P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2025.v38i02.07

Indian Journal of
Plant Genetic Resources

RESEARCH ARTICLE

Genetic Divergence and Associations Studies among Forage and Quality Characters in Guar (*Cyamopsis tetragonoloba* L.) Germplasm

Mohit Jain[1], Devinder Pal Singh[1*] and Meenakshi Goyal[1]

Abstract

The objective of the current study was to assess the extent of genetic variation among guar genotypes using morpho-agronomic data based on Principal Component Analysis (PCA) and to measure the genetic distance among these genotypes using hierarchical cluster analysis. The study consisted of 32 guar accessions collected from different regions of India. These 32 guar genotypes were grown in a randomized complete block design with three replications for two years. Analysis of variance revealed the significant differences present for the genotypes under investigation. Higher PCV and GCV values were recorded for leaf-stem ratio (L: S) followed by the number of branches per plant (B/P), stem girth (SG), dry matter yield (DMY) and green fodder yield (GFY). High heritability (>95%) was present for the characters such as plant height (PH), number of leaves (NOL/P), number of branches (B/P) and leaf-stem ratio (L:S). Heritability for quality traits was also high, *i.e.,* 92.83% for neutral detergent fiber (NDF) and 89.16% for *in vitro* dry matter digestibility. The highest genetic advance was observed for leaf stem ratio (46.98%) whereas moderate genetic advance was recorded for the number of branches (B/P), stem girth (SG), green fodder yield (GFY), number of leaves (NOL/P) and plant height (PH). The PCA reveals five principal components that contribute to the maximum variations and traits related to these components. Further, the cluster analysis based on centroid distance diversified the genotypes into five groups. Cluster-I includes nine genotypes with higher GFY followed by Cluster-III includes 10 genotypes with average GFY. The genotypes lying under Cluster-I and Cluster-III showing better plant height, stem girth, and number of branches per plant with higher crude protein, acid detergent fiber, neutral detergent fiber, *in vitro* dry matter digestibility content can be utilized in further breeding programs.

Keywords: Cluster analysis, Correlation, Genetic parameters, Guar, PCA.

[1]Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Punjab, India.

***Author for correspondence:**

devinderpal301@pau.edu

Received: 20/06/2024 **Revised:** 01/11/2024

Accepted: 24/03/2025

How to cite this article: Jain M, Singh DP, Goyal M. (2025). Genetic Divergence and Associations Studies among Forage and Quality Characters in Guar (*Cyamopsis tetragonoloba* L.) Germplasm. *Indian J. Plant Genet. Resour*. 38(2), 184-191. **DOI:** 10.61949/0976-1926.2025.v38i02.07

Introduction

Guar (*Cyamopsis tetragonoloba* L.) is an important legume crop cultivated in the *kharif* season within the northwestern regions of India. This resilient crop exhibits drought tolerance, demands minimal agronomic inputs, and thrives in sandy to sandy loam, light-textured soils. Guar cultivation is not limited to India; other countries such as Brazil, South Africa, and Australia also embrace it for its grains, vegetables, fodder, and industrial applications (Patel *et al.*, 2018). Guar fodder holds great nutritional value for livestock, boasting a composition of 10 to 18% crude protein, 25 to 43% crude fiber, 1.5 to 2.3% ether extract, and 35 to 48% nitrogen-free extract, along with high dry matter digestibility (Mahanta *et al.*, 2001). Furthermore, guar meal, a byproduct, is rich in protein content, ranging from 29 to 46%, making it a valuable feed for farm animals (Rodge, 2008; Kgasudi *et al.,* 2020). Despite the vital role of guar in animal feed, there is a noticeable lack of information regarding the enhancement of fodder yield and its associated traits. (Patel *et al*., 2018)

Fodder yield, as a quantitative characteristic, relies on various component traits. In breeding programs, the selection of promising crop genotypes hinges on multiple features, with the primary focus being on the final fodder yield and its quality. Understanding the relationships between yield and its contributing traits holds paramount importance in this context (Mohammadi *et al*., 2003; Rabiei *et al*., 2004). This information can be estimated by correlation analysis which provides associations for yield with other correlated traits. A correlation study is used in selection programs when highly heritable traits are associated with an important trait such as yield (Bizeti *et al*., 2004). Further, Hence, the present study was undertaken to assess the genetic variability and associations among fodder yield, its components and quality parameters. The genetic variability and association studies reveal the traits interrelated to the fodder yield. The genotypes then were subjected to the principal component analysis based on the correlations. The PCA suggests that the contribution of the traits in the variability and portion of the variability present among genotypes due to associated traits. Further, the genotypes were classified into groups based on their performance and similarity. The variable genotypes were placed in different groups so that the selection of parental lines for any breeding program could be easily done.

