P.ISSN: 0971-8184 II E ISSN: 0976-1926
DOI: https://doi.org/10.56093/ijpgr.v39i1.176030

Indian Journal of
Plant Genetic Resources

RESEARCH ARTICLE

Exploring Genetic Diversity and Yield-Contributing Traits in Sorghum (*Sorghum bicolor*) using D^2 Statistics and Principal Component Analysis

Anamika Dhar[1*], B Meena Kumari[2], D Kavithamani[2], P Meenakshi[3] and GG Kavithashree[4]

Abstract

Sorghum is a vital cereal crop with immense potential for grain and fodder, especially in semi-arid regions. This study evaluated the genetic diversity among 96 sorghum genotypes using Mahalanobis D^2 statistics and principal component analysis to identify key traits contributing to yield and other agronomic characteristics. The field experiment was conducted at the Millet breeding station, TNAU, Coimbatore, with two replications. The genotypes were grouped into 10 clusters, with distinct clusters showing unique trait combinations valuable for targeted breeding goals. For example, genotypes such as IS 28517, IS 29114, and TNSS 223 are ideal for biomass production because of their tall, late-maturing traits, whereas IS 10939 and AS 3883 are promising for high seed weight and high yield, respectively. Principal component analysis (PCA) identified traits such as leaf width, panicle weight, plant height, and flag leaf length as major contributors to genetic variability. The distribution of genotypes in the PCA biplot highlighted specific associations between yield-related traits and genotype groupings, offering insights for selecting parents for hybridization. This research provides valuable information for sorghum breeding programs aimed at enhancing productivity and resilience in dryland regions, thereby supporting food security and sustainable agriculture.

Keywords: Genetic diversity, Genetic resources, Hybridization, Multivariate analysis, Sorghum

[1]Department of Genetics and Plant Breeding, TNAU, Coimbatore, Tamil Nadu, 641003, India.

[2]Department of Millets, TNAU, Coimbatore, Tamil Nadu, 641003, India.

[3]Department of Biochemistry, TNAU, Coimbatore, Tamil Nadu, 641003, India.

[4]Department of Food Science and Nutrition, TNAU, Coimbatore, Tamil Nadu, 641003, India.

***Author for correspondence:**
meghakvkls@gmail.com

Received: July 20, 2025
Revised: February 9, 2026
Accepted: February 12, 2026

How to cite this article: Dhar A, BM Kumari, D Kavithamani, P Meenakshi and GG Kavithashree (2026) Exploring Genetic Diversity and Yield-Contributing Traits in Sorghum (*Sorghum bicolor*) using D^2 Statistics and Principal Component Analysis). *Indian J. Plant Genet. Resour*. 39(1): 92-99.

DOI: https://doi.org/10.56093/ijpgr.v39i1.176030

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench], the fifth most vital cereal crop worldwide, originated and was domesticated in northeastern Africa, with some of the earliest evidence of its domestication found in eastern Sudan around the 4th millennium BC. From there, it spread to other regions like India, China and eventually to North America. This widely cultivated species has been classified into five primary races—bicolor, durra, kafir, guinea, and caudatum—and ten intermediate races, reflecting its broad genetic diversity and adaptability (Harlan and de Wet, 1972). In India, sorghum is grown during both the *kharif* and *rabi* seasons, serving a dual purpose by providing both grain and fodder to farming communities (Swamy *et al*., 2018). Rabi-season sorghum is particularly valued for its superior grain quality, as it is primarily grown for human consumption and has a higher market price than kharif sorghum (Prasad *et al*., 2020). Sorghum is the fifth most significant cereal crop in India, after wheat, rice, maize and pearl millet and sorghum is cultivated extensively in semiarid, rainfed regions. The major sorghum-producing states include Maharashtra, Karnataka, Tamil Nadu, Rajasthan, and Madhya Pradesh. Sorghum displays substantial variability in plant morphology, panicle and grain characteristics, and physiological responses to selection pressures and is strongly influenced by environmental factors (Ezeaku *et al*., 1997). Given that rice and wheat are staple foods for much of the global population, sorghum, as a C4 crop, holds great potential for dryland agriculture, optimizing dryland usage and increasing farmer incomes (Dhar *et al*., 2024). Known as "the king of coarse cereals" and a "nutri-cereal," sorghum has a remarkable nutritional profile and is rich in unsaturated fats, proteins, fibre, and minerals such as potassium, phosphorus, calcium, and iron (Thant *et al*., 2020).

