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Quantification of genetic variability and nutritional traits in forage sorghum germplasm for crop improvement

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Abstract

This comprehensive study investigates the genetic variability, heritability and genetic advance of selected agro-morphological and biochemical traits in 42 forage sorghum accessions grown in the Tarai region of Uttarakhand during the Kharif season of 2024. The experiment was designed as a randomized block with three replications to evaluate differences among germplasm for traits such as days to 50% flowering, plant height, leaf area, fodder yield, total soluble solids, crude protein and HCN content. Results demonstrated significant variability in all traits, with high heritability (>70%) observed for key yield and quality traits, including test weight, total soluble solids and crude protein. Traits with high heritability and genetic advance, such as green fodder yield (45.83%) and seed number per panicle (77.28%), suggest strong additive gene action and the potential for effective improvement through selection. This study provides crucial insights into the genetic potential of forage sorghum germplasm for enhancing forage yield and quality in the region, thereby facilitating targeted breeding strategies for sustainable livestock production.

Keywords: Forage sorghum, genetic variability, heritability, genetic advance, agro-morphological traits, biochemical traits

Introduction

Sorghum (*Sorghum bicolor* L. Moench) was originated in African native which ranks fifth among the cereals after wheat, rice, maize and barley. It has been cultivated in many countries throughout the world like Africa, America, Australia and Asia. (Mabelebele *et al.* 2015) ^[16]. It is well suited for cultivation in arid and semi-arid regions. It is one of the important multipurpose crops which is grown for grain and forage purpose Sorghum can be grown in both *rabi* and *kharif* season. In northern India, it is grown mostly in *kharif* season but in southern India, it is grown throughout the year. It is the fast-growing habit, high yield, good palatability, regeneration potential and drought tolerance which makes it the good choice for fodder for that community of farmers which are completely relies on livestock. (Rohila *et al.*, 2022) ^[22]. In America and Oceania, sorghum is primarily used as feeding cattle and poultry but in other countries it also used as a raw material in the making of starch and alcohol (Pérez *et al.*, 2010) ^[19]. Sorghum is a genus of about 25 species of flowering plants in the grass family. Sorghum also called great millet, Indian millet, milo, durra, orshallu. It is high in carbohydrates with 10 percent protein, 3.4 percent fat, and contains calcium, small amounts of iron, vitamin B1 and niacin.

Forage is essential to the diet of ruminants and significantly influences their nutritional intake; thus, variations in its quality can greatly impact digestive efficiency, the need for additional concentrate feed and the overall health and performance of the animals. It is estimated that one ton of good pasture can provide up to 150 kg total digestible nutrients. Sorghum fodder contains more than 50% digestible nutrients with 8% proteins, 45% nitrogen free extracts and 2.5% fat. Its dietary value is equivalent to corn as its protein level is same as corn silage but slightly less in energy. Animals feeding ability enhanced due to its palatability and juicy character. But there is a need to produce high yielding sorghum genotypes (Ali *et al.* 2022) ^[1].

Numerous generations of farmers have domesticated, intensified, diversified and improved the genetic resources through conscious and unconscious selection.

Landraces and improved cultivars are examples of human-selected variability that offer essential and crucial raw materials for agricultural improvement in both the current and future generations around the world. The significance of genetic resources has been acknowledged by the inter-governmental platform associated with the Food and Agricultural Organization (FAO) of the United Nations as a “common heritage of mankind” that must be accessible without limitations (FAO, 1983). There is an enormous amount of genetic variation in sorghum [*Sorghum bicolor* (L.) Moench]. The Biodiversity Act (2002) describes “landrace” as cultivar that is primitive and has been grown by ancient farmers and their generations. A significant amount of genetic diversity can be found in regions where the crop was first domesticated (in Africa) and the regions where it was introduced early (in Asia). Both cultivated species and wild crop progenitors in Africa exhibit genetic diversity Gebrekidan, 1982^[7]. DeWet and Harlan (1971)^[6] documented the distribution of both the wild relatives and the main cultivated varieties of the crop across Africa. Nevertheless, this natural genetic diversity faces numerous threats from natural selection, habitat destruction, and often the short-sighted agricultural practices of humans. Landraces and wild relatives of cultivated sorghum found in these diversity centres have provided valuable sources of resistance to emerging pathogens, insect pests, and other challenges such as high temperatures and drought, as well as traits that enhance food and fodder quality, livestock feed, and industrial applications. Sorghum germplasm collections differ in quantity and type across different regions globally. Nonetheless, the condition of the germplasm held at the

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in Patancheru, India, as well as in the USA, Africa and China, is significant to examine due to the scale of the crop improvement initiatives (Rosenow *et al.*, 2000)^[22] in these locations.