Materials and Methods

The current study was carried out at the Forage, Millet and Nutrition section of the Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana in summer 2022 and summer 2023. The breeding material consists of 32 genotypes of guar (Table 1). These genotypes

Table 1: Genotypes of Guar studied

S.no	*Genotype*	*Origin/pedigree*	*Originating Source*
1	PG1	Derivative of the cross between AG112x Strain 197	PAU, Ludhiana
2	PG2	Derivative of the cross between AG 112 x Strain 203	PAU, Ludhiana
3	PG3	Derivative of the cross between AG 112 x Strain 242	PAU, Ludhiana
4	PG4	Selection from the local material	PAU, Ludhiana
5	PG5	Selection from indigenous material of Punjab	PAU, Ludhiana
6	PG6	Derivative of the cross between G80 x Strain 200	PAU, Ludhiana
7	PG7	Derivative of the cross between G80 x Strain 226	PAU, Ludhiana
8	HG-2-20	Derivative of the cross between HG 365 x FS 277	CCS, HAU, Hisar
9	HFG119	Pure line selection from local germplasm	CCS, HAU, Hisar
10	G80	Derivative of the cross between FS-277 x Strain 119	PAU, Ludhiana
11	HG365	Derivative of the cross between Durgajai x Hisar Local	CCS, HAU, Hisar
12	RGC1055	Derivative of the cross between RGC 1013 x RGC 986	RAU, Bikaner
13	RGC1066	Derivative of the cross between RGC 936 x RGC 197	RAU, Bikaner
14	RGC 1031	Derivative of the cross between RGC 936 x RGC 986/P10	RAU, Bikaner
15	RGC 1017	Derivative of the cross between Naveen x HG 75	RAU, Bikaner
16	RGC 936	Derivative of the cross between EC x 248 x RGC 401	RAU, Bikaner
17	AG 112	Derivative of the cross between (325x F.S.277)	PAU, Ludhiana
18	AG111	Derivative of the cross between (323x F.S.277)	PAU, Ludhiana
19	RGC 1038	Derivative of the cross between RGC 516 x HG 75	RAU, Bikaner
20	GAUG 34	Mutant of Kutch	GAU, Dantewada, Gujarat
21	Durgapura safed	An indigenous material adapted from Rajasthan	RAU, Bikaner
22	HFG 156	Selection from local germplasm	CCS HAU, Hisar
23	HG 182	Selection from local germplasm	CCS, HAU, Hisar
24	Bundel Guar 1	Selection from indigenous material of Rajasthan	IGFRI, Jhansi
25	Bundel Guar2	Selection from indigenous material of Jodhpur	IGFRI, Jhansi
26	Bundel Guar 3	An indigenous material collected from Durgapura	IGFRI, Jhansi
27	RGC 197	Local germplasm collection from Nagaur	RAU, Bikaner
28	Durgajai	Single plant selection from local germplasm,Nagaur, Rajasthan	RAU, Bikaner
29	RGC 1033	Derivative of the cross between RGC 1013 x RGC 986	RAU, Bikaner
30	RGC 986	Derivative of cross between EC 516 x HG 75	RAU, Bikaner
31	HG 870	Selection from local germplasm	CCS HAU, Hisar
32	HG 884	Derivative of the cross between HG 75 x FS 296	CCS, HAU, Hisar

were grown in RBD with three replications over two years and data was recorded for nine morphological traits *viz.* green fodder yield (GFY) (Kg/plot), dry matter (DM) (%), dry matter yield (DMY) (Kg/plot), days to flower (DTF), plant height (PH) (cm), branches/plant (B/P), number of leaves per plant (NOL/P), stem girth (SG) (cm), leaf stem Ratio (L:R) and four quality traits were estimated related to the fodder quality *viz.*, crude protein (CP) (%), acid detergent fiber (ADF) (%), neutral detergent fiber (NDF) (%), *in-vitro* dry matter Digestibility (IVDMD) (%).

Statistical Analysis

The data were subjected to analysis of variation among genotypes and environments. Genetic parameters (phenotypic and genotypic variance, heritability in a broad sense and genetic advance (percent of mean) for each trait were estimated. The phenotypic and genotypic correlation between fodder yield and other traits were computed using R-software. All correlation coefficients were worked out for all the possible combinations of traits. The principal component analysis gives the estimate of the contribution of each trait to the fodder yield in the population under study using Minitab 17 software. Further, the genotypes were divided into clusters using the centroid method based on the similarity among the genotypes using facto extra package in R-software (R Core Team, 2021).