Understanding the genetic diversity of a crop is crucial for breeders, as it allows for the selection of appropriate parental lines for breeding programs and the introduction of genes from more distantly related germplasms (Bucheyeki *et al*., 2009). In general, parents that exhibit greater genetic divergence are expected to produce hybrids with greater heterotic potential and create a broad spectrum of variability in segregating generations (Prasad and Sridhar, 2019). To analyse genetic variation, D^2 statistics are used to classify genotypes and measure genetic distance among clusters. Principal component analysis (PCA) further aids in identifying the most yield-contributing agronomic traits, which can then be emphasized in breeding efforts. Consequently, the present study aimed to evaluate genetic diversity among sorghum genotypes and identify the key traits that contribute to grain yield.

Materials and Methods

The experimental material consisted of 96 diverse sorghum genotypes, including two checks (CO 32 and K 13) collected from the Department of Millets, TNAU, Coimbatore and ICRISAT Hyderabad (Table 1). These genotypes were selected to represent wide genetic variability in terms of geographical origin, agro-morphological traits, maturity duration, and yield potential. The inclusion of landraces, breeding lines, exotic accessions, and two standard checks ensured adequate diversity for assessing genetic divergence and identifying superior parents for breeding programmes. The field experiment was carried out in a randomized block design (RBD) with two replications at Millets Breeding Station, TNAU, Coimbatore, between 11°N latitude and 77°E longitude during Rabi 2023-24. Each line was sown in 4-meter rows with 45 cm x 15 cm spacing. All the recommended agronomical practices for sorghum were followed to raise a good crop during the season. Five randomly selected plants of each genotype were observed for fourteen yield and yield-contributing traits, i.e., days to 50% flowering (DFF), number of leaves per plant (NL), leaf length (LL), leaf width (LW), flag leaf length (FLL), flag leaf width (FLW), plant height (PH), stem girth (SG), panicle length (PL), panicle width (PW), panicle weight (PWT), days to maturity (DM), hundred seed weight (HSW), and single-plant yield (SPY). The recorded data were then subjected to statistical analysis. To assess the genetic diversity present in the sorghum accessions, Mahalanobis' D^2 statistics were performed in WINDOSTAT ver. 7.1, and multivariate principal component analysis was performed in the AGRICOLAE package of R software.

Table 1: List of the ninety-six sorghum genotypes evaluated in the study

Entries	Origin	Entries	Origin
T Kallupatti local	India	SD 2033	-
IS 22794	Ethiopia	IS 23460	Yemen
IS 29640	USA	IS 30383	China
IS 10718	Ethiopia	IS 30450	India
IS 29690	India	IS 30507	Korea
IS 20594	Ethiopia	IS 1212	China
CO 4	India	IS 1233	China
IS 1052	India	IS 10477	USA
Erichanampatti local	India	IS 3937	India
IS 1141	Sudan	IS 3971	India
ICSB 23	India	IS 5286	India
SH 92	India	IS 5603	India
SH 29	India	IS 10304	India
SH 25	India	IS 10472	Ethiopia
N 14	Sudan (also referred as IS 18331)	IS 10939	USA

SH 24	Kenya	IS 19003	Ethiopia
IS 1137	India	IS 19534	Sudan
SH 16	India	IS 19824	India
E 96	Ethiopia	IS 21770	Sudan
SEB 12002	India	CO 32	India
A 6072	Ethiopia	APK 1	India
AS 3883	India	K 13	India
IS 9283	India	M35-1	India
CO 26	India	IS 1219	China
IS 3076	Deccan region of India	SD 2033	Sudan
Kottathur local	India	IS 23460	India
IS 30536	Korea	IS 30383	China
SD 12885	USA	IS 30450	China
CS 113	Sudan	IS 30507	Republic of Korea
SD 8375	Sudan	IS 1212	China
Paiyur 2	India	IS 1233	China
IS 2883	Italy	IS 10477	USA
IS 12804	Turkey	IS 3937	USA
IS 24578	Lebanon	IS 3971	India
IS 24617	Lebanon	IS 5286	India
IS 24629	Lebanon	IS 5603	India
IS 24632	Lebanon	IS 10304	USA
IS 28517	Yemen	IS 10472	USA
IS 29114	Yemen	IS 10939	USA
IS 511	Mexico	IS 19003	Sudan
IS 869	USA	IS 19534	Sudan
IS 932	Sudan	IS 19824	India
IS 2940	USA	IS 21770	Sudan
IS 3932	USA	CO 32	India
RS 29	India	APK 1	India
RC 585	-	K 13	India
IS 20575	Sudan	M35-1	India
IS 27786	Morocco	IS 1219	China

