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Assessment of genetic variability, heritability and genetic advance in *kharif* sorghum [*Sorghum bicolor* (L.) Moench] crosses

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Abstract

The present study, entitled “Genetic Studies in Kharif Sorghum [*Sorghum bicolor* (L.) Moench],” was carried out to evaluate the magnitude of genetic variability and to estimate heritability and genetic advance among forty-five sorghum crosses along with one check variety. The experiment was conducted during the *kharif* season of 2025 following a Randomized Block Design with three replications. Data were collected for thirteen quantitative traits of agronomic importance. The analysis of variance indicated significant differences among the crosses for all the characters evaluated, demonstrating the existence of considerable genetic diversity within the experimental material. For each trait, the phenotypic coefficient of variation (PCV) exceeded the corresponding genotypic coefficient of variation (GCV), indicating the influence of environmental factors on trait expression. Among the characters studied, panicle weight exhibited comparatively high GCV and PCV values, reflecting substantial genetic and phenotypic variability for this trait. High broad-sense heritability estimates were recorded for all the characters under investigation. In particular, panicle length, panicle width, panicle weight, fodder yield per plant, number of grains per panicle, 1000-seed weight, and grain yield per plant showed high heritability in association with high genetic advance as a percentage of the mean. The combined occurrence of high heritability and high genetic advance suggests a substantial contribution of additive genetic effects in the inheritance of these traits. Consequently, these characters can serve as effective selection criteria in sorghum improvement programmes, offering considerable scope for genetic enhancement through selection.

Keywords: Sorghum, genetic variability, heritability, genetic advance, GCV & PCV

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is an important cereal crop cultivated widely in tropical and semi-arid regions of the world (Assefa *et al.*, 2020)^[3]. Ethiopia is considered a major centre of origin and genetic diversification of sorghum and remains an important reservoir of its genetic resources (Desalegn Yalew, 2022)^[7]. Globally, sorghum ranks fifth among cereals after wheat, maize, rice and barley, with a production of 57.30 million metric tons from 39.85 million hectares (FAO, 2023)^[9]. It is grown in more than 100 countries, with Africa accounting for nearly 70 per cent of the global area. Sorghum belongs to the family Poaceae and is a C4 crop with 2n = 20 chromosomes. It is predominantly self-pollinated and is well adapted to moisture-stressed and semi-arid environments. The crop is widely used as food, feed and fodder, particularly in Africa and Asia. In India, sorghum is an important dual-purpose crop, providing both grain and fodder. Its grain is used for food products and various industrial purposes, while the fodder is utilized as green fodder, hay and silage. Its nutritional value, dietary fibre and diverse applications further enhance its importance as a food and industrial crop.

Despite its adaptability and multipurpose utility, sorghum cultivation has declined due to the increasing adoption of alternative cereal and commercial crops. However, its drought tolerance and suitability to rainfed conditions make it valuable for sustainable agriculture. Genetic improvement is therefore essential to enhance productivity and economic returns from the crop.

Genetic variability is the basis of crop improvement and provides opportunities for selecting superior genotypes. Phenotypic and genotypic coefficients of variation (PCV and GCV) indicate the extent of variability, while heritability measures the proportion of phenotypic variation attributable to genetic differences. Genetic advance (GA) and genetic advance as percentage of mean (GAM) help predict the expected response to selection. The combined evaluation of heritability and genetic advance is useful for identifying traits governed predominantly by additive genetic effects.

Hence, the present investigation was undertaken to assess genetic variability, heritability and genetic advance for yield and its contributing traits among kharif sorghum crosses and to identify the potential of the evaluated material for further selection and genetic improvement.

Materials and Methods

The study involved forty-six sorghum entries, comprising forty-five crosses and one standard check. The experiment was conducted during the Kharif season of 2025-26 at the experimental farm of the Sorghum Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The experimental material was evaluated in a Randomized Block Design (RBD) with three replications. Inter- and intra-row spacing of 45 cm and 15 cm, respectively, was maintained to ensure uniform crop establishment and optimum plant growth. Throughout the crop season, all recommended agronomic and plant protection practices were adopted uniformly across the experimental units. Data were recorded for thirteen quantitative traits, including days to 50% flowering, days to maturity, plant height (cm), number of leaves, leaf length (cm), leaf width (cm), panicle length (cm), panicle breadth (cm), panicle weight (g), number of grains per panicle, fodder yield per plant (g), 1000-seed weight (g), and grain yield per plant (g). Observations were obtained from representative plants in each experimental unit, and trait-wise mean values were calculated for statistical analysis.

