Research Article

Assessing the genetic diversity of Indian *Kharif* sorghum landraces through agro-morphological characterization (*Sorghum bicolor* L. Moench)

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How to Cite

Pugahendhi, N. *et al.* (2023). Assessing the genetic diversity of Indian *Kharif* sorghum landraces through agro-morphological characterization (*Sorghum bicolor* L. Moench). *Journal of Applied and Natural Science*, 15(2), 624 - 638. https://doi.org/10.31018/jans.v15i2.4477

Abstract

The agro-morphological characterization of local germplasm provides insight into existing diversity, enables the identification of desirable traits, and enhances crop improvement. The present study evaluated 96 kharif sorghum (Sorghum bicolor L. Moench) landraces and 6 checks using 20 agro-morphological traits at two locations, ICAR-IIMR in Hyderabad and Experimental Farm at Annamalai University in Annamalai Nagar, using alpha lattice design with 2 replications during 2021 kharif to assess genetic diversity. Results showed significant genetic variability among the 20 traits (P<0.01), providing opportunities for improvement. The high genotypic (GCV) and phenotypic components of variance (PCV) exhibited among the traits indicated their genetic determination and potential for improvement through breeding programs. High heritability and genetic advance also indicated the presence of additive genes, offering reliable improvement through trait selection. The correlation analysis showed a strong positive relationship between grain yield and several desirable traits, including panicle length, width, primary branch length, hundred seed weight, number of leaves, and total tillers per plant, indicating that grain yield can be improved by selecting accessions with desirable characteristics for these traits. The Cluster analysis using Euclidean distance revealed (four distinct clusters), with Cluster I being the most differentiated. These clusters may serve as valuable resources for hybridization programs. The PCA analysis indicated that the first three PCs accounted for 43.26% of the total variation and highlighted the key agro-morphological traits driving diversity. The results of this study demonstrated the significant genetic diversity among *kharif* sorghum landraces, providing a promising opportunity for varietal development programs.

Keywords: Agro-morphological characterization, Cluster analysis, Genetic variability, *Kharif* sorghum landraces, PCA analysis

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench), a cereal crop belonging to the Poaceae family's Andropogoneae tribe, is globally significant and ranks fifth after rice, wheat, barley, and maize (Pezzali *et al*., 2020). This crop is widely cultivated due to its ability to thrive in extreme climates, its drought tolerance, high yield potential, minimal nutrient requirements, and ease of cultivation (Adebowale *et al*., 2020). Approximately 500 million people in Sub-Saharan Africa and Asia rely on sorghum as a staple food grain, with India being the largest producer globally, followed by Nigeria (Bakare *et al*., 2021). In India, sorghum is the third most important cereal and is grown in three seasons - *Kharif*, Rabi, and Summer (Kumar *et al*., 2020) - in the major states of Maharashtra, Karnataka, Andhra Pradesh, and Tamil Nadu.

Sorghum is a multi-purpose crop, serving as a source of food, fodder, feed, and fuel, and it has a high sugar content (Sharma *et al.,* 2020). It is also one of the most nutritious cereal crops, with high mineral and fiber con-

tent and being gluten-free, surpassing rice and maize. Despite its importance, most sorghum production is rainfed, making it dependent on rainfall patterns and amounts and making crop improvement a priority in drought-prone areas of India (Sankar *et al.*, 2021).

India is a secondary center of origin for sorghum and boasts a diverse range of germplasms (Reddy *et al.*, 2021). Wild and cultivated forms of sorghum bicolor also display significant diversity in agronomic traits (Kavithamani *et al.*, 2019), making the characterization of germplasm diversity crucial for enhancing the crop's genetic architecture and improving the crop. The greater the diversity within a crop species, the more resources breeders have to create new and improved varieties better suited to changing climates and evolving pest and disease pressures. Landraces are a valuable source of genetic variability that plant breeders can use to develop improved varieties with better yields, nutrition, and climate adaptation (Dwivedi *et al.*, 2016; Godwin *et al.*, 2019). India's landraces have greater phenotypic and genetic richness (Elangovan *et al.*, 2009, 2012; Vara Prasad and Sridhar, 2019), making evaluation of their genetic diversity essential for crop improvement.

This study aimed to characterize Indian *Kharif* sorghum (*Sorghum bicolor* L. Moench) landraces based on their agro-morphological traits, assess their genetic divergence, and provide valuable information for improving the sorghum crop, particularly in the context of Kharif sorghum production.

MATERIALS AND METHODS

Experimental design and layout

90 *Kharif* sorghum landraces and 6 checks (CSV 15, CSV 20, CSV 27, CSV 17, CSV 21F, and CSV 24SS) were included in the study (Table 1). The accessions were collected from the Genebank at ICAR-Indian Institute of Millets Research (IIMR) in Rajendranagar, Hyderabad. The experiments were conducted during the *Kharif* season of 2021 at two locations: ICAR-IIMR in Hyderabad (Latitude 17.0° N, Longitude 78.0° E, Altitude 536 m above MSL) and the Experimental Farm at the Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University in Annamalai Nagar, Tamilnadu (Altitude 5.7 m above MSL, Latitude 11.0° N, Longitude 79.0° E). Hyderabad had an average rainfall of 853 mm and average minimum and maximum temperatures of 21°C and 30°C, while Annamalai Nagar had an average rainfall of 1400 mm and average minimum and maximum temperatures of 24°C and 32.7°C (https://mausam.imd.gov.in/).

