Research Note Electronic Journal of Plant Breeding, Vol.17(2):227-233

Assessment of genetic variability of quality, yield, and its attributing traits in sorghum (*Sorghum bicolor* (L.) Moench)

Vaishnavi, C. P. Chetariya, Reginah Pheirim*, Prajyot Waghmode and Alka Soharu

https://doi.org/10.37992/2026.1702.030

Abstract

Sorghum (2n=2x=20) being the fifth most important cereal crop in the world with high adaptability and tolerance to various biotic and abiotic stresses. Understanding genetic variability and association studies aids in enhancing the fodder yield of sorghum and identifying promising genotypes. The experiment was conducted at Lovely Professional University, Phagwara, Punjab, using a randomized block design with three replications. The assessment of genetic variability revealed significant differences among the studied genotypes for traits such as stem thickness, total soluble solids (TSS), and leaf area. These traits also demonstrated high heritability and genetic advance, indicating their potential for selection in crop improvement programs. Correlation and path coefficient analysis identified TSS, leaf length, and stem thickness as the most influential traits for green fodder yield. On the other hand, traits like leaf area and chlorophyll content had negative impacts on yield. Genetic divergence analysis grouped the genotypes into 12 clusters, with significant inter-cluster distances suggesting the potential for selecting diverse parents for breeding. Clusters VIII and X showed the highest inter-cluster distance, indicating significant genetic differentiation. The study highlights the presence of considerable genetic diversity, identifying SOR14520, and SOR14579 as the best genotypes for sorghum improvement. Selection for traits like TSS, stem thickness, and leaf area in these genotypes can significantly enhance green fodder yield.

Keywords: Sorghum, Fodder yield, Genetic variability, Association study, Genetic Divergence.

Sorghum (*Sorghum bicolor* (L.) Moench is one of the important cereals in the world, which can be used as grain and fodder. It belongs to the Poaceae family and has a chromosome number of 2n=20. It is a C4 crop with high photosynthetic efficiency (Mohammedi *et al*., 2023). Sorghum stands first among the cereals as fodder crop due to its wide adaptability and tolerance to various biotic and abiotic factors (Devi *et al*., 2018). Fodder sorghum is an important crop for livestock feed due to its adaptability, high yield potential, and nutritional benefits. A significant quantity of green biomass produced by fodder sorghum may be fed to animals. Sorghum feed is high in carbohydrates and gives animals a solid source of energy. Additionally, it has important elements including fibre, protein, and minerals that support the general health and productivity of animals. Due to its very short development cycle, sorghum may be harvested more than once within a single growing season. Its rapid growth habit provides a constant supply of fresh fodder, making it particularly valuable during periods of high livestock feeding demand. But out of the total net area that is under sorghum cultivation, not more than 5 % of land is utilized for fodder sorghum (Arvinth *et al*., 2021). Therefore, the production of fodder sorghum could not meet the demand. With the rapid growth of population and urbanization, it is almost impossible to increase the area under cultivation, hence there is a need to develop high yielding varieties.

It is evident that there is still space for development in the yield potential of sorghum, based on the gap between the biomass production potential and the current production rate. Many studies have been taken up by various researchers for assessing the genetic variability (Surashe *et al*., 2022) and genetic divergence of sorghum. The search for better parents with broad genetic base having good heterotic potential and the genes to withstand various biotic and abiotic stresses is still going on. Therefore, broadening the genetic base through the exploration of new genetic diversity and the efficient utilization of available variability offers significant potential for developing superior, high-yielding

Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab, India

Corresponding author : Reginah Pheirim, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab, India
***E-Mail:** pheirimreginah4@gmail.com

How to cite this artilce: Vaishnavi, Chetariya,C. P., Reginah Pheirim, Prajyot Waghmode and Alka Soharu. 2026. Assessment of genetic variability of quality, yield, and its attributing traits in sorghum (*Sorghum bicolor* (L.) Moench). *Electronic Journal of Plant Breeding*. 17(2): 227-233.
doi:10.37992/2026.1702.030

