

INTEGRATED ASSESSMENT OF GENETIC VARIABILITY, TRAIT ASSOCIATIONS AND MULTIVARIATE ANALYSIS OF GENETIC DIVERSITY IN SORGHUM (*SORGHUM BICOLOR* (L.) MOENCH)

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ABSTRACT

Understanding genetic diversity and trait relationships is crucial for effective utilization of sorghum germplasm. Fifty genotypes were evaluated across *kharif* and summer seasons in an RBD with two replications for genetic variability, trait associations, and divergence. Pooled ANOVA revealed significant genotypic variation and genotype $\times$ environment interactions for key phenological and yield traits, indicating differential seasonal responses. Grain yield per plant exhibited the widest range 17.8 – 86.4 g plant⁻¹ and high genotypic and phenotypic coefficients of variation 29.07 % and 36.90%, respectively. High heritability coupled with high genetic advance was recorded for days to 50% flowering, panicle width, thousand-grain weight and grain yield, indicating selection potential. Grain yield was positively correlated with panicle weight, leaf width, thousand-grain weight, leaf length and panicle width, but negatively correlated with days to 50% flowering and maturity. Path analysis identified panicle weight (0.309) and leaf width (0.247) as the major positive direct contributors to yield. Four principal components with eigenvalues greater than one explained 60.75% of the variation. Ward's hierarchical clustering using Euclidean distance grouped the genotypes into six distinct clusters, with cluster V comprised maximum of 14 genotypes and cluster VI was found to be solitary. Clusters II and VI were superior for grain yield per plant, thousand grain weight and leaf width. Panicle weight, leaf width and earliness are identified as useful selection criteria and clusters II and VI as valuable sources for sorghum improvement. These findings aid in identifying promising traits and genotypes for developing high-yielding, early-maturing, and widely adaptable sorghum cultivars.

KEYWORDS: Sorghum germplasm, Genetic diversity, Cluster analysis, Pooled ANOVA, Path coefficient analysis.

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) is the world's fifth most significant cereal crop behind wheat, rice, corn and barely plays pivotal role in sustaining agricultural systems in arid and semi-arid regions, contribute significantly to global food and nutritional security (Gebre *et al.*, 2025). Sorghum is well adapted to high temperatures, drought conditions, and nutrient-deficient soils, making it a promising sustainable crop with significant potential for carbon sequestration and strengthening climate-resilient agricultural systems in climate-vulnerable regions (Taylor *et al.*, 2025; Engida 2023). It is grown in around 40.58 million hectares globally, with an average yield of 1.52 tonnes ha⁻¹ and an annual production of almost 62.42 million metric tonnes (USDA, 2025). The United States, Nigeria, Sudan, India, and Ethiopia are the main producers of sorghum. India alone contributes between 4 and 5 million tonnes per year (Aruna and Cheruku. 2019). Given the increasing demand for scarce freshwater resources, the expanding utilization of marginal agricultural land, and shifting climatic conditions, sorghum can significantly contribute to feeding the world's most vulnerable populations. This solid findings regarding sorghum make it an ideal plant species for examining evolutionary relationships among other grass species and for conducting diverse research under changing climatic conditions to guarantee food security (Hossain *et al.*, 2022).

Genetic variation is essential for the advancement of varieties in existing populations. An enhanced emphasis should be set for the collection and analysis of germplasm for existing and prospective plant breeding programme to mitigate genetic loss. Understanding the genetic heterogeneity of a crop generally assists the breeder in identifying desirable parental lines for the breeding scheme and enables gene introgression from distantly related genetic resources. The interbreeding of a wider variety of genotypes or accessions would generate superior hybrids capable of withstanding abiotic and biotic stressful conditions (Ahalawat *et al.*, 2018). In sorghum-based agricultural systems, utilizing genetic variation is essential for increasing productivity, stability, and resilience (Mwamahonje *et al.*, 2024). Due to the steady loss of native germplasm and the growing

dominance of newer hybrids, most of the genetic varieties found in traditional landraces of sorghum remains neglected. Therefore, it is essential to systematically conserve and characterize valuable genetic resources. These genetic resource management activities will increase the potential for improvement and expand the genetic base of breeding operations. The improved sorghum genotypes that were durable, high-yielding, and had desired characteristics for cultivation in the future (Sauer *et al.*, 2022). Flowering traits, plant stature, panicle dimensions, thousand grain weight and grain yield illustrate complex quantitative traits of yield that are significantly influenced by environmental factors and regulated by multiple genes. Identifying key factors that either directly or indirectly influence yield improvement requires understanding of the variability and underlying relationships among these traits (Somu *et al.*, 2025).

Sorghum landraces that have evolved through long-term cultivation under rainfed and resource-limited conditions (Anbazhagan *et al.*, 2022). These landraces possess valuable traits such as tolerance to drought, heat, and poor soil fertility, along with grain qualities preferred by local communities. They serve as an important source of genetic diversity and novel alleles for improving adaptability, stability, and yield (Marone *et al.*, 2021). Sorghum performance is greatly impacted by environmental variability, particularly in rainfed ecosystems, evaluating genotypes over different growing seasons is especially crucial. It is possible to evaluate the consistency of genotypic performance and to separate the impacts of environment and genotype-by-environment interaction by conducting studies in relation to successive seasons. This method provides a solid foundation for finding stable and high-yielding genotypes by ensuring a more accurate evaluation of genetic parameters such as genotypic variation, heritability, and genetic advance (Aruna *et al.*, 2021).

