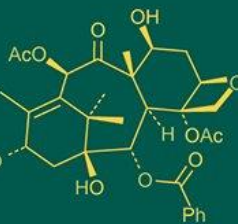
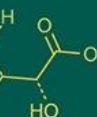
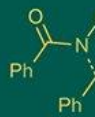


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Genetic Variability, Heritability and Genetic Diversity Analysis in Forage Sorghum (*Sorghum bicolor* L. Moench) Genotypes

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Abstract

The aim of this study is to determine the chemo-profile of aqueous extract of *Nauclea latifolia* using GC-MS. The GC-MS analysis of the plant extract was performed by using GC-MS QP-2010 (Shimadzu) and the mass spectra of the compounds found in the extract were matched with the data in the library of the National Institute of Standards and Technology (NIST). The result revealed the presence of eighteen compounds. The most prevailing compounds were 9-Octadecenoic acid (Z) - methyl ester, Oleic acid, and Benzamide 2-bromo-N-[2-(3-fluorophenyl)-5-benzoxazolyl] having a percentage area of 16.93%, 14.01%, and 9.18% respectively. The least abundant compound was 5-Methyl-2-phenylindolizine (0.66%). Some of these phytochemicals' bioactivities include anti-inflammatory, antibacterial, and antimalarial activities. As a result, the leaf extract has the potential to be a source of novel treatments. The results of this investigation thus validate the plant's traditional usage for medicine.

Keywords: Forage sorghum, genetic variability, heritability, genetic advance, Mahalanobis D^2 analysis, genetic diversity, cluster analysis, green fodder yield, plant breeding

Introduction

Forage sorghum (*Sorghum bicolor* L. Moench) is a major warm-season fodder crop grown widely across tropical and subtropical regions due to its high biomass yield, rapid growth, strong regeneration capacity, and resilience to drought and heat. Its broad adaptability and efficient water-use make it indispensable for livestock production, especially in rainfed and resource-constrained systems. The crop provides green fodder, silage and hay, meeting critical nutritional needs of dairy and meat animals. In the face of climate change, shrinking grazing lands, and rising demand for quality fodder, breeding high-yielding and widely adapted sorghum cultivars has become a key priority in forage improvement programs. The success of any plant breeding program hinges on the availability of genetic variability within the breeding material. Variability forms the foundation for selection, enabling identification of superior genotypes with desirable agronomic traits. To quantify this variability and predict selection efficiency, breeders rely on quantitative genetic parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance. Beyond variability studies, evaluating genetic diversity within available germplasm is equally vital for designing effective breeding strategies. The success of hybridization programs depends on selecting genetically diverse parents that can generate broad variability and superior recombinants in segregating generations. Crosses between divergent parents often result in greater heterosis and increase the likelihood of recovering transgressive segregants with desirable yield-related traits. Thus, identifying genetically diverse parental lines is a crucial step in forage sorghum improvement. Among multivariate techniques, Mahalanobis' D^2 statistics is widely used because it simultaneously considers multiple quantitative traits, providing a reliable measure of genetic relationships among genotypes. The use of Tocher's clustering method enables grouping of genotypes into distinct clusters, estimation of intra- and inter-cluster divergence, evaluation of cluster means for key traits, and determination of the relative contribution of individual characters to total divergence. This information helps breeders select suitable parental combinations for hybridization, thereby improving the efficiency of crop improvement programs.

Several studies have reported substantial genetic variability and diversity in forage sorghum for yield and its component traits, highlighting significant opportunities for genetic improvement through selection and hybridization. However, the magnitude of variability and divergence often differs across breeding materials and environments, underscoring the need for continuous evaluation of newly available germplasm. Characterizing diverse genotypes for heritable variation and genetic divergence is therefore essential for identifying elite parental lines and developing effective breeding strategies aimed at enhancing forage productivity.

Materials and Methods

Experimental Site

The field experiment was carried out during the Kharif 2023 season at the Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology (SVPUA&T), Meerut, Uttar Pradesh, India. The site is situated at approximately 29.01° N latitude and 77.45° E longitude, with an elevation of about 237 m above mean sea level. The region experiences a subtropical climate, characterized by hot summers, moderate to heavy monsoon rainfall, and cool winters. The experimental plots consisted of well-drained alluvial soil of medium fertility, which is well-suited for the cultivation of forage sorghum.

Plant Material and Experimental Design

The experimental material consisted of 35 genetically diverse forage sorghum (*Sorghum bicolor* L. Moench) genotypes, obtained from the Department of Genetics and Plant Breeding, SVPUA&T, Meerut. These genotypes represented a wide spectrum of variability for forage yield and associated agronomic traits. The trial was conducted using a Randomized Complete Block Design (RCBD) with three replications. Each genotype was planted in a single-row plot, following the recommended spacing and agronomic practices for forage sorghum. Standard crop management measures—including fertilizer application, irrigation, weed control and plant protection—were uniformly implemented across all plots to minimize environmental variation and ensure reliable comparisons.