Interactions between genotype and environment are essential for the development and evolution of plant varieties, as they influence the stability of genotypic values across various environments. Heritability acts as an indicator of how traits are passed from parents to their offspring and is significant for forecasting outcomes in breeding initiatives.

Materials and Methods

The instructional dairy farm, Nagla, associated with Govind Ballabh Pant University of Agriculture and Technology Pantnagar, U.S. Nagar, Uttarakhand, served as the site for the field experiment in during the *Kharif* season of 2024. Pantnagar is geographically located at an elevation of 243.84 meters above mean sea level, at latitude 29.50° N and longitude 79.30° E. This area, situated at the foothills of the Shivalik range of the Himalayas, is part of a region locally referred to as Tarai and is classified as humid sub-tropical. The region lies at the foothills of the Shivalik range of the Himalayas and is also known as Tarai, with the same classification of humid sub-tropical. There were 42 accessions and 2 check varieties (Pant Chari-5 and Pant Chari-6) which were evaluated for its variability parameters. The accessions were sown in in randomized block design with three replications during *kharif* 2024. The field was divided into 132 blocks using 3 replications for each genotype and each replication consists of 6 rows each of 4 m length and 0.25 m row to row distance. The details of accessions are shown below in the table 1.

Table 1: Name of the accessions under the study

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1.	EJ 19	12.	IS 14333	23.	EJN 39	34.	IS 25733
2.	EJ 26	13.	EJN 73	24.	EJN 40	35.	IS 29691
3.	EJ 30	14.	IS 15008	25.	IS 21622	36.	ICSR 93023
4.	EJ 42	15.	ESRK 10	26.	IS 21977	37.	UTMC 571
5.	Raj 9	16.	IS 20399	27.	IS 23586	38.	NSSV 259
6.	Raj 21	17.	IS 20703	28.	IS 22241	39.	SSV 84
7.	SEVS-1	18.	IS 20740	29.	IS 23586	40.	SSG 212
8.	IS-313	19.	IS 20782	30.	IS 23948	41.	SSG 304
9.	E1	20.	IS 21021	31.	IS 25419	42.	JJ 1041
10.	E7	21.	IS 21461	32.	Malwan	43.	Pant Chari-5 (Check)
11.	E28	22.	IS 21602	33.	IS 2549	44.	Pant Chari-6 (Check)

All the required standards required for agronomic and plant protection practices were followed during the full cropping season. The data on qualitative and quantitative descriptors were recorded. Five plants were tagged in each replication for the assessment of the traits. Brix percentage of each accession was estimated by refractometer. The quantitative data was analysed statistically using R-studio. The analysis of variance was calculated with the method suggested by Panse and Sukhatme (1985)^[18]. The genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated as per Burton (1952)^[4], while classification of GCV and PCV were followed by Johnson *et al.* (1955)^[12], heritability in broad sense and genetic advance (GA) as suggested by Allard (1960)^[2].

Results and Discussion

The 42 accessions along with 2 check varieties were characterized and evaluated for 10 agro-morphological and 3 biochemical characters. Wider range of variability was recorded for both qualitative and quantitative characters. The observed were analysed using R-studio. Table 2. is representing the General mean, range, C.D. and C.V. of different traits in forage sorghum germplasm. The range varied for each trait indicating that there is good amount of variability present in the accessions. The characters like days to 50% flowering (57.81-88.81), plant height (235.17-387.33), number of leaves per plant (12.33-22.33), leaf area (261.52-572.72), total soluble solids (4.73-9.93), HCN content (53.28-121.37), dry fodder yield (1.27-3.61) and

green fodder yield (3.71-10.10) are depicting a wide range of variation which is directly indicating towards the higher amount of variability. The highest coefficient of variance was observed in dry fodder and green fodder yield. This higher amount of coefficient of variance representing the

more scope for the improvement programme. Also leaf area and plant height showed high C.D. value which means that there are the traits which are varying across the accessions and are the main cause of variation.

Table 2: General mean, range, C.D. and C.V. of different traits in forage sorghum germplasm.