The development of locally tailored cultivars that combine resilience with high yield potential has become a major focus of sorghum improvement efforts in recent years. Therefore, a thorough evaluation of native germplasm is necessary to find important sources of variation for important agronomic and yield-related variables. Landraces from traditional sorghum-growing regions show significant morphological variability in terms of plant height, panicle length and width, seed colour, and grain size, which reflects adaptation to various microenvironments. Sorghum is primarily cultivated in India during the *kharif* and *rabi* seasons, which are well adapted to the prevailing agro-climatic conditions and agricultural seasons across the country. Subsequent to the rainy season, sorghum is commonly grown as a dual-purpose crop for its superior grain and forage yield. It acts as a significant source of nourishment and income for numerous families in India. A range of environmental, agricultural, and societal factors combine to impact sorghum productivity during the rainy season. India endures frequent droughts and considerable variations in rainfall, which can severely affect agricultural output and crop yields (Hayes *et al.*, 2023). Genetic diversity provides the fundamental basis for crop improvement through systematic hybridisation and selection. Additionally, landraces have distinctive trait combinations that provide improved grain quality and stress tolerance qualities that are crucial in situations with shifting climates and scarce resources (Pugahendhi *et al.*, 2023). Finding suitable donor lines for upcoming breeding initiatives requires a thorough assessment of genetic variability in morphological and yield-related variables among various sorghum germplasm. Breeders can create effective selection techniques by identifying genotypes with stable and desirable trait combinations. The creation of better cultivars suited to dryland environments is aided by these discoveries.

Genetic diversity must be characterized thorough statistical methods. Promising genotypes were chosen for next breeding initiatives using statistical techniques including multivariate analysis and D² statistics. According to Chatfield and Collins (1981), principal components analysis should not be deemed significant if their eigenvalues are less than one. Multivariate approaches can be excellent tools for evaluating genetic variance in order to create breeding programs that contain desirable diversity and more successful strategies for germplasm selection. Further information about the genetic diversity of sorghum genotypes must be obtained using multivariate studies. Accordingly, the present investigation was undertaken to evaluate and characterize diverse sorghum genotypes collected from established sorghum-growing regions across two successive growing seasons. Quantifying the degree of genetic variability, evaluating the heritable components for important morphological and yield-related variables, and identifying promising genotypes with high yield potential and consistent performance under changing environmental conditions were the goals. It is anticipated that the results of this study would offer sorghum enhancement initiatives meant to boost resilience and productivity in semi-arid areas.

MATERIALS AND METHODS

Experimental material

The experimental material consisted of 50 sorghum genotypes collected from farmer's field across diverse sorghum growing locations (Table 1) including two released check varieties *viz.*, Paiyur 2 and CO 4 from Department of Plant Breeding and Genetics, Madurai. Paiyur 2, is a short-duration, dual-purpose red sorghum variety from the Regional Research Station, Paiyur, TNAU, Coimbatore. It is rich in iron, zinc and B-complex vitamins, making it a healthy grain choice. CO 4 was released by Tamil Nadu Agricultural University, Coimbatore, is a high-yielding variety possessing compact panicles, bold grains, and wide adaptability for both grain and fodder purposes (TNAU, Agritech portal).

The field experiment was conducted during two consecutive growing seasons the *kharif* (June 2024 to October 2024) and Summer (February 2025 to June 2025) at Agricultural College and Research Institute, Madurai (9.9701°N latitude, 78.2041°E longitude), Tamil Nadu, India. The experiment was laid out in a Randomized

Block Design (RBD) with two replications. Each genotype was sown in two rows of 3 m length, maintaining a spacing of 45 cm between rows and 15 cm between plants within a row. Standard agronomic practices include recommended fertilizer application, irrigation scheduling, and plant protection measures, were uniformly followed to ensure optimal crop growth and minimize environmental variability.

Table 1: List of sorghum genotypes used for the experiment

S. No.	Genotype Code	Genotypes
1.	G1	ACM(RS)-22-001
2.	G2	ACM(RS)-22-002
3.	G3	ACM(RS)-22-003
4.	G4	ACM(RS)-22-004
5.	G5	ACM(RS)-22-005
6.	G6	ACM(RS)-22-006
7.	G7	ACM(RS)-22-007
8.	G8	ACM(RS)-22-008
9.	G9	ACM(RS)-22-009
10.	G10	ACM(RS)-22-010
11.	G11	ACM(RS)-22-011
12.	G12	ACM(RS)-22-012
13.	G13	ACM(RS)-22-013
14.	G14	ACM(RS)-22-014
15.	G15	Kallupatti local
16.	G16	Aviyoor local
17.	G17	Ramanujapuram local 1
18.	G18	Mangulam local
19.	G19	Kariyapatti local
20.	G20	Kodangipatti local
21.	G21	Mukkulam local
22.	G22	Pullur local
23.	G23	Ramanujapuram local 2
24.	G24	Andipatti local
25.	G25	Valayankulam local
26.	G26	Kovilangulam local 1
27.	G27	Kovilangulam local 2
28.	G28	Kovilangulam local 3
29.	G29	Kovilangulam local 4
30.	G30	Kovilangulam local 5
31.	G31	Kovilangulam local 6
32.	G32	Kovilangulam local 7
33.	G33	Kovilangulam local 8
34.	G34	Kovilangulam local 9
35.	G35	Kovilangulam local 10
36.	G36	Kovilangulam local 11
37.	G37	Kovilangulam local 12
38.	G38	Kovilangulam local 13
39.	G39	Kovilangulam local 14
40.	G40	Uthirakadikaval local
41.	G41	Perungamanallur local
42.	G42	Vettambadi local
43.	G43	Nachipudur local
44.	G44	Valavanthi combai local
45.	G45	Muthukapatti local
46.	G46	Allikundam local
47.	G47	Kottathur local
48.	G48	Thirumalaipatty local
49.	G49	Paiyur
50.	G50	CO4

Data collection

Observations were recorded on key developmental, morphological, and yield-contributing traits following the 2007 DUS guidelines issued by the Protection of Plant Varieties and Farmers' Rights Authority (PPV & FRA), Government of India, New Delhi. Data on morphological traits were recorded at the flowering stage, which included days to 50% flowering (days), plant height (cm), and stem girth (cm). Leaf morphological characteristics such as leaf length (cm), leaf width (cm), and number of leaves per plant were also measured at this stage. At physiological maturity, data were collected on reproductive and yield-related traits, including panicle length (cm), panicle width (cm), panicle weight (g), grain yield per plant (g), Days to maturity (days) and Thousand grain weight (g). These observations were recorded from five randomly selected plants in each genotype and the mean values were used for subsequent statistical analyses.

