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ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN FORAGE SORGHUM (*SORGHUM BICOLOR* L. MOENCH)

Mayank Tiwari*, S.K Singh, Rahul Singh Chauhan and Shubham Kumar
Department of Genetics & Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture and Technology,
Meerut, Uttar Pradesh-250110, India
*Corresponding author E-mail: 912mayanktiwari@gmail.com

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ABSTRACT

Sorghum is one of the most important fodder crops in the rainfed conditions of India and in Uttar Pradesh. This investigation was carried out at Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India, involving 35 genotypes of forage sorghum, using a randomized block design, in three replications, during *Kharif* 2022 to estimate the genetic variability, heritability and genetic advance. Observations were recorded for ten characters, namely days to 50% flowering (DF 50%), plant height (cm) (PH), leaf breadth (cm) (LB), leaf length (cm) (LL), number of leaves per plant (NLPP), total soluble solids (%) (TSS), leaf area (cm^2) (LA), stem girth (mm) (SG), leaf-stem ratio (LSR) and green fodder yield per plant (g) (GFYPP). Analysis of variance exhibited highly significant differences among the genotypes for all the traits, indicating a wide spectrum of variability among the genotypes. The estimated genetic advance expressed as a percentage of the mean was high (>20%) for all ten characters, indicating a favourable response to selection based on *per se* performance for these traits. High heritability (>60%) in broad sense was observed for all the ten traits. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high (>25%) for green fodder yield per plant, indicating a greater scope for selection of superior genotypes for these attributes. Based on the ten characters, the 35 genotypes were grouped into five clusters. PH contributed the highest percentage to diversity, followed by LSR, DF 50%, NLPP and LB, while SG and GFYPP contributed a smaller percentage to genetic divergence.

***Keywords* :** Fodder sorghum, genotypic coefficient of variation, intra- and inter-cluster D^2, phenotypic coefficient of variation, genetic diversity.

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is extensively grown for fodder in Rajasthan, Punjab, Haryana, Uttar Pradesh, Delhi and Gujarat. Sorghum originated in Africa. It is incredibly drought-tolerant and ranks among the top five cereal crops after wheat (*Triticum aestivum*), rice (*Oryza sativa*), maize (*Zea mays*) and barley (*Hordeum vulgare*) (Dalton *et al.*, 2021). Because of its drought tolerance capacity, sorghum is a great option for cultivation in arid and semi-arid regions. It is one of the main multipurpose crops cultivated for grain and fodder. Sorghum yields in India differ from state to state owing to differences in rainfall patterns, soil composition and seasonality. It can be grown throughout the year in the southern region, but only during the *rabi* and *kharif* seasons in the northern regions. The livestock sector depends on sorghum because of its rapid growth habit, high yield, capacity for regeneration, improved palatability, digestibility and resistance to drought (Neha *et al.*, 2022). In Uttar Pradesh, the overall area, production and productivity of sorghum are 3.81 million hectare, 4.23 million tonnes and 1110 kg/ha, respectively, and 0.17 million hectare, 0.27 million tonnes and 1578 kg/ha, respectively, in India (Anonymous, 2022). Studies on genetic variability offer fundamental knowledge on the genetic characteristics of a population, which can be used to develop breeding strategies for crop improvement. These investigations are also useful in understanding the type and magnitude of variability that may be attributed to various causes, the crop's sensitivity to environmental factors, the heritability of traits, and the genetic advance that can be achieved through practical breeding. The degree of genetic diversity and heritability in the source material determines the extent of any crop improvement programme. The environment also affects heredity; therefore using heritability statistics alone might not be helpful in identifying the traits that need to be chosen. However, heritability predictions are more accurate when combined with the anticipated genetic advance. Genetic advance aids in the development of appropriate breeding strategies, whereas heritability provides information on the degree of inheritance of quantitative traits.

Materials and Methods

The experimental material consisted of 35 diverse genotypes of forage sorghum (Table 1) obtained from previous research conducted in the Department of Genetics and Plant Breeding at Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh, India.