Results and Discussion

Analysis of Variance

The mean square for the genotypes was significant for GFY, DM%, DMY, DTF, PH, B/P, NOL/P, CP, ADF, NDF and IVDMD traits indicating that significant differences were present between genotypes for these traits (Table 1). The pooled analysis of variance for thirteen traits showed significant differences for all traits except stem girth and leaf-stem ratio (Table 2). Hence, the presence of a large amount of variability might be due to diverse sources of material taken for the present study. This indicated that there is ample scope for the selection of promising lines from the present gene pool for green fodder yield and its attributing traits. The germplasm characterization showed a high extent of phenotypic variability presented in Table 3. These results were in agreement with the findings of Sultan *et al.* (2012) and Manivannan *et al.*, (2015) Hence, the presence of a large amount of variability might be due to the diverse sources of material taken for the present study. The average recordings for each trait are tabulated in Table 2.

Genetic Parameters

Highly significant differences were observed for all the traits indicating that the variation was genetic and provides a good chance of improvement in studied guar genotypes. The genotypic coefficient of variability (GCV %) and phenotypic coefficient of variability (PCV %), broad sense heritability and expected genetic advance (as percentage of mean) for various studied traits are presented in Table 3. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimation for nine morpho-agronomic traits and four quality traits revealed that the estimated values of PCV were slightly higher than the GCV values for all traits indicating little influence of environment on expression of traits. Identical results were reported for fodder traits in maize (Kapoor and Batra, 2015; Chaudhary *et al.*, 2016), oats (Sahu and Tiwari, 2020), cowpea (Sahu, 2021; Chawla *et al.,* 2024) and barley (Singh and Singh, 2011). Slightly higher PCV than GCV values were recorded for Leaf-Stem ratio (24.00) (23.40) followed by branches per plant (15.91) (15.57), stem girth (14.00) (13.55), dry matter yield (13.10) (11.76) and green fodder yield (12.97) (12.18), respectively. That indicates the presence of exploitable genetic variability for B/P, SG and GFY. The higher PCV and GCV values for Leaf-Stem ratio were recorded by Singh *et al.,* (2023a) in cowpea. However, low phenotypic and genotypic coefficients were observed for dry matter% (4.35) (2.97) and IVDMD% (4.00) (3.78).

GFY

green fodder yield (q/ha), DM: dry matter (%), DMY: Dry Matter Yield, DTF: days to flowering, PH: plant height (cm), B/P : Branches per plant, NOL: number of leaves per plant, SG: stem girth, L:R: leaf-stem ratio, CP: crude protein (%), ADF: acid detergent fiber (%), NDF: neutral detergent fiber (%), IVDMD: *in-vitro* dry matter digestibility (%)

Perusal from Table 3 indicates that high heritability was present for the characters such as Plant Height (99.22%) followed by Number of Leaves per Plant (96.15%), Branches per Plant (95.78%) and Leaf-Stem Ratio (95.05%), heritability

Table 2: Pooled analysis of variance for different forage traits over the years

Source	*DF*	*GFY*	*DM*	*DMY*	*DTF*	*PH*	*B/P*	*NOL/P*	*SG*	*L:R*	*CP*	*ADF*	*NDF*	*IVDMD*
Year	1	2.92	0.75	0.05	38.91	14.93	2.87	203.9	0.08	0.09	3.39	19.62	35.62	20.81
Rep within year	4	2.70	0.61	0.07	76.85	15.05	0.30	68.27	00	00	4.52	7.95	3.13	5.29
Genotypes	31	3.20**	0.66**	0.06	49.70**	238.6*	3.42*	233.15*	0.03	0.08	3.34*	21.59**	34.94**	17.84**
Genotypes x Year	31	2.84**	0.72**	0.04	50.23**	198.4	4.45**	201.9*	0.01	0.03	3.30*	18.52*	29.58**	15.90**
Pooled error	124	1.33	0.4	0.0	26.84	221.81	3.27	198.6	0.002	0.001	3.18	15.87	21.54	10.53

**,* significant at 1% and 5% respectively

Table 3: Pooled descriptive statistics for forage and quality traits in guar

Trait	h^2*(%)*	*GA*	*%GA*	*PCV*	*GCV*	*GM*	*CV*
GFY	88.25	1.96	23.57	12.97	12.18	8.30	4.44
DM	46.65	0.56	4.18	4.35	2.97	13.45	3.18
DMY	80.63	0.24	21.76	13.10	11.76	1.12	5.77
DTF	87.04	7.64	11.81	6.59	6.15	64.63	2.37
PH	99.22	18.28	22.44	10.98	10.93	81.46	.97
B/P	95.78	2.14	31.39	15.91	15.57	6.81	3.27
NOL/P	96.15	17.69	22.63	11.42	11.20	78.18	2.24
SG	93.67	0.19	27.02	14.00	13.55	0.70	3.52
L:S	95.04	0.33	46.98	24.00	23.40	0.71	5.35
CP	78.37	1.84	13.28	8.23	7.28	13.86	3.83
ADF	86.06	4.99	14.94	8.43	7.82	33.43	3.15
NDF	92.83	6.69	16.15	8.44	8.14	41.41	2.26
IVDMD	89.16	4.65	7.35	4.00	3.78	63.24	1.32

for quality traits was also high for NDF (92.83%). The values for broad sense heritability ranged from 46.65% (DM) to 99.22% (PH), However, the heritability for GFY was 88.25%. The heritability for other traits such as DMY, DTF, SG, ADF and IVDMD was also high. Similar results were reported by Phogat *et al*., (2017) for leaf-stem ratio. The highest genetic advance was observed for the Leaf-Stem ratio (46.98%) whereas moderate genetic advance was recorded for B/P (31.39%), SG (27.02%), GFY (23.57%), NOL/P (22.63%) and PH (22.44%).