Statistical analysis

Data were recorded from five randomly selected plants of each genotype in every replication. The replicated data were subjected to analysis of variance (ANOVA) for each season as well as for pooled data across seasons using R software (version 4.0.3). The analyses were performed with the aid of the 'Metan' package (Olivoto and Lucio, 2020) to assess the extent of genetic variability among genotypes. From the pooled ANOVA table, genotypic variance (σ^2G), phenotypic variance (σ^2P), and error variance (σ^2E) were estimated for each trait. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated to quantify the relative magnitude of variability. Broad-sense heritability (h^2) was estimated as the ratio of genetic variance (σ^2G) to total phenotypic variance ($\sigma^2P = \sigma^2G + \sigma^2E$) following the method of Allard (1960). Pearson's correlation coefficients were computed among all pairs of traits to determine the strength and direction of genetic associations using the 'agricolae' package in R. Path coefficient analysis was carried out following the method of Wright (1921) as detailed by Dewey and Lu (1959) to partition the correlation coefficients into direct and indirect effects of individual traits on grain yield per plant. Further, Euclidean distance matrices were generated from standardized quantitative data to assess cluster analysis among genotypes. A dendrogram depicting the clustering pattern was constructed using the 'pheatmap' and 'ggplot2' packages in R to visualize relationships among genotypes and identify groups with similar phenotypic performance.

RESULTS

Pooled Analysis of Variance

The pooled analysis of variance revealed significant genetic variability among the evaluated 50 sorghum genotypes for most of the traits (Table 2). Genotypic effects were highly significant for days to 50% flowering, days to maturity, leaf length, number of leaves, panicle width, thousand-grain weight and grain yield per plant. Significant genotypic differences were also recorded for panicle length, stem girth and panicle weight, demonstrating the availability of adequate genetic variability for selection and crop improvement. However, plant height and leaf width exhibited non-significant genotypic effects.

The environmental effect was highly significant for days to maturity, panicle width and grain yield and significant for stem girth and panicle weight indicating that the expression of these traits was considerably influenced by seasonal environmental conditions. The genotype $\times$ environment ($G \times E$) interaction was highly significant for days to 50 % flowering, days to maturity, leaf width, panicle length, panicle width, panicle weight, thousand grain weight and grain yield per plant whereas stem girth exhibited a significant interaction. The relative performance of the genotypes for these traits varied between environments. In contrast, the non-significant $G \times E$ interactions observed for plant height, leaf length and number of leaves indicate that these traits were expressed relatively consistently across the evaluated environments (Table 2).

Similar findings were reported by Enyew *et al.* (2021), who observed substantial genotypic variation and environmental responses for grain yield and panicle weight in sorghum. They also reported considerable $G \times E$ interaction effects for these traits, whereas days to flowering, panicle length, panicle width and plant height were predominantly governed by genotypic variation. Likewise, Nagesh Kumar *et al.* (2021) reported that variation in grain and fodder yields was strongly influenced by genotype, environment and their interaction. These findings support the results of the present investigation and demonstrate the importance of evaluating sorghum genotypes across multiple seasons to distinguish stable genetic effects from environment-dependent responses.

The experimental coefficients of variation ranged from 2.24% for days to 50% flowering to 11.24% for Stem girth, indicating acceptable experimental precision and reliability of the recorded observations. Grain yield per plant exhibited a mean of 47.36 g plant⁻¹ with a CV of 9.35% (Table 2). The significant genotypic variability observed for most traits provides considerable scope for selection, while the pronounced $G \times E$ interaction for grain yield and several associated traits highlights the importance of stability analysis for identifying consistently high-yielding and environmentally adaptable sorghum genotypes. In the present investigation, a significant genotype $\times$ environment interaction was identified for most of the quantitative traits, which is in accordance with earlier reports in red sorghum where differential response of genotypes across environments were observed, though genotypic effects contributed a greater proportion (50.2%) of variation in grain yield were reported by Rajesh kumar *et al.* (2025).

Table 2: Combined ANOVA Revealing the Effects of Environment, Genotype, and Genotype × Environment Interaction on Yield and Associated Traits in Sorghum

	DFF	DM	PH	LL	LW	NL	PL	SG	PWI	PW	TGW	GYP
ENV	4.59	357.38**	0.59	6.85	16.53	7.00	0.009	117.508**	58.88*	29.71*	0.42	968.95*
REP(ENV)	3.02	1.17	1.46	1.07	3.48*	1.53	1.48	0.25	1.91	1.05	5.33**	0.84
GEN	11.99***	5.40***	12.36	3.83***	1.48	2.48***	2.17**	3.85***	2.39**	1.67*	5.56***	2.63***
GEN x ENV	18.22***	15.19***	0.36	1.14	11.61***	0.44	10.73***	8.63***	1.52*	15.88***	4.05***	23.62**
RESIDUALS	4.93	9.618	279.45	11.45	0.08	0.99	2.63	0.229	0.13	14.57	2.58	19.62
CV (%)	2.24	2.46	6.31	4.57	4.19	8.14	7.09	7.03	11.24	5.32	6.1	9.35
MEAN	99.17	125.92	265.05	74.06	6.98	12.22	22.91	6.81	3.22	71.8	26.38	47.36