The field was arranged in an Alpha Lattice Design with two replications, rows sown 2 m in length, and placed 60 cm apart with 15 cm between plants. Standard local cultivation practices were followed.

Agro-morphological traits studied

Five randomly selected plants were used to record observations on 20 agro-morphological quantitative traits (Table 2) using the trait descriptors provided by IBPGR -International Board for Plant Genetic Resources (IBPGR and ICRISAT, 1993).

Statistical analysis

The mean values from the two locations were used. Means were compared using Fisher's protected Least Significant Differences at a significance level of 0.05% (Gomez and Gomez, 1984, Jimmy *et al.*, 2017). An F-test was used to evaluate the homogeneity of error variances for each character across the two locations, which were found to be homogeneous for all characters studied. The R (Version 3.4.2) software was used to perform descriptive statistics, combined analysis of variance, genetic variability parameters, genetic correlations, cluster analysis, and principal component analysis (PCA). The variability package was used to compute genetic parameters and correlations, while the Euclidean distance matrix and the Ward2 method were used to perform cluster analysis and produce a dendrogram (Balkaya *et al.*, 2010). Principal component analysis (PCA) was performed to identify patterns of morphological variation using the FactoMineR package.

RESULTS AND DISCUSSION

Analysis of variance and Coefficient of variation

Table 3 presents the results of the combined analysis of variance for the twenty agro-morphological quantitative traits of ninety *kharif* sorghum landraces and six checks. The results indicated a significant (P<0.01) difference between the accessions for all traits studied, revealing a high level of genetic diversity among the *kharif* sorghum landraces. The interaction between location and plant height, panicle length, days to maturity, and grain yield was also significant (P<0.05), suggesting that the phenotypic expression of the lines varied between the two locations.

The grain yield showed significant (P<0.05) variations between locations and highly significant (P<0.01) differences across genotypes, indicating that the variation in growing conditions and heterogeneity in genotypes affect yield performance. This is consistent with earlier studies by Sulieman *et al.*, 2020; Ahmed *et al.*, 2021 and Kifle *et al.*, 2021 which were also conducted in Ethiopian sorghum growing regions and reported that location significantly affects sorghum yield performance in this area.

Genotype-environment interactions were highly significant (P<0.01) for all traits studied, except for the number of internodes, internode length, total tillers per plant, and green fodder yield per plant. This significant difference in genotype-environment interactions implies

that different genotypes respond differently in the two locations, similar to the findings by Biradar *et al.*, 2020; Desai *et al.*, 2021 and Ravi *et al.*, 2021.

Higher coefficients of variation (>30%) are generally associated with higher experimental inconsistency, which is important to recognize when comparing experimental variations in trials with parameters in various units (Taylor *et al.*, 1999). Hence, grain yield (CV=14.19%) has the most significant potential for improvement through selection.

Previous studies on the collection of sorghum landraces by Patil *et al.* (2020); Kumar *et al.* (2021) and Basava *et al.* (2021) have reported significant diversity in traits and significant variations in the landraces. These results suggest that the landraces remain genetically diversified, providing opportunities as a genetic resource for breeding programs and improvement.

Analysis of genetic variability parameters

Assessing genetic variability, heritability, and genetic advance in germplasm is essential for identifying superior genotypes (Tilahun *et al.,* 2021). Environmental factors play a significant role in determining quantitative traits, making it crucial to understand the magnitude and nature of variation and their interaction to improve them through breeding. Table 4 presents the mean and range values, genotypic and phenotypic variance, phenotypic and genotypic coefficients of variability, heritability in a broad sense, genetic advance, and genetic advance as a percent of the mean for each trait.

The relative ratios of genotypic and phenotypic coefficients of variation determine the level of variability. For every trait studied, the phenotypic variance (VP) and phenotypic coefficient of variation (PCV) were found to be more significant than the genotypic variance (VG) and genotypic coefficient of variation (GCV), respectively (Table 4). This suggests that the observed variation is primarily due to environmental factors affecting trait expression (Kotal *et al.*, 2010; Bhagasara *et al.*, 2017). However, for most traits, the difference between PCV and GCV is minimal, except for leaf width, panicle width, hundred seed weight, potential tillers per plant, and grain yield, indicating low environmental influence and a significant role of genetics in character expression. These findings align with previous studies by Narkhede *et al.* (2000) for panicle length and Singh *et al.* (2013) for fodder yield per plant. Therefore, the phenotype-based selection is likely adequate for most traits.

Traits such as plant height, panicle length without peduncle, panicle length of branches, neck of panicle, hundred grains seed weight, stem: juice brix, number of leaves per plant, number of internodes per plant, the total number of tillers per plant, potential number of tillers per plant, green fodder yield per plant, dry fodder yield per plant, and grain yield per plant had higher GCV and PCV values ranging between 24.74 and 83.89 (Deshmukh *et al.*, 1986). These traits indicate a greater potential for genotype improvement through selection and hybridization. Similar findings were reported for sorghum crops by Jain *et al.*, 2010; Elangovan *et al.*, 2012; Elangovan *et al.*, 2015; Tesfaye, 2017; Ranjith *et al.*, 2017; Zinzala *et al.*, 2018; Gedifew and Tsige, 2019 and Sejake *et al.*, 2020 for the majority of traits evaluated.