Results and Discussion

D^2 analysis

According to the Mahalanobis D^2 analysis, the D^2 values measure the degree of diversity and determine the pertinent contribution of each constituent character to total divergence. The genotypes studied were grouped into different clusters on the basis of genetic distance among the genotypes.

In this study, 96 genotypes, including two checks, were grouped into 10 different clusters using Tocher's method (Fig. 1) on the basis of their relative distances, i.e., D^2 values. The dendrogram can be a useful visualization tool for understanding the structure of the data and identifying natural groupings among the observations. Among the 10 clusters, a large number of genotypes (64) fell into Cluster I, implying greater similarity among these genotypes, which indicates a lack of sufficient divergence within this group. Cluster II consisted of 16 genotypes, followed by cluster V with 7 genotypes and cluster III with 3 genotypes. In contrast, the presence of solitary clusters (III, IV, VI, VII, VIII, and X) containing only one genotype in each cluster suggested that these genotypes are quite distinct from the others, potentially harbouring unique traits that could be valuable for breeding programs (Table 2).

Table 2: Clustering of ninety-six sorghum genotypes by Tocher's method into 10 different clusters

Clusters	Number of genotypes	Genotypes
Cluster I	64	IS 2883, IS 23460, IS 22794, SEB 12002, IS 20575, IS 19003, IS 19824, ICSB 23, Erichanampatti local, IS 3971, IS 1141, Kottathur local, CO 4, T Kallupatti local, IS 20594, E 96, SD 12885, IS 1052, CO 32, IL 46, A 6072, IS 27786, MR 99, IS 10477, IS 511, IS 10472, M35-1, IS 3932, ICS PIRMER, IS 2940, K

		13, ART 3015, IS 29690, SH 16, IS 24629, IL 497, IS 19534, IS 869, COS 28, IS 932, IS 10304, SH 92, SH 25, Paiyur 2, CO 30, IS 3937, IS 5603, SD 8375, IS 1219, IS 30450, IS 30507, IS 5286, IS 21770, SH 24, IS 1212, ISHAT 2001, SD 2033, IS 24617, IS 24632, IS 24578, AKZ 354, IS 1233, IS 3076, N 14
Cluster II	16	TNS 695, TNS 704, CO 26, TNS 702, IS 29322, APK 1, TNSS 225, TNSS 227, IS 1137, IS 9283, SAR 39, SH 29, CS 113, A 404, RS 29, SB 103
Cluster III	1	IS 30536
Cluster IV	1	IS 30383
Cluster V	7	IS 29640, ICSB 29, IS 12804, CO 27, TNFS 230, TNFS 239, IS 10718
Cluster VI	1	IS 10939
Cluster VII	1	RS 627
Cluster VIII	1	RC 585
Cluster IX	3	IS 28517, IS 29114, TNSS, 223
Cluster X	1	AS 3883

The mean values of ten clusters for 96 genotypes (Table 3) revealed notable genetic diversity across traits, which is valuable for breeding objectives. Cluster IX presented the highest means for plant height (252.85 cm), days to 50% flowering (75.83 days), number of leaves per plant (10.67), flag leaf length (64.43 cm), and days to maturity (113.83 days). Thus, the genotypes present in this cluster, such as IS 28517, IS 29114, and TNSS 223, were late-maturing, tall, and had more leaves, making them promising for improving the biomass of forage and silage crops. Cluster VI had the highest hundred-seed weight (4.25 g), indicating that genotype IS 10939 has strong grain yield potential. Cluster X presented the greatest means for leaf length (87.12 cm), stem girth (2.15 cm), panicle weight (102.30 g), and single-plant yield (78.24 g), identifying genotype AS 3883 as ideal for high-yield, dual-purpose varieties for grain and fodder (Greater plant height- 224.5 cm). Cluster VII presented low values for days to 50% flowering, panicle length, panicle width, and single-plant yield, indicating early maturity and suitability for short-duration crops. Cluster VIII exhibited maximum mean values for leaf width (10.50 cm) and flag leaf width (9.47 cm), which indicated the potential for increased photosynthesis and biomass. Cluster IV had the highest mean panicle length (32.67 cm), and the solitary nature of this cluster suggested that the genotype within this cluster was quite distinct and could possess unique traits not found in the other clusters. Hence, the genotypes linked with these clusters can be utilized as parents in a breeding plan, as observed by Navya *et al*., (2021) in a similar study.