The results obtained through the estimation of GCV along with heritability revealed that selection is the most suitable method for the improvement of Green Fodder Yield and its contributing traits. Thus, the study of genetic parameters like the GCV, PCV and heritability provides a transparent picture of the magnitude of variability present in a set of germplasm. Generally, high heritability estimates coupled with high genetic advance% were observed for PH, GFY, and L: R and B/P. From the results, it can be concluded that these traits are controlled by additive types of gene action and could be improved through selection. These results for PH and GFY are in agreement with Sultan *et al., (*2021)

Correlation

Correlation studies usually explain the influence of one trait on another trait. The phenotypic and genotypic correlation coefficients were estimated using agro-morphological data and quality parameter data for all the possible combinations of traits. Correlation coefficients revealed both positively significant and negatively significant associations between traits. The selection of one trait can improve the positively correlated traits and, there must be linkage drag between negatively correlated traits. For simultaneous improvement of such negatively correlated traits, these negative correlations must be broken using other breeding strategies.

Phenotypic and Genotypic Correlation

The magnitude of genotypic correlations was higher than that of phenotypic correlations for most of the characters. (Table 4). GFY showed significant positive phenotypic and genotypic correlation with other agro-morphological traits viz. DMY (0.96) (0.94 and PH (0.27) (0.25) respectively, and only phenotypic correlation for SG (0.21) and for quality parameters significant and positive phenotypic and genotypic correlation were present for ADF % (0.51) (0.42) and NDF% (0.60) (0.55) respectively and phenotypic correlation for CP (0.23) only. The negative and significant phenotypic associations were present for DM % (-0.22) and IVDMD % (-0.50) with GFY and the negative and significant genotypic association was present for only IVDMD % (-0.50) similar results for associations were recorded by Singh *et al., (*2023b) in guar, however, the results were not in agreement with association present for IVDMD %. Further, the agro-morphological traits like DMY, PH and SG show positive and significant association with each other, in addition to B/P. DMY showed positive phenotypic and genotypic associations with B/P (0.24)(0.27), ADF % (0.45) (0.36) and NDF % (0.57) (0.51) respectively, and DMY showed positive phenotypic association with SG (0.21) and showed a negative association with IVDMD % (-0.54) (-0.47). PH showed significant and positive phenotypic and genotypic correlation with B/P (0.21) (0.21) and SG (0.22) (0.21) respectively. As studied by Sultan *et al 2021*, the PH showed similar associations with Branches per Plant. B/P showed positive and significant phenotypic and genotypic correlation with SG (0.28) (0.25) and negative and significant association with L:R (-0.25) (-0.23). Similar findings in correlation analysis were also reported positive although low correlations between dry matter yield and cell wall components such as acid detergent fiber and neutral detergent fiber and negative correlations between dry matter yield and *in vitro* dry matter digestibility by Singh *et al.,* 2023b. Both genotypic and phenotypic correlations showed similar trends for the traits associated with GFY. The green fodder yield is a quantitative and complex character that is dependent on many yield-contributing characters. Therefore, due to more effect of environmental fluctuations on yield, direct selection for yield as such will not be effective. Thus, the selection of such traits showing positive associations with each other can be helpful in the selection for the improvement of green fodder yield (Patel *et al., 2018).* The results were in agreement with the findings of Sultan *et al., 2021*, that the selection for fresh forage yield should be effective for the selection of traits such as Plant Height and branches per plant. The result for correlations may vary due to the selection of different genotypes for the study. However the PH showed association with B/P, so the selection for B/P would be equally effective. Therefore selection for the traits such as PH, SG, B/P, CP, ADF, NDF and IVDMD would be effective for the improvement of GFY.

