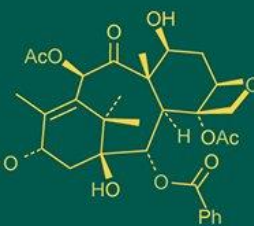
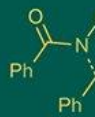


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(7): 1811-1815
www.biochemjournal.com
Received: 01-04-2026
Accepted: 05-05-2026

Manojkumar HG
Department of Genetics and
Plant Breeding, Sardar
Vallabhbhai Patel University
of Agriculture and Technology,
Meerut, Uttar Pradesh, India

Mitali Srivastava
Department of Genetics and
Plant Breeding, Sardar
Vallabhbhai Patel University
of Agriculture and Technology,
Meerut, Uttar Pradesh, India

SK Singh
Department of Genetics and
Plant Breeding, Sardar
Vallabhbhai Patel University
of Agriculture and Technology,
Meerut, Uttar Pradesh, India

Corresponding Author:
Manojkumar HG
Department of Genetics and
Plant Breeding, Sardar
Vallabhbhai Patel University
of Agriculture and Technology,
Meerut, Uttar Pradesh, India

Characterization of genetic diversity in forage sorghum (*Sorghum bicolor* L. Moench) for fodder improvement

Manojkumar HG, Mitali Srivastava and SK Singh

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i7Sv.9308>

Abstract

The present study entitled-“Characterization of Genetic Diversity in Forage Sorghum (*Sorghum bicolor* L. Moench) for Fodder Improvement” was undertaken during Kharif season at Crop Research Center (C.R.C), Sardar Vallabhbhai Patel University, Meerut. A set of thirty seven sorghum genotypes were evaluated to investigate the scope and scale of genetic divergence using Mahalanobis's D^2 Statistics on ten important quantitative traits. The experimental material was evaluated in a Randomized Block Design (RBD) with 3 replications in a 5-meter long and 4-row patch. Plants were spaced 10 cm apart and rows were spaced 30 cm apart. In each replication, five randomly selected plants were tagged and observations were recorded. Analysis of variance showed significant amount of variability for all the traits under study. Based on D^2 values thirty seven sorghum genotypes were partitioned into six distinct clusters based on ten morphological attributes. Cluster I was the largest comprising of fourteen genotypes while Cluster II was smallest with three genotypes. The peak intra-cluster variability (2.38) recorded for cluster I while smallest within group distance (0.02) was noted in case of cluster IV. The highest degree of inter-group distance was observed between cluster II and cluster IV (5.81) and the shortest distance between any two clusters was observed between cluster I and cluster VI (2.71). Green fodder yield per plant was the maximum contributor towards genetic diversity whereas minimum contribution of character towards genetic divergence was recorded for days to 50% flowering.

Keywords: Forage sorghum, genetic diversity, cluster analysis, D^2 statistics

Introduction

Sorghum is the best crop for semi-arid tropical regions, fits in well with sustainable agricultural models, and is a staple food for the world's poorest and most food insecure population. The cultivation and use of sorghum are prevalent worldwide; an estimated 42 million hectares of sorghum harvesting land are used worldwide. Although there is a growing global demand for sorghum production, India's production is failing to keep pace with the demand. In terms of both acreage and output, sorghum ranks fifth globally among cereal crops, after rice, wheat, maize, and barley. Sorghum is grown over an area of 39.7 m.ha. and produces around 63.5 m.t. worldwide in roughly 105 countries. Of the world's sorghum production, half is produced in Africa (50.2%), followed by the America (32.4%) and Asia (13.4%). In India, its cultivation encompasses an area of around 4.0 million hectares for food, feed, and fodder purposes, producing 4.6 million tons of grain annually (FAO, 2024) [7].

