The Pharma Innovation Journal 2023; 12(12): 3008-3015

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(12): 3008-3015

www.thepharmajournal.com
Received: 01-10-2023
Accepted: 08-11-2023

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Genetic divergence and principal component analysis for fodder and biochemical traits in fodder maize (*Zea mays* L.)

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Abstract
Despite being a dual-purpose crop, very few studies have been done so far on maize for improving fodder quality and yield. The present investigation was carried out with 48 fodder maize genotypes analyzed for genetic variability, diversity (Mahalanobis's D^2) and principal components (PCA) in fodder maize. The observations were recorded for 13 different characters including biochemical traits like CP, NDF and ADF. The highest GCV (19.90%) and PCV (24.09%) was observed for green fodder yield per plant and it also had high heritability along with high genetic advance, indicating that selection for this trait would be fruitful. In PCA, three PCs extracted collectively contributed 72.5% of the total variability. Hence, the genotypes that recorded higher PC scores in PC1, PC2 and PC3 could be utilized in the further hybridization program to enhance the fodder yield in maize. D^2 analysis grouped 48 genotypes in nine different clusters. The maximum inter-cluster distance was present between clusters 5 (GWC-0320) and 9 (AFMC-1) [D = 14.60] followed by clusters 2 (Origin Mexico-6360) and 9 (AFMC-1) [D = 14.56]. Thus, crosses should be made among them to exploit better heterosis for enhancing green fodder yield in maize.

Keywords: Forage maize, Genetic variability, Diversity studies, Mahalanobis's D^2 analysis, Principal Component Analysis (PCA)

Introduction
Fodder maize, also known as silage corn or fodder corn, plays a pivotal role in the global agricultural landscape. Maize as a forage crop serves as a critical source of high-quality feed for livestock, contributing significantly to sustainable and efficient livestock production systems. Its unique characteristics, high nutritional value and good adaptability make it an indispensable resource for meeting the growing demand for animal feed. Unlike other cereal crops, such as wheat and barley, fodder maize possesses superior energy content, making it an excellent energy source for livestock. Additionally, its higher digestibility and abundant supply of carbohydrates make it highly palatable and well-suited as feed for dairy animals (Lauer, 2018) [12]. Fodder maize is characterized by its high content of starch, fibre, protein, vitamins and minerals; that contributes to the health and performance of livestock. The starch content provides a readily available source of energy which is essential for growth, reproduction and milk production. The fibre component plays a crucial role in maintaining rumen health and promoting proper digestion. Moreover, the protein content in fodder maize offers a balanced amino acid profile to livestock (Grant, 2013) [7].

There are many multivariate techniques available for the analysis of genetic diversity in germplasm accessions, breeding lines and populations. The principal component analysis is one of the important multivariate techniques invented by Karl Pearson in 1901, which extracts the relevant information from confusing data sets (Gorban *et al.*, 2008) [6]. PCA provides a pathway for reducing complex data set to lower dimensions sometimes in hidden, simplified structures that underlying them, with little effort. It is appropriate to use principal component analysis to assess a number of observed variables and to create a smaller set of artificial variables (referred to as principal components) that will largely explain the variation present in the population. The principal components can then be employed as a predictor or criteria variables in subsequent studies. The estimation of genetic diversity is commonly employed by breeders as an alternative to the course of germplasm selection since it enables lines to be organised into different clusters that, when crossed with each other would provide the most promising results and save time as well as resources.

The classification of genotypes based on diversity analysis will allow the breeder to choose the parents with the greatest genetic diversity for the hybridization programme. Assessment of genetic divergence helps in reducing the number of breeding lines that have to be maintained by plant breeders. The genetic distance between different genotypes can be measured using D^2 statistics given by Mahalanobis (1936) [13]. D^2 analysis is a very useful method for measuring the degree of genotypic divergence between biological populations. It also determines how much each component contributed to the overall divergence at both the intra and inter-cluster levels. Hence, the objective of the current investigation was to study the variability parameters; to estimate the genetic diversity using Mahalanobis's D^2 analysis and to perform principal component analysis for 48 fodder maize genotypes.

Materials and Methods

Experimental site

The experiment was carried out in *Kharif*-2021 at Main Forage Research Station, Anand Agricultural University, Anand (22° 35' N, 72° 55' E), Gujarat, India. The experimental site has sandy loam soil with a pH range of 8.1 to 8.5. It has low levels of organic matter, nitrogen and cation exchange capacity, but is relatively rich in potash and has a medium level of phosphorus.

