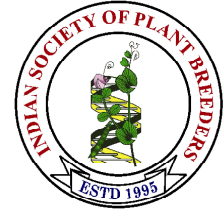


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Research Article

Genetic studies on green fodder yield and quality traits in fodder maize (*Zea mays* L.)

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Abstract

An experiment was conducted to evaluate the genetic divergence in 93 inbreds of fodder maize through genetic variability, D^2 and principal component analysis. Observations were recorded on ten biometrical traits and a quality trait. The variability analysis revealed higher GCV and PCV for green fodder yield per plant and higher heritability coupled with high genetic advance for the traits viz., plant height, leaf length and green fodder yield per plant. Hence, the variability study indicated that the direct selection for the above traits would be effective. Diversity analysis sorted the 93 inbred into eleven clusters. In case of inter cluster distance, maximum distance was obtained between cluster VIII and X followed by cluster VI and VIII and VIII and XI indicating that these cluster pairs have a more genetic divergence and the inbreds of these clusters could be utilized in a fodder maize hybridization programme. The D^2 analysis suggests that the inbreds viz., GETM30, GETM84, GETM12, and GETM81 were distinct and diversified and classed as promising inbreds based on the cluster mean and divergence. These genotypes could be utilized in a fodder maize hybridization programme to obtain heterotic fodder maize hybrids apart from getting the desired segregants in later generations. According to the principle component (PC) analysis, out of 11 PC groups, four PCs recorded more than one Eigen value, which contributes 70.30% of the total variability. However, the variability for green fodder yield and its attributing traits were higher in PC1, PC2, PC3 and PC4 and hence, the inbreds that recorded higher PC scores in these components could be utilized in the further hybridization programme to enhance the biomass yield in fodder maize.

Keywords: Fodder maize inbreds, variability, diversity, PCA

INTRODUCTION

Maize, also known as corn (*Zea mays* L.), is a major versatile crop used all over the world. It is a member of the Maydeae tribe of the Poaceae family, genus *Zea*, with somatic chromosomal number $2n=20$. According to Vavilov (1926), the most likely centre of origin for maize is Mexico or Central America, with a secondary origin in South America. Maize is recognized as the "Queen of Cereals" around the world because it has the highest genetic potential towards yield of all cereals. It is a major source of food, animal feed, poultry feed, and industrial raw materials (starch, protein, oil, alcoholic beverages,

food sweeteners). Fodder maize is a fast-growing, succulent, sweet-tasting, high-yielding, nutritional, and toxic-free crop that may be fed to animals at any stage of development (Devi, 2002). Fodder maize can be stored as hay/silage for use during lean season would be crucial for safeguarding the interests of small dairy farmers. The nutritional quality of fodder maize is significantly superior for cattle, particularly from the tasseling stage onwards. Green fodder supplies adequate energy and proteins for growth of animals, efficient reproduction and ample milk production (Takawale *et al.*, 2009). The livestock sector

has grown at a Compound Annual Growth Rate (CAGR) of 8.15% over the last five years ending 2020. Growth in the liquid milk segment, which accounts for over half of the dairy industry, is likely to remain stable (6-7%). A revival in economic activities, increasing per capita consumption of milk and milk products, changing dietary preferences and rising urbanization in India, has driven the dairy industry to grow by 9-11% in current financial year (Indian dairy sector-Press news, 2021). In India, the net shortfall of 35.6% in green fodder, 10.95% in dry fodder, and 44% in concentrate feed supplies. Green and dry fodder demand is predicted to rise dramatically by 2050, reaching 1,012 million tonnes and 631 million tonnes, respectively (IGFRI Vision, 2050). As the green fodder deficit is very high, there is an urgent need to identify the elite genotypes of fodder crops having increased biomass. The present study is focused on identifying the best inbreds in fodder maize to develop hybrids or composites with higher biomass.

