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RESEARCH ARTICLE

# Multivariate Analysis of Fodder Maize (*Zea mays* L.) Germplasm Lines under Temperate Niches

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## Abstract

An experiment was conducted following randomised complete block design (RCBD) with three replications to assess the genetic variability among germplasm lines of fodder maize. A total of 16 traits were taken including yield and quality attributes. The statistical analysis of the data demonstrated existence of significant genetic variation among all the evaluated maize germplasm lines for each trait under study. The phenotypic coefficients of variation (PCV) estimates were invariably higher than their corresponding genotypic coefficient of variation (GCV) values thereby suggesting the environmental influence. Fresh leaf weight per plant exhibited high genotypic and phenotypic coefficient of variation. Selection of superior fodder maize germplasm lines based on their performance for green fodder yield per plant, grain yield per plant, fresh stem weight per plant and stem girth will be effective as these traits showed high heritability coupled with high genetic advance. Plant height, fresh leaf weight per plant and stem girth exhibited considerable direct effects, coupled with highly significant and positive correlation with green fodder yield per plant indicating true correlation between them, therefore, selecting these traits would greatly enhance green fodder yield per plant. Principal component analysis revealed that five out of 16 principal components recorded Eigen values greater than one and could explain 88.33% of the total variability. Based on PC1 scores, the germplasm lines KDFM-86, KDFM-79, KDFM-76 and KDFM-55 were identified as potential contributors of variability, which can be used in crossing programs to transfer key traits related to yield.

**Keywords:** Cluster analysis, Fodder, PCA, *Zea mays* L.

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## Introduction

Maize (*Zea mays* L.) is an important cereal crop belonging to the tribe Maydeae of the grass family Poaceea (Dhoot *et al.,* 2017). It is a dual purpose crop that produces kernels for human consumption as well as fodder for livestock (Borkhatariya *et al.,* 2022). It is considered an ideal forage because it grows quickly, produces high yields, is palatable, is rich in nutrients and helps to increase body weight and milk quality in cattle (Sattar *et al.,* 1994). Because of the size and dispersion of its foliage, maize is better than most other cereal crops at utilising sunlight being a C4 plant and develops more quickly (Warman, 2003). As fodder for livestock, maize is excellent, highly nutritive and sustainable (Hukkeri *et al.,* 1977, Iqbal *et al.,* 2006). Maize holds sufficient nutritional quality when we compare it to other non-leguminous fodders (Mahdi *et al.,* 2011).

India has the largest livestock population in the world and is the top producer of milk, accounting for 23% of global milk production. Despite India's largest livestock population and its global position with highest milk production, the productivity of Indian cattle is low compared to the global average and even lower than the European countries (Rajendra and Mohanty, 2004). Milk production is heavily reliant on the availability of high quality fodder. An insufficient supply of high quality feed and fodder is the primary factor lowering milch animal productivity in India

(Kumari *et al*., 2022). There is currently a net deficiency of 35.6% green fodder, 10.95% dry fodder and 44% concentrate feed materials in the country (Singh *et al.,* 2022).

Maize is commonly grown as a *Kharif* fodder in the north-western regions of India. Its quality is much better than sorghum and pearl millet, since both sorghum as well as pearl millet possess anti- quality components such as hydrocyanic acid and oxalate, respectively. Secondly, baby corn is ready for harvest approximately 2 months after sowing (Chaudhary *et al*., 2012). Maize contains high concentrations of protein and minerals and possesses high digestibility (Gupta *et al.,* 2004). It also possesses excellent ensiling characteristics as it contains sufficient quantities of soluble sugars required for proper fermentation (Allen *et al.,* 2003). On an average, it contains 9-10% crude protein (CP), 60 to 64% neutral detergent fibre (NDF), 38 to 41% acid detergent fibre (ADF), 23 to 25% hemi-cellulose, and 28 to 30% cellulose on the dry matter basis when harvested at milk to early dough stage (Kumar *et al.,* 2020).

The achievement of any programme aimed at improving crops is subjected to the nature and magnitude of genetic variability present in the quantitative and qualitative traits, as this increases the likelihood of identifying and selecting desirable types. The mean values, genotypic and phenotypic coefficient of variation, heritability, correlation coefficients and path coefficient analysis of the traits are some of the essential attributes that ascertain the potency of a breeding program. Multivariate analysis is the most popular approach for assessing the genetic diversity to study the pattern of variation and their genetic relationships within collections of germplasms. Principal component analysis and Cluster analysis are preferred tools and has made it possible to choose genetically diverse parents for breeding programme. The diversity analysis plays a crucial part in selecting divergent parents for hybridisation in order to maximize heterosis effectively. Based on the above consideration, a study was taken to evaluate the genetic diversity among fodder maize germplasm lines to select the best line that can be exploited in future maize breeding programme.