Experimental design and material

A randomized complete block design (RBD) with three replications was used to evaluate 48 different fodder maize genotypes (list given in Table 1). Each genotype was planted in a single row that was 5.0 m long, 30 cm apart and had a 10 cm plant-to-plant spacing. The experiment was surrounded by border rows to prevent damage and border effects. The crop was successfully raised by following all the suggested agronomic and plant protection practices.

Observations recorded and characters investigated

Five randomly selected plants from each entry were observed for thirteen different characteristics *viz*; days to 50% tasselling, days to 50% silking, number of leaves per plant, plant height (cm), stem thickness (cm), leaf length (cm), leaf width (cm), leaf: stem ratio, dry matter content (%), crude protein content (%) [CP], neutral detergent fibre content (%) [NDF], acid detergent fibre content (%) [ADF] and green fodder yield per plant (g). The sample collected from each genotype was chopped, air-dried for three days and then dried in the oven at 100º C till the attainment of constant weight; after that dry matter content was measured. Finally, the sample was powdered and scanned with "FOSS NIR System" (Model: 5000 composite) following the standard analytical protocol to determine all the quality parameters like CP, NDF and ADF.

Table 1: List of fodder maize genotypes used in this study

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1	IC-77541	17	BAIF-119	33	AFM-24
2	IC-130725	18	BAIF-155	34	AFM-25
3	IC-130791	19	BAIF-252	35	AFM-28
4	IC-130917	20	Narendra Moti	36	AFM-29
5	IC-131213	21	GS-2	37	AFM-30
6	GDRM-2	22	GWC-0320	38	AFM-31
7	GDRM-41	23	GWC-0511	39	AFM-32
8	EC-286987	24	GDRFG-1627	40	AFM-33
9	Mexico Accession-3969	25	GDRFG-1643	41	AFM-34
10	Mexico Accession-4081	26	AFM-9	42	AFM-35
11	NP96K-2416	27	AFM-11	43	AFM-36
12	NP96K-5720	28	AFM-18	44	AFMC-1
13	Origin Mexico-6350	29	AFM-19	45	AFMC-2
14	Origin Mexico-6360	30	AFM-20	46	AFMC-3
15	Origin Mexico-6371	31	AFM-22	47	AFMC-4
16	HYD-997-1517	32	AFM-23	48	J-1006

Statistical analysis

Variability parameters were estimated using the "Variability" package (Popat *et al.*, 2020) [20] in the R-studio. Principal components are generally extracted using two different methods; either from correlation matrix or covariance matrix. In the present investigation correlation matrix was used to extract the principal components and the analysis was carried out using Minitab software. Mahalanobis's D^2 statistics (Mahalanobis, 1936) [13] was used to analyze the data followed by Tocher's approach as described by Rao (1952) [21] to determine the group constellation. The computation of average intra-cluster and inter-cluster distances was executed as per Singh and Chaudhary (1985) [23]. The D^2 analysis was carried out using IndoStat Software.

Results and Discussion

Variability parameters

All the data of thirteen biometrical and quality traits of fodder maize genotypes were subjected to an analysis of variance. ANOVA revealed significant differences among genotypes for all the thirteen traits studied. The broad range of mean values were observed for the traits like days to 50% tasselling (44.00-55.00), days to 50% silking (50.00-62.00), number of leaves per plant (11.40-14.60), plant height (157.40-259.00 cm), stem thickness (0.80-1.60 cm), leaf length (41.20-76.80 cm), leaf width (3.82-7.30 cm), leaf: stem ratio (0.32-0.91), dry matter content (12.10-23.20%), crude protein content (4.85-5.19%), neutral detergent fibre content (63.53-82.06%), acid detergent fibre content (36.77-45.04%) and green fodder yield per plant (138.40-410.00 g) in 48 genotypes of fodder maize (Table 2).

Phenotypic variance was higher than genotypic variance for the green fodder yield and its contributing traits, suggesting that these characters are influenced by the environmental factors. The quantity of genetic and non-genetic variation is determined by estimating genotypic and phenotypic

coefficients of variation as suggested by Burton (1952) [3]. The highest PCV was observed for green fodder yield per plant (24.09%); it also had maximum GCV of 19.90%. Naharudin *et al.* (2021) and Rathod *et al.* (2021) [22] also found the highest GCV and PCV for green fodder yield. Moderate GCV and PCV were obtained for the leaf: stem ratio (13.48 and 18.83%). Further, moderate PCV was observed for stem thickness (12.79%), leaf length (11.25%), leaf width (11.93%) and dry matter content (10.88%). The current findings are in accordance with Kapoor (2017) [10] and Rathod *et al.* (2021) [22]. Higher and moderate magnitude of GCV and PCV for the traits given above indicated presence of high degree of variability and better scope for selection. All the other traits showed lower GCV and PCV. The difference between PCV and GCV was highest for leaf: stem ratio, indicating that this trait has greater influence of the environment on it. Similar results were obtained by Rathod *et al.* (2021) [22].