Data Recording

Observations were recorded on thirteen quantitative characters from five randomly selected competitive plants in each replication, while observations on flowering were recorded on a plot basis. The traits studied were: Days to 50% flowering, Plant height (cm), Leaf breadth (cm), Leaf length (cm), Stem girth (mm), Leaves per plant, Internodes per plant, Nodes per plant, Leaf area (cm²), Leaf-stem ratio, Total soluble solids (°Brix), Protein content (%) and Green fodder yield per plant (g). The mean values of individual observations were used for statistical analyses.

Statistical Analysis

Analysis of Variance

The recorded data were analyzed using analysis of variance (ANOVA) following the procedure outlined by Panse and Sukhatme (1985) [9] to assess the significance of differences among genotypes for all quantitative traits. The treatment effects were tested using the F-test at both the 5% and 1% probability levels, ensuring a rigorous evaluation of genetic variability across the studied genotypes.

Estimation of Genetic Variability

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following the method proposed by Burton and De Vane (1953) [11]. These parameters were employed to quantify the extent of genetic and phenotypic variability among the sorghum genotypes. The magnitude of GCV and PCV was interpreted using the standard classification of low, moderate, and high variability, thereby providing a clear measure of the variability present in the population.

Estimation of Heritability and Genetic Advance

Broad-sense heritability (H^2) was estimated following the procedure outlined by Lush (1940) [9]. The expected genetic advance (GA) under selection was computed according to Johnson *et al.* (1955) [6], assuming a selection intensity of 5%. Genetic advance was further expressed as a percentage of the population mean (GAM). The combined interpretation of heritability and genetic advance provided insights into the nature of gene action controlling different traits and helped assess the effectiveness of phenotypic selection in forage sorghum improvement.

Genetic Diversity Analysis

Genetic divergence among the thirty-five forage sorghum genotypes was assessed using Mahalanobis' D^2 statistics (Mahalanobis, 1936) [10]. Based on generalized squared distances, the genotypes were classified into distinct clusters using Tocher's method (Rao, 1952) [13]. Intra- and inter-cluster distances were computed to evaluate the degree of genetic divergence among clusters. Cluster mean values were estimated for all quantitative traits to identify groups with desirable agronomic characteristics, while the relative contribution of each trait to total genetic divergence was determined to highlight the most influential characters driving diversity. This analysis provided a comprehensive understanding of genetic relationships among the genotypes and facilitated the identification of suitable parental combinations for hybridization in forage sorghum improvement programs.

Results

Analysis Of Variance

The analysis of variance (ANOVA) revealed highly significant differences ($P \leq 0.01$) among the thirty-five forage sorghum genotypes for all thirteen quantitative traits, confirming the presence of substantial genetic variability in the experimental material. Significant treatment mean squares were observed for days to 50% flowering (30.54), plant height (2040.52), leaf breadth (0.821), leaf length (82.90), stem girth (4.524), leaves per plant (4.819), internodes per plant (4.411), nodes per plant (2.884), leaf area (3348.42), leaf-stem ratio (0.0023), total soluble solids (5.218), protein content (1.011), and green fodder yield (16826.39). The highly significant variation observed across all traits demonstrates the existence of adequate genetic variability among the evaluated genotypes, thereby providing ample scope for effective selection and genetic improvement in forage sorghum.

Genetic Variability, Heritability and Genetic Advance

The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability, genetic advance (GA), and genetic advance as percent of mean (GAM) revealed considerable variability among the forage sorghum genotypes. For all traits, PCV

values were slightly higher than the corresponding GCV estimates, suggesting only a minor environmental influence on trait expression and indicating that most of the observed variation was genetic in origin. Among the studied traits, green fodder yield per plant exhibited the greatest variability, with GCV and PCV values of 22.62% and 22.73%, respectively. High variability was also recorded for leaf area, leaf-stem ratio and internodes per plant, total soluble solids, and leaves per plant, reflecting substantial exploitable variation in these economically important traits. Moderate variability was observed for plant height, stem girth, leaf breadth, leaf length, protein content, and nodes per plant. In contrast, the lowest variability was recorded for days to 50% flowering (GCV 3.07%; PCV 3.52%), indicating comparatively limited variation for this phenological trait. The estimates of broad-sense heritability (H^2) ranged from 40.76% for nodes per plant to 99.03% for green fodder yield per plant. Very high heritability was observed for green fodder yield (99.03%), plant height (93.52%), stem girth (86.89%), leaves per plant (84.73%), leaf area (82.48%), and leaf-stem ratio (80.33%). Relatively high heritability was also recorded for days to 50% flowering (75.95%), total soluble solids (72.23%), and internodes per plant (66.54%). Moderate heritability estimates were noted for leaf breadth (57.31%), leaf length (51.50%), and protein content (49.17%), while nodes per plant exhibited the lowest heritability (40.76%). These results indicate that most major yield-related traits are predominantly governed by genetic factors rather than environmental influences. The estimates of genetic advance as percent of mean (GAM) varied considerably across traits. The highest GAM was recorded for green fodder yield (46.37%), followed by leaf area (23.81%), leaf-stem ratio (21.94%), leaves per plant (19.85%), total soluble solids (19.58%), internodes per plant (19.48%), stem girth (15.69%), plant height (16.01%), leaf breadth (13.22%), nodes per plant (10.27%), leaf length (9.46%), protein content (9.27%), and days to 50% flowering (5.51%). The combination of high heritability and high GAM observed for green fodder yield, plant height, stem girth, leaves per plant, leaf area, and leaf-stem ratio suggests the predominance of additive gene action. This indicates that direct phenotypic selection for these traits would be highly effective in forage sorghum improvement programs.