S. No.	Character	Mean	Range		C.D.	C.V.
			Minimum	Maximum		
1.	Days to 50% flowering	72.18	57.81	88.81	3.61	8.67
2.	Plant height (cm)	326.63	235.17	387.33	27.25	10.22
3.	Number of leaves per plant	17.08	12.33	22.33	1.40	10.01
4.	Leaf length (cm)	76.03	60.67	89.17	4.62	7.45
5.	Leaf breadth (cm)	7.14	5.75	8.70	0.56	9.60
6.	Leaf area (cm ²)	407.34	261.52	572.72	46.79	14.07
7.	Stem girth (cm)	1.84	1.42	2.32	0.17	11.59
8.	T. S. S. (%)	7.40	4.73	9.93	0.46	7.80
9.	HCN content (ppm)	85.65	53.28	121.37	9.68	13.84
10.	Crude protein (%)	7.49	5.97	9.10	0.33	5.36
11.	Test weight (g)	19.36	13.36	27.40	0.58	3.69
12.	Dry fodder yield (kg/plot)	2.3	1.27	3.61	0.65	17.42
13.	Green fodder yield (kg/plot)	6.53	3.71	10.10	1.81	17.04

ANOVA for each character was also performed, and it was found to be significant for the treatment mean sum of square, which means that there is enough amount of variability present in the accession which is due to the genetic factors not by a random chance. All the replications mean sum of square for all the traits were found non-significant which means that out accessions don't get deviated when planted in different replication blocks. Low

error means sum of square also depicting that there is less influence of environmental variation which is indicating that the variability came out to be more precise as it is completely depending upon the genotypic proportion. Similar results were also reported by Bhatt (2003) ^[5], Kour and Pradhan (2016) ^[15], Sen *et al.* (2019) ^[24] and Kumar *et al.* (2020) ^[14].

Table 3: Analysis of variance (ANOVA) depicting mean sum of squares for 13 traits in sorghum

S. no.	Source of variation	Replication MSS	Treatment MSS	Error MSS
	Degree of freedom	2	43	39.16
1.	Days to 50% flowering	29.43	224.66**	1113.46
2.	Plant height (cm)	266.06	3441.42**	2.92
3.	Number of leaves per plant	5.01	19.60**	32.06
4.	Leaf length (cm)	14.37	163.01**	0.47
5.	Leaf width (cm)	0.18	1.61**	3283.59
6.	Leaf area (cm ²)	13.63	14281.71**	0.05
7.	Stem girth (cm)	0.06	0.22**	0.32
8.	T. S. S. (%)	0.31	7.29**	140.60
9.	HCN content (ppm)	356.66	1107.60**	0.17
10.	Crude protein (%)	0.01	2.13**	45601.14
11.	Seeds per panicle	23859.44	1025914.05**	0.51
12.	Test weight (g)	0.73	42.08**	554.94
13.	Dry fodder yield (kg/plot)	0.243	1.282 **	0.160
14.	Green fodder yield (kg/plot)	2.701	9.295**	1.239

** Significant at 1% level of significance

Genotypic variance, phenotypic variance and environmental variance were also calculated along with GCV, PCV, broad sense heritability and genetic advance as percentage which is presented in Table 3. It was found to be less difference between phenotypic coefficient of variance and genotypic coefficient of variance means there is low environmental coefficient of variance which is indicating that the variability present among the accessions is less influenced with the environmental factors. Highest value of PCV was found for seeds per panicle (50.6) followed by dry fodder yield (31.79), green fodder yield (30.32), HCN content (25.12), TSS (21.97) and leaf area (20.47). Moderate value of PCV was found for traits like test weight (19.58), stem girth (17.46), number of leaves per plant (17.05), days to

50% flowering (13.92), plant height (13.31), leaf width (12.91), crude protein (12.12) and leaf length (11.44). Similarly, Highest value of GCV was found for seeds per panicle (47.4) followed by dry fodder yield (26.59), green fodder yield (25.08), HCN content (20.96) and T.S.S. (20.59). Moderate value of PCV was found for traits like test weight (19.58), stem girth (17.46), number of leaves per plant (17.05), days to 50% flowering (13.92), plant height (13.31), leaf width (12.91), crude protein (12.12) and leaf length (11.44). Similarly, Moderate value of PCV was found for traits like test weight (19.58), number of leaves per plant (17.8), leaf area (14.86), stem girth (13.09), days to 50% flowering (10.89) and crude protein (10.79). Traits viz., plant height (8.53), leaf width (8.63) and leaf length (8.69)

were found to have low value of GCV. Similar results were also reported by Kalpande *et al.* (2014) [13], Singh *et al.* (2016) [25], Malik *et al.* (2015) [17], Kour and Pradhan (2016) [15] and Sen *et al.* (2019) [24]

Heritability of these characters were found higher as the traits are highly heritable. High heritability along with high genetic advance as percentage of mean represents more gain in character in it to be put under selection pressure. As the characters total soluble solids (87.79), crude protein (79.35) and test weight (96.45) were found to be very high heritability. For genetic advance as percentage of mean leaf area (22.24), total soluble solids (39.74), test weight (38.90), dry fodder yield (45.83) and green fodder yield (42.73) showed the higher values for genetic advance as percentage of mean. Characters which are showing higher values of heritability and genetic advance as percentage of mean can be improved just by direct selection as the tendency to pass on that character is higher than the other traits. Bhatt (2003) [5] and Arunkumar *et al.* (2013) [3] observed high heritability for HCN content which perfectly aligns with the current

findings. Malik *et al.* (2015) [17] and Jain and Patel (2013) [11] also reported high heritability as observed in results. Rana *et al.* (2016) [20], Jain (2010) [10] and Kour and Pradhan (2016) [15] also observed the high heritability for green fodder yield as recorded in current study.