Table 4: Genotypic and phenotypic correlations among forage yield traits

Trait		*GFY*	*DM %*	*DMY*	*DTF*	*PH*	*B/P*	*NOL/P*	*SG*	*L:R*	*CP*	*ADF*	*NDF*	*IVDMD*
GFY	PC	1												
	GC	1												
DM	PC	-0.23*	1											
	GC	-0.11	1											
DMY	PC	0.96**	0.02	1										
	GC	0.94**	0.23*	1										
DTF	PC	-0.11	0.58**	0.05	1									
	GC	-0.10	0.39**	0.04	1									
PH	PC	0.27**	-0.38**	0.18	-0.02	1								
	GC	0.25*	-0.26**	0.17	-0.01	1								
B/P	PC	0.19	0.31**	0.27**	0.02	0.21*	1							
	GC	0.17	0.22*	0.24**	0.04	0.21*	1							
NOL/P	PC	0.15	-0.16	0.11	-0.26**	0.17	0.10	1						
	GC	0.14	-0.07	0.11	-0.22**	0.17	0.10	1						
SG	PC	0.21*	-0.02	0.21*	-0.23**	0.22*	0.28**	0.00	1					
	GC	0.19	-0.01	0.18	-0.20	0.21*	0.25*	0.00	1					
L:R	PC	0.05	0.13	0.10	0.43**	-0.08	-0.25*	-0.24*	-0.55**	1				
	GC	0.04	0.06	0.07	0.39**	-0.08	-0.24*	-0.23*	-0.53**	1				
CP	PC	0.23*	-0.51**	0.09	-0.22*	-0.03	-0.26*	0.04	-0.00	0.02	1			
	GC	0.20	-0.32**	0.08	-0.15	-0.02	-0.19	0.07	-0.00	0.00	1			
ADF	PC	0.51**	-0.27**	0.45**	-0.54**	0.06	0.00	-0.12	0.21*	0.00	0.22*	1		
	GC	0.42**	-0.15	0.36**	-0.45**	0.06	0.03	-0.10	0.19	-0.00	0.23*	1		
NDF	PC	0.60**	-0.20	0.57**	-0.29**	0.15	-0.01	0.03	0.13	0.19	0.23*	0.84**	1	
	GC	0.55**	-0.09	0.51**	-0.23*	0.14	-0.00	0.03	0.10	0.18	0.24*	0.78**	1	
IVDMD	PC	-0.57**	0.13	-0.54**	0.44**	0.06	-0.02	-0.04	-0.04	-0.04	-0.02	-0.80	-0.77**	1
	GC	-0.50**	0.03	-0.47**	0.38**	0.06	-0.03	-0.05	-0.03	-0.02	-0.07	-0.80	-0.73**	1

Principal Component Analysis

The principal component analysis (PCA) was performed to reduce the data set for 13 morpho-agronomic traits under investigation. The eigenvalues for all traits were determined along with the proportion of each principal component contributing to the variation. Five principal components (PCs) had an eigenvalue of more than 1 (Table 5).

These five PCs contributed 79.1% of the total variability amongst the genotypes selected under investigation. The remaining components contributed only 20.9% towards the genetic diversity. Pavithra *et al.,* (2022) also recorded 70.30% variability in four principal components in 93 inbreds of

Table 5: The Principal Components and their proportions

	PC1	*PC2*	*PC3*	*PC4*	*PC5*	*PC6*
Eigenvalues	3.954	2.043	1.926	1.350	1.016	0.899
Proportion	0.304	0.157	0.148	0.104	0.078	0.069
Cumulative proportion	0.304	0.461	0.609	0.713	0.791	0.861

Table 6: Traits contributing to the principal components

Trait	*PC1*	*PC2*	*PC3*	*PC4*	*PC5*	*PC6*
GFY	**0.411**	0.132	0.186	**-0.287**	-0.016	-0.206
DM	-0.152	**0.337**	**0.408**	**0.333**	-0.153	-0.169
DMY	**0.371**	0.232	**0.307**	-0.193	-0.050	-0.253
DTF	**-0.243**	**0.425**	0.246	-0.258	0.191	-0.140
PH	0.120	-0.207	0.189	**-0.524**	0.287	0.536
B/P	0.062	-0.094	**0.543**	0.050	-0.038	0.098
NOL/P	0.072	-0.273	0.086	**-0.304**	**-0.767**	-0.033
SG	0.149	**-0.363**	**0.311**	0.172	**0.429**	-0.231
LSR	-0.029	**0.563**	-0.203	-0.233	0.029	0.219
CP	0.150	-0.091	**-0.368**	**-0.281**	0.146	**-0.619**
ADF	**0.429**	0.040	-0.142	**0.283**	0.132	0.150
NDF	**0.433**	0.173	-0.089	0.059	0.031	0.133
IVDMD	**-0.413**	-0.137	0.070	**-0.294**	0.202	-0.152