Sorghum [*Sorghum bicolor* (L.) Moench], $2n = 2x = 20$, is a C_4 plant belonging to the *Poaceae* family that is widely used for food, feed, and fodder. In India, it is cultivated over an area of around 4.24 million hectares for food, feed, and fodder purposes, yielding 4.78 million tons of grain annually. The world's greatest population of cattle is found in India, an agricultural nation. The availability of green feed is crucial for the security of animals. In India, pastures make up just 3.4% of the total land area, and cattle are typically kept on subpar pasture grasses or are stall-fed, mostly agricultural waste. India already lacks enough dry fodder (22%), green fodder (62%), and concentrates (64%). Given that sorghum is still regarded as a crop for marginal environments, a number of crop improvement initiatives were created to optimize biomass output as a result of its many applications as fodder (Prasanth *et al.*, 2021) [17].

According to the 21st livestock census (2024), India is home to 20% of the world's livestock population in just 2.4% of the country's total land area (68.0 million in Uttar Pradesh), meaning that these shortages will only become worse (BAHS, 2024). The main reason for low productivity and output of fodder is that farmers do not have access to better forage crop types with high-quality fodder. A supply of nutrient-rich fodder is essential to the success of any dairy enterprise. Compared to other kharif and summer season fodder crops, forage sorghum is a more palatable, nutrient-dense feed with excellent dry matter yield and digestibility. India's sorghum output is inadequate despite the growing global demand for the crop. There are several reasons why sorghum isn't more widely used. The most notable and significant factor is the dearth of adequate sorghum varieties. Breeders work to create new cultivars that are extremely effective and adaptable to all types of environments. The ideal variety is one that can thrive in a variety of growing environments within a certain producing region. In other words, as production circumstances improve, the cultivars must be able to withstand a variety of stressors and perform well in terms of yield (Erdurmus *et al.*, 2021) ^[6]. The degree of variation between or within species is referred to as genetic diversity. The necessity of optimal parental variety in order to produce superior genotypes in the segregating generations has been underlined by a number of researchers. A potential and ongoing source for creating new and improved crop

varieties is the genetic heterogeneity of both cultivated species and their wild relatives. In order to evaluate this level of diversity, group distance based on numerous characters was calculated using D^2 statistics. It is now one of the key methods for evaluating genetic divergence based on a variety of phenotypes. The use of these methods for evaluating genetic diversity in plant breeding was proposed by Rao (1952) ^[19]. Genetic divergence has been highlighted as being crucial for increasing yield potential through hybridization. In addition to serving as a limiting factor for assessing the level of divergence across various populations, Mahalanobis generalized distance (D^2) is also useful for choosing genetically diverse parents for a successful breeding program. Considering all these aspects, a research study was carried out to analyse genetic diversity in sorghum.

Materials and Methods

The current study, " D^2 analysis in forage sorghum (*Sorghum bicolor* L. Moench)," was carried out during the kharif season at the Sardar Vallabhbhai Patel University of Agriculture & Technology Crop Research Centre in Meerut. The Crop Research Center is located in the North Western Plain Zone, at an elevation of roughly 297 meters above mean sea level with 29°01'N latitude and 77°45'E longitude. The experimental material included thirty-seven different forage sorghum genotypes. Table 1 provides information about the experimental material.

Table 1: List of forage sorghum genotypes

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1.	SSG-59-3	14.	Pusa Chari-6	27.	SSV-84
2.	HJ-513	15.	UP Chari-2	28.	HC-136
3.	CSV-21	16.	Pusa Chari-23	29.	Pusa Chari-9
4.	G-48	17.	Pant Chari-2	30.	IC-056030
5.	MP Chari	18.	Rajasthan Chari-2	31.	IC-0568396
6.	Pratap Chari-1080	19.	Jawahar Chari-6	32.	IC-0347571
7.	UP Chari-3	20.	CSV-15	33.	IC-0597651
8.	HC-171	21.	CSV-17	34.	IC-0347568
9.	Pant Chari-8	22.	Pant Chari-7	35.	UP Chari-4
10.	Varsha	23.	Pant Chari-5	36.	UP Chari-1
11.	Rajasthan Chari-1	24.	Pant Chari-4	37.	IC-0597638
12.	HC-260	25.	Pant Chari-3		
13.	IC-0347570	26.	Pusa Chari-615		