The higher the coefficients, the more evolvable the trait is. Studies on sorghum landraces have indicated that traits with higher GCV estimates have significant potential for improvement through selection (Tura *et al.*, 2021 and Kamara *et al.* (2020). However, heritability and genetic advance assessments are necessary to evaluate the amount of genetic variation. When considering both heritability and genetic advance, predicting the effectiveness of selection and the presence of additive genes in the attribute becomes possible. In this study, all traits except leaf width, days to maturity, and grain yield had high heritability and high genetic advance as a percent of the mean, indicating low environmental effect and a high breeding value. Direct phenotypic selection could be efficient for genetic improvement in this scenario. Similar observations of high heritability coupled with high genetic advance were made in studies by Deepalakshmi and Ganesamurthy (2007); Kannababu *et al.* (2013); Elangovan *et al.*(2015); Ranjith *et al.* (2017) and Gedifew and Tsige (2019) for most of the traits studied. In these studies, grain yield, leaf width, and days to maturity showed low heritability estimates, which were attributed to the impact of environmental factors as these traits were polygenic. Despite this, Teklewold *et al.* (2021) reported that grain yield, leaf width, and days to maturity exhibited low heritability estimates, consistent with previous studies by Hamad and Dagash (2017). It is important to note that previous studies on diverse germplasm recorded higher heritability and genetic advance than the present study, which mainly focused on landraces. These findings suggest that heritability estimates can vary depending on the germplasm used and environmental conditions and that careful consideration of these factors is necessary when designing breeding programs for sorghum.

Correlation analysis

The Pearson correlation analysis of the traits is presented in Fig. 1. Positive correlations were found between grain yield and several other traits, including panicle length (r=0.22), panicle width (r=0.15), primary branch length (r=0.11), hundred seed weight (r=0.46), number of leaves (r=0.11), total tillers per plant (r=0.20), dry fodder yield (r=0.10), and green fodder yield (r=0.14). Previous research has shown that selecting one desirable trait can improve other associated

Table 1. List of sorghum genotypes used in the study

Accession No	IC Number	Landrace Name	Race	Area of Collection
E 153	IC 568370	Poru	Guinea	Gujarat
E 158	IC 568375	Sundia	Durra	Gujarat
E 159	IC 568376	Rajka Jowar	Kafir	Gujarat
E 163	IC 568380	Char	Durra	Gujarat
E 173	IC 568390	Wagad	Durra	Gujarat
E 178	IC 568395	Gundri	Durra	Gujarat
E 186	IC 568447	Sudan Grass	Caudatum	Madhya Pradesh
E 193	IC 568454	Khandwa	Durra	Madhya Pradesh
E 195	IC 568456	Baidara Boria	Durra	Madhya Pradesh
E 197	IC 568458	Hathikunta	Durra	Madhya Pradesh
E 202	IC 568463	Sabet Baidara	Durra caudatum	Madhya Pradesh
E 205	IC 568466	Zunku	Durra caudatum	Madhya Pradesh
E 210	IC 568471	Chatkul	Guinea	Madhya Pradesh
E 223	IC 568484	Dugdugu	Durra caudatum	Madhya Pradesh
E 225	IC 568486	Kadhgav Deshi	Durra caudatum	Madhya Pradesh
E 228	IC 568489	Basmati Jowar	Durra	Madhya Pradesh
E 249	IC 568510	Devla	Durra	Madhya Pradesh
E 106	IC 415797	Jonnari	Guinea	Uttar Pradesh
E 109	IC 415800	Jonndi	Durra	Uttar Pradesh
E 101	IC 415792	Sabet Deshi	Durra	Uttar Pradesh
E 4	IC 338971	Gudli Local	Guinea caudatum	Rajasthan
EG 2	IC 541309	Manjal Cholam	Caudatum	Tamil Nadu
EG 10	IC 541327	Kari Cholam	Durra bicolor	Tamil Nadu
EG 11	IC 541318	Karareddu Cholam	Durra bicolor	Tamil Nadu
EG 20	IC 541327	Vellai Nattu Cholam	Durra	Tamil Nadu
EG 24	IC 541331	Kovilpatti Cholam	Durra	Tamil Nadu
EG 35	IC 541342	Senkatan Cholam	Durra	Tamil Nadu
EG 39	IC 541346	Pei (Thalaiviracham) Cholam	Guinea	Tamil Nadu
EG 40	IC 541347	Senjolam	Kafir	Tamil Nadu
EG 48	IC 541355	Makkatai Cholam	Durra	Tamil Nadu
EG 54	IC 541361	Vailkattu Cholam	Durra	Tamil Nadu
EG 55	IC 541362	Nattu Cholam	Durra	Tamil Nadu
E 203	IC 568464	Peeli Baidara	Durra	Madhya Pradesh
GGUB 20	IC 319863	Chikni Jowar	Durra caudatum	Madhya Pradesh
GGUB 21	IC 319864	Pili Local	Durra	Madhya Pradesh
GGUB 22	IC 319865	Dhavali Jowar	Durra	Madhya Pradesh
GGUB 27	IC 319870	Katrae	Durra	Madhya Pradesh
GGUB 30	IC 319873	Lahi Jowar	Durra	Madhya Pradesh
GGUB 31	IC 319874	Barsati Jowar	Durra	Madhya Pradesh
GGUB 32	IC 319875	Badi Jowar	Durra	Madhya Pradesh
GGUB 34	IC 319877	Meethi Jowar	Guinea caudatum	Madhya Pradesh
GGUB 37	IC 319880	Chikni Pilia	Durra	Madhya Pradesh
GGUB 38	IC 319881	Kale Tonsa Ki Jowar	Durra caudatum	Madhya Pradesh
GGUB 48	IC 319891	Ramtak Local	Durra caudatum	Madhya Pradesh
GGUB 50	IC 319892	Charsi Local	Durra caudatum	Madhya Pradesh