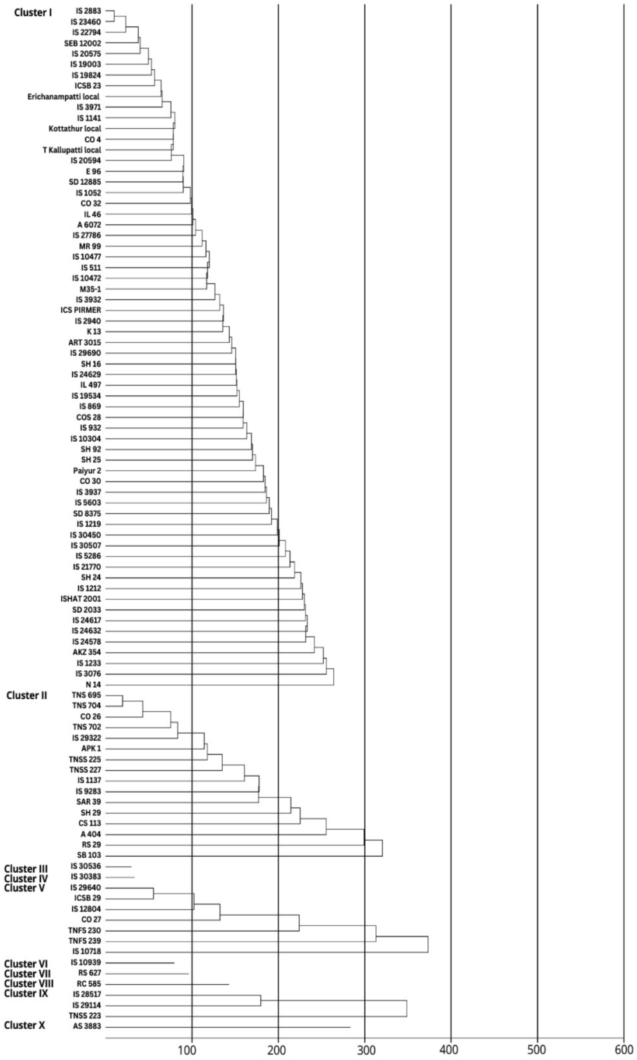

Fig. 1: Dendrogram showing the clustering pattern of 96 genotypes by Tocher's method.

The analysis of intracluster and intercluster distances offers valuable insights for breeding strategies (Table 4). The highest intracluster distance in Cluster IX (20.22) highlighted considerable variability, indicating potential for selection within this group containing the genotypes IS 28517, IS 29114, and TNSS, 223. Clusters with zero intracluster distances, such as III, IV, VI, VII, VIII, and X, represent solitary clusters. The largest intercluster distances were observed between Clusters VI and X (46.91) and between Clusters VII and X (44.71), suggesting significant genetic divergence. Therefore, IS 10939, AS 3883 and RS 627 could be selected as parental materials for hybridization programs. The overall larger intercluster distances than intracluster distances suggested substantial diversity across groups, which aligns with the findings of Prasad and Biradar (2018), Thant *et al*., (2020), Navya *et al*., (2021), Verma *et al*., (2022) and Bhadouriya and Bhadouriya (2024).

