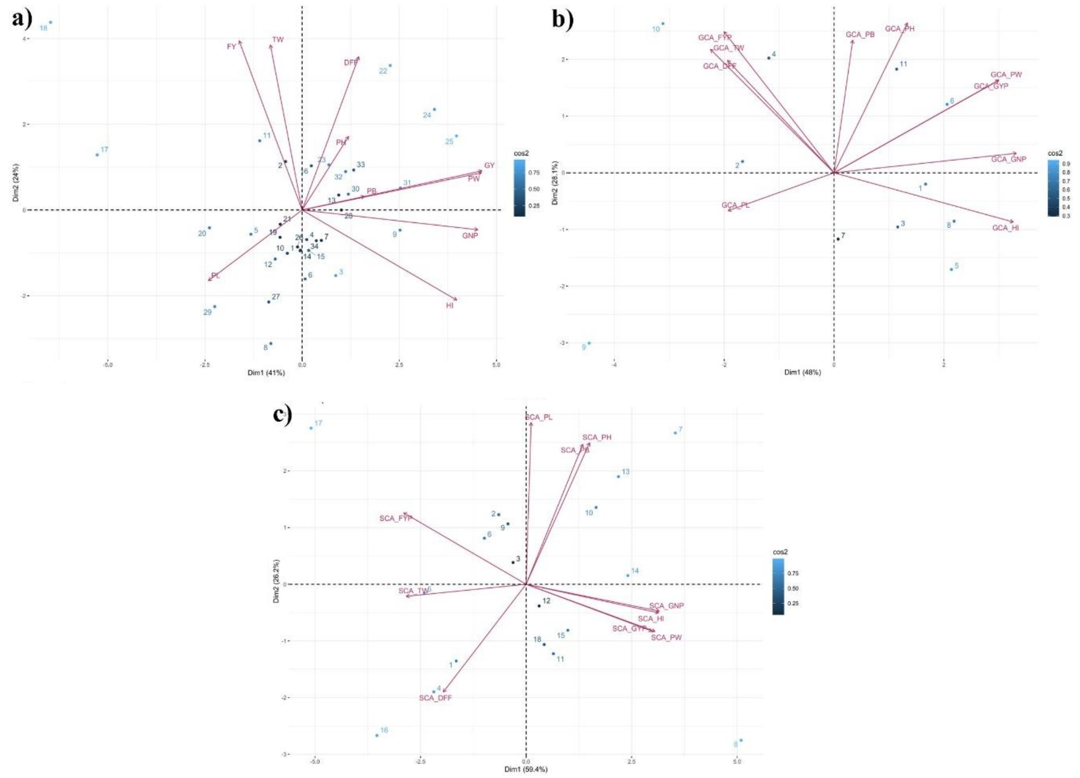

Fig.1. Biplot diagrams from principal component analysis (PCA) are presented for mean values (a), GCA values of parents (b), and SCA values of hybrids (c)

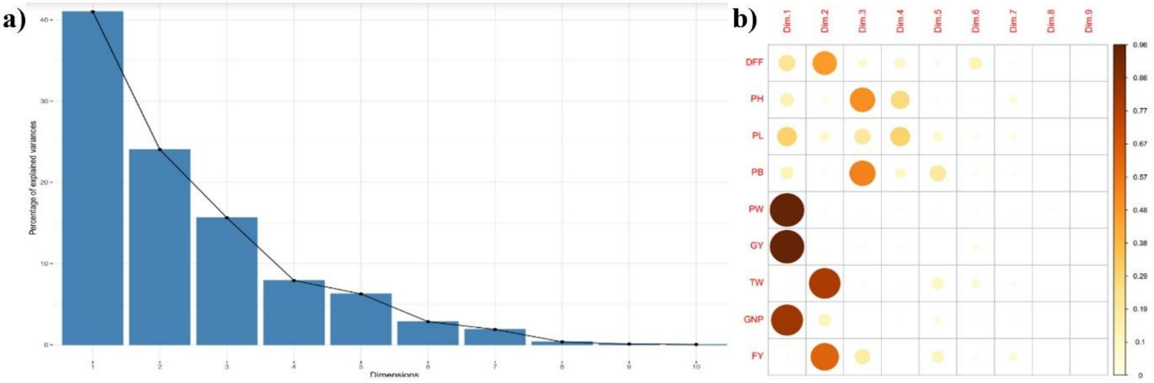

Fig. 2. a) Scree plot indicating eigen values variations, b) Correlation plot showing the contribution of each trait to principal components

and its attributes. BJMS 1A × Sb ABM was noted as the superior cross in terms of heterobeltiosis for grain yield per plant. The inheritance patterns revealed a predominance of non-additive gene action (dominance), suggesting that heterosis breeding would be advantageous for achieving rapid improvements in *rabi* sorghum. Additionally, PCA biplot analysis highlighted a high level of genetic variation and pinpointed the traits contributing to this diversity, making these findings valuable for selecting parents to enhance various morphological traits.

REFERENCES

Abraha, M.T., Shimelis, H., Laing, M. and Assefa, K. 2016. Performance of tef (*Eragrostis tef* (Zucc.) Trotter) genotypes for yield and yield components under drought-stressed and non-stressed conditions. *Crop Sci*., **56**(4): 1799–1806. [Cross Ref]

Anonymous. 2023. U.S. Department of Agriculture. Foreign Agricultural Service. World Agricultural Production. Available from: https://ipad.fas.usda.gov/

Arunachalam, V. 2001. Quantitative genetics from the perspective of Mendelian and molecular breeding. *Crop Improv.,* **28**(2): 129–156.