Table 1. Contd…..

GGUB 51	IC 319893	Aathner Mohali	Durra caudatum	Madhya Pradesh
GGUB 54	IC 319895	Satpari	Durra	Madhya Pradesh
GGUB 55	IC 319896	Kantolli	Guinea caudatum	Madhya Pradesh
GGUB 56	IC 319897	Safeda	Durra caudatum	Madhya Pradesh
GGUB 57	IC 319898	Gudagi	Durra	Madhya Pradesh
GGUB 58	IC 319899	Pili Safed	Durra	Madhya Pradesh
GGUB 61	IC 319902	Mehara Jowar	Durra	Madhya Pradesh
GGUB 62	IC 319903	Pilimotia	Durra	Madhya Pradesh
GGUB 63	IC 319904	Murga Jowar	Durra	Madhya Pradesh
GGUB 64	IC 319905	Somkath Safea	Durra	Madhya Pradesh
GGUB 65	IC 319906	Arom Safed	Durra caudatum	Madhya Pradesh
GGUB 67	IC 319907	Safed Jowar	Durra	Madhya Pradesh
GGUB 68	IC 319908	Mehara Jowar	Durra	Madhya Pradesh
EB 1	IC 332460	Deshi Sabet	Durra caudatum	Madhya Pradesh
EB 2	IC 332461	Deshi Dhawli	Durra caudatum	Madhya Pradesh
ERN 13	IC 568528	Kamal Parva	Durra	Gujarat
ERN 23	IC 568538	Chachadia	Durra	Gujarat
ERN 26	IC 568541	Solapuri	Durra	Gujarat
ERN 29	IC 568544	Gundri	Durra	Gujarat
E 219	IC 568480	Zunku Basmati	Durra	Madhya Pradesh
E 1	IC 338968	Jowari Local	Durra	Rajasthan
EJ 42	IC 339022	Deshi Chari	Durra bicolor	Rajasthan
EA 1	IC 345243	Irungu Cholam	Bicolor	Tamil Nadu
EA 2	IC 345244	Vella Cholam	Durra	Tamil Nadu
EA 4	IC 345246	Karum Cholam	Bicolor	Tamil Nadu
EA 6	IC 345248	Matthappu Cholam	Guinea caudatum	Tamil Nadu
EA 10	IC 345252	Irungu Cholam	Bicolor	Tamil Nadu
EA 11	IC 345253	Sevappu Cholam	Guinea	Tamil Nadu
EG 1	IC 541308	Periya Manjal Cholam	Durra bicolor	Tamil Nadu
E 143	IC 415834	Bani	Durra caudatum	Gujarat
ER 3	IC 0585137	Jondi	Durra	Gujarat
EJN 11	IC 0585181	Utavali	Caudatum	Tamil Nadu
EJN 26	IC 0585196	Maklani	Durra	Tamil Nadu
ERS 3	IC 0585208	Sivappu Irunggu	Bicolor	Madhya Pradesh
ERP 65	IC 0622100	Sivappu Cholam	Caudatum	Madhya Pradesh
ELS 30	IC 0621995	Nattu Tella Jonna	Guinea	Andhra Pradesh
ELS 16	IC 0621989	Jonnari	Guinea	Andhra Pradesh
SEA 14	IC-0627117	Nandyal Tella Jonna	Durra	Andhra Pradesh
ER 79	NA	Senvholam	Caudatum	Tamil Nadu
EUK 51	NA	Mandi Jowar	Durra	Madhya Pradesh
EUK 32	NA	Khantroli	Caudatum	Madhya Pradesh
ELG 25	IC 568361	Mariyal Jola	Durra	Madhya Pradesh
EUK 12	NA	Gharia	Caudatum	Madhya Pradesh
EUK 9	NA	Khangda	Durra	Madhya Pradesh
EUK 23	NA	Bajari Jowar	Durra	Madhya Pradesh
CSV 27		Grain Sorghum Variety		
CSV 20		Grain Sorghum Variety		
CSV 15		Grain Sorghum Variety		
CSV 21F		Fodder Sorghum Variety		
CSV 24SS		Sweet Sorghum Variety		
CSV 17		Early Duration Variety		