Genetic Diversity

The Mahalanobis' D^2 analysis grouped the thirty-five forage sorghum genotypes into five distinct clusters, confirming the presence of substantial genetic divergence among the germplasm. Cluster III was the largest, comprising 12 genotypes, followed by Clusters I and V with seven genotypes each, Cluster IV with five genotypes, and Cluster II with four genotypes. The unequal distribution of genotypes across clusters highlighted considerable diversity, independent of their origin. Estimates of intra- and inter-cluster distances further validated the extent of divergence. Intra-cluster distances ranged from 2.316 (Cluster II) to 2.957 (Cluster III), indicating relatively high genetic similarity among genotypes within clusters. In contrast, inter-cluster distances were consistently greater, reflecting substantial divergence between clusters. The maximum inter-cluster distance was observed between Clusters II and IV ($D^2 = 4.931$), followed by Clusters I and IV (4.729) and Clusters III and IV (4.240). These combinations are

expected to yield the greatest potential for heterotic crosses and broad genetic variability in segregating generations. Conversely, the minimum inter-cluster distance was recorded between Clusters I and III (2.653), suggesting a relatively close genetic relationship between these groups. The cluster mean analysis revealed substantial variation among clusters for all studied traits. Cluster IV recorded the highest mean values for several economically important characters, including plant height (319.46 cm), leaves per plant (11.27), internodes per plant (10.10), nodes per plant (10.03), leaf area (264.76 cm²), and green fodder yield (374.76 g), highlighting its potential as a source of superior genotypes for fodder productivity. Cluster V exhibited the highest values for leaf breadth (5.50 cm) and stem girth (13.98 mm), while Cluster II recorded the highest leaf-stem ratio (0.240) and protein content (7.58%). Cluster I showed the highest total soluble solids (11.09 °Brix), whereas Cluster III was the earliest flowering group (84.42 days) and also produced relatively high fodder yield (274.69 g). These findings suggest that clusters combining superior mean performance with high genetic divergence could serve as valuable parental sources in future breeding programs. The relative contribution of individual traits to total genetic divergence indicated that nodes per plant (11.40%) contributed the most, followed by leaf breadth (9.75%), leaf length (9.21%), protein content (9.19%), days to 50% flowering (8.47%), leaf area (7.53%), internodes per plant (7.70%), leaves per plant (7.47%), leaf-stem ratio (7.23%), total soluble solids (6.96%), stem girth (6.76%), plant height (5.47%), and green fodder yield (2.86%).

These results indicate that while green fodder yield remains the primary economic trait, variation in several morphological characters was largely responsible for the overall genetic divergence observed. Consequently, these traits should be given due emphasis when selecting parents for hybridization and population improvement programs in forage sorghum.

Discussion

The availability of sufficient genetic variability forms the foundation of any crop improvement program, as it enables effective selection and the development of superior cultivars. In the present study, the highly significant differences observed among the thirty-five forage sorghum genotypes for all quantitative traits confirmed the presence of substantial variability in the experimental material. This broad genetic variation offers excellent opportunities for improving forage yield and associated traits through selection. Comparable findings have been reported by Singh *et al.* (2023) [16], Chavhan *et al.* (2022) [12], Kumar *et al.* (2020) [8], and Shafiqurrahman *et al.* (2024) [14], who also documented significant variability among forage sorghum genotypes for yield and related traits. For all studied traits, the phenotypic coefficient of variation (PCV) was consistently higher than the corresponding genotypic coefficient of variation (GCV), although the differences were generally small. This close correspondence between PCV and GCV suggests that environmental effects had only a limited influence on trait expression, and that the observed variability was largely genetic in nature. Consequently, phenotypic performance can be considered a reliable indicator of the genetic potential of these genotypes. Similar observations have been made by Malik *et al.* (2015), Srivastava *et al.* (2019), Kumar *et al.* (2020) [8], and