Biological Diversity Act and Biological Diversity Rules. 2004. National Biodiversity Authority, pp. 57.

Borikar, S.T., Jahagirdar, J.E. and Ambekar, S.S. 2000. Adoption in relation to seasons in sorghum. In: Vasantrao Naik Memorial National Agricultural Seminar. **8**: 18–19.

Chavhan, M., Jawale, L.N. and Bhutada, P.O. 2022. Correlation and path analysis studies in *kharif* sorghum (*Sorghum bicolor* L. Moench) inbred lines. *J. Pharmacogn. Phytochem*. **11**(4): 140–144. [Cross Ref]

Elangovan, M. and Bahadure, D.M. 2013. Combining ability of new parental lines for flowering, maturity, and grain yield in *rabi* sorghum. *Electron. J. Plant Breed*., **4**(3): 1214–1218.

Falconer, D.S. 1996. Introduction to Quantitative Genetics. Pearson Education India.

Jinks, J.L. 1954. The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. *Genetics,* **39**(6): 767. [Cross Ref]

Kale, P.B. 2011. Studies on combining ability of newly developed sorghum lines. M.Sc. (Agri.) Thesis. Dr. PDKV, Akola.

Kashyap, A. and Yadav, V.K. 2020. Principal component analysis and character association for yield components in rice (*Oryza sativa* L.) genotypes of salt tolerance under alkaline condition. *Int. J. Curr. Microbiol. App. Sci.,* **9**: 481–495. [Cross Ref]

Kavithamani, D., Yuvaraja, A. and Selvi, B. 2019. Principal component analysis and grouping of sorghum (*Sorghum bicolor* L. Moench) gene pool for genetic diversity. *Electron. J. Plant Breed.,* **10**(4): 1426–1434. [Cross Ref]

Kempthorne, O. 1957. An Introduction to Genetic Statistics. John Wiley and Sons, New York, pp. 457–471.

Kenga, R., Alabi, S.O. and Gupta, S.C. 2004. Combining ability studies in tropical sorghum (*Sorghum bicolor* L. Moench). *Field Crops Res,* **88**(2–3): 251–260. [Cross Ref]

Klein, R.R., Mullet, J.E., Jordan, D.R., Miller, F.R., Rooney, W.L., Menz, M.A. and Klein, P.E. 2008. The effect of tropical sorghum conversion and inbred development on genome diversity as revealed by high-resolution genotyping. *Crop Sci*., **48**: S–12. [Cross Ref]

Mukri, G., Biradar, B.D. and Sajjanar, G.M. 2010. Effect of temperature on seed setting behaviour in *rabi* sorghum (*Sorghum bicolor* L. Moench). *Electron. J. Plant Breed.,* **1**(4): 776–782.

Nachimuthu, V.V., Robin, S., Sudhakar, D., Raveendran, M., Rajeswari, S. and Manonmani, S. 2014. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. *Indian J. Sci. Technol.,* **7**(10): 1555–1562. [Cross Ref]

Nagesh Kumar, M.V., Ramya, V., Govindaraj, M., Dandapani, A., Maheshwaramma, S., Ganapathy, K.N. and Jagadeeshwar, R. 2022. India's rainfed sorghum improvement: three decades of genetic gain assessment for yield, grain quality, grain mold, and shoot fly resistance. *Front. Plant Sci.,* **13**: 1056040. [Cross Ref]

Prabhakar, M., Elangovan, and Raut, M.S. 2010. Stability of new varieties for yield components in *rabi* sorghum. *Indian J. Agric. Sci.,* **80**(2): 106–109.

Reddy, B.V.S., Sharma, H.C., Thakur, R.P., Ramesh, S., Rattunde, F. and Mgonja, M. 2006. Sorghum hybrid parents research at ICRISAT – strategies, status and impacts. *J. SAT Agric. Res.,* **2**(1): 1–24.

Sajjanar, G.M., Biradar, B.D. and Biradar, S.S. 2011. Evaluation of crosses involving *rabi* landraces of sorghum for productivity traits. *Karnataka J. Agri. Sci.,* **24**(2): 227–229.

Sandeep, N. and Biradar, B.D. 2020. Genetic variability studies involving maintainers on maldandi and milo source of male sterility in *rabi* sorghum [*Sorghum bicolor* (L.) Moench]. *Electron. J. Plant Breed.,* **11**(2): 645–649. [Cross Ref]

Solanki, R.S., Gami, R.A., Tiwari, K.K., Patel, R.N., Parmar, L.D. and Patel, P.S. 2023. Genetic analysis in sorghum for yield and shoot fly resistance attributes. *Electron. J. Plant Breed.,* **14**(4): 1354–1368. [Cross Ref]

Somegowda, V.K., Vemula, A., Naravula, J., Prasad, G., Rayaprolu, L., Rathore, A., Blümmel, M. and Deshpande, S.P. 2021. Evaluation of fodder yield and fodder quality in sorghum and its interaction with grain yield under different water availability regimes. *Curr. Plant Biol*., **25**: 100191. [Cross Ref]

Srivastava, A. N., Singh, K. P., Mishra, A.R. and Singh, H. G. 2023. Combining ability in sorghum. *Madras Agric. J.,* **66** (8): 546–550. [Cross Ref]

Takanashi, H. 2023. Genetic control of morphological traits useful for improving sorghum. *Breed. Sci.,* **73**(1): 57–69. [Cross Ref]