NA-Not available

Table 2. Agro-morphological traits and measurement units

S.No.	Trait	Abbreviation	Unit
1	Days to 50% flowering	DFF	days
2	Plant height	PH	cm
3	Stem diameter	SD	cm
4	Leaf length	LL	cm
5	Leaf width	LW	cm
6	Panicle length without peduncle	PL	cm
7	Panicle width	PW	cm
8	Panicle length of branches	PLPB	cm
9	Neck of panicle	NOP	cm
10	Hundred grains seed weight	SW	g
11	Stem: juice brix	SJB	%
12	Number of leaves per plant	NOL	numbers
13	Number of internodes per plant	NOI	numbers
14	Internode length	IL	cm
15	Total tillers per plant	TTPP	numbers
16	Potential tillers per plant	PTPP	numbers
17	Days to maturity	DM	days
18	Green fodder yield per plant	GFYPP	g
19	Dry fodder yield per plant	DFYPP	g
20	Grain yield	GY	g

traits (Elangovan *et al*., 2009; 2020 b). By selecting landraces with superior panicle length, width, primary branch length, hundred seed weight, number of leaves, and total tillers per plant, it is possible to increase grain yield due to the strong correlations observed between these traits. Strong positive correlations were also found between leaf length and width (r=0.65), days to maturity and fifty percent flowering (r=0.80), panicle length and primary branch length (r=0.67), and dry and green fodder yield per plant (r=0.82). The positive correlation between panicle traits supports the 'multiplication and condensation hypothesis (Harlan *et al*., 1973), suggesting that selecting these traits will indirectly improve yield performance. Leaf length, width, and the number of leaves are important for yield as they impact food synthesis through photosynthesis and ultimately affect yield (Liu *et al*., 2021)

Several studies have reported significant correlations among various traits in sorghum. For instance, Katiyar *et al*. (2019) identified a strong positive correlation between panicle length and branch length, while Hussain *et al*., 2019 found a strong positive correlation between panicle length and grain yield. Furthermore, Gebre *et al*., 2021; Guleria *et al.,* 2021 and Roy *et al*. 2019 reported positive correlations between leaf area and fodder yield, indicating that leaf traits could be essential selection criteria for enhancing fodder yield in sorghum breeding programs. Elangovan *et al*., 2007 also observed predominantly positive correlations among various quantitative traits in sorghum.

Cluster analysis

Fig. 2 shows the hierarchical clustering results performed on 90 *kharif* sorghum landraces and checks based on their trait performance. The data was processed using the Euclidean distance matrix and Ward's linkage approach, resulting in four distinct clusters. The size of the individual clusters varied from 16 to 37, with Cluster I having the highest number of accessions at 37 and Cluster III having the lowest at 16.

Table 5 presents the number of accessions and genotypes for each cluster. The clustering pattern demonstrated a significant level of diversity among the sorghum landraces evaluated, as accessions from different states were grouped into separate clusters. This outcome is in agreement with previous studies (Mekbib *et al*., 2020; Bimpong *et al*., 2021; Nidhi *et al.,* 2021), and indicates a broad genetic base of the genotypes belonging to each origin. According to Table 6, Cluster I and III demonstrated the highest inter-cluster distance of 12.48, indicating that they are suitable for hybridization to generate a diverse segregating generation. As suggested by Singh *et al*. (2019) and Mekbib *et al.* (2020), identifying the most divergent clusters is crucial for selecting the ideal cluster for further hybridization and selection.

The inter-cluster distances and genotype performance were used to select genetically diverse and agronomically superior (Fikre et al., 2020; Ana et al., 2021; Girmay et al., 2021). Table 7 displays the mean values of different characters for each cluster. The data sug-

Table 3. Combined analysis of variance and Coefficient of variation (CV) for twenty agro-morphological traits evaluated at two locations during *kharif* 2021

Source	Df	DFF	PH	SD	LL	LW	PL	PW	PLPB	NOP	SW	SJB	NOL	NOI	IL	TTP	PTP	DM	GFYPP	DFYPP	GY
Environment	1	2132.88	134081.90*	0.61	262.62	0.95	1428.86*	13.86	87.12	0.32	44.42	6.10	131.06	1.206	20.12	4.38	17.94	30317.04*	160066.67	45981.26	39345.71*
Replication (ENV)	2	20.41	3971.32	0.27	853.58	11.73	15.05	7.49	0.13	4.20	0.05	0.47	16.21	3.942	3.30	2.04	0.14	16.51	3439.50	2227.14	8.44
Block (REP*ENV)	44	12.40	448.17	0.04	33.45	0.90	2.48	1.13	0.61	2.38	0.00	1.10	1.85	0.518	0.67	0.47	0.11	5.13	1310.08	455.91	12.61
Genotype	95	273.11**	7694.93**	0.34**	267.49**	2.98**	91.53**	3.06*	22.66**	98.09**	0.95*	50.30**	13.79**	12.44**	22.37**	6.06*	0.55**	301.70**	26946.19**	8743.62**	372.51**
GenotypeX-Environment	95	105.77**	847.61**	0.14**	130.01**	2.11**	14.81**	1.92*	0.77**	10.47**	0.35*	3.13**	2.92**	0.681	0.75	0.19	0.28*	165.40**	1304.01	1340.78**	313.57**
Error	146	12.25	489.56	0.06	39.71	1.18	3.08	0.90	0.44	2.24	0.00	1.15	1.35	0.700	0.89	0.53	0.13	4.61	1215.76	487.15	8.86
CV %		4.28	9.53	12.28	9.39	17.54	9.16	18.47	11.15	8.74	2.54	6.86	11.42	9.61	5.32	24.12	28.07	1.96	21.03	21.32	14.19