Table 3: Cluster mean values of 10 clusters for 14 different biometrical characters

	DFF	NL	LL	LW	FLL	FLW	PH	SG	PL	PW	PWT	DM	HSW	SPY
CLUSTER I	62.50	7.02	57.30	5.81	37.84	4.88	157.40	1.12	18.97	5.58	30.57	104.98	2.50	20.42
CLUSTER II	61.94	7.86	72.27	7.58	45.57	6.37	173.36	1.28	24.66	6.50	63.58	105.59	2.55	45.96
CLUSTER III	56.50	5.66	52.53	5.35	38.93	4.49	211.79	1.11	31.42	5.35	14.88	99.50	1.87	10.34
CLUSTER IV	66.50	7.16	56.13	5.22	40.90	3.80	191.75	1.18	32.67	5.15	30.33	109.50	2.05	22.93
CLUSTER V	55.64	6.69	56.41	4.89	38.99	4.58	198.11	1.10	28.05	8.15	19.73	97.36	1.64	13.89
CLUSTER VI	59.50	7.34	42.92	4.07	27.45	3.15	103.89	1.09	19.00	4.91	23.20	104.50	4.25	17.99
CLUSTER VII	51.50	8.66	78.92	7.40	48.30	7.37	106.33	1.12	17.78	3.68	17.25	91.50	1.45	9.00
CLUSTER VIII	73.50	8.84	77.05	10.50	59.19	9.47	118.89	1.38	27.05	9.52	92.90	113.50	2.46	57.70
CLUSTER IX	75.83	10.67	79.59	9.23	64.43	8.10	252.85	2.06	20.33	9.34	65.61	113.83	3.36	37.87
CLUSTER X	65.50	7.66	87.12	10.12	53.30	7.74	224.50	2.15	31.13	8.05	102.30	105.50	2.62	78.24

Note: DFF=Days to 50% flowering (days count), NL=number of leaves per plant (numbers count), LL=leaf length (cm), LW=leaf width (cm), FLL=flag leaf length (cm), FLW=flag leaf width (cm), PH=plant height (cm), SG=stem girth (cm), PL=panicle length (cm), PW=panicle width (cm), PWT=panicle weight (g), DM=days to maturity (days count), HSW=hundred seed weight (g/100 seed), and SPY=single plant yield (g).

Table 4: Average intracluster and intercluster distances (D^2 values) among the 10 clusters

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	13.54	21.09	17.48	16.86	20.88	18.88	17.95	29.49	33.14	40.44
Cluster II	21.09	15.09	24.62	19.87	27.01	27.32	25.67	19.74	28.46	27.34
Cluster III	17.48	24.62	0.00	9.12	15.82	25.65	17.77	35.45	38.73	42.29
Cluster IV	16.86	19.87	9.12	0.00	19.03	24.01	19.80	30.37	35.40	37.16
Cluster V	20.88	27.01	15.82	19.03	17.60	29.55	21.42	34.39	38.36	43.68
Cluster VI	18.88	27.32	25.65	24.01	29.55	0.00	27.73	35.69	36.04	46.91
Cluster VII	17.95	25.67	17.77	19.80	21.42	27.73	0.00	34.54	40.46	44.71
Cluster VIII	29.49	19.74	35.45	30.37	34.39	35.69	34.54	0.00	25.82	24.51
Cluster IX	33.14	28.46	38.73	35.40	38.36	36.04	40.46	25.82	20.22	29.65
Cluster X	40.44	27.34	42.29	37.16	43.68	46.91	44.71	24.51	29.65	0.00

Principal component analysis

A multivariate statistical approach known as principal component analysis (PCA) was performed for 96 sorghum genotypes across 14 biometric traits. PCA was used to assess the genetic diversity of the sorghum genotypes and their relationships with the observed attributes on the basis of the correlation between the traits and the pattern of variation in the genotypes. A scree plot displays the eigenvalues and percentage of variation associated with each principal component (Fig. 2). Three major principal components, i.e., PC1, PC2 and PC3, were extracted because they had eigenvalues greater than one (Brejda *et al*., 2000), which collectively explained 67.38% of the total variation (Table 5). PC1 contributed 44.77% of the variance and was heavily influenced by traits such as leaf width, panicle weight, and plant height, indicating that these traits are key drivers of genetic diversity. PC2, accounting for 12.36%, was strongly associated with panicle length and width, indicating that panicle size plays a significant role in genotype differentiation. PC3 explained 10.25% of the variance and was influenced mainly by plant height, days to flowering, and panicle dimensions.