Shafiqurrahman *et al.* (2024) ^[14], who also reported narrow differences between PCV and GCV for key quantitative traits in sorghum. The high estimates of GCV and PCV recorded for green fodder yield, leaf area, leaf–stem ratio, internodes per plant, and leaves per plant highlight the presence of considerable exploitable genetic variability for these economically important traits. The high variability observed for yield-related characters suggests that these traits have been subjected to relatively less selection pressure, thereby offering greater scope for genetic improvement. Since green fodder yield is a complex quantitative trait influenced by multiple components, the existence of substantial variability in these characters provides opportunities for simultaneous improvement of fodder productivity through selection. Similar findings have been reported by Jain and Patel (2013), Dev *et al.* (2019) ^[3], Sumonthant *et al.* (2021) ^[17], and Singh *et al.* (2023) ^[16]. Heritability estimates provided valuable insights into the proportion of phenotypic variation that is heritable and transmissible to subsequent generations. In this study, high heritability was observed for green fodder yield, plant height, stem girth, leaves per plant, leaf area, and leaf–stem ratio, indicating that these traits are predominantly controlled by genetic factors. However, heritability alone cannot reliably predict the response to selection, as it does not differentiate between additive and non-additive gene effects. Therefore, simultaneous consideration of heritability and genetic advance offers a more dependable basis for identifying traits amenable to genetic improvement.

The combination of high heritability and high genetic advance as percent of mean (GAM) observed for green fodder yield, leaf area, leaf–stem ratio, stem girth, leaves per plant, and plant height suggests the predominance of additive gene action governing these traits. Since additive effects are largely fixable through selection, direct phenotypic selection is expected to be highly effective in improving these characters in forage sorghum breeding programs. Conversely, traits such as protein content and leaf length, which exhibited moderate heritability coupled with relatively low genetic advance, are likely influenced by non-additive gene effects and environmental factors. For these traits, simple selection may be less effective, and alternative breeding approaches may be required. These observations corroborate the findings of Rana *et al.* (2016), Singh *et al.* (2017), Dev *et al.* (2019) ^[3], Kumar *et al.* (2020) ^[8], Sumonthant *et al.* (2021) ^[17], and Chavhan *et al.* (2022) ^[2], who also reported that high heritability combined with high genetic advance is indicative of additive gene action in forage sorghum.

The assessment of genetic divergence is crucial, as the success of hybridization programs largely depends on the selection of genetically diverse parents. In the present study, Mahalanobis' D^2 analysis grouped the thirty-five forage sorghum genotypes into five distinct clusters, confirming the existence of substantial genetic diversity within the experimental material. The distribution of genotypes across clusters, irrespective of their pedigree or geographical origin, suggests that geographical origin is not always a reliable indicator of genetic divergence. This may be attributed to factors such as germplasm exchange, natural selection, and breeding practices, which often result in genetically similar genotypes originating from different regions. Comparable findings have been reported by Patankar *et al.* (2005) ^[12], Elangovan *et al.* (2014) ^[4],

Khadakabhavi *et al.* (2014) ^[7] and other researchers working on sorghum diversity. The magnitude of inter-cluster distances was consistently greater than intra-cluster distances, reaffirming the presence of wide genetic divergence among clusters. The maximum divergence observed between Clusters II and IV indicates that genotypes from these groups are the most genetically distinct and therefore constitute promising parents for hybridization. Crosses involving such divergent parents are expected to produce greater heterosis and wider segregation, thereby enhancing the probability of recovering transgressive segregants with superior forage yield and desirable agronomic traits. Similar conclusions have been drawn in earlier studies, where greater inter-cluster divergence was considered a key criterion for parent selection. The cluster mean analysis further revealed that different clusters exhibited superiority for different agronomic traits. Cluster IV showed superior mean performance for green fodder yield, plant height, leaf area, leaves per plant, internodes per plant, and nodes per plant, suggesting favorable allelic combinations for fodder productivity. Cluster V was superior for leaf breadth, leaf length, and stem girth, while Cluster II recorded higher leaf–stem ratio and protein content. Cluster I excelled in total soluble solids, whereas Cluster III was the earliest flowering group and also produced relatively high fodder yield. The identification of clusters that combine high genetic divergence with superior mean performance provides valuable guidance for selecting parental combinations capable of generating broad variability and high-performing segregants in future forage sorghum breeding programs.

The analysis of trait contributions to total genetic divergence revealed that nodes per plant, leaf breadth, leaf length, protein content, and days to 50% flowering contributed more to overall divergence than green fodder yield itself. This finding underscores the importance of morphological and developmental traits in differentiating forage sorghum genotypes. Consequently, these characters should be given due consideration during parental selection for hybridization, as they can facilitate the development of genetically diverse populations with enhanced forage productivity.