Table 2: Estimates of different variability parameters for different traits in fodder maize

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	H^2 (%)	GA	GAM
1	DT	48.05±0.65	44.00-55.00	5.47	5.94	84.69	4.979	10.36
2	DS	55.03±0.7	50.00-62.00	4.37	4.88	79.90	4.423	8.04
3	NOL	13.03±0.24	11.40-14.60	3.56	4.72	56.72	0.719	5.52
4	PH	215.27±8.98	157.40-259.00	3.88	8.20	22.39	8.138	3.78
5	ST	1.16±0.07	0.80-1.60	8.38	12.79	42.92	0.131	11.31
6	LL	59.47±2.34	41.20-76.80	8.97	11.25	63.57	8.760	14.73
7	LW	5.58±0.28	3.82-7.30	8.46	11.93	50.24	0.688	12.35
8	LSR	0.59±0.05	0.32-0.91	13.48	18.83	51.22	0.117	19.87
9	DM	17.92±0.81	12.10-23.20	7.61	10.88	48.95	1.965	10.97
10	CP	5.08±0.03	4.85-5.19	0.20	0.88	5.00	0.005	0.09
11	NDF	73.5±1.59	63.53-82.06	0.37	3.75	0.96	0.054	0.07
12	ADF	41.45±1.02	36.77-45.04	0.20	4.23	0.22	0.008	0.02
13	GFYPP	221.57±17.37	138.40-410.00	19.90	24.09	68.24	75.022	33.86

DT= days to 50% tasselling, DS= days to 50% silking, NOL= number of leaves per plant, PH= plant height (cm), ST= stem thickness (cm), LL= leaf length (cm), LW= leaf width (cm), LSR= leaf: stem ratio, DM= dry matter content (%), CP= crude protein content (%), NDF= neutral detergent fibre content (%), ADF= acid detergent fibre content (%), GFYPP= green fodder yield per plant (g), GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, H^2= Heritability (broad sense), GA= Genetic advance, GAM= Genetic advance as percentage of mean

Heritability is the ratio of genotypic variance to the total variance and it is a good index to check the transmission of traits from parents to their offspring (Falconer, 1960). The trait days to 50% tasselling (84.69%) recorded the highest estimate of heritability followed by days to 50% silking (79.90%) and green fodder yield per plant (68.24%). Rathod *et al.* (2021) [22] observed the same pattern during the experiment. Wali *et al.* (2019) also obtained high heritability for days to 50% silking. Naharudin *et al.* (2021) [15] found high heritability for days to 50% tasselling, days to 50% silking and green fodder yield per plant. Also, for leaf length (63.57%), high heritability was observed, which was similar to the results obtained by Rathod *et al.* (2021) [22] and Kapoor (2017) [10]. Number of leaves (56.72%), stem thickness (42.92%), leaf width (50.24%), leaf: stem ratio (51.22%) and dry matter content (48.95%) showed moderate heritability. All the biochemical traits (CP, NDF and ADF) as well as plant height exhibited low heritability, indicating that environmental factors like soil fertility, irrigation, *etc*. play an important role in determining biochemical traits in fodder maize.

Genetic advance is an estimate of genetic gain under selection. High genetic advance as percent of mean was observed for green fodder yield per plant (33.86%). While moderate genetic advance as percent of mean was estimated for days to 50% tasselling (10.36%), stem thickness (11.31%), leaf length (14.73%), leaf width (12.35%), leaf: stem ratio (19.87%) and dry matter content (10.97%). Other traits had low genetic advance as percent of mean. The results were in accordance with Kapoor and Batra (2015) [11] for NDF; Kapoor (2017) [10] for number of leaves and stem thickness; Chandel and Guleria (2019) for leaf width; Naharudin *et al.* (2021) [15] for days to 50% silking, green fodder yield per plant, number of leaves and NDF; Rathod *et al.* (2021) [22] for days to 50% silking, leaf: stem ratio and CP. Heritability estimates along with genetic advance are more useful in predicting the gain under selection than heritability estimates alone (Johnson *et al.*, 1955) [9]. The trait green fodder yield showed high heritability estimates accompanied with high genetic advance percent of mean which might be due to additive gene action and direct selection for such trait is rewarding in crop improvement. Naharudin *et al.* (2021) [15] and Rathod *et al.* (2021) [22] observed the similar results. Parmar *et al.* (2022) also found high heritability coupled with high genetic advance for green fodder yield, while working with forage crop. High heritability coupled with moderate genetic advance was found for days to 50% tasselling and stem thickness; thus, selection for these traits may be fruitful.