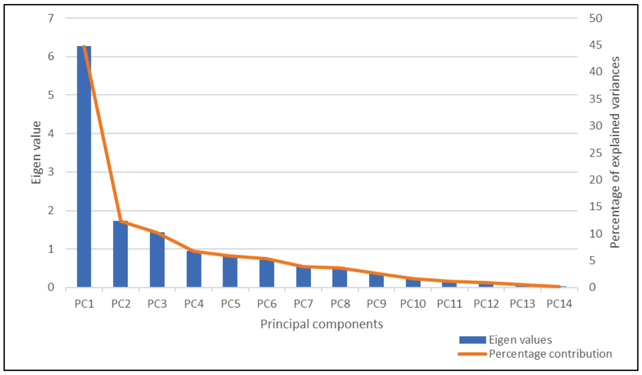

Fig. 2: Scree plot showing the eigenvalue and percentage contribution of each principal component towards divergence.

Similarly, Pugahendhi *et al*., (2023) reported that the first three principal components accounted for 43.26% of the total variation and highlighted the key agro-morphological traits driving diversity among 96 kharif sorghum genotypes using 20 agro-morphological traits. However, the factor loadings of traits on each principal component (PC) provided insights into how each trait contributes to the observed variability among the genotypes (Table 5). The traits with positive loadings on PC1—such as leaf width, flag leaf width, panicle weight, flag leaf length, single plant yield, stem girth, days to 50% flowering, and plant height—were key drivers of genetic divergence among the sorghum genotypes, highlighting their importance for phenotypic variability. Genotypes with higher values for these traits showed strong associations with PC1 variance. The results were in accordance with the findings of Pugahendhi *et al*., (2023) for traits such as days to 50% flowering, plant height, and leaf dimensions; by Boukrouh *et al*., (2023) for grain yield, panicle weight, and plant height; and by Malini *et al*., (2023) for flowering and maturity timing. Overall, flag leaf length, plant height, panicle length, and panicle width presented positive loadings across all three principal components, indicating that they are key contributors to genetic divergence and phenotypic differentiation among sorghum genotypes. The consistent influence of these genes suggested that they are valuable traits for selection in sorghum breeding programs.

Table 5: Relative contribution and factor loading of each biometrical trait towards divergence in the 3 major principal components

	Principal components		
Variables	Pc1	Pc2	Pc3
Eigen values	6.268	1.731	1.435
Variance %	44.773	12.364	10.253
Cumulative variance %	44.773	57.137	67.39
Trait	**Factor loadings**		
DFF	0.229	-0.413	0.384
NL	0.221	-0.210	-0.054
LL	0.328	0.165	-0.161
LW	0.359	0.043	-0.159
FLL	0.335	0.095	0.143
FLW	0.346	0.120	-0.089
PH	0.119	0.232	0.568
SG	0.287	-0.05	0.088
PL	0.112	0.343	0.181
PW	0.206	0.339	0.288
PWT	0.341	0.044	-0.295
DM	0.215	-0.47	0.321
HSW	0.123	-0.466	-0.162
SPY	0.318	0.065	-0.327

Note: DFF=Days to 50% flowering, NL=number of leaves per plant, LL=leaf length, LW=leaf width, FLL=flag leaf length, FLW=flag leaf width, PH=plant height, SG=stem girth, PL=panicle length, PW=panicle width, PWT=panicle weight, DM=days to maturity, HSW=hundred seed weight, and SPY=single plant yield.

PCA also provided valuable insights into the relationships among biometric traits (Fig. 3), as shown by vector angles. An acute angle between days to 50% flowering and days to maturity indicated a strong positive correlation, which is useful for selecting early-maturing types. Similarly, positive correlations were