Overall, the present investigation demonstrated the existence of substantial exploitable genetic variability and wide genetic divergence among the evaluated forage sorghum genotypes. The combination of high heritability and high genetic advance for major yield-related traits indicates that direct phenotypic selection would be effective for genetic improvement. Furthermore, the identification of genetically divergent clusters with superior mean performance provides a strong foundation for selecting parents in future hybridization programs aimed at developing high-yielding forage sorghum cultivars with improved agronomic performance and broader adaptability.

Table 1: Average intra and inter cluster (D^2 value) distance in thirty five genotype of forage sorghum (*Sorghum bicolor* L.Moench).

Clusters	I	II	III	IV	V
I	2.499				
II	3.642	2.316			
III	2.653	3.916	2.957		
IV	4.729	4.931	4.240	2.696	
V	3.813	3.022	3.655	3.382	2.640

Bold values are intra cluster distance

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

Cluster	No. of genotypes	Genotypes
I	7	CSV-21, GFS-5, CSV-15, Pusa Chari 09, MP Chari, Pant Chari-7 and Rajasthan Chari-2
II	4	CSV-17, Pant Chari-4, Varsha and Pratap Chari-1080
III	12	Pusa chari-23, IC-0347568, Rajasthan Chari-1, SSV-84, SSG-59-3, IC-7570, G-48, HJ-513, Pusa Chari-615, Pant Chari-3, IC-8396 and IC-0597651
IV	5	HC-171, IC-0597638, HC-136, UP Chari-1 and UP Chari-3
V	7	Pant Chari-2, HC-260, UP Chari-4, UP Chari-2, Pusa Chari-6, Jawahar Chari 6 and Pant Chari-8

Table3: Cluster mean values for thirteen characters in forage sorghum (*Sorghum bicolor* L.Moench).

Cluster	Days to 50% flowering	Plant Height (cm)	Leaf Breadth (cm)	Leaf length (cm)	Stem girth (mm)	Leaves per plant	Internodes per plant	Nodes per plant	Leaf area (cm ²)	Leaf stem ratio	Total soluble solids	Protein content (%)	Green fodder yield (g)
I	85.71	267.32	4.50	65.63	13.34	9.21	7.53	8.53	214.91	0.180	11.09	7.21	266.86
II	90.50	262.90	5.02	61.74	13.10	10.72	8.87	9.87	205.12	0.240	10.90	7.58	224.46
III	84.42	274.73	4.72	61.94	11.83	9.71	7.91	8.95	205.68	0.200	8.83	6.65	274.69
IV	88.27	319.46	5.02	65.46	12.34	11.27	10.10	10.03	264.76	0.170	10.13	6.46	374.76
V	88.19	276.80	5.50	66.15	13.98	11.26	9.30	9.90	234.01	0.200	9.07	7.34	298.18

*Minimum cluster mean values **Maximum cluster mean values

Table 4: Contribution of different characters in creating diversity in forage sorghum (*Sorghum bicolor* L.Moench) based on Mahalanobis's D^2 analysis

Genotypes	% Contribution
Days to 50% flowering	8.47
Plant Height (cm)	5.47
Leaf Breadth (cm)	9.75
Leaf length (cm)	9.21
Stem girth (mm)	6.76
Leaves per plant	7.47
Internodes per plant	7.70
Nodes per plant	11.40
Leaf area (cm ²)	7.53
Leaf stem ratio	7.23
Total soluble solids	6.96
Protein content (%)	9.19
Green fodder yield (g)	2.86

Table 5: Estimates of variability parameters for thirteen characters in forage sorghum (*Sorghum bicolor* L. Moench).

Genotypes	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	Genetic advance (as % of mean)
Days to 50% flowering	3.07	3.52	75.95	4.78	5.51
Plant Height (cm)	8.03	8.31	93.52	44.61	16.01
Leaf Breadth (cm)	8.47	11.19	57.31	0.65	13.22
Leaf length (cm)	6.40	8.92	51.50	6.06	9.46
Stem girth (mm)	8.17	8.76	86.89	2.00	15.69
Leaves per plant	10.47	11.37	84.73	2.04	19.85
Internodes per plant	11.60	14.22	66.54	1.66	19.48
Nodes per plant	7.81	12.23	40.76	0.96	10.27
Leaf area (cm ²)	12.72	14.01	82.48	52.75	23.81
Leaf stem ratio	11.88	13.26	80.33	0.04	21.94
Total soluble solids	11.18	13.16	72.23	1.91	19.58
Protein content (%)	6.42	9.15	49.17	0.65	9.27
Green fodder yield (g)	22.62	22.73	99.03	132.80	46.37

Table 6: Analysis of variance (ANOVA) for thirteen characters of thirty five genotypes in forage sorghum (*Sorghum bicolor* L. Moench).