** Significant at the 1% probability level and *Significant at the 5% probability level; CV % - Coefficient of variation; Df-degrees of freedom

gests significant variance across clusters for most of the evaluated characters, with Cluster I having the highest mean values for all significant yield components and Cluster III having the lowest. Crossbreeding between these divergent groups is expected to lead to a more diverse genetic basis in the base population and reveal hidden variability. The resulting progeny is predicted to be highly variable, offering more opportunities for identifying and releasing transgressive segregants as new varieties or for use in sorghum crop improvement.

Principal component analysis

Principal component analysis (PCA) is a powerful tool for analyzing genetic variation by determining the key characteristics that significantly impact overall genetic variation and their relative importance in a breeding program (Teshome *et al.*, 2021). Brejda et al., 2000 recommended selecting eigenvalues greater than one that contributes at least 10% of the variation. In the current study, the PCA analysis showed that seven of the 20 components had eigenvalues greater than one, resulting in a total variability of 71.38% (Table 8).This result is consistent with the findings of Nago *et al. (*2020); Mekonnen *et al.* (2021) and Wolde *et al.* (2021) who reported that the first three components are crucial in representing variation patterns among landraces, and the traits related to these components are most useful in discriminating different landraces.

The first component, accounting for 23.33% of the total variation, was positively associated with various characteristics such as days to 50% flowering, plant height, stem diameter, leaf length, leaf width, panicle length without peduncle, panicle width, panicle length of branches, neck of panicle, number of leaves and internodes per plant, internode length, days to maturity, green and dry fodder yield per plant. The second component was dominated by six traits: days to 50% flowering, hundred grains seed weight, stem: juice brix, number of leaves and days to maturity, and grain yield per plant. The third component showed a positive correlation with plant height, leaf length, leaf width, hundred grains seed weight, stem: juice brix, number of internodes and tillers per plant, internode length, green and dry fodder yield per plant, and potential number of tillers per plant. These three components significantly impact yield and its related traits, which are crucial in making selections during sorghum crop improvement. Improving certain traits in a given component will directly improve other yield traits in the same component as long as they have a positive effect. This finding is in line with previous studies by Kassahun *et al.* (2020); Kadam *et al.* (2021); Asfaw *et al.* (2021); Gebretsadik *et al.* (2021) and Singh *et al.* (2021), who reported highly significant genetic variation across sorghum accessions

Table 4. Parameters of genetic variability for twenty agro-morphological traits evaluated at two locations during *kharif* 2021

Traits	Mean	Range		Variance		Co-Variance		H2b %	GA	GAM %
		Min	Max	σ2g	σ2p	GCV%	PCV%			
DFF	81.86	51	110	111.26	161.84	12.88	15.53	68.75	18.02	22.01
PH	232.25	90	370	3302.59	4392.33	24.74	28.53	75.19	102.65	44.20
SD	1.93	1	3.1	0.13	0.21	18.61	23.81	61.09	0.58	29.97
LL	67.12	36	92.13	97.43	170.05	14.70	19.42	57.3	15.39	22.93
LW	6.20	2.7	9.8	0.75	2.23	13.97	24.07	33.72	1.04	16.72
PL	19.16	6.5	38	39.82	51.70	32.93	37.52	77.04	11.41	59.54
PW	5.13	2	11	0.86	2.20	18.05	28.88	39.06	1.19	23.25
PLPB	5.96	1.5	16.5	10.89	11.76	55.36	57.54	92.57	6.54	109.72
NOP	17.14	6.1	32	46.55	51.53	39.80	41.88	90.34	13.36	77.94
SW	1.78	0.25	3.31	0.33	0.60	32.46	43.62	55.4	0.89	49.78
SJB	15.60	7.2	25	24.24	26.05	31.56	32.71	93.05	9.78	62.72
NOL	10.16	4	16.2	5.64	8.14	23.38	28.08	69.36	4.08	40.13
NOI	8.00	3	14	5.89	6.56	27.87	29.41	89.8	4.74	54.40
IL	17.76	9.5	25	10.74	11.62	18.44	19.19	92.41	6.49	36.53
TTPP	3.00	1	7	2.81	3.24	55.52	59.58	86.81	3.22	106.56
PTPP	1.00	1	3	0.15	0.39	30.51	48.65	39.33	0.51	39.43
DM	109.00	71	140	69.09	232.62	7.59	13.93	29.7	9.33	8.52
GFYPP	165.77	40	420	12557.70	14388.47	67.60	72.36	87.28	215.66	130.10
DFYPP	103.54	20	330	3903.43	4840.18	60.33	67.18	80.65	115.58	111.62
GY	20.98	1.06	20.98	62.57	309.93	37.68	83.89	20.19	7.32	34.89