The experiment was set up using a randomized block design with three replications, with each genotype serving as a treatment. The experiment was planted in a 5-meter-long, 4-row patch. Plants were spaced 10 cm apart, and rows were spaced 30 cm apart. To produce a competitive and robust crop stand, all cultural treatments necessary for a strong feed sorghum crop were used. During harvest, five competitive plants were chosen at random from each plot, and observations were made on these plants for several attributes. However, observations were made on a plot-by-plot basis over the days leading up to 50% blooming. For statistical analysis, the average of these five plants with regard to various plant characteristics was utilized. Observations on ten yield and yield attributing characters-Days to 50% flowering, Plant height (cm), Leaf breadth (cm), Leaf length (cm), Stem girth (mm), Leaves per plant, Leaf area (cm²), Leaf stem ratio, Total soluble solids (%) and green fodder yield (g) were recorded. In this experiment statistical analysis was followed and replication wise mean data of thirty seven genotypes for ten

characters are used for the statistical and biometrical analysis for the parameters-Analysis of variance as per the methods given by Panse and Sukhatme (1957) ^[14] and Genetic divergence analysis was done as per the Mahalanobis D^2 (1928) ^[11] statistics followed by the Rao (1952) ^[19].

Results and Discussion

Analysis of variance showed that the highly significant mean differences were observed for all the ten characters under study i.e., days to 50% flowering, plant height, leaf breadth, leaf length, stem girth, leaves per plant, leaf area, leaf stem ratio, total soluble solids and green fodder yield per plant which indicated that substantial variability was present in the sorghum accessions selected for study and were suitable for further genetic and selection parameters. High amount of genetic variability for many of these traits has also been reported earlier by Parashuram *et al.* (2022) ^[15], Bhadouriya & Bhadouriya (2024) ^[4] and Boratkar *et al.* (2025) ^[5].

Based on D^2 values thirty seven genotypes of sorghum were grouped into six clusters using ten component characters. Cluster I was the largest, comprising of fourteen genotypes followed by Cluster V with eight genotypes, Cluster III represented by six genotypes, Cluster VI have five genotypes, Cluster II with three genotypes, which concluded that in general, there was parallelism between genetic and geographic diversity. Cluster IV have one genotype which independently diverged from others (Table-2). Fourteen genotypes grouped under Cluster I which indicated their

proximity and narrow genetic base. This view point has been supported by the works of Rajappa *et al.* (2024) [18], Ahmad *et al.* (2025) [1] and Gebre *et al.* (2025) [8]. Genotypes belonging to cluster I (G-48, Pratap Chari-1080, Varsha, IC-0347570, UP Chari-2, CSV-17, Pant Chari-7, Pant Chari-4, IC-056030, IC-0568396, IC-0597651, UP Chari-4 and UP Chari-1, UP Chari-4 and UP Chari-1) observed maximum genetic diversity within the cluster as compared to the genotypes belonging to other clusters.

Table 2: Distribution of thirty seven genotypes of forage sorghum (*Sorghum bicolor* L. Moench)

Clusters	No. of genotypes	Genotypes
I	14	G-48, Pratap Chari-1080, Varsha, IC-0347570, UP Chari-2, CSV-17, Pant Chari-7, Pant Chari-4, IC-056030, IC-0568396, IC-0597651, UP Chari-4 and UP Chari-1.
II	3	CSV-21, Pant Chari-8 and IC-0597638.
III	6	SSG-59-3, HJ-513, Rajasthan Chari-1, Pusa Chari-23, Pant Chari-3 and Pusa Chari-615.
IV	1	MP Chari
V	8	HC-171, Pusa Chari-6, Pant Chari-2, Rajasthan Chari-2, Jawahar Chari-6, CSV-15, SSV-84 and IC-0347568.
VI	5	UP Chari-3, HC-260, Pant Chari-5, HC-136 and Pusa Chari-9.