Source of variation	DF	Days to 50% flowering	Plant Height (cm)	Leaf Breadth (cm)	Leaf length (cm)	Stem girth (mm)	Leaves per plant	Internodes per plant	Nodes per plant	Leaf area (cm ²)	Leaf stem ratio	Total soluble solids	Protein content (%)	Green fodder yield (g)
Replication	2	1.18	337.43	0.239	57.6	0.289	0.578	0.772	0.107	47.92	0.0050	2.903	0.316	290.06
Treatment	34	30.54**	2040.52**	0.821**	82.9**	4.524**	4.819**	4.411**	2.884**	3348.42**	0.0023**	5.218**	1.011**	16826.39**
Error	68	2.24	34.75	0.129	15.8	0.164	0.208	0.493	0.769	168.83	0.0001	0.458	0.208	41.12
Total	104	11.47	696.30	0.357	38.6	1.592	1.722	1.779	1.448	1205.99	0.0009	2.061	0.472	5533.40

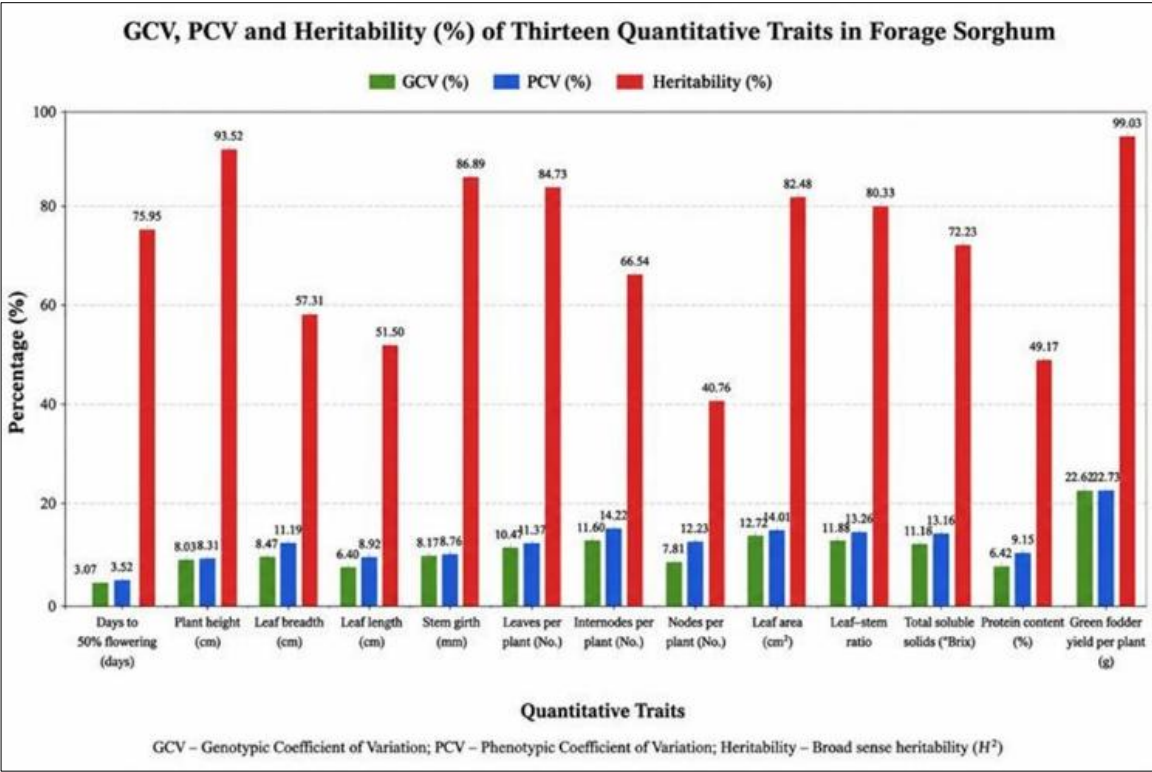


Fig 1: "GCV, PCV and Heritability (%) of Thirteen Quantitative Traits in Forage Sorghum"