Received:16.11.2025 **Revised**: 03.07.2026 **Accepted**: 06.07.2026

sorghum genotypes. Effective utilization of existing genetic resources is the most important step in any crop improvement programme. In order to know the extent of variation present, estimation of various genetic variability parameters is of prime importance. Genotypic Coefficient of Variation (GCV) represents the proportion of total variation that is attributed to genetic differences among individuals, whereas Phenotypic Coefficient of Variation (PCV) includes both genetic and environmental variances. The heritability coupled genetic advance estimates indicate that the traits are governed by additive gene action and selection for those traits to improve the performance of the crop will be effective. The association studies reveal the relation between various traits and how the other quantitative traits are affecting the yield, directly as well as indirectly. Mahalanobis's D^2 analysis helps in identifying how closely or distantly the genotypes are related. This information can be utilized for selection of parents in the crop improvement programme. Therefore, the present study was conducted to assess the genetic variability, character association and genetic divergence among the 30 genotypes of fodder sorghum.

This research was conducted at Genetics and Plant breeding Research field of Lovely Professional University in the summer of 2024. The experimental material comprises of thirty fodder sorghum genotypes obtained from Indian Institute of Millet Research, Rajendranagar, Hyderabad, Telangana. Each genotype was sown in two lines of three-meter long with a spacing of 10 x 30 cm. These thirty genotypes were sown in three replications in a Randomized Block Design. The observation were recorded for 10 quantitative traits that are attributed to yield *viz*., plant height (cm), chlorophyll content (mg), leaf length (cm), leaf width (cm), leaf area (cm^2), number of leaves, stem thickness (cm), stem juiciness (%), total soluble solids (%), and green fodder yield (g/plant). The analysis of variance was carried out according to the procedure suggested by Panse and Sukhatme (1985). GCV and PCV were estimated according to Burton and De Vane (1953). Heritability and Genetic advance were calculated as per the methods suggested by Allard (1960) and Johnson *et al*. (1955). Correlation Coefficient analysis was performed as per the procedure suggested by Al-jibouri *et al*. (1958) and path coefficient analysis as per Dewey and Lu (1959). Genetic Divergence analysis was done according to Mahalanobis's D^2 statistics (1936).

Analysis of variance revealed highly significant ($p \leq 0.01$) differences among the 30 genotypes for all ten traits studied (**Table 1**), confirming the presence of substantial genetic variation that can be exploited for crop improvement. Similar results were reported by Nikhil *et al*. (2024) in forage sorghum, Arvinth *et al*. (2021) in forage sorghum, and Kumar *et al*. (2020) in forage sorghum.

The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all traits (**Table 2**), indicating predominant genetic control with minor environmental influence. High GCV and PCV values were recorded for stem thickness (15.01%; 16.50 %), total soluble solids (14.77 %; 16.26 %), green fodder yield (14.64 %; 17.66 %), and leaf area (14.53 %; 16.28 %), suggesting these traits have high genetic variability and are reliable candidates for selection. Moderate values were observed for stem juiciness, chlorophyll content, and leaf width, while plant height, number of leaves, and leaf length recorded the lowest values, indicating greater environmental susceptibility. Similar results in forage sorghum were reported by Santosh *et al*. (2020), Santosh and Pandey (2020), Kumar *et al*. (2020) and Harshdeep *et al*. (2019).

High heritability coupled with high genetic advance as percentage of mean (GAM) was recorded for stem thickness (82.75 %; 28.13 %), total soluble solids (82.52 %; 27.64 %), and leaf area (79.73 %; 26.73 %), indicating the predominance of additive gene action and the effectiveness of direct selection for these traits **(Table 2).** High heritability with moderate GAM was observed for leaf width (85.54 %; 24.24 %), stem juiciness (72.80 %; 22.69 %), and chlorophyll content (71.15 %; 22.07 %). Green fodder yield exhibited low heritability (68.72 %) with high GAM (25.00 %), while plant height