For genetic advance as percentage of means, Seeds per panicle (77.28) recorded maximum value of genetic advance as percent of mean followed by dry fodder yield (45.83), green fodder yield (42.73), TSS (37.74), test weight (38.90), HCN content (36.03), leaf area (22.24) and stem girth (20.20). Similar results have also been reported by Godbharle *et al.* (2010) [8], Seetharam and Ganesamurthy (2013) [23] and Swamy *et al.* (2018). Moderate value of genetic advance as percentage of mean exhibited by crude protein (19.81), days to 50% flowering (17.56), leaf length (13.59), leaf width (11.89) and plant height (11.26). Moderate estimates of genetic advance expressed as percentage of mean in sorghum has been reported by Seetharam and Ganesamurthy (2013) [23] for the leaf length.

Table 4: Estimates of variance components, PCV, GCV, heritability, genetic advance and genetic advance as percent of mean for 13 traits in forage sorghum

S. no.	Character	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Environmental variance (σ^2_e)	PCV (%)	GCV (%)	Heritability (%)	Genetic Advance	Genetic advance as per cent of mean
1.	DTF	61.83	101.00	39.164	13.92	10.89	61.22	12.67	17.56
2.	PH	775.99	1889.45	1113.458	13.31	8.53	41.07	36.78	11.26
3.	NLPP	5.56	8.48	2.922	17.05	13.80	65.55	3.93	23.02
4.	LL	43.65	75.71	32.059	11.44	8.69	57.65	10.33	13.59
5.	LW	0.38	0.85	0.470	12.91	8.63	44.71	0.85	11.89
6.	LA	3666.04	6949.63	3283.58	20.47	14.86	52.75	90.59	22.24
7.	SG	0.0574	0.1027	0.0453	17.46	13.09	55.9	0.37	20.20
8.	TSS	2.32	2.64	0.327	21.97	20.59	87.79	2.94	39.74
9.	HCN	322.33	462.93	140.60	25.12	20.96	69.63	30.86	36.03
10.	CP	0.65	0.82	0.161	12.12	10.79	79.35	1.48	19.81
11.	TW	13.86	14.37	0.510	19.58	19.23	96.45	7.53	38.90
12.	DFY	1293.13	1848.07	554.938	31.79	26.59	69.97	61.97	45.83
13.	GFY	13700.57	20022.86	6322.294	30.32	25.08	68.42	199.45	42.73

Note: DTF- days to 50% flowering, PH- plant height (cm), NLPP- number of leaves per plant, LL- leaf length (cm), LW- leaf width (cm), LA- leaf area(cm²), SG – stem girth (cm), TSS – total soluble solids (%), CP – crude protein (%), TW – test weight (g), DFY – dry fodder yield (kg/plot), GFY – green fodder yield (kg/plot)

Conclusion

The present investigation revealed substantial genetic variability among the 42 forage sorghum accessions and two check varieties evaluated under the Tarai conditions of Uttarakhand. Significant differences among genotypes for all agro-morphological and biochemical traits indicated the presence of ample genetic diversity that can be effectively utilized in sorghum improvement programmes. High estimates of heritability coupled with moderate to high genetic advance for traits such as green fodder yield, dry fodder yield, total soluble solids, crude protein content, test weight and seed number per panicle suggested the predominance of additive gene action and the effectiveness of direct selection for these characters.

The narrow differences between phenotypic and genotypic coefficients of variation for most traits indicated limited environmental influence on trait expression, thereby enhancing the reliability of selection based on phenotypic performance. Among the evaluated traits, green fodder yield, dry fodder yield, total soluble solids, crude protein content and test weight emerged as important selection criteria for developing high-yielding and nutritionally superior forage sorghum cultivars.

Overall, the identified superior germplasm accessions constitute valuable genetic resources for future breeding programmes aimed at enhancing forage productivity and quality. The findings provide a strong foundation for the development of improved sorghum cultivars suited to the Tarai region and other similar agro-climatic conditions, thereby contributing to sustainable livestock production and fodder security.

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