The maximum intra cluster distance (2.38) was recorded for cluster I followed by cluster II (2.32), cluster V (2.25), cluster III (2.03), cluster VI (1.91) while minimum intra cluster distance (0.02) was noted in case of cluster IV (Table-3). Maximum inter cluster distance revealed between cluster II and cluster IV (5.81) followed by cluster III and V (5.25), cluster IV and cluster VI (5.21) and the minimum inter cluster distance was found between cluster I and cluster VI (2.71). These results are in accordance with the findings of Pal *et al.* (2022) [13], Arvinth *et al.* (2024) [2], Patel *et al.* (2024) [16] and Santosh & Pandey (2024) [20].

Table 3: Average intra and inter cluster (D^2 value) distance in thirty seven genotypes of forage sorghum (*Sorghum bicolor* L. Moench)

Clusters	I	II	III	IV	V	VI
I	2.38	3.70	2.86	4.79	3.85	2.71
II		2.32	4.95	5.81	3.60	3.63
III			2.03	3.81	5.25	3.93
IV				0.02	4.74	5.21
V					2.25	2.87
VI						1.91

In this, Days to 50% flowering had highest mean (Table-4) for cluster number I (86.29) and lowest mean for cluster number III (72.56). For cluster number IV (321.97), plant height was maximum; for cluster number II (263.33), it was minimum. In the cluster numbers III and II, leaf length recorded the highest mean (83.44), and the lowest (44.93). Cluster number V shows the maximum leaf breadth (791) and cluster number III shows the minimum leaf breadth (633). Cluster VI recorded the highest means (460.35) and cluster II recorded the lowest means (242.19) for leaf area. According to the stem girth data from cluster numbers IV (18.57) and II (13.73), cluster number IV reported a maximum mean and cluster II reported a minimum mean. Cluster number VI (15.22) had the highest number of leaves per plant, while cluster number II (10.73) had the lowest number of leaves per plant. The leaf stem ratio produced a maximum mean (5.53) for cluster number IV and a minimum mean (1.86) for cluster number III. Cluster number III had the highest mean (TSS) (10.89), while cluster number II had the lowest (8.90). Green fodder yield observed maximum mean for cluster number IV (836.71) and minimum mean for cluster number II (209.00).

Table 4: Cluster means values for ten characters in forage sorghum (*Sorghum bicolor* L. Moench)

Characters	Days to 50% flowering	Plant height (cm)	Leaf breadth (cm)	Leaf length (cm)	Stem girth (mm)
I	81.24	258.46	4.99	72.20	11.29
II	81.89	255.91*	5.33	71.89*	13.59**
III	77.67*	282.42	4.26*	76.59	10.74*
IV	88.67**	329.78**	4.74	85.45**	11.33
V	85.62	294.02	5.85	77.64	13.36
VI	79.33	258.22	5.88**	74.20	12.44

Characters	Leaves per plant	Leaf area (cm ²)	Leaf stem ratio	Total soluble solids (%)	Green fodder yield per plant (g)
I	11.80	260.23	5.29*	9.27	200.22
II	12.33**	268.95	8.22**	10.72**	299.89**
III	10.17*	243.92*	6.53	8.05*	183.68
IV	10.33	260.03	6.78	9.73	172.98*
V	12.26	333.02**	5.58	10.06	291.20
VI	10.87	326.15	5.82	8.70	239.31

In the present investigation, green fodder yield per plant was the maximum contributor towards genetic diversity (12.78) followed by leaf length (12.27), leaves per plant (11.45), plant height (10.40), leaf breadth (10.11), stem girth (9.36), total soluble solids (9.33), leaf stem ratio (8.92) and leaf area (8.32) whereas minimum contribution of character

towards genetic divergence was recorded for days to 50% flowering (7.07) as given in Fig-1. These results are somewhat in accordance with the findings of Kumar *et al.* (2023) [10], Kiran *et al.* (2024) [9] and Navyashree *et al.* (2024) [12].

