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Research Article

Exploring genetic variability in fodder quality of forage sorghum in the North – Eastern regions of India

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Abstract
This study investigated genetic variability, character association, and genetic diversity in ninety-five forage sorghum genotypes, evaluated using a randomized block design for seven fodder quality traits. Analysis of variance revealed significant differences among genotypes for all traits. Genotypes such as G90 (424B), G23 (334B), G87 (CSV21F), G76 (330B), and G45 (373B) exhibit desirable fodder quality traits. Notably, G90 (424B) and G47 (NSS5B) stand out for their superior green forage yield per plant and fodder quality, making them prime candidates for varietal development programs. Crude protein emerged as a crucial selection factor for fodder quality. Green forage yield per plant showed minimal association with the other quality traits. A strong positive correlation was observed among in vitro organic matter digestibility, metabolic energy, crude protein, and ash content. D^2 analysis identified five clusters, with genotypes from clusters V and IV recommended for crossing to produce superior transgressive segregants for fodder quality. Acid detergent fibre, crude protein, and ash content significantly contributed to genetic divergence. Considering these selected traits and genotypes, they could be invaluable in future sorghum forage breeding programs aimed at enhancing fodder quality traits.

Keywords: Correlation, genetic diversity, Path analysis, Sorghum Fodder quality

INTRODUCTION

Sorghum is the world's fifth-most important grain crop and a major food crop on the Asian and African continents. In India, which houses 20% of the global livestock population, sorghum is a significant fodder source. (Tonapi *et al.,* 2020). Addressing livestock production challenges and population growth necessitates managing fodder, crop wastes, and feed deficits through productivity enhancements or land expansion. Forage sorghum can bridge the demand-supply gap for fodder, and a diverse genetic base is crucial for sustainable production, providing higher genetic gain and resilience in crop improvement programs. Plant breeders must harmonize forage sorghum crop fodder and feed production and nutritional quality to maintain a balanced diet (Godfray *et al.,* 2010). Breeders should possess knowledge of quality traits, their interactions, and genetics in order to improve forage sorghum. Sorghum forage exhibits higher *in vitro* dry matter digestibility compared to grain sorghum genotypes, with seasonal variations. Forage is chemically analysed by separating it into two fractions: the neutral detergent fibrous fraction and the acid detergent fibrous fraction. Cellulose, hemicellulose, and lignin are components of neutral detergent fiber, which affects the digestibility of feed (Wang *et al.,* 2016). The acid detergent fibre content has an impact on nutritional digestibility and nitrogen balance (Obregón-Cano *et al.*, 2019; Miranda *et al.,* 2020). Sorghum breeders use both traditional and biotechnological approaches to create new varieties or hybrids with desired stem traits, such as being genetically stable, easy to digest, high in dry matter yield, crude protein, sugar content, and low levels of hydrocyanic acid (Rosati *et al.,* 2019; Ping *et al.,* 2018).

The demand for fodder in nonconventional regions like Assam is increasing due to limited cultivation, leading to fodder scarcity (Bora *et al.,* 2020). This demand is driven by the growing dairy and meat industries' need for high-quality green and dry fodder (Talukdar, 2006). Assessing the genetic potential of existing genotypes is crucial for optimizing high-quality fodder production to meet the rising demand for livestock products. Genetic variability studies explore crop variability, heritability of traits, and potential for genetic improvement through breeding (Chavhan *et al.,* 2022). Understanding genetic parameters is crucial for plant breeders in selecting appropriate methods to enhance plant traits, estimating the potential improvement through selection, and assessing the significance of different genetic effects (Allard, 1960; Patil *et al.,* 2022). Yield, a multifaceted character, results from the interplay of various traits, and studying trait associations can facilitate indirect selection for yield improvement (Somegowda *et al.,* 2021). The study of path coefficient analysis is necessary to consider both the causal association and the magnitude of the relationship. To enhance the genetic improvement of fodder quality in sorghum, it is crucial to possess knowledge and information on genetic architecture and genetic diversity. This includes the implementation of effective breeding strategies and the incorporation of genes from distantly related germplasm (Rohila *et al.,* 2022). Transgressive segregants and hybrids with improved fodder quality were produced through the crossing of genetically diverse genotypes. This is the first attempt to study the genetic parameters, including genetic variability, diversity and trait association, of forage quality sorghum in the Assam condition to improve dairy product production, strengthen farmers' needs and provide livelihood security.

MATERIALS AND METHODS

Planting material and experimental design: This study involved 95 genotypes of forage sorghum in total and presented in **Table 1**, the field experiment was carried out using a fully randomized block design with two replications at Assam Agricultural University (AAU), Jorhat during *Kharif* season, 2021. The genotypes were planted with a spacing of 40 × 10 cm. Each plot consisted of a single row that was 3 m long and contained 15 plants of each genotype. The experiment followed conventional agronomic practices and implemented protection measures.