To breed the fodder maize composites or hybrids, adequate information on the extent of genetic divergence among the available fodder maize inbred lines is necessary. Understanding genetic variability is important for progress in breeding programme. Since, it helps in the choice of the best yield traits either for selection or hybridization. In this view, an attempt was made to evaluate the degree and extent of genetic divergence for several green fodder yield contributing traits among the available fodder maize inbred lines.

MATERIALS AND METHODS

An experiment was conducted at Department of Forage Crops, Tamil Nadu Agricultural University, Coimbatore during *Rabi*, 2021 to evaluate the genetic diversity in fodder maize inbreds lines. The experiment material comprised of 92 domestic fodder maize inbreds and a check variety African tall. The inbreds were raised in a randomized block design (RBD) with two replications in which each genotype was sown in one row of 4 m length, with a distance of 30 cm × 20 cm. To raise a good crop, one plant per hill was maintained and other agronomic practices and plant protection measures were followed as recommended. For quantitative analysis in each genotype, five randomly selected plants from the rows of a plot were tagged. On five selected plants from each lines, observations were recorded on 11 traits *viz.*, days to 50% flowering (DFF), plant height (PH), number of leaves per plant (NOL), leaf length (LL), leaf width (LW), number of nodes per plant (NON), stem girth (SG), leaf stem ratio (LSR), green fodder yield per plant (GFY), dry matter content (DM %) and crude protein (CP %). Biometrical data observed from five plants were averaged replication wise and the mean value was used for statistical analysis. Variability parameters were studied in terms of phenotypic and genotypic variance which was arrived using standard methods. PCV and GCV were estimated by following the method of Sivasubramanian and Menon (1973). Heritability (h^2) in broad sense and genetic advance

(GA) were worked out based on the method suggested by Allard (1960) and Johnson *et al.* (1995), respectively. Genetic diversity was estimated by multivariate analysis using Mahalanobis D^2 statistics. The genotypes were grouped into different clusters by following Tocher's method (Rao, 1952) and principal component analysis was done according to Rao (1964). Mahalanobis D^2 analysis was carried out by using STAR 2.0.1 version software (<http://bbi.irri.org>). The principal component analysis was performed using OPSTAT software package (<http://www.202.141.47.5/opstat/index.asp>).

Genetic variability studies provide basic information about the genetic properties of the population on which breeding procedures are used for further improvement of the crop. All the data of eleven biometrical and quality traits of fodder maize inbreds were subjected to an analysis of variance. ANOVA revealed significant differences across genotypes for all the traits studied. The wide range of mean values were observed for the traits *viz.*, days to 50 % flowering (52.50 - 64.50 days), plant height (116.31 - 224.35 cm), number of leaves per plant (7.79 - 14.89), leaf length (43.13 -104.93 cm), leaf width (5.27 - 9.78 cm), number of nodes per plant (4.83 - 9.83), stem girth (4.94 -9.47 cm), leaf stem ratio (0.17 - 0.37), crude protein (7.74 -13.62 %), dry matter content (18.09 - 23.85 %) and green fodder yield (128.56 - 491.40 g/plant) in 93 fodder maize inbred lines (**Table 1**). Phenotypic variance was higher than genotypic variance for the green fodder yield and its associated traits, indicating that these traits are influenced by the environmental factors. The highest genotypic and phenotypic variance was recorded for green fodder yield per plant (5724.66 and 5830.58, respectively) followed by plant height (594.95 and 632.46, respectively) and leaf length (173.60 and 198.20, respectively) with lesser difference value exist between the genotypic and phenotypic variance. Less difference in the estimates of genotypic and phenotypic variance suggested that the variability present among the genotypes was mainly due to genetic reason with minimal influence of environment. Similar results were reported by Rathod *et al.* (2021) in fodder maize. The quantity of genetic and non-genetic variation is determined by estimating genotypic and phenotypic coefficients of variation as suggested by Burton (1952). Higher GCV and PCV magnitudes for these traits indicated a high degree of diversity and more scope for selection. The obtained results of higher GCV and PCV for green fodder yield (23.74 and 23.96%) revealed that the green fodder yield trait is controlled by additive gene action and hence the selection might be effective (**Table 1**). Moderate GCV and PCV were obtained for the traits such as plant height (13.89 and 14.32 %), number of leaves (12.39 and 15.23 %), leaf length (16.67 and 17.82 %), leaf width (10.10 and 12.73 %), number of nodes (12.37 and 15.55 %), stem girth (13.87 and 16.61%), leaf stem ratio (12.35 and 14.45%) and crude protein (12.51 and 14.18 %). Similar findings for plant height and leaf length were reported by Kapoor and Batra (2015) and