The experimental data were analyzed statistically to assess the significance of variation among the evaluated entries. Analysis of variance was performed according to the procedures outlined by Panse and Sukhatme (1967)^[17]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated following Burton and Devane (1953)^[6]. Broad-sense heritability was estimated as described by Allard (1960)^[1], while the magnitude of heritability and genetic advance was interpreted using the criteria proposed by Johnson *et al.* (1955)^[11]. The resulting genetic parameters were used to determine the extent of genetic variability and evaluate the prospects for selection and improvement of the traits under investigation.

Results and Discussion

The analysis of variance presented in Table 1 revealed statistically significant differences among the crosses for all thirteen quantitative traits evaluated in the present investigation. The significant genotypic variation observed for each character indicates that the experimental material was genetically diverse with respect to the traits under study. The existence of such variability is an essential prerequisite for effective selection, as the presence of differences among crosses enables the identification of

superior material for use in future breeding programmes. The significant variation observed in the present material therefore provides considerable scope for genetic improvement of *kharif* sorghum for important growth, yield and yield-associated characters. Similar evidence of significant variation among sorghum genotypes has been reported by Nikam *et al.* (2021)^[16], Kariyannavar *et al.* (2022)^[12], and Pugahendhi *et al.* (2023)^[18]. The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance (GA), and genetic advance as percentage of mean (GAM) are presented in Table 2. The PCV estimates were consistently higher than the corresponding GCV estimates for all the characters. This difference indicates that, although genetic factors contributed substantially to the observed variation, environmental conditions also had some influence on the phenotypic expression of the traits. The magnitude of the difference between PCV and GCV is useful in understanding the extent to which environmental variation contributes to the total phenotypic variability. In the present study, the differences between the two estimates were comparatively small for several characters, suggesting that the expression of these traits was influenced to a considerable extent by genetic factors. Such traits may consequently provide a more reliable response to selection under similar environmental conditions.

The highest levels of GCV and PCV were recorded for panicle weight, grain yield per plant, fodder yield per plant, number of grains per panicle, and 1000-seed weight. The relatively high variability associated with these characters indicates the presence of substantial genetic differences among the crosses. From a breeding perspective, traits exhibiting high genetic variability are particularly valuable because selection can be more effective when a wider range of genetic expression is available within the breeding material. The observed variation for these yield and yield-related traits therefore provides opportunities for selecting crosses with superior grain and fodder production potential. Similar results have been reported by Swamy *et al.* (2018)^[24], Shivaprasad *et al.* (2019)^[22], and Yali and Nepir (2026)^[25], who also observed greater variability for important yield-associated traits in sorghum.

Moderate estimates of GCV and PCV were observed for plant height, number of leaves, leaf length, leaf width, panicle length, and panicle breadth. The occurrence of moderate variability suggests that sufficient genetic differences were present for these traits, although the magnitude of variation was lower than that observed for panicle weight and other major yield-related characters. Such characters can still contribute effectively to selection when considered together with their heritability and genetic advance estimates. Moderate variability for these traits also suggests that gradual improvement may be possible through appropriate selection pressure over successive generations. The present findings are in accordance with the reports of Swamy *et al.* (2018)^[24], and Badhe *et al.* (2024)^[4].

In comparison, days to 50% flowering and days to maturity exhibited relatively lower estimates of GCV and PCV. The lower magnitude of variation suggests that the crosses possessed comparatively less diversity for these developmental characters. Since flowering and maturity are strongly influenced by genetic constitution as well as environmental conditions, the narrow range of variation observed in the present material may restrict the extent of

improvement achievable through selection. Nevertheless, the high heritability observed for these traits indicates that the available variation was largely transmissible and could still be utilized where specific flowering or maturity duration is desired. Similar comparatively low variability for phenological traits has been reported by Bahaa *et al.* (2020)^[5] and Netram *et al.* (2024)^[15].

