International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating: 5.29
IJABR 2025; 9(7): 924-927
www.biochemjournal.com
Received: 15-04-2025
Accepted: 19-05-2025

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Genetic variability studies in kharif sorghum [*Sorghum bicolor* (L.) Moench]

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DOI: https://www.doi.org/10.33545/26174693.2025.v9.i7l.4856

Abstract

The present investigation entitled "Genetic Variability Studies in Kharif Sorghum [*Sorghum bicolor* (L.) Moench]" was undertaken to assess the extent of genetic variability, heritability, and genetic advance among thirty-five sorghum genotypes, including one check. The experiment was conducted during Kharif 2024 using a Randomized Block Design with three replications. Observations were recorded on thirteen quantitative characters. Analysis of variance revealed significant differences among the genotypes for all the traits under study, indicating the presence of adequate genetic variability. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits. High values of GCV and PCV were observed for panicle weight.

The high estimates of heritability in broad sense were observed for all the traits studied. Traits such as panicle length, panicle breadth, panicle weight, fodder yield per plant, 1000-seed weight and grain yield per plant demonstrated high heritability coupled with high genetic advance as percentage of mean. This suggests the predominance of additive gene action and indicates that these traits have a high potential for improvement through selection.

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

Introduction

Sorghum is a major multipurpose crop in India, holding the fifth position worldwide among cereal food crops, following rice, wheat, maize, and barley in terms of production. It is grown widely in various countries, including those in Africa, Americas, Brazil, China, Russia, and Peru. In India, sorghum is mainly cultivated in regions like Maharashtra, Karnataka, Madhya Pradesh, Andhra Pradesh, and Rajasthan. It is an annual diploid crop with 20 chromosomes (2n = 20), and it belongs to the grass family *Poaceae* and the tribe *Andropogoneae*. It is typically self-pollinated but can show cross-pollination of up to 30%, classifying it as an often cross-pollinated crop. Its grains are used to produce bread, snacks, beer, as well as to extract wax, alcohol, starch, dextrose, syrup, edible oil, and other industrial by-products, making sorghum a highly versatile crop. It is widely known for its adaptability to diverse agro-climatic conditions. Physiologically, sorghum is a C4 plant and has high photosynthetic efficiency, moderate water-use efficiency, and a low respiration rate (Arunkumar, 2013) [3]. The productivity of sorghum is still lower than its potential (Gebregergs and Mekbib, 2020) [10]. The ideal areas for sorghum cultivation in India usually receive annual rainfall of 500 to 1000 mm, alongside temperatures between 26 °C and 32 °C. Due to its strong drought resilience, sorghum serves as an essential crop in regions with limited and unpredictable rainfall. Plains and plateaus located below 1000 metres in elevation offer ideal conditions for effective farming.

Sorghum is a resilient crop that plays a key role in ensuring food and fodder security, especially in rainfed and drought-prone regions. To enhance its yield and adaptability, it is important to assess the available genetic variability. A clear understanding of genetic differences, trait inheritance and their interrelationships is essential for effective crop improvement. The success of selection largely depends on the extent of variability within a population. Estimating genetic parameters that is variability, heritability and genetic advance provides valuable insights into the nature and magnitude of genetic variation. Therefore, the present study was undertaken to evaluate genetic variability, heritability, and genetic advance for yield and related traits in sorghum (*Sorghum bicolor* (L.) Moench) grown during the Kharif season.

Materials and Methods

The experimental material consisted of thirty-six sorghum entries, including thirty-five genotypes along with one check variety. The study was conducted during the Kharif season 2024-25 at the experimental field of the Sorghum Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, using a Randomized Block Design (RBD) with three replications. A spacing of 45 cm between rows and 15 cm between plants was maintained. All recommended agronomic and plant protection practices were followed to ensure healthy crop growth.

Data were collected on 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). The mean values of these observations were computed and analyzed statistically. Analysis of variance and summary statistics were done as per Panse and Sukhatme (1967) [19]. PCV and GCV were computed based on Burton and Devane (1953) [7], broad-sense heritability as per Allard (1960) [1], and heritability along with genetic advance were categorized according to Johnson *et al.* (1955) [12].

Results and Discussion

Table 1 presents the results of the analysis of variance, which revealed significant differences among all thirteen traits. This indicates the presence of substantial genetic variability in these traits under study. These findings are in agreement with those reported by Nikam *et al.* (2021) [18], kariyannanavar *et al.* (2022) [13], Khandebharad *et al.* (2022) [14], and Pugahendhi *et al.* (2023) [20]. The data were further analyzed to estimate the variability parameters, including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance as percent of mean. The results shown in Table 2 indicated that the genotypic coefficient of variation was lower than the phenotypic coefficient of variation for all traits, although the differences between them were relatively small. The small differences between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) suggest that the traits exhibit relative resistance to environmental fluctuations. High genotypic and phenotypic coefficient of variation were recorded for panicle weight, making it an ideal trait for direct selection. Comparable findings were noted by Swamy *et al.* (2018) [26], Shivaprasad *et al.* (2019) [24], and Kariyannanavar *et al.* (2022) [13]. Moderate GCV and PCV were observed for number of leaves, panicle length, panicle breadth, fodder yield per plant, 1000 seed-weight and grain yield per plant, suggesting potential for improvement through selection. These findings are supported by Shinde *et al.* (2010) [23] for number of leaves, panicle length, panicle breadth, and fodder yield per plant; Swamy *et al.* (2018) [26] and Nikam *et al.* (2021) [18] for 1000-seed weight; and Badhe *et al.* (2024) [4] for grain yield per plant. On the other hand, low GCV and PCV were noted for days to 50% flowering, days to maturity, plant height, leaf length, leaf width, and number of grains per panicle. These outcomes match findings Bahaa *et al.* (2020) [5] for plant height, leaf length, and leaf width, and by Netram *et al.* (2024) [17] for days to 50% flowering and days to maturity.