σ2e-Environment variance,σ2p-Phenotypic variance; σ2g-genotypic variance;
ECV%-environment coefficient variation; GCV%-genotypic coefficient variation;
PCV%-phenotypic coefficient variation; GA-Genetic advance; H^{2}b %- broad sense heritability; GAM %-genetic advance percent of mean(GAM); Days to 50% flowering (DFF), Plant height (PH); Stem diameter(SD); Leaf Length (LL), Leaf Width (LW), Panicle length without peduncle (PL); Panicle Width(PW); Panicle length of branches (PLPB); Neck of Panicle (NOP), Hundred grains seed weight (SW); Stem: juice brix(SJB); Number of leaves per plant (NOL); Number of internodes per Plant (NOI), internode length (IL); The total number of tillers per plant (TTPP); Potential number of tillers per plant (PTPP), Days to maturity (DM), green fodder yield per plant (GFYPP; Dry fodder yield per Plant (DFYPP), and Grain yield per plant (GY).

Table 5. Clustering based on Ward's Euclidean hierarchial analysis

Clusters	Total number.of genotypes	Name of genotypes
I	37	EUK 32, EG 35, GGUB 58, CSV 15, ERP 65, E 158, CSV 17, GGUB 55, ERN 23, ERN 26,EG 10, EG 55, ERN 13, EA 1, EJN 11, ER 79, GGUB 27, GGUB 38, EG 48, EA 2, EG 24, EJ 42, GGUB 56, EUK 51, E 1, GGUB 21, E 163, EUK 23, EA 11, EJN 26, GGUB 62, E 159, E 173, GGUB 31, GGUB 61, EG 11, GGUB 54
II	18	E 205, E 225, E 197, E 195, GGUB 57, EA 6, EG 1, GGUB 32, GGUB 50, ERN 29, EUK 9, SEA 14, CSV 24SS, ELS 30, CSV 20, EG 2, EG 20
III	16	GGUB 37,E 186, GGUB 30, GGUB 64, CSV 27, E 203, ELG 25, E 228, E 249, E 202, E 223, E 219, GGUB 20, GGUB 67, EB 1,GGUB 22
IV	25	ELS 16, E 109, EG 54, EG 39, E 106, E 178, ERS 3, E 153, E 210,EA 10, ER 3, GGUB 48, EB 2, GGUB 65, GGUB 34, GGUB 63, EUK 12, GGUB 68, EG 40, E 101, E 193, E 143, EA 4, E 4, GGUB 51

Table 6. Inter-cluster distance between four cluster based on Ward's Euclidean hierarchical analysis

Clusters	I	II	III	IV
I	0.000			
II	9.18	0.000		
III	12.48	11.28	0.000	
IV	10.26	9.22	11.21	0.000

Fig. 1. *Correlation among twenty agro-morphological traits evaluated at two locations during kharif 2021*

Fig. 2. *Dendrogram constructed using Ward's Euclidean hierarchical analysis method*

Table 7. Cluster-wise mean values of twenty agro-morphological characters in 4 clusters

Traits	Clusters			
	I	II	III	IV
DFF	75.85	78.50	85.78	87.83
PH	206.29	224.17	271.55	219.30
SD	1.77	1.82	2.15	1.97
LL	63.00	62.63	75.40	65.18
LW	5.97	5.87	6.84	5.92
PL	19.08	15.08	21.35	19.99
PW	4.83	4.56	5.78	5.18
PLPB	5.73	4.20	6.80	6.74
NOP	18.05	14.81	18.00	16.84
SW	1.98	1.66	1.80	1.63
SJB	15.70	19.23	14.40	13.75
NOL	8.32	9.98	11.11	11.55
NOI	7.63	9.12	10.59	8.38
IL	18.09	17.52	19.36	15.24
TTPP	4.14	2.55	2.62	2.49
PTPP	1.63	1.13	1.22	1.10
DM	103.43	106.43	113.14	115.54
GFYPP	116.63	184.97	221.72	135.20
DFYPP	79.32	111.76	134.21	85.20
GY	22.56	20.73	18.91	22.02

Table 8. Coefficient and vector association with the first 3 principal components