Table 1. Estimates of genetic parameters for different traits in fodder maize.

Traits	Range of mean values	GV	PV	GCV (%)	PCV (%)	H ² (%)	GA	GAM (%)
DFF	52.5 - 64.5	4.86	5.55	3.95	4.22	87.66	4.25	7.62
PH	116.31 - 224.35	594.95	632.46	13.89	14.32	94.06	48.73	27.76
NOL	7.79 - 14.89	1.97	2.97	12.39	15.23	66.12	2.35	20.75
LL	43.13 - 104.93	173.60	198.20	16.67	17.82	87.58	25.40	32.15
LW	5.27 - 9.78	0.63	1.00	10.10	12.73	62.97	1.30	16.52
NON	4.83 - 9.83	0.90	1.42	12.37	15.55	63.24	1.55	20.26
SG	4.94 - 9.47	0.96	1.37	13.87	16.61	69.74	1.68	23.86
LSR	0.17 - 0.37	0.00	0.00	12.35	14.45	73.02	0.06	21.74
CP	7.74 - 13.62	1.45	1.87	12.51	14.18	77.76	2.19	22.72
DM	18.09 - 23.85	1.05	1.88	4.89	6.54	55.94	1.58	7.54
GFY	128.56 - 491.40	5724.66	5830.58	23.74	23.96	98.18	154.44	48.47

DFF – Days to 50 % flowering, PH - Plant height (cm), NOL – Number of leaves per plant, LL - Leaf length (cm), LW - Leaf width (cm), NON - Number of nodes per plant, SG- Stem girth (cm), LSR-Leaf stem ratio, DMY- Dry matter content (%), GFY- Green fodder yield (g/plant), CP – Crude protein(%),PV- Phenotypic variation, GV- Genotypic variation, PCV- Phenotypic coefficient of variation, GCV – Genotypic coefficient of variation, h²- Heritability (broad sense), GA- Genetic advance, GAM - Genetic advance as percentage of mean

for crude protein by Chakrovorty and Neog (2015) and Murugan *et al.* (2010) for green fodder yield by Gayosso-Barragán *et al.* (2020) in fodder maize.

Heritability is the ratio of genotypic variance to the total variance. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1960). The trait green fodder yield (98.18%) recorded the highest estimate of heritability followed by plant height (94.06%), days to 50 % flowering (87.66%), leaf length (87.58%), crude protein (77.76%), leaf stem ratio (73.02%), stem girth (69.74%), number of nodes per plant (63.24%) and leaf width (63.97%). Similar results for plant height reported by Prakash *et al.* (2019) and for plant height, green fodder yield, and stem girth also reported by Ali *et al.* (2015) in fodder maize. It indicates that improvement of these characters would be effective through phenotypic selection due to additive gene action.

Genetic advance is a measure of genetic gain under selection. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al.*, 1955). High heritability coupled with high genetic advance were recorded for the trait green fodder yield (98.18% and 154.44, respectively) followed by plant height (94.06% and 48.73, respectively) and leaf length (87.58% and 25.40, respectively). It indicates that the genes for these traits are controlled by additive gene action and selection may be effective. Similar results were reported by Ali *et al.* (2015). Therefore, the genetic variability studied in the inbreds of fodder maize indicated that the direct selection for green fodder yield, plant height and leaf length would be effective.