Trait phenotyping: A total of seven fodder quality traits were recorded on five randomly selected competitive plants of each genotype in each replication. These traits included ash content % (AC), acid and neutral detergent fibre % (ADF and NDF), acid detergent lignin % (ADL), metabolizable energy (ME-MJ/kg DM), crude protein % (CP), and in-vitro organic matter digestibility % (IVOMD). Harvested fodder was dried, chopped, and ground. Samples were scanned using a Fourier transformation near infrared spectrometer (FT-NIR) on a BUCHHI NIRMasterTM Essential (Switzerland) with the software package BUCHI NIRWare and specific sorghum calibration equations developed and validated by conventional laboratory analysis (Blümmel *et al.,* 2010).

Statistical analysis:The studies utilized various statistical methods, including analysis of variance (Panse and Sukhatme, 1967), PCV and GCV (Burton, 1952), heritability (Allard, 1960), genetic advance (Johnson *et al*., 1955), correlation analysis (Singh and Choudhary, 1981), path coefficient analysis (Dewey and Lu, 1959), and D^2 analysis (Mahalanobis, 1936; and Singh, 1981). All the analyses in this study were performed in R Studio, using R version 4.1.2 (R Core Team, 2021). The variability package (Popat *et al.,* 2020) was utilized for analyzing ANOVA, genetic variability parameters, and correlation studies. The ggplot2 package, version 3.3.4 (Wickham, 2016), was utilized to create visualizations using ggplot and biotools package (da Silva, 2021) and FactomineR (Le *et al.,* 2008) were used for carrying out D^2 and cluster analysis.

RESULTS AND DISCUSSION

Analysis of variance for fodder quality traits: Variance analyses for 95 forage sorghum genotypes across seven fodder quality traits are detailed in **Table 2.** Significant variations were observed among the genotypes, indicating substantial genetic variability in forage yield and quality attributes (Chavhan *et al.,* 2022; Somegowda *et al.,* 2021).

Mean performance: The average performance of 95 forage Sorghum genotypes for seven fodder quality traits is presented in **Table 3**. Higher average values for ash content, crude protein content, metabolizable energy, and *in vitro* organic matter digestibility were observed, which are the desirable traits in fodder. On the other hand, lower mean values were noticed in neutral detergent fibre content, acid detergent lignin content, and acid detergent fibre content. The G90 (424B) genotype showed favourable mean performances for neutral detergent fibre content (60.59 %), acid detergent lignin content (5 %), metabolizable energy (7.38), crude protein (12%), and in-vitro organic matter digestibility (50.51%). In addition, G23 (334B), G87 (CSV21F), G76 (330B), and G45 (373B) were desired for most of the fodder quality traits. Adopting a comprehensive breeding strategy requires selecting genotypes that excel in both forage yield and quality traits. Genotypes G90 (424B) and G47 (NSS5B) emerged as the most desirable, exhibiting higher green forage yield per plant and superior fodder quality. These genotypes are promising candidates for breeding programs focused on enhancing both yield and quality, thus ensuring a balanced feed ration. Similar findings were reported by Chavhan *et al.* (2022).

Genetic Variability, skewness and Kurtosis studies: Understanding genetic parameters are crucial for plant breeders to make informed decisions about selection methods, predict selection gains, and assess the

Table 1. List of genotypes included in the present study (Source - BVB, IIMR, Hyderabad)