High heritability was recorded for traits such as days to 50% flowering, days to maturity, plant height, 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, suggesting the influence of additive gene action and the potential for effective selection. Similar findings had been reported by Shinde *et al.* (2010) [23] for number of grains per panicle; Santosh *et al.* (2020) [22] for leaf width; Dhutmal *et al.* (2020) [9] for fodder yield per plant; Nikam *et al.* (2021) [18] for panicle length, panicle breadth, panicle weight, and 1000-seed weight; and Angadi *et al.* (2025) [2] for days to 50% flowering, days to maturity, plant height, number of leaves, leaf length, and grain yield per plant.

Traits such as panicle length, panicle breadth, panicle weight, fodder yield per plant, 1000 seed-weight and grain yield per plant exhibited high genetic advance as percent of mean, indicating high genetic gain through selection. These findings are consistent with those reported Shinde *et al.* (2010) [23] for panicle breadth; Swamy *et al.* (2018) [26] for panicle length, panicle weight, 1000-seed weight, and grain yield per plant; and Khandebharad *et al.* (2022) [14] for fodder yield per plant., and others.

Overall, high heritability coupled with high genetic advance in key traits such as panicle length, panicle breadth, panicle weight, fodder yield per plant, 1000 seed-weight and grain yield per plant confirms the prevalence of additive gene action, making them highly responsive to selection and valuable for crop improvement. Similar findings had been reported by Shinde *et al.* (2010) [23] for panicle breadth; Goswami *et al.* (2020) [11] for panicle length, 1000-seed weight, and grain yield per plant; and Rathod *et al.* (2023) [21] for fodder yield and panicle weight.

Table 1: Analysis of variances for thirteen characters in Sorghum

Sr. No	Characters	Replication	Treatment	Error
1	Degree of freedom Days to 50% Flowering	2 3.593	35** 56.428**	70 2.069
2	Days to maturity	0.454	36.170**	1.463
3	Plant height (cm)	0.731	666.378**	2.398
4	Number of leaves	0.620	8.524**	1.439
5	Leaf length (cm)	0.778	55.038**	2.073
6	Leaf width (cm)	0.028	1.612**	0.016
7	Panicle length (cm)	2.234	38.968**	1.183
8	Panicle breadth (cm)	0.056	3.181**	0.034
9	Panicle weight (g)	5.528	440.114**	2.899
10	Number of grains per panicle	458.259	60,037.825**	1,083.021
11	Fodder yield (g)	7.442	710.442**	2.692
12	1000 seed weight (g)	0.069	68.304**	1.216
13	Grain yield per plant (g)	2.004	96.309**	1.064

Table 2: Parameters of genetic variability for yield and yield contributing characters in sorghum genotypes

Sr. No.	Characters	Range	Mean	GCV (%)	PCV (%)	Heritability (bs) (%)	Genetic Advance (GA)	Genetic Advance as percent of mean (%)
1	Days to 50% flowering	69.33-83.67	77.48	5.49	5.80	89.75	8.31	10.72
2	Days to maturity	113.67-127.33	120.32	2.83	3.00	88.77	6.60	5.49
3	Plant height (cm)	169.33-242.67	218.94	6.80	6.83	98.93	30.48	13.92
4	Number of leaves	9.33-17.67	13.66	11.25	14.28	62.13	2.50	18.27
5	Leaf length (cm)	61.33-81.33	70.50	5.96	6.30	89.49	8.19	11.62
6	Leaf width (cm)	5.70-8.60	7.71	9.46	9.60	97.04	1.48	19.19
7	Panicle length (cm)	19.07-33.03	26.57	13.36	13.97	91.41	6.99	26.31
8	Panicle breadth (cm)	5.10-8.70	6.91	14.84	15.07	96.88	2.08	30.08
9	Panicle weight (g)	33.00-70.33	52.33	23.07	23.30	98.05	24.63	47.05
10	No. of grains per panicle	1121.67-1702.67	1447.40	9.69	9.95	94.78	281.14	19.42
11	Fodder yield per plant (g)	111.93-169.53	138.89	11.06	11.12	98.87	31.46	22.65
12	1000 seed weight (g)	20.46-33.81	27.75	17.04	17.50	94.84	9.49	34.19
13	Grain yield per plant (g)	29.67-47.40	38.64	14.58	14.83	96.76	11.42	29.55

Conclusions

The present study revealed a considerable amount of genetic variability among the sorghum genotypes. The phenotypic coefficient of variation (PCV%) exceeded the genotypic coefficient of variation (GCV%) for all traits examined, indicating the impact of environmental influences. The character panicle weight showed comparatively higher estimates of both genotypic and phenotypic coefficients of variation, indicating a high level of variability and ample scope for effective improvement. High heritability coupled with high genetic advance as a percent of mean was observed for traits such as panicle length, panicle breadth, panicle weight, fodder yield per plan, 1000 seed-weight and grain yield per plant. This suggests the involvement of additive gene action and indicates that direct selection based on these traits would be effective for genetic improvement.

Acknowledgments

I sincerely thank Dr. V. V. Kalpande, my research guide, for his valuable guidance and support throughout the conduct of this research. I also extend my gratitude to the Sorghum Research Unit in Akola for providing the seed material and the necessary facilities essential for the successful completion of this research.

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