*, ** and *** significant and highly significant at 0.05, 0.01 and 0.001 probability levels, respectively: REP-Replication; ENV-Seasons; GEN-Genotype; REP-Replications DFF-Days to 50% flowering(days); LL-Leaf length(cm); LW-Leaf width(cm); NL-Number of leaves; PL-Panicle length(cm); SG-Stem girth(cm); PWI-Panicle width(cm); PH-Plant height(cm); PW-Panicle weight(g); GYP-Grain yield per plant (g); TGW-Thousand grain weight(g); DM-Days to maturity(days)

Genetic Parameters for Quantitative Traits in Sorghum Germplasm

Considerable variability was observed among the evaluated sorghum genotypes for all quantitative traits (Table 3). Grain yield per plant exhibited the widest range (17.8–124.6 g), followed by plant height (192.2–307.4 cm) and panicle weight (39.6–113.96 g), indicating sufficient variability for selecting superior genotypes. Similar findings were reported by Gebregergs *et al.* (2020), who observed substantial variation in yield and yield-contributing traits and emphasized their importance in sorghum improvement. The phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all traits, indicating environmental influence on trait expression. Grain yield recorded high GCV and PCV values of 29.07 and 36.90%, respectively, demonstrating considerable variability and scope for yield improvement. Panicle width showed moderate GCV (17.46%) and high PCV (20.28%), while days to 50 % flowering, days to maturity, panicle length and thousand grain weight exhibited moderate GCV and PCV. Narrow differences between GCV and PCV for days to 50 % flowering, days to maturity, plant height, leaf length and thousand grain weight indicated comparatively low environmental influence, whereas wider differences for grain yield, panicle length, leaf width and panicle weight suggested greater environmental effects. Adedugba *et al.* (2023) similarly reported higher PCV than GCV for most sorghum traits, while Ngidi *et al.* (2024) observed high variability for grain yield and other productivity-related traits.

Broad-sense heritability ranged from 32.69% for leaf width to 91.66% for days to 50% flowering. High heritability was recorded for days to 50 % flowering (91.66%), thousand grain weight (82.04%), days to maturity (81.49%), plant height (80.50%), panicle width (74.08%), leaf length (73.95%) and grain yield (62.06%), indicating a substantial genetic contribution to their expression. Moderate heritability was observed for stem girth (58.18%), panicle length (54.10%), panicle weight (40.14%), number of leaves (39.99%) and leaf width (32.69%), suggesting that both genetic and environmental factors influenced these traits. These findings agree with Gebregergs *et al.* (2020), who reported high heritability for several yield-related traits in sorghum.

High heritability coupled with high genetic advance as a percentage of the mean was observed for days to 50 % flowering (91.66% and 31.32%), panicle width (74.08% and 30.95%), thousand grain weight (82.04% and 24.49%) and grain yield per plant (62.06% and 47.18%). This combination suggests the predominance of additive gene action and indicates that direct phenotypic selection would be effective for improving these traits. Ngidi *et al.* (2024) and Thamizhiniyan *et al.* (2022) also reported high heritability with high genetic advance for grain yield and biomass-related traits. In contrast, Adedugba *et al.* (2023) reported lower heritability for grain yield per plant because of its greater environmental sensitivity, which may be attributed to differences in genetic material and experimental environments. Days to maturity, plant height, panicle length, stem girth and panicle weight recorded moderate Genetic advance mean, suggesting a moderate response to selection. Leaf length showed high heritability but low Genetic advance mean, whereas leaf width and number of leaves exhibited moderate heritability with low Genetic advance mean, indicating limited improvement through direct selection.

The high heritability and genetic advance mean recorded for grain yield per plant, days to 50 % flowering, panicle width and thousand grain weight demonstrate that these traits are reliable selection criteria for developing high-yielding sorghum genotypes.

Table 3: Genetic Parameters for Quantitative Traits in Sorghum Germplasm

TRAIT	RANGE	MEAN	GCV (%)	PCV (%)	h^2 (%)	GAM
DFF	70-124	99.165	15.8788	16.5854	91.6609	31.3168
DM	96-154	125.92	10.0719	11.1571	81.4922	18.7299
PH	192.2-307.4	265.0516	6.4083	7.1422	80.5047	11.8446
LL	62.3-93.6	74.062	4.1189	4.7898	73.9505	7.2966
LW	4.9-8.6	6.9819	4.9757	8.7022	32.6923	5.8606
NL	10.1-15.4	12.2232	3.3242	5.2564	39.993	4.3305
PL	14-38.25	22.91	12.6117	17.147	54.0966	19.1084
SG	2.1-4.25	3.2165	8.1894	10.7363	58.1832	12.8682
PWI	3.02-10.6	6.8098	17.4579	20.2832	74.0821	30.954
PW	39.6-113.96	71.8012	8.6738	13.691	40.1367	11.32
TGW	19.9-42.6	26.382	13.1261	14.4917	82.041	24.4917
GYP	17.8-124.6	47.3616	29.0728	36.9044	62.0608	47.1805

GCV-Genotypic coefficient of variation; PCV-phenotypic coefficient of variation; h^2 -Hertiability; GAM-Genetic advance as percent of mean; GEN-Genotype; REP-Replications DFF-Days to 50% flowering(days); LL-Leaf length(cm); LW-Leaf width(cm); NL-Number of leaves; PL-Panicle length(cm); SG-Stem girth(cm); PWI-Panicle width(cm); PH-Plant height(cm); PW-Panicle weight(g); GYP-Grain yield per plant (g); TGW-Thousand grain weight(g); DM-Days to maturity(days)