Genotype Code	Genotype Name	Pedigree Information	Genotype Code	Genotype Name	Pedigree Information
G1	403B	(NSSB 1003 X NSSB 26)-3-1	G49	339B	(NSSB 1003 x ICSB 342)-3-2-3
G2	415B	(NSSB 1003 x ICSB 342)-1-3-1	G50	360B	(ICSB 687 x ICSB 702)-6-1-1
G3	349B	(ICSB 342 x ICSB 467)-3-1-3	G51	436B	(ICSB 687 x ICSB 702)-4-3-3
G4	321B	(NSSB 1002 X 296B)-7-1	G52	419B	(ICSB 338 x ICSB 342)-2-3-2
G5	445B	44121B x NSS 20B-5	G53	375B	44121B x NSS 20B-5
G6	370B (whIte)	(90001B x NSSB 1005)-4-1-2	G54	410B	(NSSB 1002 x NSSB 1005)-1-1-3
G7	353B	(ICSB 342 x ICSB 467)-10-1-1	G55	296B	Karad Local x IS 3922
G8	336B	(NSSB 1002 x NSSB 1005)-3-5-3	G56	CSV27	(GJ 38 x Indore 12) - 2 - 1 - 2 - 1 GJ 38 = GJ 35 x E 35 - 1
G9	301B	(NSSB 2 X 2219B)-3-1	G57	408B	(27B X NSSB 1002)-2-3
G10	412B	(NSSB 1002 x NSSB 1005)-3-5-3	G58	NSS1003B	Pedigree not available
G11	354B	(ICSB 342 x ICSB 687)-1-3-2	G59	329B	(NSSB 1003 X NSSB 26)-3-2
G12	ICS56B	(Serere elite x IS 9530)-2	G60	NSS7B	Pedigree not available
G13	429B	(ICSB 342 x ICSB 687)-1-3-2	G61	435B	(ICSB 687 x ICSB 702)-4-2-1
G14	NSS11B	Pedigree not available	G62	ICS27B	Pedigree not available
G15	402B	(NSSB 1003 X NSSB 26)-2-2	G63	442B	(90001B x NSSB 1005)-6-3-1
G16	428B	(ICSB 342 x ICSB 467)-10-2-2	G64	2219B	kafir shallu seletion
G17	CSV33MF	EMS mutant of CO FS 29	G65	325B	(NSSB 1002 X NSSB 23)-10-1
G18	384B	(NSSB 5 X 2219B)-5-1	G66	313B	(NSSB 6 X (CSV 17 X PKV 809))-10-2
G19	308B	(NSSB 5 X 2219B)-4-2	G67	PC615	Pusa chari 40 × Pusa Chari 67
G20	370B(Black)	(90001B x NSSB 1005)-4-1-2	G68	444B	44121B x NSS 13B-3
G21	323B	(NSSB 1002 X 296B)-12-1	G69	352B	(ICSB 342 x ICSB 467)-9-1-2
G22	NSS23B	Pedigree not available	G70	335B	(NSSB 13 x ICSB 699)-1-1-1
G23	334B	(27B X NSSB 1002)-2-3	G71	NSS1002B	Pedigree not available
G24	413B	(NSSB 1002 x NSSB 1005)-5-1-2	G72	351B	(ICSB 342 x ICSB 467)-8-2-1
G25	337B	(NSSB 1002 x NSSB 1005)-5-1-2	G73	CSV-20	SPV 946 x Kh 89 -246
G26	345B	(ICSB 338 x ICSB 342)-6-1-1	G74	377B	94001B x 41735-1
G27	359B	(ICSB 687 x ICSB 702)-4-3-3	G75	342B	(ICSB 4 x NSSB 13)-4-1-2
G28	367B	(ICSB 702 x ICSB 697)-5-3-1	G76	330B	(NSSB 1003 X NSSB 26)-9-1
G29	2077B	IS 2046 selection	G77	MP CHARI	K- 49 x J-57
G30	388B	(NSSB 6 X (CSV 17 X PKV 809))-8-2	G78	369B	(90001B x NSSB 1005)-3-1-1
G31	NSS10B	Pedigree not available	G79	355B	(ICSB 683 x NSSB 8)-2-2-3
G32	322B	(NSSB 1002 X 296B)-8-1	G80	382B	(NSSB 2 X 2219B)-3-2
G33	311B	(NSSB 6 X (CSV 17 X PKV 809))-4-2	G81	RS29	Pedigree not available
G34	389B	(NSSB 6 X (CSV 17 X PKV 809))-10-2	G82	467B	[((ICSB 11 × ICSV 700) × PS 19349B) × ICSB 13]4-1
G35	NSS1B	Pedigree not available	G83	Red B	Pedigree not available
G36	302B	(NSSB 2 X 2219B)-3-2	G84	327B	(NSSB 1003 X NSSB 26)-2-2
G37	338B	(NSSB 1003 x ICSB 342)-1-3-1	G85	CSV33MF	Derived from COFS29
G38	363B	(ICSB 687 x ICSB 702)-9-1-3	G86	CSV32F	HC 260 x B 35
G39	385B	(NSSB 5 X 2219B)-8-2	G87	CSV21F	GSSV 148 x SR 897
G40	346B	(ICSB 338 x ICSB 342)-7-3-1	G88	UPMC503	Selection from IS 5977
G41	NSS1008B	Pedigree not available	G89	348B	(ICSB 342 x ICSB 467)-2-3-3
G42	365B	(ICSB 686 x NSSB 1)-1-1-1	G90	424B	(ICSB 342 x ICSB 467)-2-3-3
G43	407B	(27B X NSSB 20)-1-3	G91	314B	(NSSB 15 X 296B)-2-1
G44	309B	(NSSB 5 X 2219B)-5-1	G92	PCD-8-1-2	
G45	373B	(ICSB 702 x (27BxSSV 84))-10-3-1	G93	307B	(NSSB 5 X 2219B)-4-1
G46	CSV30F	NSS 223 x NARI 111	G94	409B	(27B X NSSB 1002)-8-2
G47	NSS5B	Pedigree not available	G95	SSG-59-3	Non sweet sudan grass × IS-263
G48	358B	(ICSB 687 x ICSB 702)-4-2-1			

Table 2. Mean squares from analysis of variance for forage quality and its attributing traits of 95 forage sorghum genotypes

Source of Variation	DF	AC	NDF	ADF	ADL	ME	CP	IVOMD
Replication	1	0.23662	0.3892	0.248	0.002083	0.011464	0.4869	0.152
Genotype	94	2.323***	9.601 ***	35.615***	0.121***	0.102***	5.696***	3.958***
Error	94	0.101	0.336	0.416	0.019	0.013	0.211	0.305