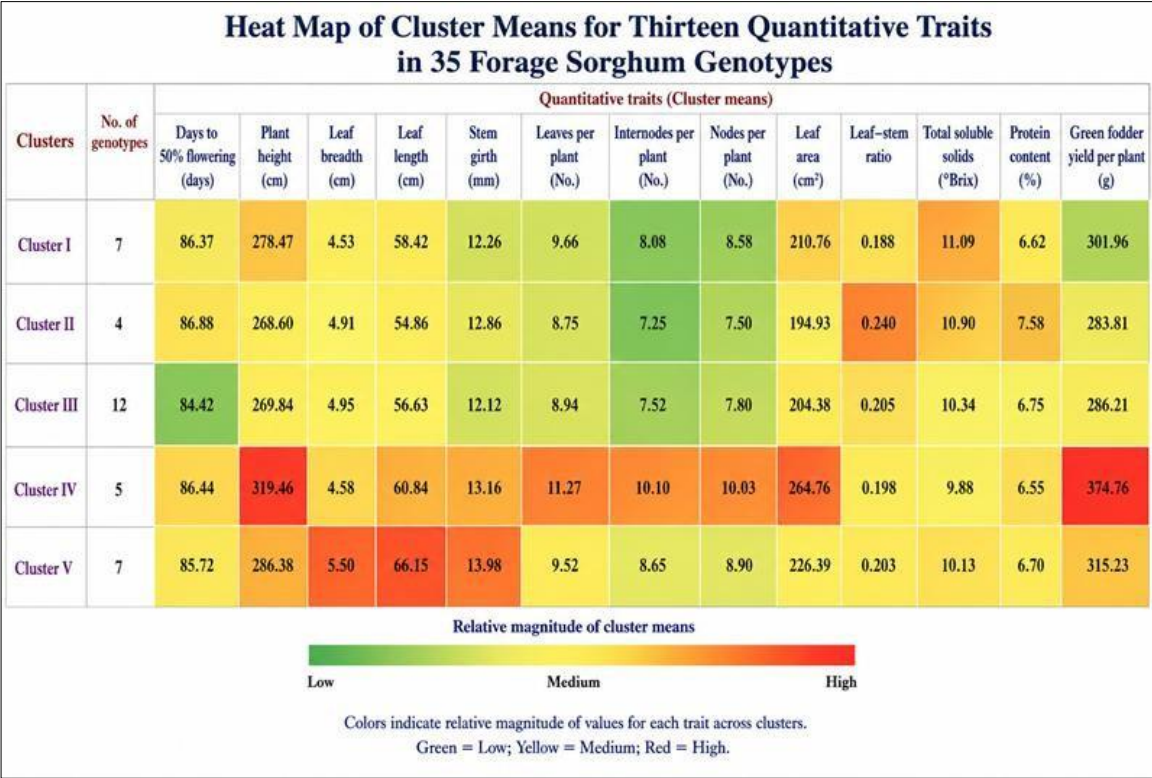


Fig 2: "Heat Map of Cluster Means for Thirteen Quantitative Traits in 35 Forage Sorghum Genotypes"

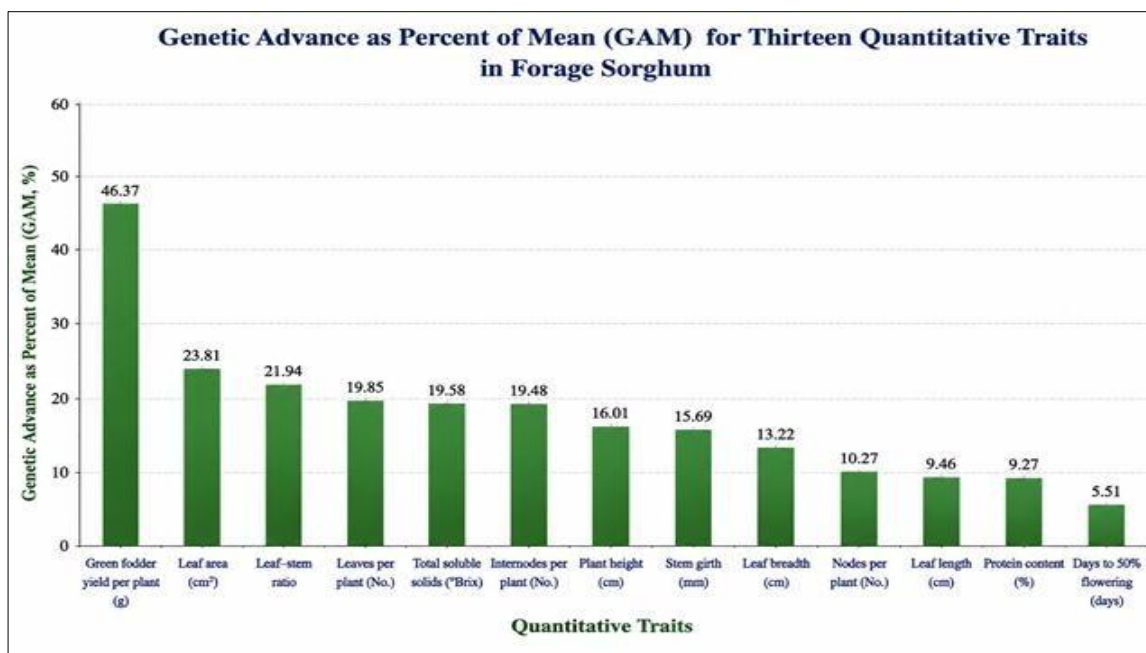


Fig 3: Genetic Advance as Percent of Mean (GAM) for Thirteen Quantitative Traits in Forage Sorghum