Principal component analysis

Principal component analysis, also known as canonical vector analysis, is a type of multivariate analysis in which canonical vectors or roots representing various axes of differentiation and the proportion of variation accounted for by each axis, respectively, are produced (Rao, 1952). It shows the significance of the largest contributor to overall variation on each differentiation axis (Nadarajan *et al.*, 2020).

In this investigation, out of total 13, three principal components (PCs) extracted had eigenvalue >1. Earlier scientists, Sinha *et al.* (2019) observed four PCs with greater eigenvalues (>1) after studying 14 traits and Al-Naggar *et al.* (2020) identified five PCs with >1 value out of 21 characters studied, while Pavithra *et al.* (2022) [18] found four PCs with eigenvalue >1 from 11 traits. Three components, PC1, PC2 and PC3 together contributed 72.5% of the total variability amongst the fodder maize genotypes assessed for green

fodder yield and its related traits (Table 3). While the remaining components contributed only 27.5% of the total diversity present among the fodder maize genotypes. PC1 contributed 44.4% towards the variability followed by PC2 (19.4%) and PC3 (8.7%). Most of the traits except dry matter content, NDF and ADF showed positive factor loadings on PC1 (Table 3). The maximum factor loading was observed from stem thickness followed by days to 50% tasselling and green fodder yield per plant.

The second principal component (PC2) represented CP, leaf: stem ratio and days to 50% tasselling with their positive loadings. While the minimum and negative loading was observed from dry matter content in PC2. The PC3 was explained by variation among fodder maize genotypes mainly due to number of leaves, plant height and stem thickness with their positive loadings and most negative loading exhibited by leaf: stem ratio.

Table 3: Principal components for fodder yield and its contributing traits of fodder maize

Parameters	PC1	PC2	PC3
Eigenvalue	5.773	2.519	1.130
Proportion	0.444	0.194	0.087
Cumulative	0.444	0.638	0.725
Days to 50% tasselling	0.366	0.008	-0.224
Days to 50% silking	0.327	-0.047	-0.267
Number of leaves per plant	0.197	-0.006	0.462
Plant height (cm)	0.354	-0.149	0.163
Stem thickness (cm)	0.371	-0.123	0.163
Leaf length (cm)	0.348	-0.100	-0.096
Leaf width (cm)	0.343	-0.127	-0.072
Leaf: stem ratio	0.046	0.219	-0.738
Dry matter content (%)	-0.126	-0.519	-0.144
Crude protein content (%)	0.064	0.447	0.011
Neutral detergent fibre content (%)	-0.167	-0.489	-0.068
Acid detergent fibre content (%)	-0.194	-0.378	-0.164
Green fodder yield per plant (g)	0.362	-0.190	-0.026

Principal components, PC1 and PC2 were scaled, thus values are symmetrically distributed between the trait scores and genotype scores. The trait scores are depicted in the loading plot (Figure 1) and genotype scores are depicted in the score plot (Figure 2). A genotype by trait biplot was also created by plotting the PC1 scores against the PC2 scores for each genotype and each trait (Figure 3). The genotype by trait biplot effectively reveals the interrelationships among different traits and also provides the better image for visual comparison between different genotypes based on multiple traits at a time. The results of the genotype by trait biplot explained 63.80% of the total variation as PC I and PC II collectively contribute that proportion of the variation.