*** - Significance level at (p < 0.001); Where, AC= Ash Content (%), NDF= Neutral Detergent Fibre Content (%), ADF= Acid Detergent Fibre Content (%), ADL= Acid Detergent Lignin Content (%), ME= Metabolizable Energy (%), CP= Crude Protein (%) and IVOMD= In vitro organic matter digestibility (%)

Table 3. Mean performances of 95 forage sorghum genotypes for seven fodder quality traits

Genotype	AC	NDF	ADF	ADL	ME	CP	IVOMD	GFYP
G1	15.11	60.02	49.52	5.43	7.18	6.62	49.44	142.36
G2	15.27	70.74	57.32	5.89	6.50	6.47	43.23	204.82
G3	13.92	61.56	56.58	5.31	7.13	8.00	49.50	313.00
G4	12.88	67.29	57.68	5.70	6.65	8.11	46.72	302.48
G5	11.80	67.54	52.04	6.31	6.45	6.33	46.01	155.68
G6	14.57	64.42	67.62	5.67	6.80	6.81	46.33	193.09
G7	13.56	64.39	55.57	5.58	6.80	7.55	46.61	246.83
G8	12.42	65.67	54.77	5.68	6.70	7.66	47.13	286.28
G9	11.83	64.92	50.31	5.78	6.76	5.37	46.95	228.23
G10	12.88	63.55	53.72	5.64	7.01	5.72	47.43	337.13
G11	12.54	63.99	50.61	5.61	6.81	6.52	46.73	194.53
G12	12.49	63.46	48.66	5.59	6.90	7.16	47.01	137.50
G13	13.34	62.06	47.71	5.38	7.17	8.08	49.68	215.12
G14	13.37	62.68	52.43	5.33	7.08	6.11	49.00	317.89
G15	13.46	64.15	54.56	5.52	6.81	8.18	47.44	314.33
G16	13.37	63.77	52.56	5.52	6.89	6.14	48.53	314.22
G17	13.29	67.62	51.21	5.82	6.61	4.53	46.52	108.16
G18	13.59	60.93	52.55	5.02	7.19	7.84	48.64	267.86
G19	12.77	61.39	46.25	5.36	7.08	7.11	48.06	211.21
G20	11.02	59.45	43.79	5.63	7.33	8.18	48.28	169.93
G21	10.90	65.23	46.61	5.76	6.55	7.99	46.16	222.92
G22	12.85	61.56	45.45	5.40	7.08	8.89	48.25	319.26
G23	15.13	61.62	54.76	5.16	7.34	11.94	50.44	283.28
G24	13.05	61.51	45.99	5.64	6.93	10.88	48.15	225.94
G25	11.55	64.89	45.96	5.83	6.69	8.91	47.16	256.13
G26	13.06	65.85	54.31	5.58	6.86	7.33	48.29	204.12
G27	12.59	62.62	46.53	5.51	6.87	9.06	47.39	116.39
G28	11.65	64.56	47.50	5.62	6.72	8.03	47.28	266.82
G29	13.48	63.44	48.27	5.39	7.11	9.12	49.17	150.39
G30	14.05	65.46	56.34	5.83	6.56	7.88	46.27	336.77
G31	12.28	62.83	46.31	5.52	6.87	8.06	47.51	230.98
G32	15.07	65.47	57.17	5.51	6.84	8.16	47.00	344.05
G33	15.51	70.53	53.06	5.68	6.72	10.89	44.62	328.04
G34	13.88	63.40	55.32	5.50	6.98	9.84	48.38	306.30

Table 3. Continued…..

