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Genetic Diversity and Principle Component Analyses for Fodder Yield and their Component Traits in Genotypes of Forage Sorghum (*Sorghum bicolor* L. Moench)

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Abstract: In the current set of an experiment twenty eight forage sorghum genotypes including two checks were evaluated for understanding genetic diversity for fodder yield and their component traits in forage sorghum. For evaluation of these traits, correlation, principal component (PC) and diversity analysis employed to obtain suitable parents that can be exploit for further breeding programs. Green and dry fodder yield was significantly and positively correlated with stem girth, leaf width, leaf length, number of leaves/plant, plant height and days to 50% flowering. The positive correlation among these fodder yield contributing traits suggested that these traits are important for direct selection of high fodder yielding genotypes. By performing analysis for PCs it was observed that variance for Eigen value was maximum (3.844) in PC-1 followed by PC-II (1.455) and least for PC-III (1.076). First three PC scored 70.89% variation and variance percentage was maximum in PC-I (42.72%) followed by PC-II (16.17%) and PC-III (11.97%). The total variation was mainly due to variation in the fodder yield and their contributing traits i.e. green fodder yield, dry fodder yield, stem girth, leaf width, number of leaves/plant, leaf length, and days to 50% flowering. The twenty eight genotypes were grouped into four clusters on the basis of average linkage. Cluster-I contained 3 genotypes, cluster-II contained 9 genotypes, cluster-III contained 14 genotypes and cluster-IV contained 2 genotypes. Distribution pattern of all the genotypes into four clusters showed the presence of considerable genetics diversity among the genotypes for most of the traits under consideration. Varieties of cluster first and second was superior in terms of green and dry fodder yield, third cluster for early maturity and forth for brix per cent and these genotypes can use as release new cultivar and for further breeding programs.

Key words: Genetic diversity, fodder sorghum.

Sorghum is the fifth most important cereal crops in the world after wheat, rice, maize and barley. It is widely grown for providing protein for many people in Asia and Africa, malt production of non-alcoholic drinks, flour production and animal feed and fodder in semi-arid tropics (Agarwal *et al*., 2004; Ajirlou *et al*., 2013). Sorghum is high tolerance to high temperature and better ability to stand during drought conditions. It also has potential to sequestrate carbon, thereby contributing to reduction of greenhouse gases. Its high resistance to drought makes it a suitable fodder crop for semi-arid areas especially in light of its higher productivity under dry conditions compared to corn (Tabosa *et al*., 1999). House (1985) noted that cultivated sorghums are highly variable and suggested that to enhance the productivity levels of sorghum, prior information on the nature and the magnitude of genetic diversity present in breeding material is a pre-requisite.

Precise information on the nature and degree of genetic diversity help plant breeder in selecting the parents for targeted hybridization. It provides the raw materials from which desirable alleles for improved agronomic traits of interest can be selected and subsequently incorporated into elite lines. The purpose of principal component analysis is to reduce the volume of data. Watson and Eyzaguirre (2002) also reported that PCA of morphological characterization results could identify a few key or minimum descriptors that effectively account for the majority of the diversity observed, saving time and effort for future characterization efforts. Principal components approach is very helpful in deciding which agronomic traits of crop contributing most to yield, subsequently, these agronomic traits

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should be emphasized in the breeding program. In order to determine genetic variation genotype classifications and genetic distance among them the cluster analysis is done. Cluster analysis identifies and classifies objects individuals or variables on the basis of the similarity of the characteristics they possess. It seeks to minimize within-group variance and maximize between-group variance. It is also helpful for parental selection in the breeding program and crop modeling. Therefore, the present study was done to evaluate the genetic diversity among forage sorghum genotypes specifically for green and dry fodder yield to select the best genotypes can be exploited in future forage sorghum breeding program.