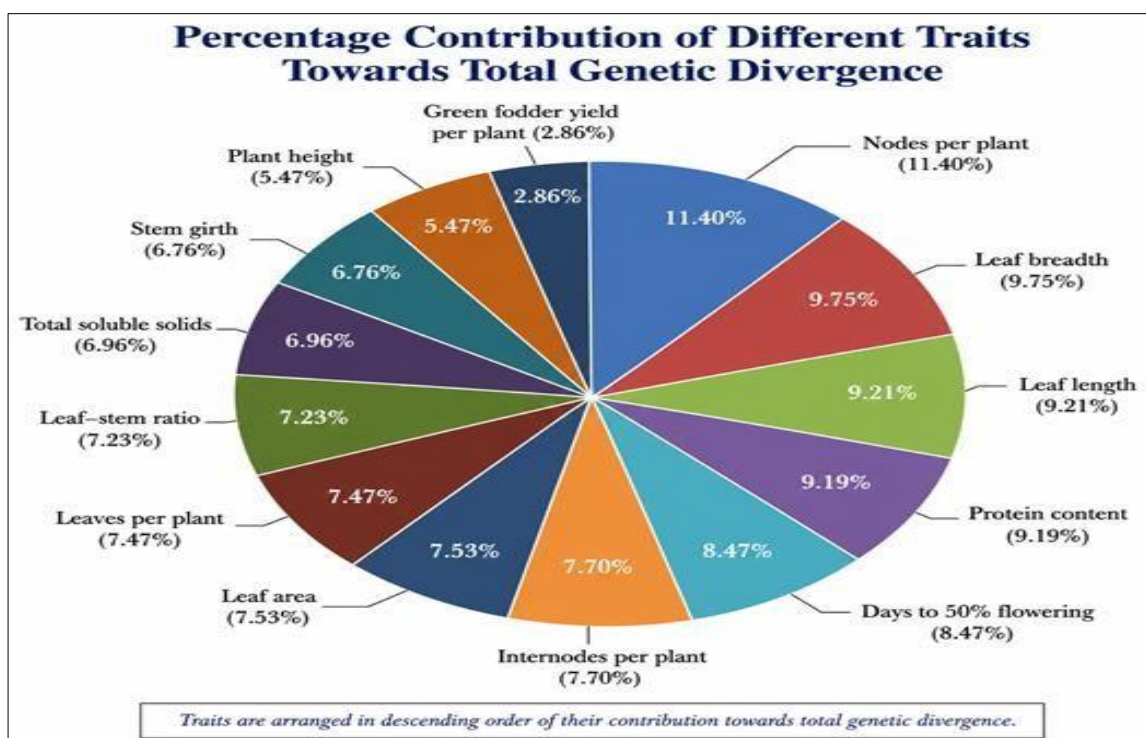


Fig 4: "Percentage Contribution of Different Traits Towards Total Genetic Divergence"

Conclusion

The present investigation demonstrated the existence of substantial genetic variability and diversity among thirty-five forage sorghum (*Sorghum bicolor* L. Moench) genotypes evaluated under Kharif 2023 conditions. The highly significant differences observed across all studied traits confirmed ample scope for genetic improvement through selection and hybridization. The narrow differences between genotypic and phenotypic coefficients of variation for most traits suggested minimal environmental influence, reinforcing the reliability of phenotypic performance as an indicator of genetic potential. High heritability coupled with high genetic advance as percent of mean (GAM) was recorded for green fodder yield, leaf area, leaf-stem ratio,

leaves per plant, stem girth, plant height, total soluble solids, and internodes per plant. This combination indicates the predominance of additive gene action, suggesting that direct phenotypic selection would be highly effective for improving these traits in forage sorghum breeding programs. The Mahalanobis' D^2 analysis revealed considerable genetic divergence, grouping the genotypes into five distinct clusters. The maximum inter-cluster distance between Clusters II and IV highlighted the potential of these groups as parents for hybridization, with the likelihood of generating greater heterosis and wider segregation. Notably, Cluster IV exhibited superior mean performance for green fodder yield and several yield-contributing traits, making it a valuable source of elite parental material. In addition,

traits such as nodes per plant, leaf breadth, leaf length, protein content, and days to 50% flowering contributed substantially to overall genetic divergence, underscoring their importance in parental selection.

In summary, this study identified valuable genetic resources possessing high variability, favorable heritability, and wide genetic divergence. These findings provide a strong scientific basis for selecting genetically diverse and agronomically superior parents in hybridization programs aimed at developing high-yielding forage sorghum cultivars with improved productivity and adaptability.

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