Table 7: The guar genotypes differentiated into clusters

	No. of observations	*Name of genotypes*	*Within Cluster Sum of Squares*	*Average distance from centroid*	*Maximum distance from centroid*
Cluster1	9	PG1, PG2, PG3, Bundel Guar 1, Bundel Guar 2, Bundel Guar 3, PG6,PG7, G 80(LC)	676.738	8.48875	13.1973
Cluster2	2	PG4, PG5	47.627	4.87992	4.8799
Cluster3	10	HG-2-20, HG 365, RGC 197, RGC 1031, HFG 119, RGC 1066, RGC 1033, RGC 1055, HG 870, HG 884	790.473	8.44984	14.2271
Cluster4	4	Durgajai, RGC 936, AG 112, RGC 1017	113.102	5.16596	7.3042
Cluster5	7	AG 111, RGC 1038, HG 182,GAUG 34, Durgapura safed, HFG 156	408.385	7.38486	11.3671

Table 8: Cluster centeroids

Trait	*Cluster1*	*Cluster2*	*Cluster3*	*Cluster4*	*Cluster5*	*Grand centroid*
GFY	8.96	8.62	8.01	9.10	7.39	8.30
DM	13.44	13.43	13.63	12.89	13.55	13.45
DMY(Kg/plot)	1.21	1.16	1.09	1.17	1.00	1.12
Day to flowering	66.17	67.62	65.32	56.22	65.81	64.62
Plant Height (cm)	90.15	79.53	70.80	84.27	85.69	81.46
Branches/plant	7.19	6.90	6.59	6.63	6.77	6.81
NOL/P	84.46	56.83	76.75	84.50	75.52	78.18
Stem girth (cm)	0.68	0.68	0.68	0.78	0.74	0.70
Leaf: Stem	0.79	0.87	0.76	0.49	0.62	0.71
CP(%)	13.62	14.13	13.91	14.93	13.36	13.86
ADF (%)	33.08	33.63	33.37	36.96	31.84	33.43
NDF(%)	42.73	41.67	41.20	45.00	38.10	41.41
IVDMD%	63.05	62.70	62.89	60.11	65.90	63.24

fodder maize. Priyanka *et al.,* (2022) recorded similar results in oat germplasm with 72.18% variability due to four principal components. Manoj *et al.,* (2022) recorded the 70.5% of variability present due to five PCs in 169 cowpea genotypes. Similarly, Chawla *et al.,* (2024) studied genetic diversity among 62 oats genotypes using hybrid hierarchical K means and formed four distinct clusters. Among them, cluster 1 exhibited the highest count of genotypes and also had the lowest intra-cluster distance and highest group means implying the presence of additive gene action for yield-related traits. In the present study, PC_1 contributed maximum variability towards the total variability (30.4%) followed by PC_2 (15.7%), PC_3 (14.8%), PC_4 (10.4%) and PC_5 (7.8%) (Table 5). The similar variability for principal components was estimated by Khalid *et al.,* (2017) in guar.

For PC_1, traits like GFY, DMY, ADF and NDF revealed significant and positive factor loadings, on the contrary DTF and IVDMD showed negative loadings. Traits like DM, DTF and LSR exhibited positive loadings for PC_2 while SG showed negative loadings. This revealed that traits like GFY, DM, DMY, DTF, SG, LSR and quality traits (ADF, NDF, and IVDMD) were the major contributing traits towards diversity. The maximum variability was observed in the first two PCs with GFY, DTF and LSR are major contributing traits towards phenotypic diversity.PC_3 was related to diversity among genotypes due to DM, DMY, B/P and SG with positive loadings and CP with negative loadings. PC_4 was elucidated by diversity among genotypes for DMY, ADF with positive loadings and GFY, PH, NOL/P CP and IVDMD with negative loadings. PC_5 was elucidated by diversity among genotypes for positive loadings for SG and negative loadings of NOL/P (Table 6).

Clustering using centroids

The 32 genotypes under present investigation were divided into 5 clusters (Table 7). Cluster-III comprises the largest cluster with 10 genotypes which include HG-2-20, HG 365, RGC 197, RGC 1031, HFG 119, RGC 1066, RGC 1033, RGC 1055, HG 870, and HG 884 followed by cluster-I which contains nine genotypes PG1, PG2, PG3, Bundel Guar 1, Bundel Guar 2, Bundel Guar 3, PG6, PG7, G 80(LC) followed by Cluster-V with seven genotypes including AG 111, RGC 1038, HG 182, GAUG 34, Durgapura safed, HFG 15-6 and cluster-IV includes four genotypes Durgajai, RGC 936, AG 112, RGC 1017 and the smallest group includes Cluster-II with two genotypes PG4, PG5.