Table 1 : List of Genotypes

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

In the *kharif* season of 2022, the experiment was conducted using a randomized block design with three replications. It was planted on June 28, 2022, in a 4-row plot that was five meters in length. The plant to plant distance was 10 cm, and the row-to-row spacing was 30 cm. All cultural procedures were implemented to produce a healthy crop. Observations were recorded for days to 50% flowering (DF 50 %), plant height (cm) (PH), leaf breadth (cm) (LB), leaf length (cm) (LL), number of leaves per plant (NLPP), total soluble solids (%) (TSS), leaf area (cm^2) (LA), stem girth (mm) (SG), leaf stem ratio (LSR) and green fodder yield per plant (g) (GFYPP). Statistical analyses were performed according to methods described by Dewey and Lu (1959), and Rao (1962).

Results and Discussion

Analysis of variance

The analysis of variance (ANOVA) for 35 genotypes was performed for all ten characters as stated above and the analysed data are presented in Table 2. For all the ten traits studied, including DF 50 %, PH, LB, LL, NLPP, TSS, LA, SG, LSR and GFYPP, ANOVA revealed significant differences among the genotypes used in the present investigation. This revealed that there was sufficient variability in the current set of materials for further analysis and study. A high amount of genetic variability for many of these traits has also been reported by Yucel *et al.* (2020) and Chavhan *et al.* (2022).

Table 2 : Analysis of variance (ANOVA) was performed on ten characters among thirty-five genotypes of forage sorghum [*Sorghum bicolor* (L.) Moench].

Sources of variation	d.f.	DF 50 %	PH	LB	LL	NLPP	TSS	LA	SG	LSR	GFYPP
Replication	2	4.46	166.27	0.01	0.38	0.27	0.03	49.76	0.24	0.001	102.51
Treatment	34	92.72**	1526.78**	2.15**	281.56**	7.75**	5.49**	13181.05**	14.25**	0.007**	21164.31**
Error	68	9.28	195.52	0.07	6.97	0.28	0.22	294.55	0.21	0.003	142.81

*, ** Significant at 5% and 1% level, respectively.

Variability Parameters

Fig-1 provides the estimates of heritability, genetic advance, genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) for each character. For all the characters, the phenotypic coefficient of variation was nearly equal to the genotypic coefficient of variation, indicating that there were few environmental effects influencing their expression to some degree or other. Maximum (>25%) genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for GFYPP per plant (27.320 and 27.590), while moderate (10-25%) values were noted for the LB (14.630 and 15.400), LL (13.470 and 13.970), NLPP (11.750 and 12.380), TSS (14.850 and 15.730), LA (21.110 and 21.820) SG (16.940 and 17.320) and LSR (12.450 and 14.840) whereas recorded low (<10%) values were recorded for days to 50% flowering (6.580 and 7.600) and PH (6.820 and 8.190). These findings are similar to those reported by Rana *et al.* (2016) and Ranjith *et al.* (2017).

All traits, including days to 50% flowering (74.980), PH (69.420), LB (90.310), LL (92.920), NLPP (90.000), TSS (89.110), LA (93.580), SG (95.700), LSR (70.350), and GFYPP (98.000), showed high heritability (> 60%). These results were similar to those of Nikhil *et al.* (2024) and Kumar *et al.* (2020).

The expected genetic advance expressed as a percentage of the mean was high (>20%) for LB (28.640), LL (26.750), NLPP (22.960), TSS (28.880), LA (42.060), SG (34.150), LSR (21.510), and GFYPP (55.710), while a moderate genetic advance (10–20%) was observed for days to 50% flowering (11.740) and PH (11.710). Higher genetic advance indicates a good response to selection based on per se performance for these characters. A similar result was also noted earlier by Srivastava *et al.* (2019) and Koppeti *et al.* (2022).