Table 1. Analysis of variance for ten quantitative traits in fodder sorghum

S. No.	Source of variation	Replication	Treatment	Error
	D.f	2	29	58
1	Plant height	72.06	407.58**	192.25
2	Chlorophyll content	0.08	20.47**	7.31
3	Leaf length	6.91	51.13**	21.07
4	Leaf width	0.40	0.81**	0.13
5	Leaf area	1007.72	3806.87**	892.26
6	Number of leaves	0.83	1.49**	0.52
7	Stem thickness	0.03	0.20**	0.07
8	Stem Juiciness	30.86	33.53**	11.14
9	Total Soluble Solids	0.76	2.97**	0.59
10	Green fodder yield	824.98	9082.51**	3287.96

Table 2. Genetic variability parameter among sorghum genotypes

S.No.	Character	Mean	Maximum	Minimum	GCV %	PCV %	Heritability %	GAM %
1	Plant height (cm)	192.31	292.08	163.82	9.64	12.04	64.11	15.90
2	Chlorophyll content (mg)	33.42	42.66	27.33	12.70	15.06	71.15	22.07
3	Leaf length(cm)	83.95	96.78	71.84	7.91	9.62	67.67	13.41
4	Leaf width(cm)	6.88	8.04	4.39	12.72	13.75	85.54	24.24
5	Leaf area (cm^2)	407.58	504.41	264.38	14.53	16.28	79.73	26.73
6	Number of leaves	11.63	13.54	9.85	9.87	11.65	71.90	17.25
7	Stem thickness (mm)	3.06	4.16	2.61	15.01	16.50	82.75	28.13
8	Stem Juiciness (g/g)	42.30	50.10	30.53	12.91	15.13	72.80	22.69
9	Total Soluble Solids (%)	11.28	14.01	9.10	14.77	16.26	82.52	27.64
10	Green fodder yield (g/plant)	1924.07	2628.52	1504.76	14.64	17.66	68.72	25.00

(64.11 %; 15.90 %) and leaf length (67.67 %; 13.41 %) showed low heritability and low GAM, limiting the scope for effective early-generation selection. Similar results in forage sorghum were reported by Tomar *et al*. (2012) in sweet sorghum, Sami *et al*. (2013) in sweet sorghum, Iraddi *et al*. (2013) in sweet sorghum, Nikhil *et al*. (2024) in forage sorghum, and Kumar *et al*. (2020) in forage sorghum.

Correlation Coefficient Analysis

Genotypic correlation coefficients were higher in magnitude than phenotypic correlations for most trait pairs. Highly significant positive genotypic correlations with green fodder yield were observed for total soluble solids (0.9928), leaf length (0.9793), number of leaves (0.8830), stem thickness (0.8787), stem juiciness (0.8590), and plant height (0.8351), indicating that improvement in any of these traits would lead to a corresponding increase in green fodder yield **(Table 3**). Leaf width (−0.3181) showed a non-significant negative genotypic correlation with yield, while chlorophyll content (0.0328) and leaf area (0.3693) showed non-significant positive correlations, suggesting limited utility of these traits as direct selection criteria for yield improvement. These results in forage sorghum are in accordance with Vara Prasad and Sridhar (2019) in yellow pericarp sorghum, Bhusal *et al*. (2013) in forage sorghum, Iraddi *et al*. (2013) in sweet sorghum, Tariq *et al*. (2012) in forage sorghum , Iyanar *et al*. (2010) in multicut fodder sorghum, and Harshdeep *et al*. (2019) in forage sorghum.

Path Coefficient Analysis

Path coefficient analysis revealed that total soluble solids exerted the highest positive direct effect on green fodder yield at both phenotypic (0.5076) and genotypic (0.8636) levels, followed by leaf length (0.2326; 0.5422) **(Table 4**). Leaf width (0.2361), stem thickness (0.1337), stem juiciness (0.0801), number of leaves (0.0749), and plant height (0.0311) showed moderate to low positive direct effects. Chlorophyll content (−0.4438) and leaf area (−0.2739) exhibited negative direct effects on green fodder yield at the genotypic level despite showing positive phenotypic correlations with yield, indicating that these associations are largely indirect and mediated

Table 3. Phenotypic correlation coefficient (above the diagonal) and genotypic correlation coefficients (below the diagonal) between 10 traits of fodder sorghum genotypes