Materials and Methods

The plant material comprised of 28 elite entries of forage sorghum including two checks viz., CSV 21 F and GFS 5 pooled under All India Coordinated Sorghum Improvement Project, Sorghum Research Station, Sardarkrushinagar Dantiwada Agricultural University, Deesa. Gujarat (Table 1). The trial was grown in randomized block design with 3 replications during kharif 2015 at Sorghum Research Station, Deesa (latitude of 24.5°N longitude of 72°E and elevation of 136 M above the Mean Sea Level). The soil of the field was sandy in texture with pH value of 7.5 to 8.00 having good physical and chemical properties (Organic Carbon= 0.23, EC dS m^{-1} = 0.232, K_2O= 259.9 kg ha^{-1} and P_2O_5= 46.2 kg ha^{-1}). The experimental unit was a four-row plot of 5.0 m long with a row spacing of 0.30 m. NPK 80:40:00 fertilizers was applied as half basal dose of nitrogen and full dose of phosphorus at the time of sowing and half nitrogen applied after one month of sowing. The all other recommended agronomical practices were followed to raise a good crop during the season. Data were taken on days to 50% flowering, plant height (cm), number of leaves per plant, leaf length (cm), leaf width (cm), stem girth (cm), brix value (%), green fodder yield (q ha^{-1}) and dry fodder yield (q ha^{-1}). The data was subjected to correlation analysis, cluster analysis and principal component analysis (PCA) using statistical software packages of SAS 9.2. Cluster analysis was performed using average linkage clustering while tree diagram based on euclidian distances was developed by Ward's method. The first two principal components were plotted against each other to find out the patterns of variability among genotypes and characters using SAS 9.2 software.

Table 1. A list of 28 Forage sorghum genotypes with their pedigree used in this study

Entry	Pedigree	Source
DSF 0129	UPMC 503 x IS 18551	SRS, SDAU Deesa
DSF 0130	UPMC 503 x AKR 150	SRS, SDAU Deesa
DSF 0131	UPMC 503 x IS 18551	SRS, SDAU Deesa
DSF 0132	CSV 15 x S 35	SRS, SDAU Deesa
DSF 0133	Selection from GP FM 303	SRS, SDAU Deesa
DSF 0134	Selection from SRF 2812	SRS, SDAU Deesa
DSF 0135	PC 4 x EC 582510	SRS, SDAU Deesa
DSF 0136	CSV 15 x S 35	SRS, SDAU Deesa
DSF 0137	HC 171 x ICSV 700	SRS, SDAU Deesa
DSF 0138	CSV 15 x S 35	SRS, SDAU Deesa
DSF 0139	PC 4 x EC 582508	SRS, SDAU Deesa
DSF 0140	PC 4 x EC 582510	SRS, SDAU Deesa
DSF 0141	Selection from HC 308	SRS, SDAU Deesa
DSF 0142	HC 171 x ICSV 700	SRS, SDAU Deesa
DSF 0143	SPV 1624 x SL	SRS, SDAU Deesa
DSF 0144	Selection from GP FM 363	SRS, SDAU Deesa
DSF 0145	Selection from GFS 5	SRS, SDAU Deesa
DSF 0146	IS 22557 x I 12	SRS, SDAU Deesa
DSF 0147	Selection from SSG 59-3	SRS, SDAU Deesa
DSF 0148	Selection from SRF 316	SRS, SDAU Deesa
DSF 0149	Selection from ERS 31	SRS, SDAU Deesa
DSF 0150	Selection from GFS 5	SRS, SDAU Deesa
DSF 0151	UPMC 503 x IS 18551	SRS, SDAU Deesa
DSF 0152	Selection from ERS 23	SRS, SDAU Deesa
DSF 0153	Selection from Ramkel	SRS, SDAU Deesa
DSF 0154	Selection from MP Chari	SRS, SDAU Deesa
GFS 5	SPV 1087 x GSSV 148	SRS, NAU Surat
CSV 21F	GSSV 148X SR 897	SRS, NAU Surat

SRS= Sorghum Research Station.

Results and Discussions

The estimation of mean, range and CV (%) of all the characters were studied to assess the variability pattern in the material (Table 2). Among all the traits investigated, green fodder yield followed by dry fodder yield and plant

Table 2. Estimation of basic statistics for nine quantitative traits in 28 forage sorghum genotypes