Genotype	AC	NDF	ADF	ADL	ME	CP	IVOMD	GFYP
G35	12.05	65.27	48.70	5.47	6.92	5.36	48.19	446.18
G36	13.09	63.46	53.05	5.30	7.10	7.64	48.82	406.77
G37	12.68	64.51	50.00	5.59	6.83	9.89	49.07	225.50
G38	13.36	62.77	48.82	5.22	7.07	9.18	48.51	383.02
G39	14.70	66.55	53.51	5.40	6.95	7.95	48.26	259.63
G40	11.90	65.44	53.32	5.56	6.74	6.49	46.93	269.26
G41	12.77	63.56	53.51	5.67	6.91	9.89	48.11	285.54
G42	12.90	63.36	53.89	5.67	6.84	9.95	47.58	186.77
G43	13.50	64.50	54.11	5.50	6.91	8.39	47.72	280.38
G44	12.34	65.40	50.11	5.91	6.69	9.96	47.28	309.21
G45	11.75	57.63	43.50	5.51	7.43	9.71	48.04	231.55
G46	12.56	65.89	52.51	5.55	6.88	6.89	48.00	226.66
G47	12.56	60.95	45.30	5.28	7.12	6.15	49.11	362.28
G48	12.68	63.61	54.50	5.56	6.85	6.89	46.66	203.17
G49	12.24	61.88	45.83	5.45	7.10	9.86	48.02	351.79
G50	12.93	62.81	54.45	5.39	7.00	8.16	48.88	202.27
G51	12.28	63.22	45.83	5.51	7.00	8.91	47.74	189.43
G52	12.52	63.11	49.98	5.34	7.06	6.31	48.61	251.12
G53	13.63	64.22	54.49	5.56	7.04	10.03	48.72	229.01
G54	13.77	64.00	56.83	5.46	6.97	7.90	48.20	326.48
G55	13.37	65.34	54.67	5.59	6.82	7.15	48.09	193.19
G56	14.54	61.86	50.03	5.17	7.20	10.95	49.91	263.15
G57	13.82	64.05	53.95	5.57	6.94	5.88	47.96	258.36
G58	14.44	64.05	55.07	5.64	6.90	8.97	47.33	402.11
G59	13.49	64.61	53.92	5.45	7.04	9.01	48.67	241.13
G60	14.59	63.39	56.45	5.48	6.97	6.91	48.46	290.57
G61	13.36	64.62	52.75	5.56	6.85	7.07	47.54	169.04
G62	12.34	63.39	44.56	5.72	6.88	9.91	47.67	369.65
G63	13.74	63.21	50.82	5.61	6.83	10.15	48.05	447.51
G64	12.99	63.22	49.50	5.47	6.95	10.10	47.48	364.63
G65	13.31	62.52	49.13	5.58	6.81	8.05	48.04	286.61
G66	13.63	63.31	48.10	5.49	7.06	10.15	49.01	328.74
G67	11.83	61.53	44.47	5.62	7.04	9.08	46.99	102.50
G68	13.87	62.25	50.55	5.25	6.99	6.03	47.67	194.49
G69	12.68	63.97	50.34	5.50	6.91	11.00	47.07	437.76
G70	12.51	63.54	47.78	5.72	6.82	11.04	47.87	233.03
G71	12.47	66.95	54.78	5.69	6.83	7.04	48.50	195.30
G72	12.44	63.02	46.73	5.52	6.81	8.05	47.92	195.09
G73	12.81	66.12	54.80	5.72	6.88	5.56	47.38	166.72
G74	12.87	66.17	56.20	5.49	6.83	5.49	46.67	154.98
G75	13.86	68.45	56.96	5.81	6.56	5.48	44.28	313.34
G76	16.16	61.51	56.72	4.62	7.70	9.83	51.57	286.23
G77	13.48	62.74	47.78	5.46	7.09	10.22	49.39	169.08
G78	12.30	66.27	54.55	5.64	6.87	7.03	48.94	177.10
G79	12.39	62.32	46.60	5.46	6.86	7.95	48.05	262.14
G80	11.72	66.60	51.93	6.23	6.52	6.44	45.95	325.15

Table 3. Continued…..

Genotype	AC	NDF	ADF	ADL	ME	CP	IVOMD	GFYP
G81	14.73	65.43	56.78	5.56	6.91	8.19	47.38	199.95
G82	13.31	61.61	47.83	5.32	7.18	8.14	49.77	260.94
G83	13.33	62.44	51.81	5.28	7.07	6.01	49.22	212.93
G84	13.38	63.44	54.30	5.50	6.84	8.22	47.62	312.61
G85	13.29	62.97	51.97	5.45	6.98	6.07	49.18	216.83
G86	13.80	67.61	54.92	5.74	6.61	5.49	44.56	376.94
G87	16.10	60.72	57.29	4.54	7.79	9.74	52.87	215.06
G88	15.03	59.67	48.86	5.39	7.22	5.23	49.74	226.92
G89	12.46	62.74	48.56	5.53	6.97	5.70	47.23	391.70
G90	15.06	60.59	54.93	5.00	7.38	12.00	50.51	375.10
G91	11.51	63.77	45.94	5.83	6.72	8.87	47.28	346.34
G92	13.71	63.04	56.56	5.44	7.01	7.99	48.38	115.35
G93	12.54	64.36	49.66	5.59	6.83	8.79	49.62	268.18
G94	12.49	62.27	46.40	5.47	6.90	9.00	47.72	154.67
G95	11.57	63.90	47.40	5.62	6.75	8.00	47.48	377.17
Min GEN	G21	G45	G45	G87	G5	G17	G2	G67
Max GEN	G76	G2	G6	G5	G87	G90	G87	G63
Grand Mean	13.18	63.79	51.51	5.52	6.93	8.03	47.92	260.59
SEm	0.23	0.41	0.46	0.10	0.08	0.32	0.39	9.402
CD (5%)	0.63	1.15	1.28	0.27	0.23	0.91	1.10	26.403
CD (1%)	0.84	1.52	1.70	0.36	0.30	1.21	1.45	34.961
No of genotypes above GM	46	51	45	44	41	47	49	46