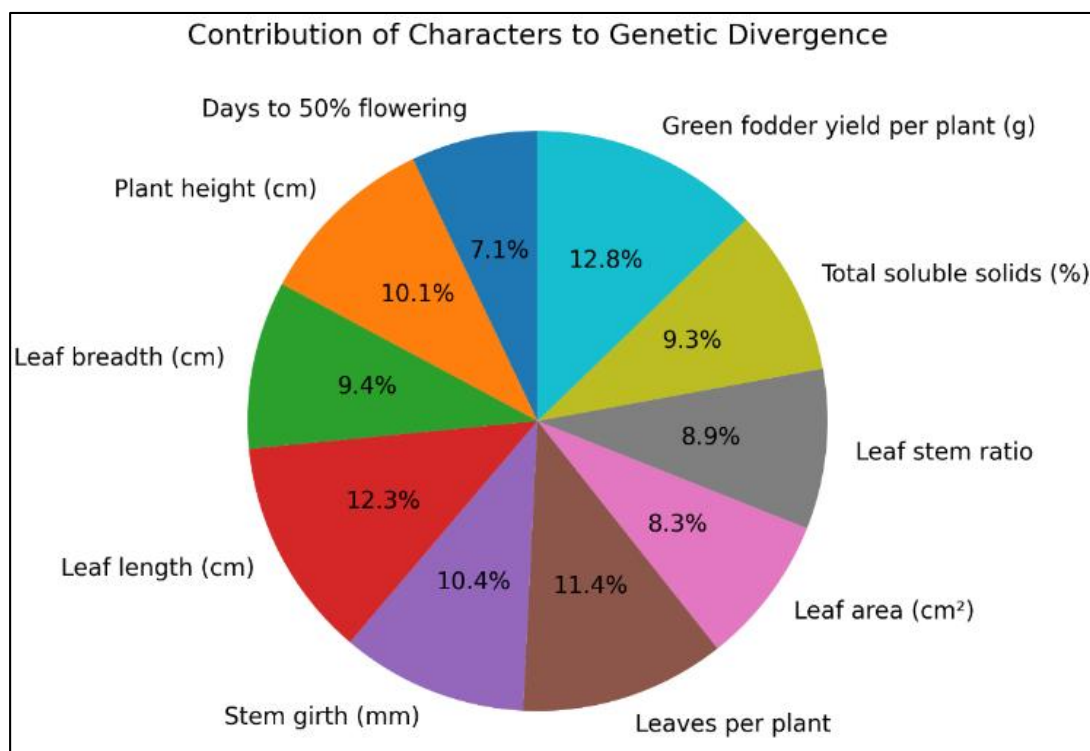


Fig 1: Percentage contribution of characters

Conclusion

Analysis of variance exhibited high significant differences among the genotypes for all the characters i.e., days to 50% flowering, plant height, leaf breadth, leaf length, stem girth, leaves per plant, leaf area, leaf stem ratio, total soluble solids and green fodder yield per plant which indicated that wide spectrum of variability among the genotypes. Genotypes belonging to cluster I (G-48, Pratap Chari-1080, Varsha, IC-0347570, UP Chari-2, CSV-17, Pant Chari-7, Pant Chari-4, IC-056030, IC-0568396, IC-0597651, UP Chari-4 and UP Chari-1) observed maximum genetic diversity within the cluster as compared to the genotypes belonging to other clusters. Hence, hybridization could be taken up among these genotypes for obtaining desirable segregants for the fodder yield and yield contributing characters. In the present investigation, green fodder yield per plant was the maximum contributor towards genetic diversity (12.78) followed by leaf length (12.27), leaves per plant (11.45), plant height (10.40), leaf breadth (10.11), stem girth (9.36), total soluble solids (9.33), leaf stem ratio (8.92) and leaf area (8.32) whereas minimum contribution of character towards genetic divergence was recorded for days to 50% flowering.