Characters	Days to 50% flowering	Plant height (cm)	Number of leaves plant^{-1}	Leaf length (cm)	Leaf width (cm)	Stem girth	Brix (%)	Green fodder yield	Dry fodder yield
Mean	72.52	320.96	12.35	80.29	7.15	5.78	13.03	605.37	226.35
Min	62.00	270.00	10.20	67.00	5.50	4.80	8.70	377.04	107.85
Max	81.00	365.00	16.66	97.00	9.00	7.50	16.40	887.19	341.42
Range	19.00	95.00	6.46	29.20	3.50	2.70	7.70	510.14	233.56
CV %	1.59	2.24	9.50	7.50	10.11	8.33	4.77	7.70	9.95
SeM	0.66	4.16	0.68	3.47	0.42	0.28	0.36	26.93	13.01
SD	5.66	28.60	1.61	7.10	0.74	0.62	2.28	139.02	58.38

height recorded maximum value of mean, range, variance and standard deviation. The descriptive statistics of nine quantitative traits indicated the existence of diversity among the genotypes. Pearson's correlation is measure of strength of linear relationship in between the characters. In the present investigation green and dry fodder yield was significantly and positively correlated with stem girth, leaf width, leaf length, number of leaves/plant, plant height and days to 50% flowering (Table 3). Such strong positive correlations recorded among the genotypes, suggest that they are heritable and genetically controlled traits which could be transmitted into desired genotypes. The finding of present study was agreed with the Jain *et al*. (2011), Jain and Patel (2012). The brix per cent was negatively correlated with the green fodder yield, dry fodder yield and leaf length. All the other yield contributing traits were also positively correlated with each other indicated that selection may be in positive direction based on these traits towards crop improvement program.

A scree plot is a simple line segment plot that shows the fraction of total variance in the data. It is a plot, in descending order of magnitude, of the eigen values of a correlation matrix. According to Chatfied and Collins (1980), components with an eigenvalue of <1 should be eliminated so that fewer components are dealt with. Sharma (1998) reported that PCA reflects the importance of the largest contributor to the total variation at each axis of differentiation. It was further reported by Fenty (2004) that PCA reduces a large set of variables to come up with smaller sets of components those summaries the correlations. The Scree plot of the PCA (Fig. 1) shows that the first three eigenvalues correspond to the whole percentage of the

Table 3. Pearson phenotypic correlation coefficient between nine quantitative traits in forage sorghum

Characters	Days to 50% flowering	Plant height	Number of leaves/plant	Leaf length	Leaf width	Stem girth	Brix %	Green fodder yield
Days to 50% flowering	1.000							
Plant height	0.401**	1.000						
Number of leaves/plant	0.431**	0.164	1.000					
Leaf length	0.068	-0.135	0.165	1.000				
Leaf width	0.386**	0.139	0.155	0.378**	1.000			
Stem girth	0.286*	0.196	0.305**	0.430**	0.684**	1.000		
Brix %	-0.119	0.060	-0.190	-0.388**	-0.071	-0.233	1.000	
Green fodder yield	0.309**	0.236*	0.287*	0.357*	0.569**	0.737**	-0.300*	1.000
Dry fodder yield	0.274*	0.278*	0.332**	0.322**	0.523**	0.711**	-0.254*	0.933**