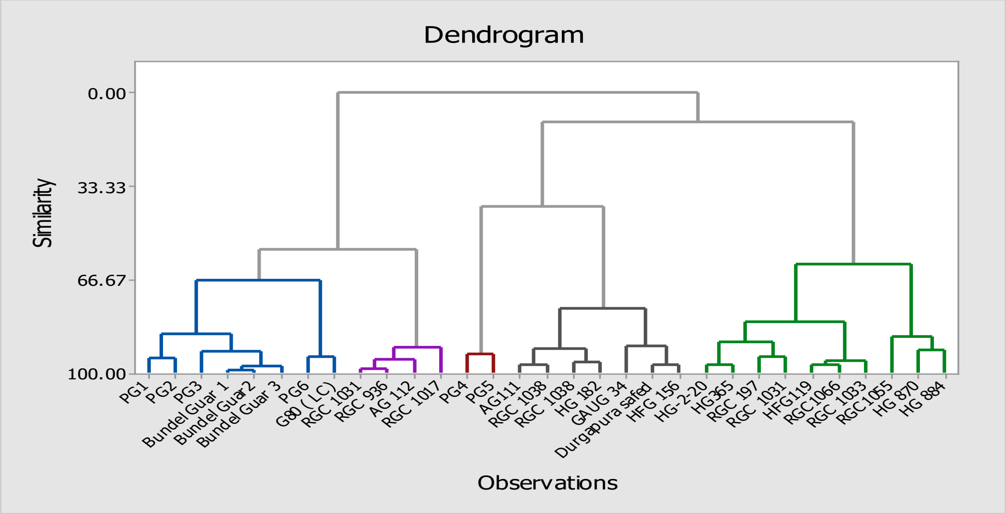

Fig. 1: The dendrogram showing the genotypes divided into five clusters

A perusal of Table 8 indicates Cluster-I comprising genotypes with higher GFY with maximum DMY, PH, B/P, late flowering, and higher quality parameters such as IVDMD, ADF and NDF content and with lower CP. Cluster two is the smallest comprising of two genotypes with higher CP and IVDMD. Cluster-III was the largest group comprising 10 genotypes with average GFY, medium in PH, late DTF and medium CP, ADF, NDF and IVDMD content. Cluster-IV comprises the genotypes with the highest GFY, NOL/P, early DTF, average PH, and B/P, and are suitable for quality traits with higher CP, ADF and NDF. Cluster-V consists of genotypes with lower GFY and quality parameters. The dendrogram reveals the description of genotypes divided into clusters (Fig. 1)

Conclusion

The findings of this study indicated that there is some range of variability present in the genotypes. Understanding the magnitude of variability and the degree of association between different traits is important to provide a base for effective selection for forage yield improvement in 32 genotypes of guar. The analysis of variance revealed significant differences among genotypes for all the traits studied. Meanwhile, a higher variation was present for L: R ratio followed by B/P, SG and GFY. Therefore, there is a large scope for simultaneous improvement in these traits as well as other green fodder yield components through selection. High heritability (h2) estimates coupled with high genetic advance% (GA %) were observed for PH, GFY, L:R, and B/P indicating that these traits are controlled by additive gene effects and these traits could be improved through selection. Correlation coefficients for green fodder yield components exhibited various trends of association among themselves. Therefore, selection for PH, SG, B/P, CP, ADF, NDF and IVDMD will be effective for Green Fodder Yield. Principal Components Analysis revealed five principal components (PCs) had an Eigenvalue of more than 1. These five PCs contributed 79.1% of the total variability amongst the genotypes selected under investigation. The maximum variability was observed in the first two PCs with GFY, DTF and LSR are major contributing traits towards phenotypic diversity. Further, the selection of these traits would be more effective for the improvement of fodder yield. These genotypes were divided into five clusters based on their performance. The genotypes lying under Cluster-I (PG1, PG2, PG3, Bundel Guar 1, Bundel Guar 2, Bundel Guar 3, PG6, PG7, G 80) and Cluster-III (HG-2-20, HG 365, RGC 197, RGC 1031, HFG 119, RGC 1066, RGC 1033, RGC 1055, HG 870, HG 884) can further be utilized in forage guar breeding programs.

Contributions

DPS and MJ conducted the experiments, collected and analyzed data, MG collected and analyzed forage quality data, DPS supervised the research, and MJ wrote the first draft.

Conflict of Interest

The authors declare no conflict of interest.

References

Bizeti HS, CGP deCarvalho, JRP deSouza and D Destro (2004) Path analysis under multi collinearity in Soybean. *Agron. J.* 47(5): 669-676.

Chaudhary DA, RA Kumar, A Singode, M Ganpati and B Kumar (2016) Evaluation of normal and specialty corn for fodder yield and quality traits. *Range Manag. Agrofor.* 37(1): 79-83.

Chawla R, M Jattan, DS Phogat, A Sharma, M Redhu (2024) Unravelling the hidden patterns of genetic diversity in oat(*Avena sativa* L.) accessions: Insights from novel hybrid hierarchial K-means clustering. *Indian J. Plant. Genet. Resour.*37(3): 454-459.