## Materials and Methods

### *Experimental Material*

A set of 48 fodder maize germplasm lines including three checks (African Tall, J-1006, Shalimar Fodder Maize-1) were used for evaluating yield and quality attributing traits. The experiment was laid out in randomised complete block design (RCBD) at experimental field of Division of Genetics and Plant Breeding, Faculty of Agriculture, Wadura, SKUAST-K during *Kharif,* 2022. Each genotype was sown in a 4 m row with an intra-row spacing of 15 cm and inter-row spacing of 30 cm. Recommended agronomic practices and plant protection measures were diligently followed during the crop period to raise a healthy and productive crop.

### *Observations Recorded*

A total of 16 yield and quality contributing traits *viz.,* days to 50% tasseling, days to 50% silking, plant height (cm), number of leaves per plant, leaf length (cm), leaf width (cm), stem girth (cm), fresh leaf weight per plant (g), fresh stem weight per plant (g), leaf: stem ratio, green fodder yield per plant (g), dry matter yield per plant (g), grain yield per plant (g), crude protein (CP), acid detergent fibre (ADF) and neutral detergent fibre (NDF) were analysed.

### *Statistical Analysis*

All the statistical analysis was carried out in R studio software (R studio Team, 2020). Analysis of variance was carried out using the 'Agricolae' package (de Mendiburu, 2015) of R studio. The various genetic parameters like phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability broad sense ($h^2$) and genetic advance (GA) along with correlation and path analysis were estimated using the 'Variability' package (Popat *et al.,* 2020). PCA and hierarchical UPGMA clustering were performed using 'Factoextra' package (Kaufman and Rousseeuw, 1990).

## Results and Discussion

### *Analysis of Variance (ANOVA)*

The analysis of variance (Table 1) revealed that the mean sum of squares due to germplasm lines were highly significant for all the traits under study. This indicates the existence of substantial heterogeneity among the 48 fodder maize germplasm lines studied, with regard to all the analyzed characters and offers an opportunity for further study and assessment of variability parameters. Similar results of significant mean sum of squares due to genotypes for all the traits studied were observed by Mallikarjuna *et al.* (2011); Nataraj *et al.* (2014); Mani and Deshpande (2016); Shazia *et al.* (2017); Khan *et al.* (2018) and Vanjare *et al.* (2021). The notable findings revealed substantial genetic variation resulting from natural genetic variation or crossbreeding which can be exploited through selection.

### *Genetic Variability Study*

High magnitude of PCV and GCV (>20%) were observed for fresh leaf weight per plant and grain yield per plant and lowest (<20%) for neutral detergent fiber as represented in Figure 1. In this study, PCV was found to be greater in magnitude than its corresponding GCV (Table 2) for all the analyzed characters indicating that the detected differences are both the product of genotype and environmental effect. However, the narrow range of differences suggests that environmental effects have a relatively minimal impact on the expression of these characters. Similar findings have been observed for PCV and GCV by Borad (1993) for fresh leaf weight per plant in sorghum, Dar *et al.* (2014) for days to 50 per cent tasseling, days to 50 per cent silking and grain yield per plant in maize; Kapoor and Batra (2015) for leaf width and

neutral detergent fiber in maize; Rathod *et al.* (2021) for days to 50 per cent tasseling , days to 50 per cent silking and leaf width in maize; Naharudin *et al.* (2021) for number of leaves per plant and neutral detergent fiber in maize.

Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance are usually more helpful than heritability alone in predicting the resultant effect for selecting the best genotypes. Figure 2 represents the Heritability and genetic advance value of different fodder traits. High magnitude of broad sense heritability with high magnitude of genetic advance as percent of mean was exhibited by fresh stem weight per plant, grain yield per plant, green fodder yield per plant and stem girth. Moderate magnitude of heritability with high genetic advance was exhibited by dry matter yield per plant and leaf:stem ratio. Above results indicate the presence of additive gene action and selection may lead towards improvement for these characters. Hence, it offers improved prospects for selecting maize plant material with these traits. These results are in agreement with Singh *et al.* (2017) for green fodder yield per plant in sorghum; Gayosso Barragan *et al.* (2020) for stem girth; Magar *et al.* (2021) for grain yield per plant; Rathod *et al.* (2021) and Pavithra *et al.* (2022) for stem girth and green fodder yield per plant in maize. Low heritability along with low genetic advance for the characters indicates the influence of environment upon these characters and selection would be ineffective in such cases.