|	PC1	PC2	PC3
Eigenvalue	4.341	2.276	2.03
Variability contribution (%)	21.707	11.380	10.174
Cumulative variance contribution (%).	21.707	33.088	43.262
Coefficient vector			
DFF	0.285	0.321	-0.113
PH	0.325	-0.231	0.170
SD	0.280	-0.042	-0.041
LL	0.322	-0.068	0.204
LW	0.202	-0.084	0.265
PL	0.116	-0.240	-0.511
PW	0.253	-0.1497	-0.139
PLPB	0.127	-0.233	-0.517
NOP	0.073	-0.294	-0.146
SW	-0.062	0.0767	0.219
SJB	-0.148	0.0197	0.200
NOL	0.340	0.099	-0.089
NOI	0.209	-0.076	0.190
IL	0.109	-0.261	0.100
TTPP	-0.211	-0.379	0.059
PTPP	-0.202	-0.389	0.107
DM	0.257	0.364	-0.095
GFYPP	0.265	-0.097	0.231
DFYPP	0.249	-0.151	0.227
GY	-0.080	0.236	-0.048
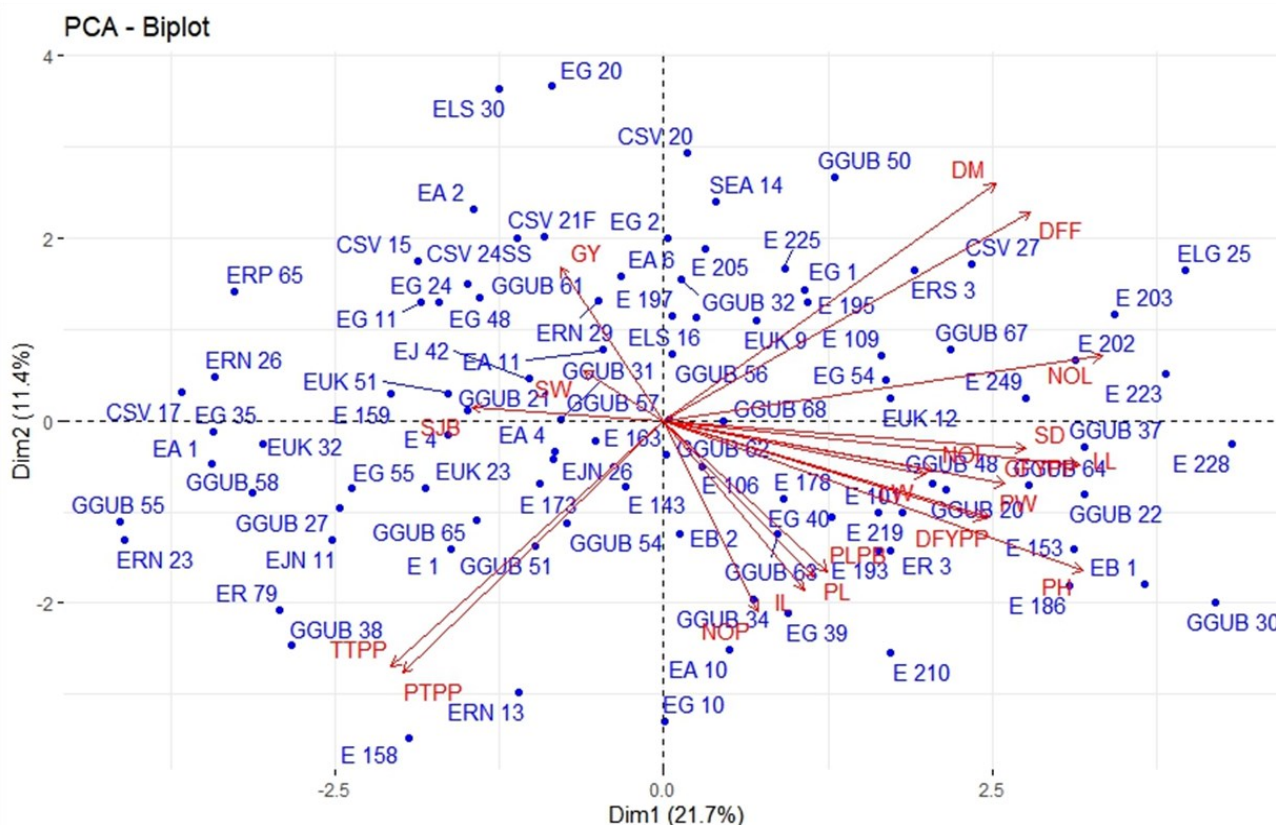
Fig. 3. *PCA biplots of the first two principal components (PC1 and PC2)*

in several quantitative agro-morphological traits.

Fig. 2 shows a biplot of the first two principal components for 20 agro-morphological characteristics. The best genotypes were selected based on these two components, which condensed the agro-morphological traits for simultaneous assessment. Jain, (2011) also used biplot analysis to estimate genetic diversity in sorghum and found that genotypes were distributed over the four quadrants, indicating significant genetic diversity. Saba *et al*. (2021) reported that PCA of morphological characterization results could identify essential descriptors that account for most of the observed diversity.

Conclusion

The characterization of a crop's agro-morphology is crucial for maximizing the potential of its genetic diversity in breeding programs. The present findings showed a vast genetic diversity in Indian *kharif* sorghum landraces for all studied traits, promising great opportunities for trait improvement. The high heritability (H2) and expected GAM% for key yield components, including panicle length, width, primary branches, seed weight, leaves, and total tillers, demonstrated the potential for improvement through selection. Further research on the interaction of these traits with the environment is necessary for enhancing sorghum yield. Four distinct

clusters were identified and a high genetic diversity among the landraces was confirmed through multivariate statistical analysis. Furthermore, the principal component analysis determined the primary sources of variation in the kharif sorghum landraces. By selecting parents based on these findings, the genetic variation in the crop can be significantly increased. Overall, the high genetic variation in the *Kharif* sorghum landraces highlights their potential use in breeding and selection programs to develop superior, high-yielding, *Kharif*-adapted cultivars.

Conflict of interest
The authors declare that they have no conflict of interest.

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