significance of genetic effects (Chavhan *et al.,* 2022; Geethanjali *et al.,* 2023). The genetic variability of 95 forage sorghum genotypes for seven fodder quality traits is presented in **Table 4**. The phenotypic co-efficient of variation (PCV) exceeded the genotypic co-efficient of variation (GCV). The highest GCV and PCV were recorded for crude protein and the lowest was recorded in *in vitro* organic matter digestibility. All the fodder quality traits have low GCV and PCV, except crude protein. These results indicated that these traits had a lower contribution to variability, and direct selection for improvement is very difficult for these traits. These results were in accordance with the results of Rana *et al.* (2016) for neutral detergent fibre content and Somegowda *et al.* (2021) for *in vitro* organic matter digestibility. The highest heritability and genetic advance as a percentage of the mean was observed for crude protein content indicating that the trait was primarily under the control of additive gene action and is less influenced by environmental factors and respond better to selection in plant breeding programmes. This result was in accordance with the results of Thant *et al.* (2021) and Deep *et al.* (2019).

Gene action for seven fodder quality traits was assessed using skewness and kurtosis to analyse trait frequency distributions, as shown in **Table 4.** In vitro organic matter digestibility exhibited near-zero skewness, indicating a normal distribution. Metabolic energy, with positive skewness, suggests slower improvement under mild selection and faster enhancement with intensive selection due to dominant and complementary gene interactions. Acid detergent lignin content displayed negative skewness, indicating dominant and duplicate gene interactions, leading to rapid improvement under both mild and intense selection. Most fodder quality traits, except crude protein content, exhibited positive skewness, implying the presence of outliers. Crude protein content showed negative kurtosis, indicating no outliers and involvement of numerous genes. These findings align with previous studies by Neelima *et al.* (2020), and Toppo and Sahu (2022).

Correlation studies : The correlation analyses of the genotypes for 7 fodder quality traits in 95 forage sorghum genotypes are presented in **Fig. 1**. The green forage yield per plant has shown little to no association with the other seven forage quality traits. This suggests that these traits have proven to be ineffective in terms of selecting for improving forage yield. The current findings are in line with the reported crude protein content and green forage yield per plant by Ali *et al.* (2022). A clear positive correlation was found among in vitro organic matter digestibility (%), metabolic energy, crude protein, and ash content. In contrast, acid detergent lignin content, acid detergent

Table 4. Genetic variability of 95 forage Sorghum genotypes for seven fodder quality traits

Trait	Range	Mean ∓ SEm	GCV (%)	PCV (%)	h2 b. s. (%)	GA	GA as % of mean	kurtosis	Skewness
AC	10.89 -16.15	13.18 ∓ .022	8.00	8.36	91.64	2.08	15.77	0.2151	0.5029
NDF	57.62 - 70.74	63.79 ∓ .41	3.37	3.49	93.23	4.28	6.71	1.2446	0.4196
ADF	43.49 - 67.62	51.51 ∓ 0.456	8.14	8.24	97.69	8.54	16.58	0.6603	0.3321
ADL	4.53 - 6.31	5.52 ∓ .097	4.10	4.80	72.93	0.40	7.21	3.4851	-0.642
ME	6.45 - 7.78	6.93 ∓ 0.081	3.05	3.48	76.90	0.38	5.50	1.7549	0.7475
CP	4.52 - 12	8.03 ∓ 0.324	20.62	21.40	92.86	3.29	40.93	-0.6132	0.1744
IVOMD	43.22 - 52.87	47.92 ∓ 0.39	2.82	3.05	85.67	2.58	5.38	1.9963	-0.0589

Where, (GCV= Genotypic coefficient of variance, PCV= Phenotypic coefficient of variance, h2 b. s. (%) = Heritability in broad sense, GA= Genetic Advance and GAM (%) = Genetic Advance as % of mean)