Correlation analysis

Correlation analysis revealed significant associations between grain yield and several yield-contributing traits (Table 4). Grain yield per plant exhibited significant positive correlations with panicle weight (0.557***), leaf width (0.373***), thousand-grain weight (0.292***), leaf length (0.224**) and panicle width (0.142*). These associations indicate that improvement in panicle weight, grain weight and leaf characteristics may contribute to increased grain yield. Panicle weight was also positively correlated with thousand-grain weight (0.302***) and panicle width (0.284***), further demonstrating the importance of panicle characteristics in yield determination. Grain yield per plant showed significant negative correlations with days to 50% flowering (−0.515***), days to maturity (−0.364***) and stem girth (−0.141*). Days to 50% flowering was negatively correlated with panicle weight (−0.485***), thousand-grain weight (−0.446***), panicle width (−0.299***) and stem girth (−0.178*). Similarly, days to maturity exhibited negative associations with panicle weight (−0.389***), thousand-grain weight (−0.418***), panicle width (−0.324***) and stem girth (−0.334***). These findings suggest that early-flowering and early-maturing genotypes generally possessed better yield components and produced greater grain yield under the evaluated conditions.

Among the other associations, days to 50% flowering was strongly and positively correlated with days to maturity (0.752***), indicating that late-flowering genotypes tend to mature later. Leaf width was positively associated with panicle weight (0.241***), while plant height showed a positive association with panicle width (0.165*). Number of leaves exhibited a significant negative association with stem girth (−0.283***). Plant height, number of leaves and panicle length showed non-significant correlations with grain yield per plant, indicating their limited direct usefulness in yield-based selection. The positive association of grain yield with panicle weight and thousand-grain weight agrees with Raheem *et al.* (2020), who identified grain weight and panicle characteristics as important contributors to sorghum yield. Jafar *et al.* (2023) also reported a positive genotypic association between panicle width and grain yield. Similar significant relationships between panicle

traits and grain yield were reported by Kebede *et al.* (2025), Sujatha *et al.* (2025), Kavipriya *et al.*, (2020) and Somu *et al.* (2025). Akshitha *et al.* (2024) observed positive associations of fodder yield with leaf width and plant height, supporting the contribution of vegetative traits to crop productivity.

In contrast, Chipvongodze *et al.* (2025) reported positive associations of grain yield per plant with flowering time, maturity and panicle length. The difference from the present results may be attributed to variation in the genetic material, environmental conditions and crop duration. Overall, panicle weight, thousand-grain weight, leaf width and earliness emerged as important traits associated with grain yield. Therefore, selecting early-flowering and early-maturing genotypes with heavier panicles and bold grains may be effective for improving grain yield in sorghum.

Path analysis

Path coefficient analysis partitioned the correlations of component traits with grain yield into direct and indirect effects (Table 5). Among the traits studied, panicle weight exhibited the highest positive direct effect on grain yield per plant (0.309), followed by leaf width (0.247), leaf length (0.086), panicle length (0.072), number of leaves (0.067) and plant height (0.028). The strong positive correlation between panicle weight and grain yield ($r = 0.557$) was therefore mainly due to its positive direct effect, confirming panicle weight as an important selection criterion for yield improvement. Leaf width also showed a positive correlation with yield ($r = 0.373$), which was largely explained by its direct effect and a favourable indirect contribution through panicle weight (0.075).

Days to 50% flowering recorded the highest negative direct effect (-0.347), followed by stem girth (-0.183), days to maturity (-0.082), panicle width (-0.034) and thousand-grain weight (-0.007). The negative association of days to 50 % flowering with grain yield ($r = -0.515$) resulted from its negative direct effect and an additional negative indirect effect through panicle weight (-0.150). The negative correlation of days to maturity with yield ($r = -0.364$) was mainly due to its indirect effect through days to 50 % flowering (-0.262), together with its negative direct effect. These findings indicate that selection for early-flowering and early-maturing genotypes may improve grain yield under the evaluated conditions.

Although thousand-grain weight had a positive correlation with grain yield ($r = 0.292$), its direct effect was slightly negative (-0.007). Its positive association was mainly caused by favourable indirect effects through days to 50 % flowering (0.155) and panicle weight (0.094). Similarly, panicle width showed a positive correlation with yield ($r = 0.142$) despite its negative direct effect (-0.034), primarily because of positive indirect contributions through DFF (0.104) and panicle weight (0.088). Therefore, thousand grain weight and panicle width should be selected together with panicle weight rather than used independently. The strong direct contribution of panicle weight agrees with the observations of Raheem *et al.* (2020), Kebede *et al.* (2025), Sujatha *et al.* (2025) who emphasized the importance of panicle traits in sorghum yield determination. Jafar *et al.* (2023) reported that grain filling rate had the highest positive direct effect on grain yield followed by harvest index. Moderate positive direct effects were also observed for biomass yield, leaf area and thousand seed weight suggesting the possibility of using these traits as selection criteria for the improvement of grain yield. However, leaf width, panicle length and panicle width had negative direct effects though they were positively associated with yield, indicating that their correlations were primarily due to indirect effects via other yield contributing traits. Therefore, selection for heavier panicles, optimum leaf width, early flowering and early maturity may be an effective strategy for improving grain yield in the evaluated sorghum genotypes. These negative effect of panicle width were supported by Somu *et al.* (2025), Verma *et al.* (2016) and Khadakhbavi *et al.* (2017).