High broad-sense heritability was recorded for all thirteen characters, including days to 50% flowering, days to maturity, plant height, number of leaves, leaf length, leaf width, panicle length, panicle breadth, panicle weight, number of grains per panicle, fodder yield per plant, 1000-seed weight, and grain yield per plant. High heritability indicates that a major proportion of the observed phenotypic variation was associated with genetic differences among the crosses. Therefore, the phenotypic performance of the crosses can provide useful information for selection, particularly when the traits are evaluated under comparable environmental conditions. However, heritability alone does not provide sufficient information regarding the expected response to selection because it does not distinguish adequately between additive and non-additive components of genetic variation. Hence, heritability estimates need to be considered together with genetic advance for making more meaningful conclusions regarding selection efficiency.

The high heritability estimates observed in the present investigation are supported by previous studies in sorghum. Shinde *et al.* (2010)^[21] reported high heritability for number of grains per panicle, while Santosh *et al.* (2020)^[20] observed high heritability for leaf width. Dhutmal *et al.* (2020)^[8] reported high heritability for fodder yield per plant, whereas Nikam *et al.* (2021)^[16] recorded high heritability for panicle length, panicle breadth, panicle weight, and 1000-seed weight. Similar findings for several growth and yield-related traits have also been reported by Angadi *et al.* (2025)^[2] and Lestari *et al.* (2026)^[14]. The consistency of these findings with earlier reports indicates that a considerable genetic component is associated with the inheritance of several agronomically important characters in sorghum.

High genetic advance as percentage of mean was recorded for plant height, number of leaves, leaf width, panicle length, panicle breadth, panicle weight, number of grains per panicle, fodder yield per plant, 1000-seed weight, and grain yield per plant. Genetic advance expressed as a percentage of the mean provides an estimate of the expected improvement that may be achieved through selection relative to the existing population mean. The high GAM values obtained for these traits indicate that substantial improvement could be expected by selecting superior individuals from the available genetic material. The presence of high GAM for several yield and yield-contributing traits is particularly encouraging because these characters are directly or indirectly associated with crop productivity.

The findings are comparable with those reported by Shinde *et al.* (2010)^[21], who observed high genetic advance as percentage of mean for panicle breadth. Swamy *et al.* (2018)^[24] reported high genetic advance for panicle length, panicle weight, 1000-seed weight, and grain yield per plant, while Khandebharad *et al.* (2022)^[13] recorded similar results for fodder yield per plant. Agreement with these earlier findings indicates that these traits may possess considerable exploitable genetic variation and can be considered

important targets in selection-oriented breeding programmes.

The combined interpretation of heritability and genetic advance provides a better understanding of the genetic basis of quantitative traits than either parameter considered independently. High heritability coupled with high genetic advance as percentage of mean was observed for plant height, number of leaves, leaf width, panicle length, panicle breadth, panicle weight, number of grains per panicle, fodder yield per plant, 1000-seed weight, and grain yield per plant. This combination generally suggests that the observed variability is associated to a considerable extent with additive genetic effects. Traits governed predominantly by additive genetic variation are expected to respond favourably to selection because desirable alleles can be accumulated through successive generations. Therefore, these characters can be given greater emphasis during the selection of superior sorghum crosses.

The presence of high heritability together with high GAM for panicle weight, number of grains per panicle, 1000-seed weight, grain yield per plant, and fodder yield per plant is of particular importance from a breeding standpoint. These traits showed not only considerable variability but also a greater likelihood of transmitting favourable performance to subsequent generations. Selection based on these characters may therefore result in appreciable genetic improvement. Similar conclusions regarding the usefulness of high heritability accompanied by high genetic advance have been reported by Shinde *et al.* (2010)^[21] for panicle breadth, Goswami *et al.* (2020)^[10] for panicle length, 1000-seed weight and grain yield per plant, and Rathod *et al.* (2023)^[19] for fodder yield and panicle weight.

The magnitude of variability, together with the estimates of heritability and genetic advance, provides useful information for determining the effectiveness of selection in the evaluated sorghum material. Traits with high variability and strong genetic control are generally more suitable for direct selection because environmental effects are relatively less likely to obscure the differences among crosses. In the present study, several growth and yield-associated characters fulfilled these criteria, indicating that the material possesses useful genetic resources for developing improved sorghum crosses. The results also suggest that selection should not be based solely on the magnitude of variability but should consider the heritability and expected genetic gain associated with individual traits.