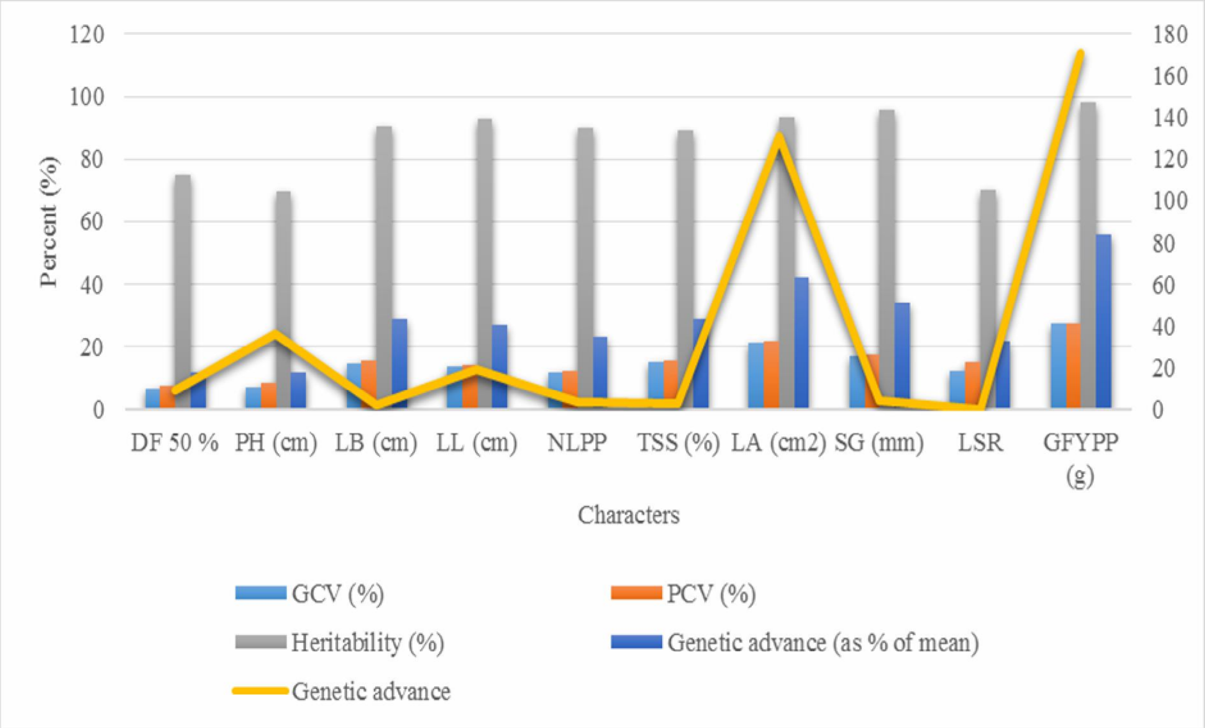

Fig. 1: Variability parameters for ten traits in forage sorghum [*Sorghum bicolor* (L.) Moench]

Inter- and intra-cluster distance

Table 3 lists the average intra- and inter-cluster D^2 values as well as the average intra and inter-cluster distances. The highest average inter-cluster D^2 value (7.410) was observed between clusters I and V, while the lowest value (2.417) was obtained between clusters I and II. Cluster II (2.194) had the highest intra-cluster distance, which was followed by Cluster I (2.181), Cluster III (1.893), Cluster IV (1.844), and Cluster V (1.325). The minimum inter-cluster D^2 value showed that clusters I and II genotypes are very closely related to one another, which is not desirable for hybridization programs; however, clusters I and V genotypes are not very closely related and the crosses among the genotypes included in these clusters may give a high heterotic response and thus better segregants to generate new material in forage sorghum. These outcomes are consistent with the conclusions of Kumar *et al.* (2022) and Kavya *et al.* (2019).

Table 3: 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	**2.181**				
II	2.417	**2.194**			
III	4.275	4.573	**1.893**		
IV	3.023	3.231	2.934	**1.844**	
V	7.401	6.616	3.817	5.275	**1.325**

Bold values are intra cluster distance

Group constellation

Thirty-five genotypes were grouped into five clusters. The clustering pattern of the genotypes is shown in Table 4. The number of genotypes in each cluster ranged from two to ten. Cluster IV was the largest cluster IV with 10 genotypes followed by cluster I with 9 genotypes, Cluster III with 8 genotype, Cluster II with 6 genotype and Cluster V with 2 genotypes which concluded that in general, there was parallelism between genetic and geographic diversity, Cluster V was represented by single genotype which independently diverged from others. The formation of solitary clusters may be due to total isolation preventing gene flow or intensive natural or human selection for diverse adaptive complexes. These genotypes may be unique and useful from a breeding perspective. Ten varieties grouped under Cluster IV indicated their proximity and narrow genetic base. These results are in accordance with the findings of Neha *et al*. (2022) and Sameera *et al.* (2021).

Table 4: Distribution of thirty- five genotypes of forage sorghum [*Sorghum bicolor* (L.) Moench].