Table 4: Correlation coefficient among quantitative traits across seasons

Trait	DFF	DM	PH	LL	LW	NL	PL	SG	PWI	PW	TGW	GYP
DFF	1.000	0.752***	0.104NS	-0.203**	-0.046NS	0.103NS	0.252***	-0.178*	-0.299***	-0.485***	-0.446***	-0.515***
DM		1.000	0.091NS	-0.087NS	0.025NS	0.171*	0.168*	-0.334***	-0.324***	-0.389***	-0.418***	-0.364***
PH			1.000	-0.062NS	0.041NS	0.090NS	-0.050NS	-0.110NS	0.165*	0.036NS	0.094NS	0.017NS
LL				1.000	0.080NS	-0.004NS	0.033NS	0.020NS	0.007NS	0.141*	0.020NS	0.224**
LW					1.000	0.073NS	0.052NS	-0.098NS	-0.088NS	0.241***	0.100NS	0.373***
NL						1.000	-0.002NS	-0.283***	0.035NS	-0.072NS	-0.025NS	0.066NS
PL							1.000	-0.038NS	-0.069NS	-0.089NS	0.121NS	-0.034NS
SG								1.000	0.120NS	0.017NS	0.081NS	-0.141*

PWI									1.000	0.284***	0.144*	0.142*
PW										1.000	0.302***	0.557***
TGW											1.000	0.292***
GYP												1.000

DFF-Days to 50% flowering(days); LL-Leaf length(cm); LW-Leaf width(cm); NL-Number of leaves; PL-Panicle length(cm); SG-Stem girth(cm); PWI-Panicle width(cm); PH-Plant height(cm); PW-Panicle weight(g); GYP-Grain yield per plant (g); TGW-Thousand grain weight(g); DM-Days to maturity(days)

Table 5: Path coefficient analysis indicating direct and indirect effects of quantitative effects on grain yield per plant

Trait	DFF	DM	PH	LL	LW	NL	PL	SG	PWI	PW	TGW
DFF	-0.347	-0.0623	0.003	-0.0176	-0.0114	0.0069	0.0182	0.0326	0.0104	-0.1501	0.0035
DM	-0.2615	-0.082	0.0026	-0.0075	0.0061	0.0115	0.0121	0.0613	0.0112	-0.1204	0.0033
PH	-0.0361	-0.0075	0.028	-0.0054	0.0102	0.006	-0.0036	0.0202	-0.0057	0.0113	-0.0007
LL	0.0704	0.0072	-0.0018	0.086	0.0197	-0.0003	0.0024	-0.0038	-0.0002	0.0435	-0.0002
LW	0.016	-0.002	0.0012	0.0069	0.247	0.0049	0.0038	0.018	0.003	0.0748	-0.0008
NL	-0.0359	-0.0142	0.0026	-0.0004	0.018	0.067	-0.0001	0.0519	-0.0012	-0.0224	0.0002
PL	-0.0875	-0.0139	-0.0014	0.0029	0.0129	-0.0001	0.072	0.007	0.0024	-0.0276	-0.0009
SG	0.0617	0.0277	-0.0031	0.0018	-0.0244	-0.019	-0.0027	-0.183	-0.0041	0.0054	-0.0006
PWI	0.104	0.0269	0.0047	0.0006	-0.0218	0.0023	-0.005	-0.0219	-0.034	0.0878	-0.0011
PW	0.1685	0.0322	0.001	0.0122	0.0598	-0.0048	-0.0064	-0.0032	-0.0098	0.309	-0.0024
TGW	0.1549	0.0346	0.0027	0.0018	0.0247	-0.0017	0.0087	-0.0149	-0.005	0.0936	-0.007

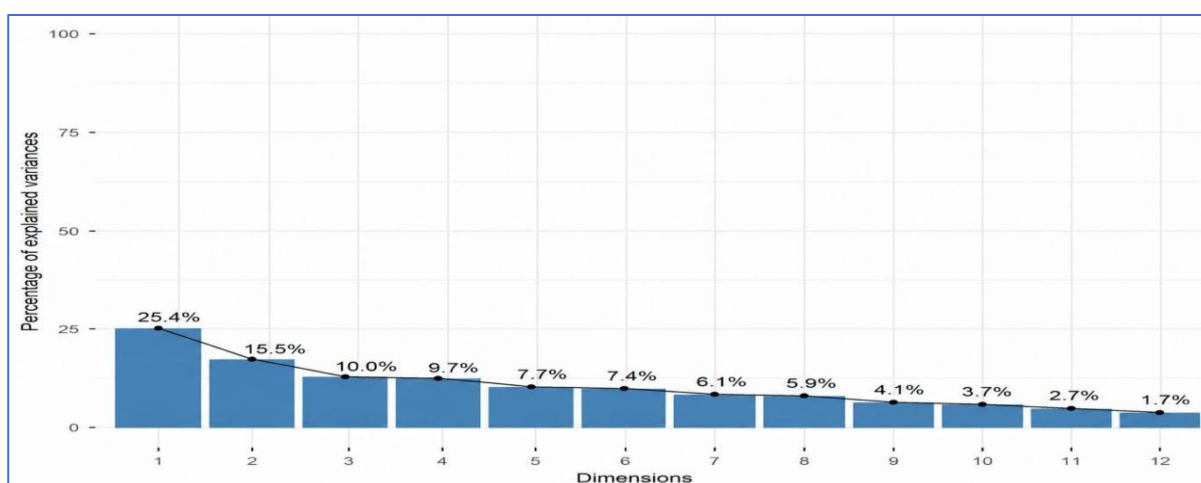
DFF-Days to 50% flowering(days); LL-Leaf length(cm); LW-Leaf width(cm); NL-Number of leaves; PL-Panicle length(cm); SG-Stem girth(cm); PWI-Panicle width(cm); PH-Plant height(cm); PW-Panicle weight(g); GYP-Grain yield per plant (g); TGW-Thousand grain weight(g); DM-Days to maturity(days)