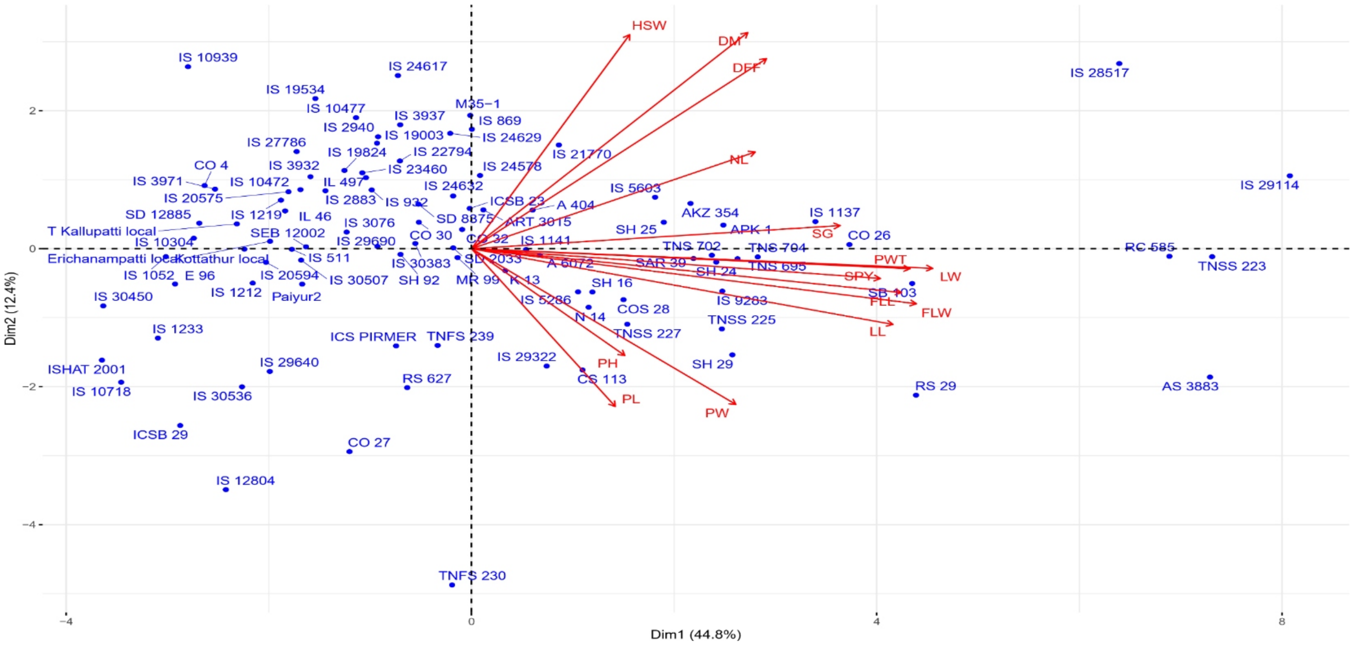

Fig. 3: PCA bi-plot showing distribution of ninety-six sorghum genotypes based on fourteen biometrical traits against two principal components.

observed between hundred-seed weight, days to maturity, days to flowering, and the number of leaves per plant. Conversely, obtuse angles between hundred-seed weight and traits such as panicle length, width, and plant height suggested that larger seed size is linked to shorter, narrower panicles and shorter plants, highlighting potential trade-offs in breeding. The acute angle between panicle length and plant height indicated a positive correlation, suggesting that taller genotypes tended to have longer panicles, supporting higher grain yields, an important factor for selecting high-yield genotypes. Additionally, single-plant yield showed a strong positive correlation with panicle weight, leaf width, flag leaf length, and width, emphasizing that these traits were crucial for increasing productivity in past sorghum breeding efforts.

The PCA biplot (Fig. 3) grouped all the sorghum genotypes according to phenotypic traits represented by the first two principal components (PC1 and PC2), revealing relationships among the genotypes on the basis of yield and yield-contributing traits. The genotypes were mostly distributed across two quadrants, indicating their similarities or differences on the basis of the fourteen traits evaluated. Genotypes such as IS 28517 and IS 29114 in the upper right quadrant exhibited traits such as high hundred-seed weight, extended days to maturity, days to 50% flowering, a greater number of leaves per plant, and thicker stems. Conversely, genotypes such as RS 29 and AS 3883 in the lower right quadrant shared characteristics such as high panicle weight, single plant yield, wider leaves, longer flag leaves, broader flag leaf width, increased leaf length, panicle width, taller plant height, and greater panicle length. This distribution highlights the trait-specific grouping among the sorghum genotypes.

Conclusion

This study assessed the genetic diversity of 96 sorghum genotypes using Mahalanobis's D^2 and principal component analyses, revealing significant variation in yield-related traits. The genotypes were clustered into 10 groups, with specific clusters offering unique traits suited to distinct breeding goals. For example, IS 28517, IS 29114, and TNSS 223 were ideal for biomass production, IS 10939 for high seed weight, AS 3883 for high yield, RS 627 and RC 585 for early maturity and enhanced photosynthesis, respectively. High intercluster distances suggest potential for heterotic hybrids, particularly between distinct genotypes such as IS 10939, AS 3883, and RS 627. PCA highlighted leaf width, panicle weight, plant height, and flag leaf traits as the primary contributors to phenotypic diversity. These findings provide a basis for selecting high-yielding, resilient genotypes, supporting sorghum productivity and sustainability in dryland regions.