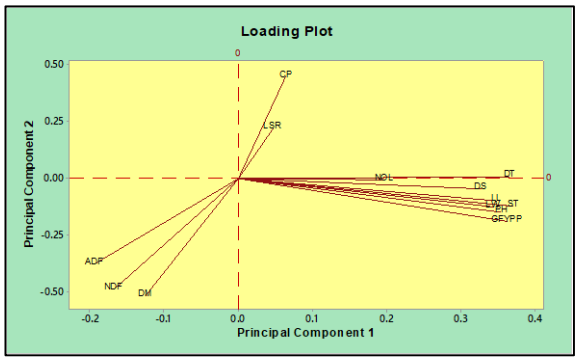

Fig 1: Loading plot of 13 different traits

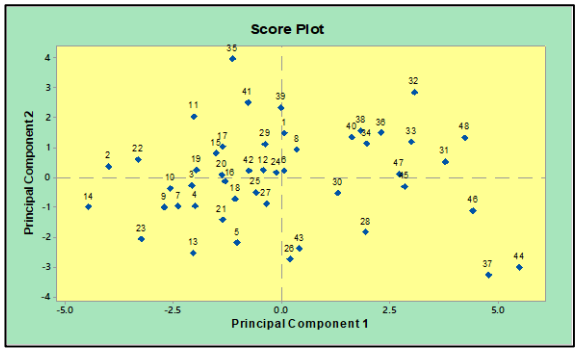

Fig 2: Score plot of 48 fodder maize genotypes

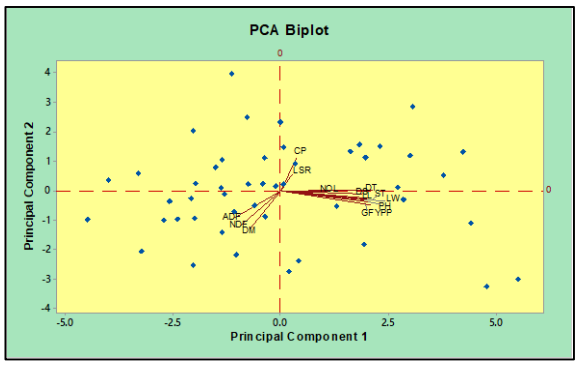

Fig 3: Genotype by trait biplot of fodder maize

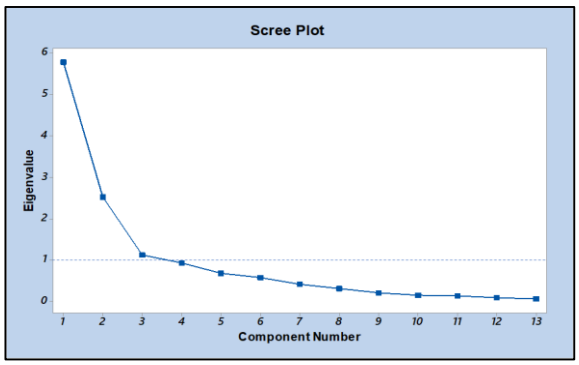

Fig 4: Scree plot of principal components

Based on the loading plot (Figure 1), dry matter content followed by NDF, CP, ADF, stem thickness, days to 50% tasselling, green fodder yield per plant and plant height had relatively long vectors either in positive or negative direction, indicating that there was relatively large variation among the genotypes for these traits. In other words, they display large amount of variation among the 48 genotypes studied, suggesting that they are the most discriminator of the morphological data under this investigation. The traits of each group which had acute (< 90°) angles between them indicate that their variations were similar, so each trait inside a specific group can be recorded instead of the other trait in the same group. Here based on the loading plot, very less angle was observed between plant height and green fodder yield; also leaf width, stem thickness, leaf length, days to 50% silking, number of leaves, days to 50% tasselling and leaf: stem ratio had < 90° angle with green fodder yield per plant suggesting that they are inter-related traits showing positive correlations. Earlier scientists, Kapoor and Batra (2015) [11] as well as Borkhatariya *et al.* (2022) also found positive correlation between them. CP had nearly right angle (= 90°) with green fodder yield per plant, indicating that variation of one trait was more or less independent of that trait (near zero correlation). Naharudin *et al.* (2021) [15] and Borkhatariya *et al.* (2022) observed non-significant correlation between CP and green fodder yield. On the contrary, dry matter content, ADF and NDF had obtuse (> 90°) angles with green fodder yield, indicating that their variations were in opposite directions and may have negative correlation.

The score plot indicates the positions of different genotypes on the bases of PC1 and PC2 (Figure 2). The genotypes present nearer to each other show more or less similar morphology. The position of the genotypes on the score plot can be used further with the PCA biplot (Figure 3) to compare the interrelationships between different traits and individual genotypes. The genotypes present in a similar direction of trait vectors may show greater values for those traits. For example, genotype numbers 48, 46, 44, 37, *etc*. had higher green fodder yield per plant as well as higher values for its related traits. While, genotype numbers 23, 13, 14, *etc*. possess good biochemical properties like ADF, NDF and dry matter content.