References

- Ahmad R, Shabbir G, Ullah SF, Ibrar D, Ilyas M, Al-Shaebi EM, *et al.* Genetic divergence among sorghum (*Sorghum bicolor* L.) genotypes grown under rainfed conditions. *Journal of Crop Health*. 2025;77(1):1-4.
- Arvinth S, Patel RN, Gami RA, Tiwari KK, Joshi AH. Morphological and molecular diversity analysis in forage sorghum (*Sorghum bicolor* (L.) Moench). *Indian Journal of Plant Genetic Resources*. 2024;37(2):206-214.
- BAHS. Release of Basic Animal Husbandry Statistics 2024. Department of Animal Husbandry and Dairying, Ministry of Fisheries, Animal Husbandry and Dairying, Government of India; 2024.
- Bhadouriya GP, Bhadouriya NS. D² analysis and principal component analysis to assess genetic divergence in *Sorghum bicolor* (L.) Moench for yield and its related attributes. *International Journal of Research in Agronomy*. 2024;7(1):322-326.
- Boratkar V, Reddy A, Gunturu PB. Principal component analysis and grouping of brown midrib sorghum advanced breeding lines for genetic diversity. *Forage Research*. 2025;51(1):29-34.
- Erdurmus C, Erdal S, Oten M, Kiremitci S, Uzun B. Investigation of forage sorghum (*Sorghum bicolor* L.) genotypes for yield and yield components. *Maydica*. 2021;66(2):1-13.
- FAO. FAOSTAT Database. Rome: Food and Agriculture Organization of the United Nations; 2024.
- Gebre W, Mekbib F, Tirfessa A, Bekele A. Phenotypic diversity of sorghum (*Sorghum bicolor* (L.) Moench) genotypes based on qualitative and quantitative traits. *Heliyon*. 2025;11(3):1-16.
- Kiran, Suvarna, Tembhurne BV, Girish G, Lakshmikanth M. Genetic diversity studies for yield and yield attributing characters in colored sorghum genotypes. *Indian Journal of Plant Genetic Resources*. 2023;36(2):208-215.
- Kumar R, Bagare V, Pathak VN, Yadav V, Singh A. Study of genetic diversity in forage sorghum (*Sorghum bicolor* (L.) Moench). *International Journal of Plant & Soil Science*. 2023;35(19):836-841.
- Mahalanobis PC. A statistical study at Chinese head measurement. *Journal of the Asiatic Society of Bengal*. 1928;25(3):301-377.
- Navyashree R, Mummigatti UV, Nethra P, Basavaraj B. Evaluation of genetic diversity in sorghum genotypes for drought tolerance using Mahalanobis' D² analysis.

- Journal of Advances in Biology & Biotechnology. 2024;27(9):90-97.
13. Pal D, Pandey PK, Verma SK, Baskheti DC, Prasad B, Gaur AK. Assessment of genetic diversity in forage sorghum (*Sorghum bicolor* (L.) Moench) for fodder yield and its component traits using D² statistics. The Pharma Innovation Journal. 2022;11(3):2190-2192.
 14. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: Indian Council of Agricultural Research; 1957.
 15. Patroti P, Madhusudhana R, Rakshit S, Sharma KK, Samdur MY, SD N, *et al.* Analysis of genetic diversity in exotic sorghum (*Sorghum bicolor*) germplasm and identification of trait-specific superior accessions for post-rainy situation. Crop Research. 2022;57(1-2):28-37.
 16. Patel M, Gami R, Tiwari KK, Kugashiya K, Patel R, Chudasama C. Genetic and molecular diversity analysis in forage sorghum (*Sorghum bicolor* (L.) Moench). Forage Research. 2024;50(2):118-125.
 17. Prasanth A, Premnath A, Muthurajan R. Genetic divergence study for duration and biomass traits in sorghum (*Sorghum bicolor* (L.) Moench). Electronic Journal of Plant Breeding. 2021;12(1):22-27.
 18. Rajappa PV, Krishnaraj PU, Hanamratti NG, Bagewadi B, Nawalagatti CM, Anisha A, *et al.* Assessment of genetic diversity in rabi sorghum landraces using D² statistics. Journal of Cereal Research. 2024;16(1):92-101.
 19. Rao CR. Use of discriminant and allied functions in multivariate analysis. Sankhyā: The Indian Journal of Statistics, Series A. 1962;24:149-154.
 20. Santosh, Pandey PK. Genetic diversity analysis for forage yield and quality traits in sorghum (*Sorghum bicolor* L. Moench) germplasm. Journal of Experimental Agriculture International. 2024;46(7):1016-1034.