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

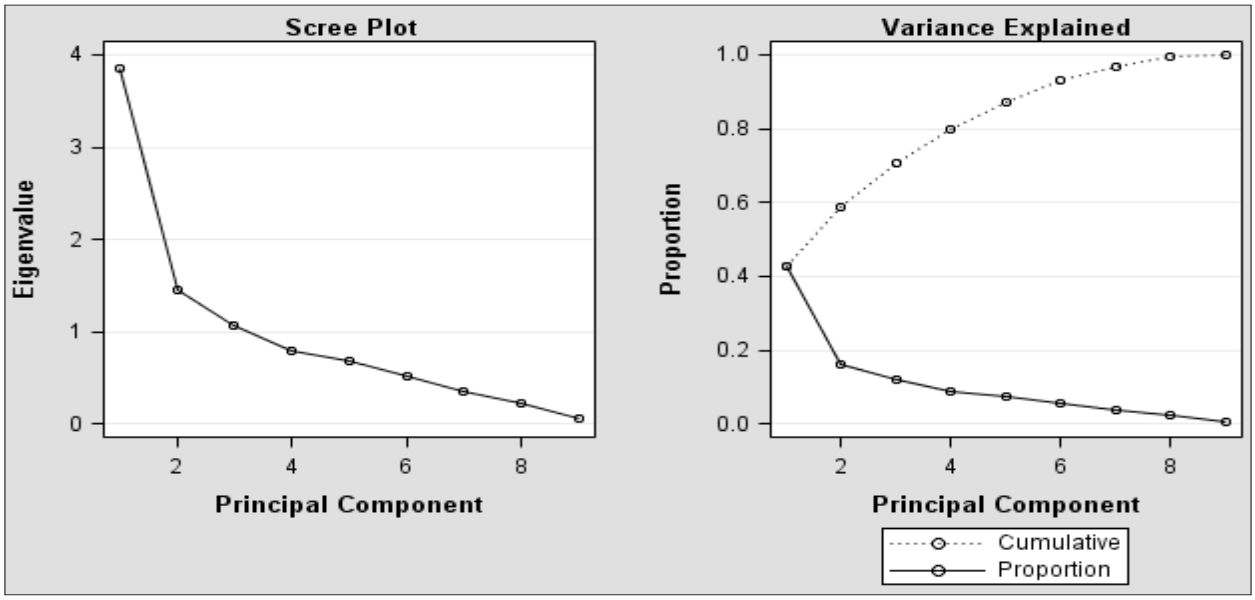

Fig. 1. Scree graph of principal component analysis of 28 genotypes of forage sorghum between Eigen values and the number of principal component.

variance in the dataset. The first three main PCAs are extracted from the complicated nine components, the total cumulative variance of these first three principal components (PC 1, PC 2 and PC 3) accounted for 70.89% of the total variation (Table 3). The Eigenvectors decreased significantly from principal component 2 from 16.17% to 11.97% (Table 4). This suggests that after principal component 3 more principal components did not describe much variation. Thus, only the first three PCs were considered.

Table 4. Eigenvectors, percentage variation, eigenvalues and cumulative variance of 9 quantitative traits in forage sorghum genotypes

Characters	Eigen vectors		
	PC_1	PC_2	PC_3
Days to 50% flowering	0.262	0.455	-0.331
Plant height	0.165	0.600	0.042
No of leaves/plant	0.243	0.216	-0.583
Leaf length	0.263	-0.489	-0.157
Leaf width	0.375	-0.019	0.319
Stem girth	0.439	-0.084	0.204
Brix %	-0.193	0.371	0.562
Green fodder yield q ha^{-1}	0.455	-0.049	0.181
Dry fodder yield q ha^{-1}	0.445	-0.009	0.179
Eigen value	3.844	1.455	1.076
% Variance	42.72	16.17	11.97
Cumulative % variance	42.72	58.89	70.89

Quantitative traits which contributed more to the first principal component (PC) accounted for 42.72% of the total variation. The second and third principal component (PC) explained 16.17% and 11.97%, respectively (Table 4). The first PCA was related to fodder yield and their contributing traits like green fodder yield, dry fodder yield, stem girth, leaf width, number of leaves/plant, leaf length, and days to 50% flowering. The second principal component was related to plant height, days to 50% flowering, brix per cent and no of leaves/plant. The third PC was related to brix per cent, stem diameter and leaf width. The first and the second PCs with a cumulative of 58.89% revealed the most variation among the populations, showing a high degree of correlation among the traits studied. Overall, the PCA analysis under this study shows that phenotypic markers are useful in genotypes of forage sorghum and able to identify few key traits that accounted for the largest variability. The present study supported by earlier workers also (Agarwal *et al*., 2004; Ali *et al*., 2009; Ali *et al*., 2011; Akatwijuka *et al*., 2016). Distribution of biometrical traits in first two components is sown in loading plot (Fig. 2). The loading plot clearly showed that green fodder yield, dry fodder yield, stem girth, leaf width, number of leaves/plant, leaf length, and days to 50% flowering contributed traits towards diversity. A scatter plot from the first two PCs (Fig. 3) generally grouped the 28