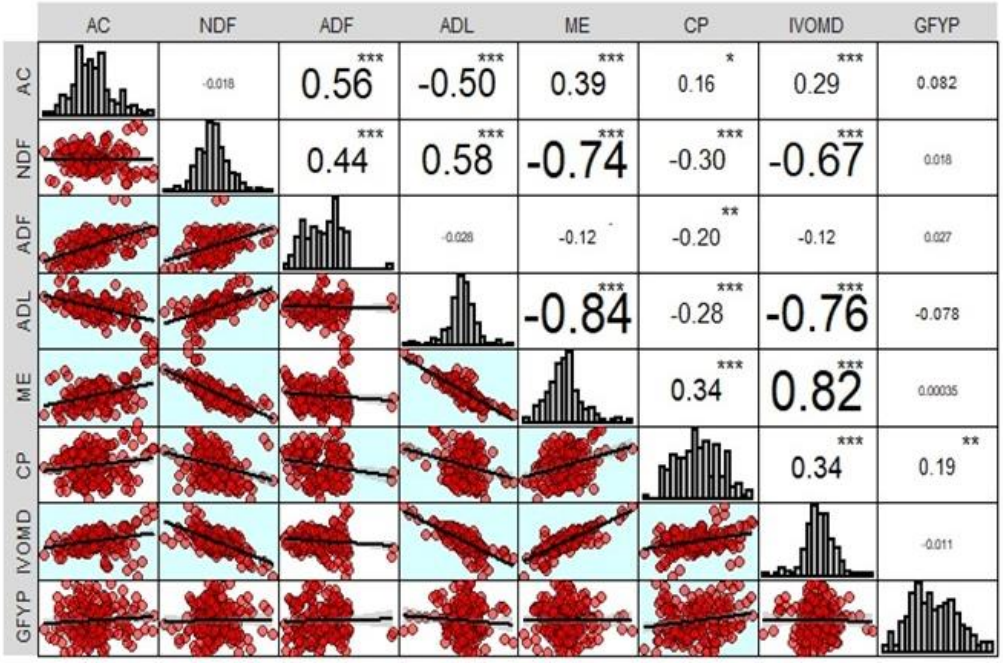

Fig.1. Genotypic correlation analysis in 95 forage sorghum genotypes for 7 fodder quality traits

fibre content, and neutral detergent fibre content showed an inverse relationship with these above-mentioned traits. The current findings align closely with the results reported by Somegowda *et al.* (2021) and Li *et al.* (2018).

Path Analysis studies for fodder quality traits : The path analyses for 7 fodder quality traits in 95 forage sorghum genotypes were summarized in **Table 5**. The result revealed that crude protein had a significant and positive affect on the green forage yield per plant. The high negative direct effect on green forage yield per plant may be attributed to the indirect influence of certain traits, such as in vitro organic matter digestibility, neutral detergent fibre content, acid detergent lignin content, and metabolic energy. Diwakar *et al.* (2016) found that protein percent had the highest direct effect on green forage yield per plant in their study. Based on the remarkably high residual value (0.903), it became evident that only a limited number of crucial factors influencing green forage yield per plant were examined in this analysis. The correlation between these traits and green forage yield per plant was positive but not statistically significant, suggesting that these traits had a minimal effect on improving green forage yield per plant. The results for crude protein content closely aligned with the findings of Diwakar *et al.* (2016) and Rana *et al.* (2016).

Genetic diversity studies : The results of Wilk's "V" statistic test revealed that significant in the analysis of variance of dispersion for 95 forage sorghum genotypes and it

Table 5. Genotypic path analysis in 95 forage sorghum genotypes for 7 fodder quality traits

Trait	AC	NDF	ADF	ADL	ME	CP	IVOMD
AC	**0.014**	-0.003	0.013	0.262	-0.214	0.030	-0.030
NDF	0.000	**-0.120**	0.010	-0.326	0.451	-0.068	0.082
ADF	0.008	-0.052	**0.022**	0.041	0.051	-0.046	0.011
ADL	-0.007	-0.075	-0.002	**-0.521**	0.503	-0.051	0.091
ME	0.005	0.096	-0.002	0.464	**-0.565**	0.071	-0.099
CP	0.002	0.033	-0.004	0.108	-0.164	**0.246**	-0.034
IVOMD	0.003	0.083	-0.002	0.399	-0.472	0.071	**-0.118**
Rg with GFYP	0.072	0.029	0.034	-0.06	-0.029	0.185	-0.036
Residual	**0.9033**						

Table 6. Analysis of variance for dispersion in 95 forage sorghum genotypes

Source of Variation	Df	Wilks criteria	approx F	num df	den df	Pr (>F)
GEN	94	0	19.8319	658	628.62	< 2.2e-16 ***
REP	1	0.94572	0.7215	7	88	0.654
Residuals	94					

*** - Significance level at ($p < 0.001$)

was presented in **Table 6**. Hence, further analysis was carried out to estimate D^2 values. The 95 forage sorghum genotypes were classified into six clusters based on their seven quality traits. These traits are presented in **Fig. 2**. Cluster I and Cluster II had the highest number of genotypes, with 33 each, while Cluster V had the lowest, with only five genotypes. Cluster III and Cluster IV each contain 12 genotypes. Cluster I was divided into four main sub-clusters, which primarily consisted of B-lines and had very limited variations. Pal *et al.* (2022) and Sejake *et al.* (2020) also reported similar results in sorghum forage quality.

The cluster mean for seven forage quality attributing traits was presented in **Table 7**. There was significant variation among the clusters in terms of the mean forage quality attributes. cluster IV exhibited the lowest mean values for metabolic energy, crude protein content, and in vitro organic matter digestibility. These traits are not ideal for superior forage quality in sorghum. On the other hand, cluster IV displayed the highest mean values for undesirable traits such as neutral detergent fibre, acid detergent fibre content, and acid detergent lignin content. cluster V exhibited the highest mean values for ash content, metabolic energy, crude protein content, and in vitro organic matter digestibility. These traits are indicative of good forage quality. In contrast, cluster V had lower mean values for undesirable traits such as neutral detergent fibre, acid detergent fibre content, and acid detergent lignin content. The genotypes with the highest and lowest mean performance for each trait were placed in their respective clusters, with high and low mean values, respectively. The genotypes of the current forage sorghum exhibited a notable level of divergence. Hybridization with accessions from the most divergent clusters (cluster V and cluster IV) is expected to yield the highest levels of transgressive segregants and maximum recombinants for the best forage quality. Pal *et al.* (2022) and Rohila *et al.* (2022) have all reported similar results in sorghum regarding forage quality. The genetic diversity resulting from various forage yields traits and individual trait contribution to the total divergence was presented in **Fig.3**. The highest contribution toward the total divergence was by the acid detergent fibre content (41.96%) and the least was by the acid detergent lignin content (0.98%). The crude protein content, ash content and neutral detergent fibre content contributed the most towards the total divergence, with higher genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as percent of the mean, respectively, that indicated direct selection for these traits might be advantageous for cluster selection and parent selection for hybridization. These results were in close conformity to the findings of Rohila *et al.* (2022) and Pal *et al.* (2022).