Scree plot generated by graphing eigenvalues and principal component numbers describe the percentage of variance related to each principal component (Figure 4). PC1 has an eigenvalue of 5.773 and a variance of 44.40%. Semi curve line obtained after the third principal component tended to become straight with little variance observed in each PC. Based on the scree plot, it is clear that the first three PCs had more than one eigenvalue indicating that it shows more variation among the fodder maize genotypes and it could be helpful for the selection of the diverse parents.

Mahalanobis's D^2analysis

The selection of parental lines from a set of genotypes can be based on their ability to trigger heterosis, which is generally determined via genetic diversity analyses. Thus, in the present experiment, 48 fodder maize genotypes were evaluated by cluster analysis and divided into nine clusters based on mean values for several quantitative and qualitative traits. The dendrogram (Figure 5) displays different clusters created using Tocher's approach.

Table 4: Average intra and inter-cluster distances for different genotypes of fodder maize

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
Cluster 1	4.83	5.98	6.14	7.70	6.46	6.15	6.87	9.45	10.97
Cluster 2		0.00	8.68	10.51	3.73	6.43	7.52	12.31	14.56
Cluster 3			0.00	4.99	9.88	6.97	8.65	6.46	8.30
Cluster 4				5.54	11.02	8.91	9.82	6.74	7.27
Cluster 5					0.00	7.25	7.67	13.16	14.60
Cluster 6						0.00	9.30	9.88	12.34
Cluster 7							0.00	13.36	13.58
Cluster 8								0.00	6.07
Cluster 9									0.00

Note: Diagonal bold values represent the intra-cluster distances, while other values represent inter-cluster distances.

Among the nine clusters, cluster 1 was the largest with 32 genotypes followed by cluster 4 with nine genotypes. One genotype each was present in clusters 2, 3, 5, 6, 7, 8 and 9. Earlier, Islam *et al.* (2020) [8] also classified 30 maize genotypes into seven clusters on the basis of Mahalanobis's D^2 analysis. Suman *et al.* (2020) identified three different clusters from 13 diverse genotypes of maize. While Pavithra *et al.* (2022) [18] identified 11 clusters out of 93 fodder maize genotypes and Peer *et al.* (2022) [19] grouped 70 genotypes of maize into 14 clusters using Tocher's method. Patel *et al.* (2022) [19] also performed D^2 analysis and identified eight different clusters from 45 genotypes in maize.

The average D^2 values of intra-cluster and inter-cluster distances are given in Table 4. The maximum intra-cluster distance was in cluster II (D = 5.54) followed by cluster I (D = 4.83). The maximum inter-cluster distance was between clusters 5 (GWC-0320) and 9 (AFMC-1) [D = 14.60] followed by clusters 2 (Origin Mexico-6360) and 9 (AFMC-1) [D = 14.56], all of these clusters had a single genotype in them. Clusters 2, 3, 5, 6, 7, 8 and 9 had no intra-cluster distances as they had a single genotype in them. The minimum inter-cluster distance was estimated among clusters 2 and 5 (D = 3.73) indicating the closer relationships among the genotypes present in it.

Genotypes belonging to the same cluster have little genetic divergence from each other, with respect to the overall influence of 13 traits. In order to have good recombination in the segregating generations, it is unlikely to make a cross between members of the same clusters. Therefore, it is suggested that crosses should be made among the genotypes from different clusters having more inter-cluster distance.

Cluster means analysed for 13 characters in fodder maize clearly indicated appreciable differences for most of the traits as shown in Table 5. Cluster 2 had a maximum value for NDF (75.80%) and ADF (43.24%). Cluster 5 had a maximum value for leaf: stem ratio (0.77) as well as the minimum value for

days to 50% tasselling (44.33), suggesting earliness. Cluster 7 exhibited the highest mean value for number of leaves (14.00) and CP (5.11%); while for days to 50% silking (51.33), it was earliest. The mean values for leaf length (72.57 cm), leaf width (6.62 cm) and green fodder yield per plant (339.00 g) were observed the highest in cluster 8. Cluster 9 showed the maximum mean values for all the remaining traits including plant height (252.40 cm), stem thickness (1.53 cm) and dry matter content (20.10%).

The percent contribution of various traits to divergence for 48 fodder maize genotypes is presented in Table 6. The present investigation revealed that the highest genetic divergence contributing character was days to 50% tasselling (40.60%) followed by days to 50% silking (10.11%) and leaf: stem ratio (10.02%). Thus, selection for these traits in the given population might be beneficial to exploit heterosis in future generations.