References

Bhadouriya GPS and NS Bhadouriya (2024) D2 analysis and principal component analysis to assess genetic divergence in

Sorghum bicolor (L.) Moench for yield and its related attributes. *Int. J. Res. Agron.* 7(1): 322-26.

Boukrouh S, A Noutfia, N Moula, C Avril, J Louvieaux, J-L Hornick, J-F Cabaraux and M Chentouf (2023) Ecological, morpho-agronomical, and bromatological assessment of sorghum ecotypes in Northern Morocco. *Sci. Rep.* 13(1): 15548.

Brejda JJ, TB Moorman, DL Karlen and TH Dao (2000) Identification of regional soil quality factors and indicators. I. Central and Southern high plains. *Soil Sci. Soc. Am. J.* 64(6): 2115-24.

Bucheyeki TL, C Gwanama, M Mgonja, M Chisi, R Folkertsma and R Mutegi (2009) Genetic variability characterisation of Tanzania sorghum landraces based on simple sequence repeats (SSRs) molecular and morphological markers. *Afr. Crop Sci. J.* 17(2). 71-86.

Dhar A, BM Kumari, D Kavithamani, NM Boopathi and P Meenakshi (2024) Understanding the advances in Sorghum grain quality improvement: An overview. *Plant Sci. Today* 11(3): 61-78.

Ezeaku IE, SC Gupta and VR Prabhakar (1997) Classification of sorghum germplasm accessions using multivariate methods. *Afr. Crop Sci.* J. 7(1): 97-108.

Harlan JR and JM de Wet (1972) A simplified classification of cultivated sorghum 1. *Crop Sci.* 12(2): 172-76.

Malini N, SH Ramakrishnan and P Vinoth (2023) Elucidation of genetic diversity and principal component analysis in sorghum genotypes for yield and its contributing traits. *J. Pharm. Innov.* 12(5): 710-14.

Navya Y, PK Singh and B Sushma (2021) Genetic variability and diversity analysis for yield attributing and biochemical parameters of sorghum (*Sorghum bicolor* L.) genotypes. *Indian J. Ecol.* 48(3): 853-58.

Prasad BHV and B Biradar (2018) Genetic diversity studies among maintainers and restorers on milo and maldandi cytoplasm from minicore collection of sorghum using D^2 statistics. *Electron. J. Plant Breed.* 9(1): 233-43.

Prasad BV and V Sridhar (2019) Genetic diversity analysis for yield parameters in yellow pericarp sorghum (*Sorghum bicolor* L. Moench) genotypes. *Int. J. Curr. Microbiol. Appl. Sci.* 7: 3077-80.

Prasad BV and V Sridhar (2020) Estimation of genetic diversity for yield parameters in yellow pericarp sorghum germplasm lines (*Sorghum bicolor* L. Moench). *J. Pharmacogn. Phytochem.* 9(1): 833-36.

Pugahendhi N, BS Kumar, M Elangovan, K Venkatesh and P Rajendrakumar (2023) Assessing the genetic diversity of Indian *kharif* sorghum landraces through agromorphological characterization (*Sorghum bicolor* L. Moench). *J. Appl. Nat. Sci.* 15(2): 624-38.

Swamy N, B Biradar, M Hosamani, G Sajjanar, V Ashwathama, A Sajjan and A Biradar (2018) Genetic diversity analysis for productivity traits in rabi sorghum (*Sorghum bicolor* L. Moench). *J. Pharmacogn. Phytochem.* 7: 1780-83.

Thant SM, P Kumari, A Guar and S Pahuja (2020) Genetic diversity study for identification of dual-purpose sorghum. *Forage Research* 46: 148-51.

Verma LK, B Biradar and A Meena (2022) Assessment of genetic diversity in *rabi* sorghum [*Sorghum bicolor* (L.) Monech] using D^2 statistics. *BFIJ* 14(1): 800-3.