Principal Component Analysis

Table 6: Principal component analysis revealing major sources of variation among quantitative traits

Component	Eigen value	Proportion of Variance	Cumulative. Proportion
PC1	3.053	25.4416	25.4416
PC2	1.8654	15.5454	40.987

PC3	1.2059	10.0494	51.0364
PC4	1.1656	9.7137	60.7502
PC5	0.9215	7.6791	68.4293
PC6	0.8879	7.3988	75.8281
PC7	0.7348	6.123	81.9511
PC8	0.7131	5.9424	87.8935
PC9	0.4889	4.074	91.9676
PC10	0.4437	3.6973	95.6649
PC11	0.3218	2.6817	98.3466
PC12	0.1984	1.6534	100



Principal component analysis was performed to summarize the variability among the sorghum genotypes and identify the major components contributing to genetic diversity (Table 6). Based on eigenvalues greater than one, the first four principal components were retained. Together, these components explained 60.75% of the total variation. PC1 contributed the highest proportion of variation (25.44%), followed by PC2 (15.55%), PC3 (10.05%) and PC4 (9.71%). The first two components jointly accounted for 40.99% of the variation, while the first three explained 51.04%. The remaining components individually contributed less than 10%, indicating their comparatively lower discriminatory importance. The concentration of variation within the first four components suggests the presence of considerable diversity among the evaluated genotypes. The scree plot and PCA biplot represent the percentage of variance explained by principal components (Fig 3 and Fig4). Gebre *et al.* (2025) similarly reported that the first three principal components accounted for 59.0% of the variation in qualitative traits, while the first six explained 76.5% of the variation in quantitative traits. Their cluster analysis also separated the genotypes into distinct and divergent groups, demonstrating the usefulness of multivariate methods for selecting genetically diverse parental materials. Premkumar *et al.* (2022) reported that the retained principal components collectively explained 74.15% of the total variation and identified ICSB 541, ICSV 15013, ICSB 52, ICSB 24001 and Macia as promising genotypes for panicle width, seed weight and grain yield. They also observed the greatest divergence between Clusters II and III, indicating the potential value of genetically distant genotypes in hybridization programmes. Enyew *et al.* (2022) likewise reported substantial genetic diversity among sorghum landraces and identified stable, high-yielding genotypes suitable for breeding. Overall, the first four principal components captured a major proportion of the variability present in the studied material. Therefore, the traits showing high loadings in these components can be considered important for genotype differentiation and the selection of diverse parents in sorghum improvement programmes.

contrast, Cluster V exhibited the lowest grain yield per plant (37.95 g) and was relatively late maturing, while the wide differences in cluster means indicate substantial phenotypic diversity that could be effectively exploited through selection and hybridization between contrasting clusters. Similarly, in the accordance with Kebede *et al.*, 2025, 158 Ethiopian sorghum genotypes were grouped into four distinct clusters based on drought-associated root and shoot traits, confirming substantial genetic diversity. Genotypes from divergent clusters could serve as promising parents for developing drought-tolerant sorghum cultivars.

Table 7: Cluster analysis of genotypes for different quantitative traits

Clusters	Genotype
1	ACM-RS-22-001, ACM-RS-22-002, ACM-RS-22-003, ACM-RS-22-004, ACM-RS-22-005, C04
2	ACM-RS-22-006, ACM-RS-22-007, ACM-RS-22-008, ACM-RS-22-009, ACM-RS-22-010, ACM-RS-22-0012, ACM-RS-22-013, ACM-RS-22-014
3	Kallupatti local, Ramanujapuram local 1, Kariyapatti local, Mukkulam local, Andipatti local, Kovilangulam local 11, Kovilangulam local 12, Kovilangulam local 14, Uthirakadikaval local, Allikundam local, Paiyur
4	Aviyoor local, Valayankulam local, Kovilangulam local 2, Kovilangulam local 1, Kovilangulam local 3, Kovilangulam local 5, Kovilangulam local 7, Kovilangulam local 6, Kovilangulam local 4
5	Mangulam local, Kondangipatti local, Ramanujapuram local 2, Kovilangulam local 8, Kovilangulam local 9, Kovilangulam local 10, Kovilangulam local 13, Perungamanallur local, Nachipudur local, Valavanthi combai local, Muthukapatti local, Allikundam local, Kottathur local, Thirumalaipatty local
6	Pullur local

Table 8: Cluster mean values for quantitative traits among sorghum genotypes

Clusters	DFF	DM	PH	LL	LW	NL	PL	PWI	SG	PW	TGW	GYP
I	77.38	109.21	244.04	75.16	6.36	11.82	22.02	7.12	3.54	76.55	28.76	60.16
II	76.78	104.50	268.03	75.01	7.51	12.23	21.21	7.79	3.32	86.92	30.27	77.09

III	102.77	133.30	271.77	74.73	6.88	12.71	19.98	6.32	2.94	64.69	25.00	37.08
IV	109.04	133.61	250.95	73.72	7.30	11.83	23.76	5.65	3.52	61.22	23.57	52.29
V	112.20	135.41	272.95	72.61	6.74	12.22	25.14	7.31	3.06	62.17	25.29	49.95
VI	117.00	134.25	284.26	78.00	7.68	12.64	37.25	7.24	2.66	72.53	32.70	62.63