Mahalanobis developed the concept of D² statistics for a measure of group distance based on several characters in 1928. This technique could be used to measure genetic diversity in plant breeding (Rao, 1952). The fundamental goal of utilizing a cluster technique to analyse data from plant breeding trials is to divide the genotypes into numerous homogenous groups, with each group having a similar response pattern (Nadarajan *et al.*, 2020). Mahalanobis D² statistics was used to calculate intra and inter cluster distances within and between the genotypes, respectively. According to Rao's description of Tocher's method, 93 inbreds of fodder maize were sorted into eleven clusters based on Tocher cut-off value 91.11 (**Table 2**). Cluster I had the most inbreds with 34, followed by cluster II, which had 29 inbreds, cluster III had nine inbreds, cluster V had seven inbreds, cluster VIII had five inbreds, cluster IX had four inbreds and cluster IV, VI, VII, X, XI was monogenotypic. Similarly Prasad, (2021) divided 19 maize genotypes into five clusters.

The average inter-cluster distance was higher than the intra-cluster distance indicating the inbred lines of different clusters have a lot of variation (**Table 3**). Cluster VIII and X (37.35) had the maximum inter cluster distance followed by cluster VI and VIII (35.45), and cluster VIII and XI (34.55), indicating that the inbred lines included in these cluster pairs have a more diverse genetic composition. The minimum inter-cluster distance was observed between the clusters VI and X (7.67), indicating that the inbred lines belonging to these clusters were comparatively less diverse. The maximum intra cluster distance observed in cluster IX (12.16) and it was minimum in cluster IV, VI, VII, X, XI (0.00) with monogenotypic.

Table 2. Distribution of 93 fodder maize inbred lines in 11 clusters.

Clusters	Number of genotypes	Genotypes
I	34	GETM79, GETM90, GETM59, GETM87, GETM68, GETM89, GETM26, GETM15, GETM51, GETM69, GETM89, GETM46, GETM47, GETM82, GETM38, GETM5, GETM20, GETM83, GETM33, GETM92, GETM52, GETM71, GETM91, GETM4, GETM88, GETM 32, GETM95, GETM41, GETM45, GETM63, GETM3, GETM74, GETM80, GETM67
II	29	GETM21, GETM40, GETM56, GETM9, GETM17, GETM1, GETM64, GETM29, GETM19, GETM65, GETM57, GETM36, GETM28, GETM2, GETM94, GETM103, GETM7, GETM53, GETM22, GETM76, GETM54, GETM31, GETM8, GETM108, GETM23 GETM61, GETM42, GETM39, GETM24
III	9	GETM14, GETM16, GETM86, GETM96, GETM49, GETM73, GETM58, GETM66, GETM6
IV	1	GETM81
V	7	GETM50, GETM62, GETM34, GETM35, GETM55, GETM37, African tall
VI	1	GETM12
VII	1	GETM27
VIII	5	GETM60, GETM85, GETM77, GETM18, GETM93
IX	4	GETM10, GETM13, GETM48, GETM102
X	1	GETM84
XI	1	GETM30

Tocher Cut-off Value = 91.11

Table 3. Average intra and inter cluster distances in fodder maize.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	8.31	14.54	10.52	9.68	16.25	22.23	14.33	16.09	14.13	23.95	21.80
II		8.85	18.35	15.03	12.07	12.08	10.73	26.78	13.74	13.53	12.97
III			9.96	13.76	19.11	26.21	17.49	13.98	17.57	28.01	24.52
IV				0.00	18.47	22.49	15.00	17.20	12.89	24.65	23.24
V					10.70	13.79	16.80	27.89	17.33	15.49	13.37
VI						0.00	15.10	35.45	18.73	7.67	9.57
VII							0.00	24.44	11.56	17.66	17.28
VIII								7.85	22.72	37.35	34.55
IX									12.16	21.02	19.87
X										0.00	11.27
XI											0.00

(Bold values represents average inter cluster distance)

Crosses involving parents from the most divergent clusters are predicted to have the most heterotic and create the greatest genetic variability. This was further supported by the fact that cluster means showed significant variation (Table 4). Cluster XI had the greatest mean values for the traits plant height, leaf length, number of nodes per plant, crude protein, and leaf stem ratio; cluster X had the highest mean values for the traits number of leaves per plant and green fodder yield per plant; and cluster VI had the highest mean values for leaf width and stem girth; and cluster IV had the highest mean value for dry matter content. There was a broad range of variation for various traits among single and multigenotypic clusters.