Overall, the results obtained from the present investigation demonstrated the existence of substantial genetic diversity among the evaluated sorghum crosses. High variability was particularly evident for panicle weight, number of grains per panicle, 1000-seed weight, grain yield per plant, and fodder yield per plant. The high heritability estimates obtained for all the characters, along with high GAM for several important traits, further indicate favourable prospects for genetic improvement through selection. Among the characters studied, panicle weight, number of grains per panicle, 1000-seed weight, grain yield per plant, and fodder yield per plant may therefore be considered important selection criteria for identifying superior crosses. Emphasis on these characters in future breeding programmes could contribute to the development of sorghum crosses with improved grain and fodder productivity while utilizing the genetic variability present in the available material.

Table 1: Analysis of variances for thirteen characters in Sorghum

Sr.no.	Traits	Replication	Treatment	Error
1	Days to 50 % flowering	1.753	49.562**	5.000
2	Days to maturity	6.355	49.653**	3.347
3	Plant height(cm)	48.981	5221.068**	359.822
4	Number of leaves	0.176	12.984**	1.323
5	Leaf length(cm)	60.734	273.382**	32.471
6	Leaf width(cm)	0.025	7.174**	0.399
7	Panicle length (cm)	2.582	25.392**	2.76
8	Panicle width(cm)	0.006	3.929**	0.372
9	Panicle weight(g)	1.121	1185.557**	31.379
10	Number of grains per panicle	14945.05	234224.67**	11956.024
11	1000 seed weight(g)	4.333	108.195**	1.703
12	Fodder yield per plant(g)	5.978	8924.036**	275.002
13	Grain yield per plant(g)	42.865	498.908**	14.943

Table 2: Estimates of Genetic Variability Parameters for Yield and Yield-Associated Traits in Sorghum Crosses

Sr. No.	Characters	Range			Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (h ²) (BS) (%)	Genetic Advance (GA)	Genetic advance as percent of mean (GAM)
		Min	Max	Mean					
1	Days to 50 % flowering	57.83	78.00	68.8	5.50	6.65	68.24	6.44	9.35
2	Days to maturity	107.64	123.00	114.29	3.44	3.79	82.18	7.34	6.42
3	Plant height(cm)	155.57	328.63	243.19	16.55	18.30	81.83	75.01	30.85
4	Number of leaves	8.40	18.23	12.5	15.77	18.26	74.61	3.51	28.06
5	Leaf length(cm)	55.10	95.47	75.01	11.95	14.16	71.29	15.57	2.76
6	Leaf width(cm)	4.68	11.68	8.16	18.49	19.84	86.83	2.90	35.49
7	Panicle length (cm)	17.49	28.96	23.44	11.74	13.72	73.99	4.85	20.71
8	Panicle width(cm)	4.61	8.76	6.26	17.39	19.94	76.11	1.95	31.20
9	Panicle weight(g)	40.35	98.61	68.81	28.50	29.64	92.46	38.85	56.46
10	Number of grains per panicle	956.18	1724.37	1322.17	20.59	22.19	86.10	520.31	39.35
11	1000 seed weight(g)	14.15	35.29	24.64	24.18	24.75	95.42	11.99	48.66
12	Fodder yield per plant(g)	111.80	322.63	207.98	25.82	27.02	91.29	105.68	50.82
13	Grain yield per plant(g)	35.02	75.25	53.27	23.35	24.45	91.19	24.46	45.93

Conclusion

The present investigation revealed the presence of considerable genetic variability among the sorghum crosses evaluated, indicating sufficient diversity for the traits under study and providing scope for further genetic improvement. The phenotypic coefficient of variation (PCV%) was higher than the corresponding genotypic coefficient of variation (GCV%) for all the characters, indicating that environmental factors contributed to the phenotypic expression of the traits. However, the relatively small differences between PCV and GCV for several characters suggested that a major proportion of the observed variation was genetically controlled. Among the traits studied, panicle weight recorded comparatively high estimates of both GCV and PCV, indicating substantial genetic variation and greater possibilities for effective selection. High heritability combined with high genetic advance as percentage of mean was observed for number of leaves, plant height, leaf width, panicle length, panicle breadth, panicle weight, number of grains per panicle, fodder yield per plant, 1000-seed weight, and grain yield per plant. The occurrence of high heritability together with high genetic advance indicates the predominance of additive genetic effects in the inheritance of these characters and suggests that selection based on phenotypic performance would be effective. Therefore,

these traits can be considered important selection criteria for identifying superior genotypes and may be given due emphasis in future breeding programmes aimed at enhancing grain and fodder productivity in sorghum.

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