DFF-Days to 50% flowering(days); LL-Leaf length(cm); LW-Leaf width(cm); NL-Number of leaves; PL-Panicle length(cm); SG-Stem girth(cm); PWI-Panicle width(cm); PH-Plant height(cm); PW-Panicle weight(g); GYP-Grain yield per plant (g); TGW-Thousand grain weight(g); DM-Days to maturity(days)

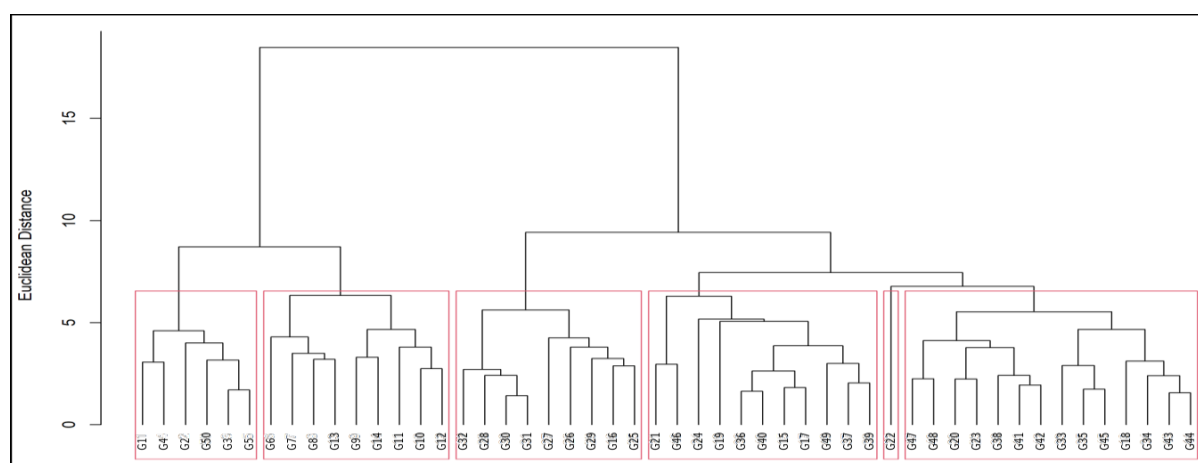


Fig 5: Hierarchical cluster analysis of sorghum genotypes based on quantitative traits

The clustered heatmap presented in Fig. 4 illustrated standardized variation in quantitative traits among the sorghum genotypes. Genotypes possessing similar trait-expression patterns were grouped together, whereas those with contrasting flowering, maturity, vegetative growth, panicle morphology and yield characteristics were separated. The hierarchical dendrogram in Fig. 5 further summarized the relative similarity among the genotypes and clearly separated them into six major clusters. Genotypes connected by shorter branches were comparatively similar, whereas those separated by longer branches exhibited greater divergence. Singh *et al.* (2015) likewise demonstrated the usefulness of hierarchical clustering and similarity indices in classifying sorghum genotypes and identifying parental materials for hybridization. The cluster mean analysis indicated that no single cluster was superior for all the quantitative traits. Cluster II was the most desirable source for early flowering, early maturity, high panicle weight and high grain yield, whereas Cluster VI was superior for panicle length and thousand-grain weight. Cluster I also combined earliness with greater leaf length, stem girth and comparatively high grain yield. Therefore, crossing superior genotypes from Cluster II with Pullur local from Cluster VI may provide opportunities to combine earliness and high panicle weight with long panicles and bold grains. Genotypes from Cluster I could also be incorporated into crossing programmes aimed at improving earliness and panicle productivity. The involvement of genetically diverse parents in hybridization programmes can increase the probability of obtaining high heterotic responses and desirable transgressive segregants through the recombination of favourable alleles. The importance of utilizing diverse parental materials to generate superior sorghum varieties has also been documented by Seetharam and Ganesamurthy (2013), Adugna (2014) and Derese *et al.* (2018) However, Behl *et al.* (1975) observed that greater heterosis may occur within an optimum or limited range of parental diversity, indicating that maximum divergence alone does not necessarily ensure superior hybrid performance. Consequently, the selection of parents should consider genetic divergence together with cluster mean performance, individual genotype performance and the breeding objective. Substantial quantitative-trait diversity among the evaluated sorghum genotypes. Cluster II contained the most promising early-maturing and high-yielding materials, while the monotypic Cluster VI represented a distinct source of long panicles, high thousand-grain weight and comparatively high grain yield. Hybridization among agronomically superior genotypes from these contrasting clusters may broaden genetic variability and facilitate the recovery of desirable recombinants for grain-yield improvement in sorghum.

CONCLUSION

The present study revealed substantial genetic variability among the 50 sorghum genotypes evaluated across two seasons. Significant genotypic and genotype $\times$ environment interaction effects demonstrated the influence of genetic constitution and seasonal conditions on trait expression. High heritability coupled with high genetic advance for days to 50% flowering, panicle width, thousand-grain weight and grain yield indicated good scope for selection. Grain yield was positively associated with panicle weight, leaf width and thousand-grain weight, whereas its negative association with flowering and maturity emphasized the advantage of earliness. Path analysis identified panicle weight and leaf width as the principal traits exerting positive direct effects on grain yield. Principal component analysis retained four components that collectively explained 60.75% of the total variation. Ward's hierarchical clustering based on Euclidean distance classified the genotypes into six genetically distinct clusters. Clusters II and VI were superior for grain yield per plant, thousand grain weight and leaf width. The distinct characteristics of these clusters indicate their potential value in hybridization programmes. Crossing superior genotypes from Clusters II and VI may combine earliness, high yield and desirable panicle traits. The identified traits and divergent genotypes provide valuable genetic resources for developing high-yielding and adaptable sorghum cultivars.

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