CHARACTER	PH	CHLOR	LL	LW	LA	N L	ST. THIC	ST.JUI	TSS	GFY
PH	1	0.3611**	0.6800**	0.0663	0.4551**	0.3899**	0.5198**	0.4116**	0.5921**	0.5500**
CHLOR	0.3848*	1	0.3658**	0.1294	0.2883	0.3111**	0.2894	0.2770	0.3792**	0.2586*
LL	0.8412**	0.1153	1	0.0045	0.5744**	0.6585**	0.7624**	0.6587**	0.8496**	0.8006**
LW	0.0057	0.0012	-0.2541	1	0.8083**	-0.0219	0.0455	0.0331	-0.0345	-0.0623
LA	0.5556*	0.1017	0.4130*	0.7889**	1	0.3787**	0.4981**	0.4329**	0.4927**	0.4180**
NL	0.9675**	0.0854	0.9286**	-0.1288	0.4237*	1	0.6150**	0.4008**	0.7110**	0.5739**
ST. THIC	0.9283**	-0.0048	0.9532**	-0.3406	0.3011	0.9052**	1	0.6429**	0.8544**	0.6863**
ST.JUI	0.6745*	-0.0127	0.8785**	-0.1453	0.4299*	0.7704**	0.9162**	1	0.6845**	0.5576**
TSS	0.8658**	-0.0171	0.8213**	-0.2582	0.3878*	0.8886**	0.8791**	0.8859**	1	0.7829**
GFY	0.8351**	0.0328	0.9793**	-0.3181	0.3693	0.8830**	0.8787**	0.8590**	0.9928**	1

* and ** Significant at 5 and 1 per cent level; PH=Plant height; CHLOR= Chlorophyll content; LL=Leaf length; LB=Leaf width; LA= Leaf area; NL = Number of leaves; ST. THIC=Stem thickness; ST. JUI=Stem juiciness; TSS= Total soluble solids; GFY= Green fodder yield

Table 4. Genotypic path coefficient analysis depicting the direct and indirect effects of various traits on green fodder yield

Traits	PH	CHLOR	LL	LW	L.A	NL	ST. THIC	ST.JUI	TSS
PH	**0.0311**	-0.1708	0.1165	0.0013	-0.1522	0.0725	0.1242	0.0541	0.7477
CHLOR	0.1198	**-0.4438**	0.0177	0.0003	-0.0278	0.0064	-0.0007	0.0010	-0.0148
LL	0.0262	-0.0512	**0.5422**	-0.0600	-0.1131	0.0695	0.1275	0.0704	0.8808
LW	0.0002	-0.00052	-0.2144	**0.2361**	-0.2161	-0.0097	-0.0456	-0.0116	-0.2230
LA	0.0173	-0.0451	0.0346	0.1862	**-0.2739**	0.0317	0.0403	0.0345	0.3348
NL	0.0301	-0.0379	0.2177	-0.0304	-0.1161	**0.0749**	0.1211	0.0617	0.7674
ST. THIC	0.0289	-0.0856	0.2481	-0.8039	-0.0825	0.0678	**0.1337**	0.0734	0.8866
ST.JUI	0.0210	0.0056	0.0433	-0.0343	-0.1178	0.0577	0.1225	**0.0801**	0.7651
TSS	0.0270	0.0076	0.0238	-0.0610	-0.1062	0.0665	0.1373	0.0710	**0.8636**

Note: Bold figures represent direct effects. PH=Plant height; CHLOR= Chlorophyll content; LL=Leaf length; LB=Leaf width; LA= Leaf area; NL = Number of leaves; ST. THIC=Stem thickness; ST. JUI=Stem juiciness; TSS= Total soluble solids; GFY= Green fodder yield

through other traits; hence, selection based on these traits alone may not effectively improve green fodder yield. The residual effect was low, indicating that the traits included in this study adequately explained the variation in green fodder yield. These results in forage sorghum were in accordance with Arvinth *et al.* (2021) in forage sorghum, Harshdeep *et al.* (2019) in forage sorghum, Khandelwal *et al.* (2015) in sorghum, Lombard *et al.* (2015) in sweet sorghum, and Khan and Sadaqat (2014) in forage sorghum.