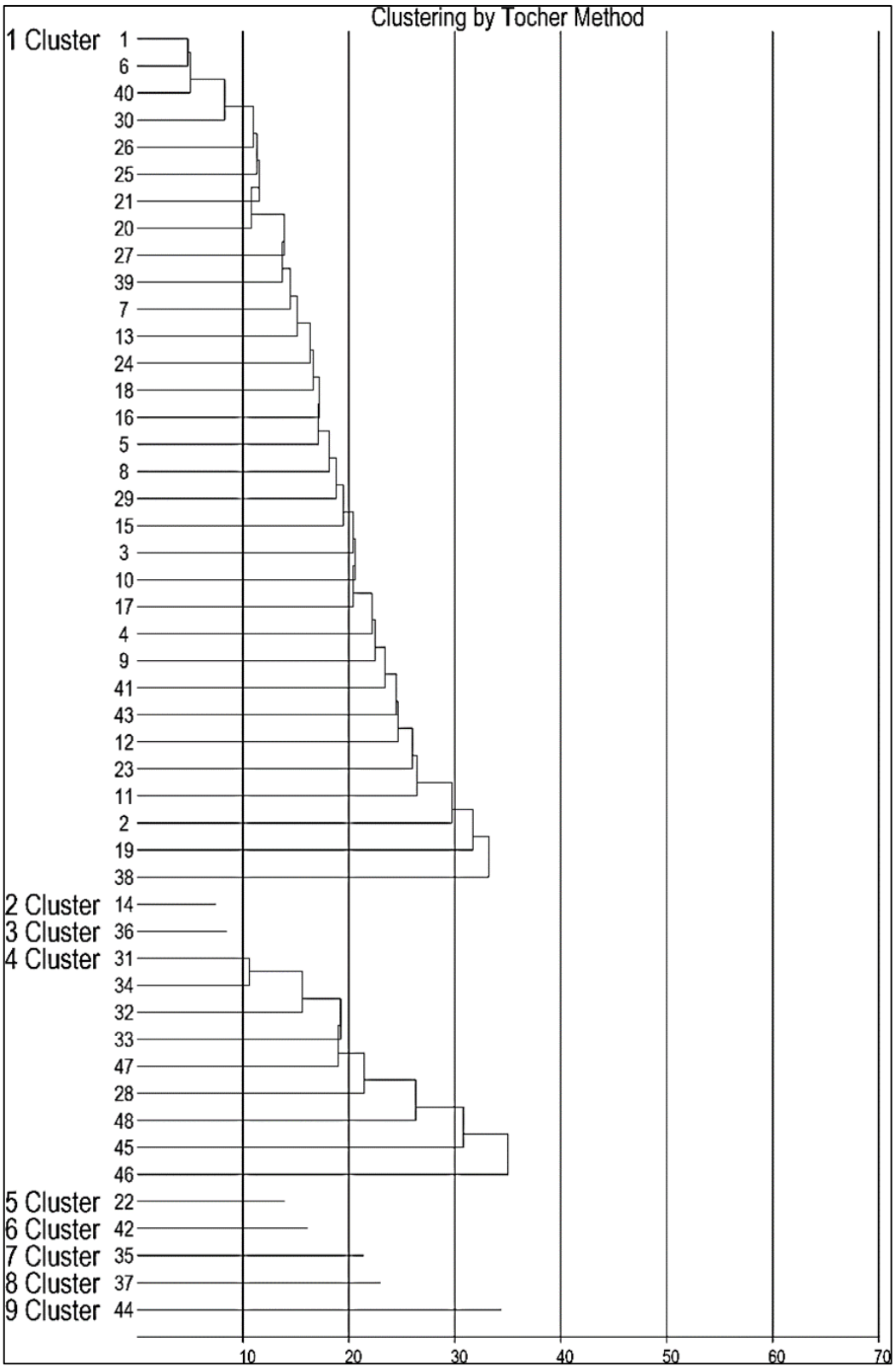

Fig 5: Dendrogram of 48 maize genotypes based on 13 characters generated using Tocher's method (Name of the genotypes as per Table 1)