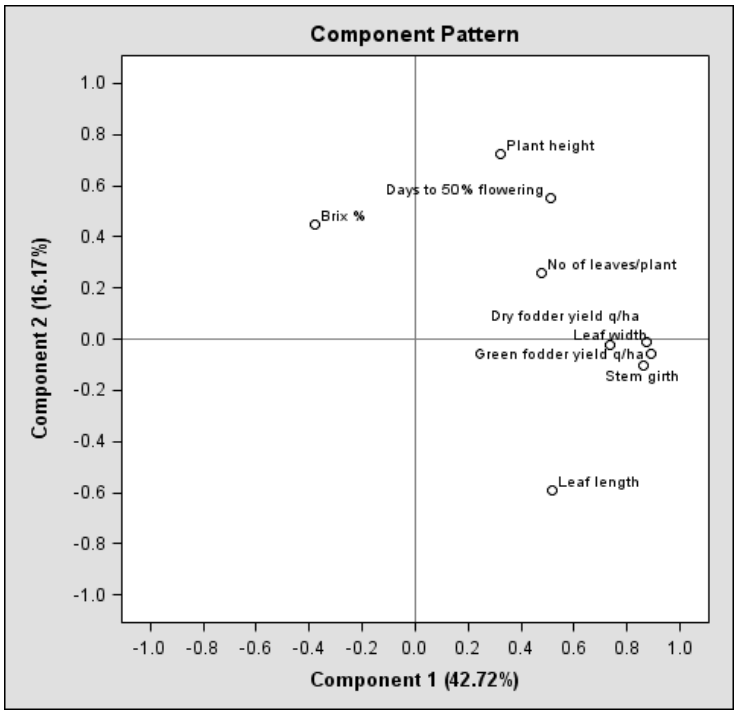

Fig. 2. Plot of the first two PCAs showing relation among various quantitative traits in forage sorghum.

genotypes in a similar way to cluster analysis (Fig. 4), using the entire data from all the traits. This showed that PCA is a reliable method in identifying few key traits contributing to the largest variation and could be a reliable method in predicting the important traits influencing clustering of different cultivars observed in Fig. 4 under cluster analysis. According to Chahal and Gosal (2002), characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. Therefore, in the present study, differentiation of the genotypes into different clusters was because of relatively high contribution of few characters rather than small contribution from each character.

The twenty eight genotypes were grouped into four clusters on the basis of average linkage

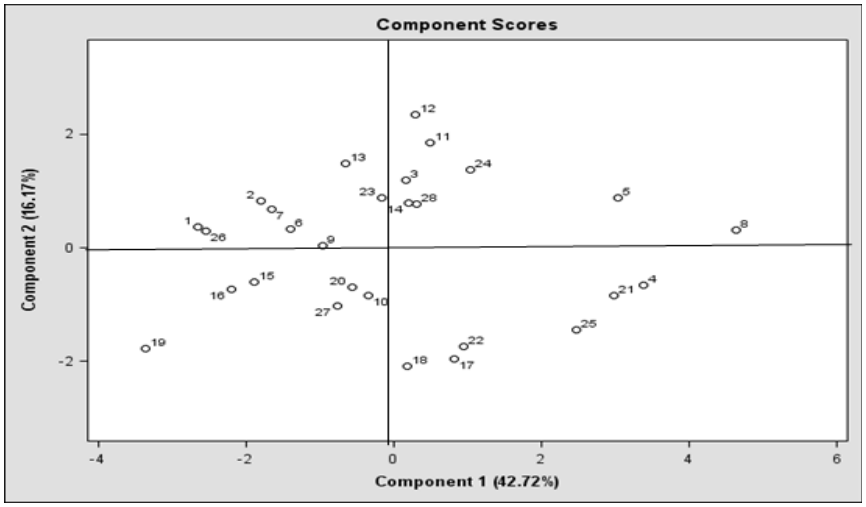

Fig. 3. Distribution of forage sorghum genotypes for first two principal components based on different quantitative traits.

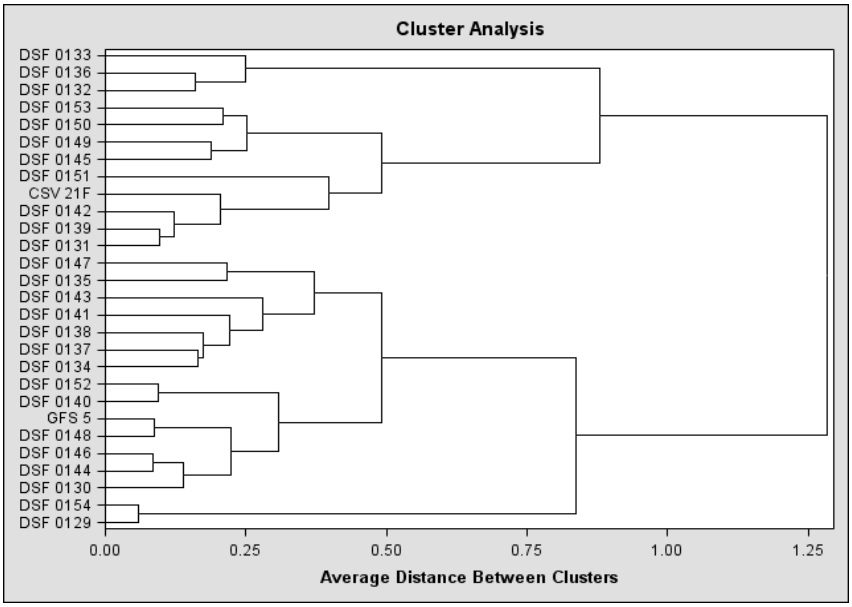

Fig. 4. The dendrogram of forage sorghum genotypes resulting from cluster analysis using ward method based on standardized data of all the traits.