Kapoor R and C Batra (2015) Genetic variability and association studies in maize (*Zea mays* L.) for green fodder yield and quality traits. *Electron. J. Plant Breed*. 6: 233-240.

Kgasudi BK, GK Rekha, KV Jyothi, K Sasikala (2020) Variability, heritability and genetic advance for yield and yield attributing characters in clusterbean (Cyamopsis tetragnoloba (L.) Taub.) genotypes . *Indian J Agric Res*. 54(2): 247-251.

Khalid M, AR Akhtar, LH Minhas, R Bukhari, SJ Zubair and MA Iqbal (2017) Screening of guar accessions [*Cyamopsis tetragonoloba* (L.) Taub.] for higher yield potential under irrigated conditions. *Afr. J. Agric. Res.* 12(37): 2788-2794.

Mahanta SK, VC Pachauri, NP Singh, UP Singh and MS Sharma (2001). Nutritional evaluation of improved varieties of forage guar. *IJAN*. 18: 330-334.

Manoj CA, Marappa, N Keerthi, A Patil, DV Naveen, S Ramesh , MSP Kanavi, GE Rao, P Venkataravana, DL Savithramma (2022) Genetic Divergence Assessment through K-Means Clustering and Principal Component Analysis for Seed Yield, Zinc, Iron and Protein Content in *Vigna unguiculata* L. Walp. *Indian J. Plant Genet. Resour.* 35(2): 178–184.

Manivannan A, CR Anandakumar, R Ushakumari and GS Dahiya (2015) Genetic diversity of guar genotypes (*Cyamopsis tetragonoloba* (L.) Taub.) based on agro-morphological traits. *Bangladesh J. Bot*. 44(1): 59-65.

Minitab 17 Statistical Software (2010) [Computer software]. State College, PA: Minitab, Inc.

Mohammadi SA, BM Prasanna and NN Singh (2003) Sequential path model for determining interrelationships among grain yield and related characters in maize. *Crop Sci***.** 43: 1690–1697.

Patel KV, DJ Parmar, RL Chavadhari, RG Machhar and HP Patel (2018) Assessment of genetic variability and character association in cluster bean (*Cyamopsis tetragonoloba* L. Taub). *Int. J. Agric. Sci*. 10 (19): 7301-7304.

Phogat DS, R Panchata, P Kumari and S Arya (2017) Variability, correlation and path analysis studies in fodder cowpea [*Vigna unguiculata* (L.)Walp]. *Trends Biosci. J.* 10(3): 1130-1132.

Pavithra A, KN Ganesan, B Meenakumari and SD Sivakumar (2022) Genetic studies on green fodder yield and quality traits in fodder maize (*Zea mays* L.). *Electron. J. Plant. Breed*. 13(2): 432-439.

Priyanka, VK Sood, A Rana, SK Sandaya, S Kumar, HK Chaudhary and A Arora (2022) Biochemical characterization of oat genotypes for β-glucan content and powdery mildew resistance. *Range Manag. Agrofor*. 43(1): 41-49.

R Core Team (2021). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

Rabiei B, M Valizadeh, B Ghareyazie and M Moghaddam (2004) Evaluation of selection indices for improving rice grain shape. *Field Crops Res*. 89: 359–367.

Rodge AB (2008) Quality and export potential of arid legumes. In. D. Kumar and Henry (eds,) Souvenir. *Scientific Publishers*. Jodhpur, India. pp. 10-17.

Sahu M (2021) Studies on genetic architecture through variability parameters and association analysis in cowpea (*Vigna unguiculata* (L.) walp). *Bangl. J. Bot*. 50(3): 557-564.

Sahu M and A Tiwari (2020) Genetic variability and association analysis in oats (*Avena sativa* L.) genotypes for green forage yield and other components. *Curr. Appl. Sci. Technol*. 39(17): 133-341.

Singh DP, M Jain and M Goyal (2023) Assessment of variability and association analysis for forage traits in cowpea (*Vigna unguiculata* (L). Walp). *Forage Res.* 48(3): 315-319.

Singh DP, RS Sohu, M Goyal, P Singh (2023) Analysis of variability and correlations among different forage traits in guar (*Cyamopsis tetragonoloba* L.). *Electron. J. Plant Breed.* 14(1): 323-328.

Singh P and K Singh (2011) Analysis of association among different morphological traits in fodder barley. *Range Manag. Agrofor*. 32: 92-95.

Sultan M, ME Walaa and ZE Ghareeb (2021) Relationship between yield and its components to detect the direct and indirect effects in some cowpea and guar genotypes. *IJSRP*. 11(1):297-307.

Sultan M, MN Yousaf, MA Rabbani, ZK Shinwari and MS Masood (2012) Phenotypic divergence in guar (*Cyamopsis tetragonoloba* L.) landrace genotypes of Pakistan. *Pak. J. Bot*. 44: 203-210.