Considerable variations among the forage sorghum genotypes for fodder quality traits, revealing better potential for breeding high yielding forage sorghum with superior fodder qualities. The genotypes such as G90 (424B), G23 (334B), G87 (CSV21F), G76 (330B), and G45 (373B) were desired for most of the fodder quality traits. G90 (424B) and G47 (NSS5B) are considered the most desirable genotypes due to their higher green

Table 7. Cluster means estimates of 7 forage quality characters in 95 forage sorghum genotypes

Trait	Cluster Name				
	I	II	III	IV	V
AC	12.65	13.28	13.20	13.41	15.40
NDF	63.35	64.39	60.96	67.24	61.26
ADF	48.47	53.54	49.12	55.35	54.75
ADL	5.57	5.52	5.36	5.84	4.90
ME	6.90	6.91	7.17	6.62	7.48
CP	9.33	6.92	7.57	6.79	10.89
IVOMD	47.96	47.82	49.00	45.71	51.06

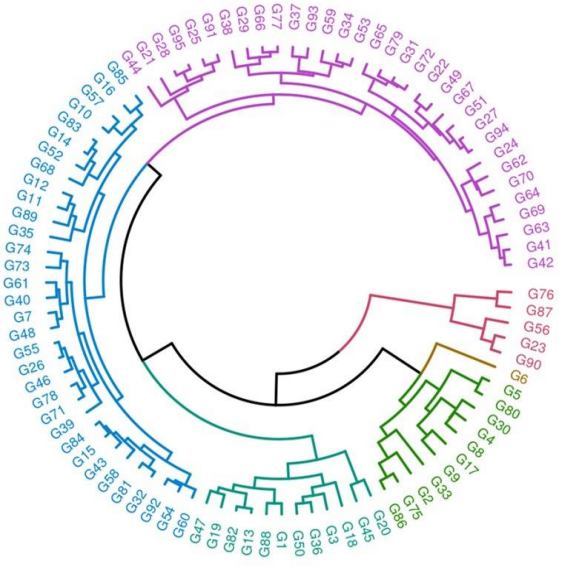

Fig.2. Dendrogram based on Mahalanobis Distance (D^2 Value) for 7 forage quality traits in 95 forage sorghum genotypes

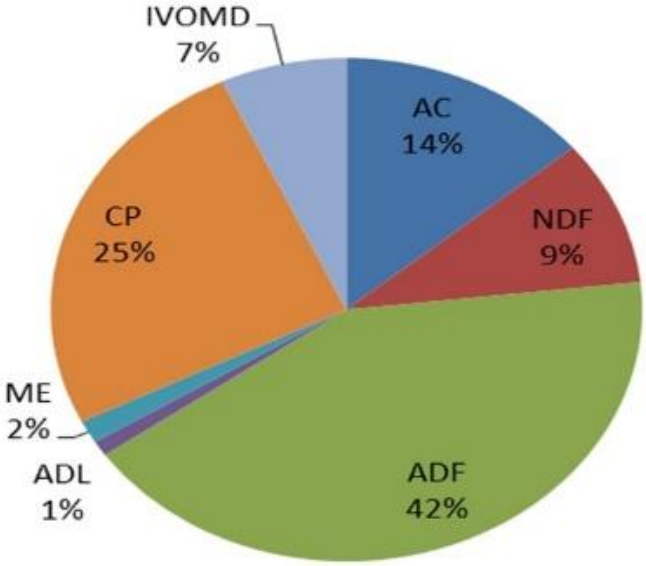

Fig.3. Relative contributions (%) of individual forage quality trait towards total divergence

forage yield per plant and superior fodder quality and hence these genotypes could be included in varietal development programme. Crude protein could be considered as an important trait during the selection of superior fodder quality genotypes, as confirmed through variability, trait association and diversity analysis. Based on the clustering pattern and mean of genotypes, crossing between genotypes in cluster V and cluster IV was expected to produce desirable transgressive segregants for fodder quality. Acid detergent fibre, crude protein, and ash content showed high contributions towards genetic divergence. Considering these traits, these selected genotypes could be utilised in varietal development programmes to develop superior fodder quality high-yielding forage sorghum cultivar.

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