and dendogram was cut at a distance of 0.75 are presented in Fig. 4. The cluster analysis sequestrates genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters. The cluster 1 having three genotypes viz., DSF0132, DSF0136 and DSF0133. The cluster 2 includes 9 genotypes viz., DSF0131, DSF0139, DSF0142, CSV 21F, DSF0151, DSF 0145, DSF0149, DSF0150, DSF0153. Cluster 3 comprised 14 genotypes includes DSF0130, DSF0144, DSF0146, DSF0148, GFS 5, DSF 0140, DSF0152, DSF0134, DSF0137, DSF0138, DSF0141, DSF 0143, DSF 0135 and DSF0147 and fourth clusters includes two genotypes DSF 0129 and DSF 0154. Distribution pattern of all the genotypes into four clusters showed the presence of considerable genetics diversity among the genotypes for most of the traits under consideration. The mean values for plant height (348.3 cm), number of leaves/ plant (12.9), leaf length (85.1 cm), leaf width (8.1 cm), stem girth (6.9 cm), green fodder yield (857.9 q ha^{-1}) and dry fodder yield (335.1 q ha^{-1}) was highest in cluster-I. Cluster-II also exhibited higher green and dry fodder yield and their component traits. Average values for fodder yield and their component traits and early flowering (70.11 days) was observed in cluster-III. The cluster-IV was superior for brix value (14.7%) (Table 5). The clustering pattern showed that there was significant genetic variability among the forage sorghum genotypes

Table 5. Mean value of the 9 quantitative traits in the 4 clusters of different genotypes of forage sorghum

Clusters	Genotypes	Days to 50% flowering	Plant height (cm)	No of leaves $plant^{-1}$	Leaf length (cm)	Leaf width (cm)	Stem girth	Brix %	Green fodder yield	Dry fodder yield
		Mean								
I	DSF0132, DSF0136, DSF0133	77.7	348.3	12.9	85.1	8.10	6.9	11.3	857.9	335.1
II	DSF0131, DSF0139, DSF0142, CSV 21F, DSF0151, DSF 0145, DSF0149, DSF0150, DSF0153	73.82	320.1	12.8	81.3	7.27	5.9	12.6	701.4	251.8
III	DSF0130, DSF0144, DSF 0146, DSF0148, GFS 5, DSF 0140, DSF0152, DSF0134, DSF0137, DSF0138, DSF0141, DSF 0143, DSF 0135, DSF0147	70.11	319.0	12.0	78.8	6.98	5.4	13.3	522.1	202.7
IV	DSF0129, DSF0154	75.85	297.5	11.9	77.9	6.50	5.25	14.7	377.3	113.4

tested that indicated the presence of excellent opportunity to bring about improvement through hybridizing genotypes from different clusters. High fodder yielding genotypes from cluster-I could be further tested for their combining ability. The genotypes from cluster-I should be crossed with cluster-III and cluster-IV to reduce the flowering time and increased brix value combined with high green and dry fodder yield. Thus the genotypes present in different clusters can be hybridized to assemble desirable traits with higher heterotic potential.

This study support that quantitative traits are useful tool for preliminary evaluation of genetic diversity in forage sorghum. Correlation studied clearly showed that the green fodder yield, dry fodder yield, stem girth leaf width, number of leaves/plant and leaf length together were the main components of fodder yield and positively correlated to each other. The present findings revealed that first three components were related to various quantitative traits mostly associated with high fodder yielding genotypes and showed that PCA is a reliable method in identifying few key traits contributing to the largest variation and could be a reliable method in predicting the important traits influencing clustering of different cultivars under cluster analysis. The cluster analysis showed that significant genetic variability among tested genotypes of forage sorghum that indicates the presence of excellent opportunity to bring about improvement through hybridization in different clusters to assemble desirable traits with higher heterotic potential and can use as release new cultivar and for further breeding program.

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