As a result, inbred lines from clusters XI may be used as a parent in hybridization programme to enhance the traits viz., plant height, leaf length, number of nodes per plant, crude protein, and leaf stem ratio; and inbred lines from cluster X may be used for improve the traits of number of leaves and green fodder yield per plant; cluster VI may be used to improving the traits of leaf width and stem girth, and IV should be chosen for the improvement of dry matter content.

The present study revealed that green fodder yield per plant is highly contributed to overall divergence (57.64%), followed by plant height (19%), days to 50%

Table 4. Cluster mean values for yield and yield contributing characters in fodder maize.

Cluster	DFF	PH	NOL	LL	LW	NON	SG	LSR	CP	DM	GFY
I	55.18	167.27	10.87	77.42	7.42	7.29	6.38	0.28	9.31	21.17	279.87
II	55.98	185.85	12.04	84.12	8.18	8.06	7.89	0.33	9.77	21.02	386.18
III	54.50	178.45	11.64	69.86	7.99	7.74	6.20	0.26	10.71	20.96	237.91
IV	55.00	131.30	9.86	89.26	7.18	7.90	6.80	0.34	8.89	22.63	288.23
V	59.71	211.94	13.26	87.89	8.26	8.71	7.68	0.31	8.42	20.18	361.19
VI	57.50	201.40	12.02	103.33	9.78	9.36	9.47	0.34	9.57	19.25	462.65
VII	53.00	163.75	10.17	61.87	8.94	8.36	8.84	0.29	10.89	18.09	380.21
VIII	54.10	135.92	9.04	53.76	7.39	6.62	5.64	0.25	9.45	20.97	157.09
IX	58.00	136.43	8.57	77.47	8.53	6.42	8.02	0.31	10.66	20.49	350.04
X	57.50	214.76	13.77	92.70	9.05	7.19	8.19	0.32	8.70	22.77	491.40
XI	59.00	223.70	12.01	104.93	8.18	9.60	8.44	0.34	13.61	21.70	438.02

DFF – Days to 50 % flowering, PH - Plant height (cm), NOL – Number of leaves per plant, LL - Leaf length (cm), LW - Leaf width (cm), NON - Number of nodes per plant, SG- Stem girth (cm), LSR-Leaf stem ratio, DMY- Dry matter content (%), GFY- Green fodder yield (g/plant), CP – Crude protein (%)

flowering (7.64 %), leaf length (5.84 %), crude protein (5.19 %), leaf stem ratio (1.24 %) and dry matter content (1.24 %) (Table 5). Similarly, higher contribution towards the genetic divergence by plant height was reported by Ganesan *et al.* (2010) in maize and Rathod *et al.* (2021) in fodder maize. The fodder maize inbreds GETM30, GETM84, GETM12, and GETM81 were distinct and diversified, and may be classed as promising inbreds based on the cluster mean and divergence. These genotypes could be utilized in a fodder maize hybridization programme to obtain heterotic fodder maize hybrids apart from getting the desired segregants in later generations.