Genetic Divergence

Genetic divergence analysis using Mahalanobis‘ D^2 statistics and Tocher‘s grouping method classified the 30 genotypes into 12 clusters (**Table 5**). Cluster II was the largest with 7 genotypes, followed by Cluster I with 6 genotypes, while Clusters VIII, IX, X, XI, and XII contained only one genotype each. The maximum inter-cluster distance was observed between Cluster VIII and Cluster X ($D^2 = 245.90$), followed by Cluster X and IX (193.94) and Cluster X and VII (186.81), suggesting that crosses between genotypes from these clusters are likely to produce maximum heterosis and broad genetic recombination (**Table 6**). The minimum inter-cluster distance was recorded between Cluster I and Cluster XII (17.47). The maximum intra-cluster distance was recorded in Cluster VII (17.36), followed by Cluster VI (14.83). Similar results estimating genetic divergence using Mahalanobis‘ D^2 statistics in forage sorghum were reported by Akshita *et al.* (2024), Nikhil *et al.* (2024), Bhadouriya and Bhadouriya, (2024), Rohila *et al.* (2022), Prasanth *et al.* (2021), Thant *et al.* (2020), Ahalawat *et al.* (2018), Diwakar *et al.* (2017), Damor *et al.* (2017), Yadav *et al.* (2017), and Sinha and Kumarvadivel (2016) in sorghum.

This study revealed significant genetic diversity in traits contributing to green fodder yield. Key traits such as total soluble solids, stem thickness, leaf area, and green fodder yield showed high genetic variability, heritability, and genetic advance, making them ideal targets for selection in crop improvement programs. Correlation

Table 5. Clustering of genotypes based on genetic divergence

Cluster	Number of genotypes	Genotype
I	6	SOR14428, SOR12500, SOR14521, SOR14646, SOR14730
II	7	SOR14326, SOR14335, SOR14338, SOR14503, SOR14579, SOR14665, SOR14678
III	3	SOR14419, SOR14444, SOR14710
IV	3	SOR14534, SOR14535, SOR14729
V	2	SOR14346, Swaraj Barsi
VI	2	Maldandi Jowar, Rajha Jowar
VII	2	SOR14731, Gauran Jowar
VIII	1	SOR14520
IX	1	SOR14541
X	1	SOR14659
XI	1	SOR14697
XII	1	Gauran-2 dehu

Table 6. Inter and Intra cluster distances among the clusters

Cluster Number	1	2	3	4	5	6	7	8	9	10	11	12
1	**12.4199**	53.7448	28.6196	29.2119	46.4304	30.3345	90.7017	111.048	83.4826	40.5081	24.5352	17.4739
2		**10.4109**	94.9943	37.2428	35.9362	80.8634	32.2723	21.0467	24.7919	149.238	78.1609	37.2538
3			**11.1667**	50.3085	46.2384	23.8077	113.081	167.67	118.202	18.3585	25.2505	22.8653
4				**13.9518**	23.6754	34.0911	57.6872	67.2265	73.052	78.7409	23.0201	24.6042
5					**11.1412**	41.2863	38.8751	63.1846	56.4747	92.4262	39.9329	19.1726
6						**14.8298**	91.6124	135.757	121.846	36.8891	21.9266	23.1532
7							**17.3606**	27.7272	31.0989	186.813	112.548	51.6142
8								**0**	29.4876	245.901	139.491	81.8805
9									**0**	193.937	132.257	58.0949
10										**0**	27.175	52.5423
11											**0**	28.6594
12												**0**

Note: Bold figures represent intra cluster distances

and path coefficient analyses identified strong positive association between green fodder yield and traits like total soluble solids, leaf length, number of leaves, and stem thickness, while traits like chlorophyll content and leaf area negatively impacted yield. Genetic divergence analysis indicated broad genetic diversity, with inter-cluster distances suggesting that selecting genotypes from distantly related clusters could enhance genetic gai. Among the 30 genotypes, SOR14520, SOR14541, SOR14579, SOR1444, Rajha Jowar, and Maldandi Jowar were identified as the most promising candidates for breeding, particularly for improving traits such as total soluble solids, stem thickness, and green fodder yield. These findings provide valuable lights for future breeding programs aimed at increasing sorghum yield and productivity.

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