Cluster Number	No. of genotypes	Genotypes
I	9	Pant Chari-4,Pant Chari-5,HJ-513,Varsha,PusaChari-615, Pant Chari-7, Pusa Chari-23, Rajasthan Chari-1 and GSF-5
II	6	MP Chari, CSV-15, SSV-84, UP Chari-4, Pratap Chari-1080 and CSV-17
III	8	Pant Chari-3, Rajasthan Chari-2, HC-136, UP Chari-3, HC-171, UP Chari-2, G-48 and CSV-21
IV	10	Jawahar Chari-6, SSG 59-3, Pusa Chari-6, Pant Chari-2, Pusa Chari-9, Pant Chari-8, IC-0597651, IC-0347571, IC-056030 and IC-0568396
V	2	HC-260 and UP Chari-1

Contribution of different characters in creating diversity

In the current study, PH (13.220) contributed the most to genetic diversity, followed by LSR (12.980), days to 50% flowering (12.610), NLPP (10.260), LB (10.070), TSS (10.020), LL (8.900), and LA (8.750). In contrast, SG (7.830) and GFYPP per plant (5.360) contributed the least to genetic divergence as given in Fig 2. To further boost fodder yield through hybridization, factors such as PH, LSR, days to 50% flowering, and NLPP were found to be highly significant contributors to genetic diversity. These factors may be used as parameters when selecting diverse parents. These results are in agreement with the findings of Singh *et al*. (2017) and More *et al*. (2018).

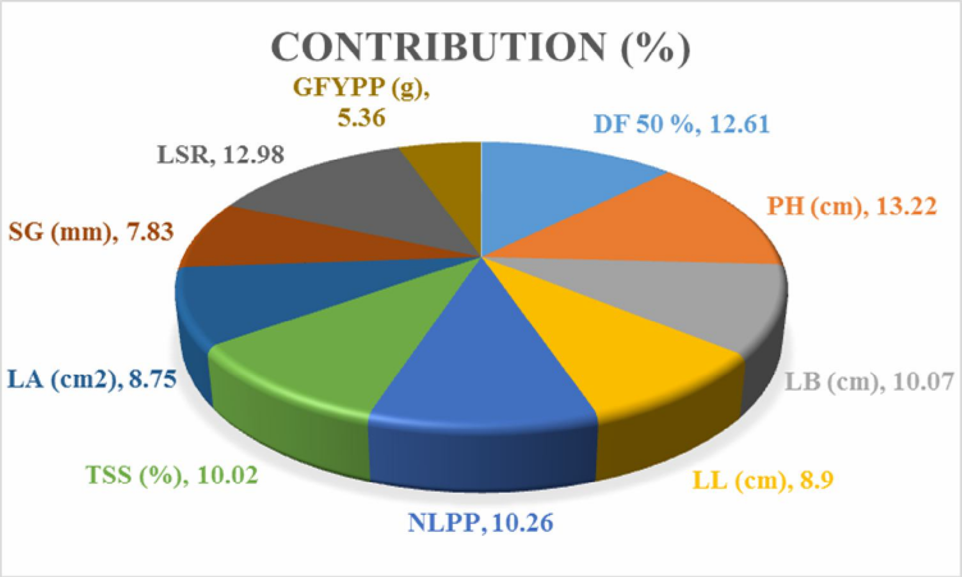

Fig. 2 : Contribution of different characters in creating diversity in forage sorghum [*Sorghum bicolor* (L.) Moench] based on Mahalanobis D^2 analysis

Conclusion

Analysis of variance for each character showed highly significant variations between the genotypes, suggesting a wide range of genetic variability in the study. High GCV and PCV values suggest that there is greater leeway to choose superior genotypes for these traits. All traits showed high heritability, indicating genotypic control of the aforementioned characteristics. Estimation of genetic advance expressed as a percentage of the mean showed that a favourable response to selection based on the inherent performance of these traits. Characters showing high heritability in conjunction with high genetic advance, as measured in percent of the mean, suggest that these characters are connected to additive gene action and selection for these attributes would be more successful. On the basis of inter-cluster distances, a hybridization program could be implemented between the varieties showing high inter-cluster distance. Hence, the identified genotypes as potential parents will be considered for selection to achieve the best results in the breeding program.

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