Table 5: Cluster means for different traits of fodder maize

	DT	DS	NOL	PH	ST	LL	LW	LSR	DM	CP	NDF	ADF	GFYPP
Cluster 1	47.03	54.07	12.96	210.86	1.13	57.46	5.42	0.58	15.20	5.08	73.84	41.70	205.82
Cluster 2	44.67	54.00	12.33	200.80	0.88	52.00	4.53	0.67	18.73	5.04	75.80	43.24	155.10
Cluster 3	50.00	58.00	13.13	225.40	1.22	57.60	5.96	0.53	15.60	5.09	71.41	40.00	261.47
Cluster 4	51.74	58.15	13.34	226.96	1.25	65.33	6.15	0.63	16.98	5.09	72.00	40.91	269.06
Cluster 5	44.33	52.00	11.80	198.47	1.02	57.27	4.93	0.77	19.63	5.07	73.33	41.55	166.53
Cluster 6	45.67	53.67	12.20	218.47	1.07	64.67	5.45	0.39	16.60	5.08	74.00	40.67	206.73
Cluster 7	46.33	51.33	14.00	208.33	1.07	52.20	5.04	0.74	14.20	5.11	71.97	39.73	165.50
Cluster 8	50.67	60.00	13.53	240.60	1.45	72.57	6.62	0.50	19.73	5.06	74.58	41.97	339.00
Cluster 9	53.67	58.67	13.67	252.40	1.53	71.60	6.10	0.56	20.10	5.05	75.59	39.81	333.03

DT= days to 50% tasselling, DS= days to 50% silking, NOL= number of leaves per plant, PH= plant height (cm), ST= stem thickness (cm), LL= leaf length (cm), LW= leaf width (cm), LSR= leaf: stem ratio, DM= dry matter content (%), CP= crude protein content (%), NDF= neutral detergent fibre content (%), ADF= acid detergent fibre content (%), GFYPP= green fodder yield per plant (g)

Table 6: Contribution of various traits towards the divergence for different genotypes of fodder maize

Characters	Times Ranked 1st	Contribution %
Days to 50% tasselling	458	40.60%
Days to 50% silking	114	10.11%
Number of leaves per plant	111	9.84%
Plant height (cm)	20	1.77%
Stem thickness (cm)	23	2.04%
Leaf length (cm)	72	6.38%
Leaf width (cm)	32	2.84%
Leaf: stem ratio	113	10.02%
Dry matter content (%)	84	7.45%
Crude protein content (%)	6	0.53%
Neutral detergent fibre content (%)	1	0.09%
Acid detergent fibre content (%)	8	0.71%
Green fodder yield per plant (g)	86	7.62%

Conclusion

The results of the present study revealed that the highest PCV was found for green fodder yield per plant (24.09%) and it also had the highest GCV of 19.90%. While high heritability along with high genetic advance recorded for the green fodder yield per plant and hence the selection for this trait would be effective. In the principal component analysis, three PCs out of total 13 PCs had eigenvalues greater than one, which collectively contributed 72.5% of the total variability present in the fodder maize genotypes. Hence, the genotypes that recorded higher PC scores in PC1, PC2 and PC3 components could be utilized in the further hybridization program to enhance the fodder yield in maize. PC1 itself had an eigenvalue of 5.773 and a variance of 44.40%. Thus, important traits contributing to PC1 like stem thickness, days to 50% tasselling, green fodder yield per plant, plant height, leaf length, leaf width and days to 50% silking should be given more emphasis while selecting better genotypes for the hybridization program to obtain better segregants. However, PC2 suggested the importance of CP as a biochemical trait and leaf: stem ratio as a quantitative trait, while practising selection in fodder maize. Clustering of the genotypes using Mahalanobis's D^2 analysis grouped 48 genotypes in nine different clusters. The maximum inter-cluster distance was present between clusters 5 (GWC-0320) and 9 (AFMC-1) [D = 14.60] followed by clusters 2 (Origin Mexico-6360) and 9 (AFMC-1) [D = 14.56]. Therefore, it is suggested that crosses should be made among the genotypes present in them to exploit better heterosis through the hybridization program to enhance green fodder yield in maize.

Future Scope

The present investigation determined variability parameters for the 48 genotypes and also identified green fodder yield per plant as a trait with high GCV, PCV, heritability and genetic advance. Thus, direct selection in the population studied could be fruitful for development of new and better variety in fodder maize. PCA provided numbers of traits including CP as important traits while practicing selection for improving fodder yield. Mahalanobis's D^2 analysis grouped fodder maize genotypes in different clusters and crossing among those genotypes belonging to the different clusters with high inter-cluster distance could be useful to exploit better heterosis for fodder yield and quality traits in maize.

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