Principal component analysis or canonical vector analysis is a sort of multivariate analysis where canonical vectors or roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively, are derived (Rao,1952). It represents the importance of the most significant

contributor to total variation on each differentiation axis (Nadarajan *et al.*, 2020)

The principle component analysis identified eleven different components in the fodder maize inbreds, with four of them, PC1, PC2, PC3 and PC4, having >1 eigen value with 70.30% of cumulative variation observed for green fodder yield and its attributing traits. The results revealed that out of the four components, PC1 contributes the higher variability (36.38%), followed by PC2 (13.98 %), PC3 (10.30%) and PC4 (9.60%) (Table 6). Gour *et al.* (2017) also obtained higher variability in PC1 with eigen value more than 1 in rice. Among the four principal components, PC1, PC2, and PC3 were contributed to green fodder yield and its attributing traits. Hence, selection of lines for increased yield PC1, PC2, and PC3 might be effective and more particularly PC1 would be the best option.

Table 5. Contribution of various traits towards the divergence for 93 fodder maize.

S.No.	Traits	Times Ranked 1 st	Contribution (%)
1	Days to 50 % flowering	327	7.64
2	Plant height	814	19.03
3	Number of leaves per plant	8	0.19
4	Leaf length	250	5.84
5	Leaf width	47	1.10
6	Number of nodes per plant	20	0.47
7	Stem girth	18	0.42
8	Leaf stem ratio	53	1.24
9	Crude protein	222	5.19
10	Dry matter content	53	1.24
11	Green fodder yield per plant	2466	57.64

Table 6. Principal components for 11 yield contributing traits of fodder maize

Parameters	PC1	PC2	PC3	PC4
Eigenvalues	4.002	1.538	1.133	1.060
Proportion	0.364	0.140	0.103	0.096
Cumulative Proportion	0.364	0.504	0.607	0.703
DFF	0.255	0.008	-0.297	0.485
PH	0.373	-0.376	0.221	-0.040
NOL	0.296	-0.454	0.307	-0.097
LL	0.293	-0.151	-0.463	0.131
LW	0.252	0.368	0.317	-0.203
NON	0.318	-0.143	0.323	-0.091
SG	0.382	0.319	0.019	-0.105
LSR	0.339	0.240	-0.335	-0.054
CP	0.023	0.547	0.289	0.059
DM	-0.030	-0.042	-0.370	-0.818
GFY	0.444	0.118	-0.124	-0.013

DFF – Days to 50 % flowering, PH - Plant height , NOL – Number of leaves per plant, LL - Leaf length , LW - Leaf width , NON - Number of nodes per plant, SG- Stem girth , LSR-Leaf stem ratio, DMY- Dry matter content, GFY- Green fodder yield , CP – Crude protein

The traits in PC1 viz., days to 50 % flowering (0.255), plant height (0.373), number of leaves per plant (0.296), leaf length (0.293), leaf width (0.252), number of nodes per plant (0.318), stem girth (0.382), leaf stem ratio (0.339), crude protein (0.023), green fodder yield per plant (0.444) showed positive contribution towards genetic divergence, while dry matter content (-0.030) showed negative contribution. However, in PC2, the traits such as days to 50 % flowering (0.008), leaf width (0.368), stem girth (0.319), leaf stem ratio (0.240), crude protein (0.547) and green fodder yield per plant (0.118) displayed positive contribution towards the genetic divergence whereas plant height (-0.376), number of leaves per plant (-0.454), leaf length (-0.151), number of nodes per plant (-0.143), dry matter content (-0.042) recorded negative contribution to the genetic divergence. In PC3, the traits such as plant height (0.221), number of leaves per plant (0.307), leaf width (0.317), number of nodes per plant (0.323), stem girth (0.019), crude protein (0.289) revealed positive contribution towards the genetic divergence, while days to 50 % flowering (-0.297), leaf length (-0.463), leaf stem ratio (-0.335), dry matter content (-0.370), green fodder yield per plant (-0.124) displayed the negative contribution towards genetic divergence. The trait days to 50 % flowering (0.485) in PC4 showed positive contribution towards the genetic divergence. Similar results for were reported by Sinha *et al.* (2019) in maize and for plant height reported by Avinash *et al.* (2016) in maize.

A scree plot (Fig.1) was created between eigen value and principal component to demonstrate the percent of total variation between them. The variation in PC1 recorded higher value (36.38%) followed by PC2

(13.98%), PC3 (10.30%) and PC4 (9.60%). These four principal components had a cumulative variance of 70.30 %. The inbreds in PC1 possess higher variability than other components, and hence it could be used for further hybridization programmes to obtain better segregants.

As a result, the inbreds viz., GETM12, GETM30, GETM37, GETM84, GETM31, GETM8, GETM7, GETM64, GETM35 and African tall in PC1 were highly and positively contributed for the green fodder yield traits, viz., days to 50 % flowering, leaf width , stem girth , leaf stem ratio, crude protein and green fodder yield per plant . The inbreds viz., GETM10, GETM13, GETM27, GETM48, GETM8, GETM32, GETM24, GETM16, GETM22, GETM80 in PC2 were highly and positively contributed for the green fodder yield per plant and its attributing traits viz., days to 50 % flowering, leaf width , stem girth , leaf stem ratio and crude protein . The inbreds viz., GETM16, GETM27, GETM86, GETM14, GETM6, GETM85, GETM53, GETM55, GETM73, GETM42 in PC3 were highly and positively contributed for the green yield attributing traits viz., plant height , number of leaves per plant, leaf width , number of nodes per plant, stem girth and crude protein (Table 6).

The research of the present study revealed that, high heritability along with high genetic advance recorded for the traits viz., green fodder yield per plant , plant height and leaf length and hence the selection for these traits for improving green fodder yielding maize inbreds would be effective. In cluster analysis, cluster VIII and X followed by cluster VI and VIII and cluster VIII and XI had the

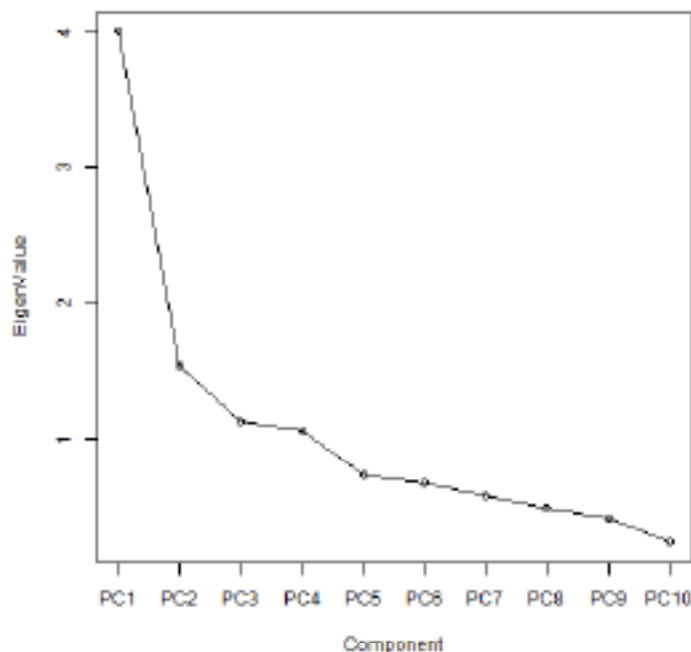


Fig 1. Scree plot of principal component analysis of fodder maize inbred lines between eigen values and principal components.

greatest inter cluster distance indicating that the inbred lines included in these cluster pairs have a more diverse genetic composition. The selection of parents for a future breeding programme from these clusters would result with higher manifestation of heterosis in hybrids and broad heterogeneity in later. In principle component analysis, out of 11 PCs, four PCs were recorded more than one eigen value which contributes 70.30% of variability among the fodder maize inbreds. The inbreds in PC1 possess higher variability than other components and hence, it could be used for further hybridization programme to obtain better segregants. The present study implies that there is a lot of scope in promising lines to be chosen for enhancing green forage yield from the current gene pool in fodder maize hybrids, composites, open pollinated varieties by using the current gene pool.

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