### *Correlation and Path Coefficient Analysis*

The correlation between all possible combinations among the characters was estimated at the genotypic level (Table 3). Genotypic correlation coefficients offer a means to quantify the genetic relationship between different traits, providing insights into which traits may be valuable for identifying more significant traits in a specific selection program. The correlation coefficients at the genotypic level obtained in the current investigation indicated that there were generally positive associations among the characters studied, which is beneficial for breeding high-yielding cultivars in fodder maize.

Green fodder yield per plant displayed a positive and highly significant correlation with dry matter yield per plant, plant height, fresh stem weight per plant, fresh leaf weight per plant, stem girth, number of leaves per plant, leaf length and leaf width but significant and positive correlation with crude protein, days to 50% silking, days to 50% tasseling and grain yield per plant. It indicated that an increase in any of these traits will increase green fodder yield per plant. A negative and non-significant correlation with leaf: stem ratio, acid detergent fiber and neutral detergent fiber were also observed. These findings are in agreement with the results of Icoz and Kara (2009) for green fodder yield and dry matter yield in maize; Kapoor and Batra (2015) for plant height, leaf length, leaf width and number of leaves per

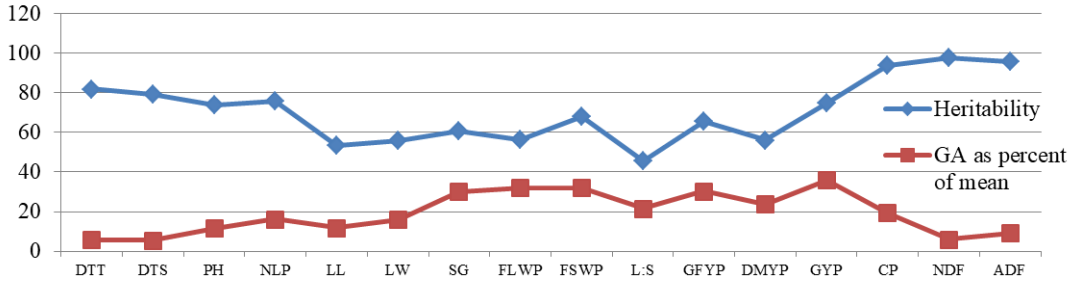
**Table 1:** Analysis of variance of 16 forage traits in fodder maize germplasm lines

| Trait | DTT | DTS | PH | NLP | LL | LW | SG | FLWP | FSWP | L:S | GFYP | DMYP | GYP | CP | NDF | ADF |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replication | 1.69 | 0.63 | 61.2 | 0.05 | 10.3 | 0.10 | 0.03 | 0.43 | 152.5 | 0.004 | 138.7 | 15.87 | 12.16 | 0.047 | 0.012 | 0.111 |
| Genotype | 18.70** | 20.49** | 782.33** | 3.75** | 172.72** | 2.89** | 0.33** | 1210.3** | 1873.6** | 0.05** | 5138.2** | 263.56** | 199.09** | 1.65** | 11.87** | 13.17** |
| Error | 1.28 | 1.66 | 82.6 | 0.36 | 39.0 | 0.60 | 0.05 | 248.3 | 255.4 | 0.01 | 764.8 | 54.3 | 20.11 | 0.03 | 0.09 | 0.18 |

**Table 2:** Estimates of PCV, GCV, heritability and genetic advance as percent of mean among 16 forage traits in fodder maize germplasm lines

| *Trait* | *DTT* | *DTS* | *PH* | *NLP* | *LL* | *LW* | *SG* | *FLWP* | *FSWP* | *L:S* | *GFYP* | *DMYP* | *GYP* | *CP* | *NDF* | *ADF* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PCV | 3.46 | 3.38 | 7.50 | 10.37 | 10.74 | 13.85 | 23.96 | 27.65 | 22.75 | 23.02 | 22.43 | 20.65 | 23.40 | 10.07 | 2.94 | 4.53 |
| GCV | 3.13 | 3.00 | 6.45 | 9.03 | 7.84 | 10.34 | 18.66 | 20.75 | 18.75 | 15.52 | 18.16 | 15.46 | 20.43 | 9.76 | 2.94 | 4.53 |
| $h^2$ | 81.91 | 79.01 | 73.83 | 75.84 | 53.33 | 55.77 | 60.64 | 56.36 | 67.96 | 45.45 | 65.59 | 56.10 | 74.79 | 93.83 | 97.55 | 95.94 |
| GAM | 5.84 | 5.50 | 11.41 | 16.20 | 11.79 | 15.91 | 29.93 | 32.10 | 31.85 | 21.55 | 30.31 | 23.86 | 36.05 | 19.48 | 5.98 | 9.14 |


**Figure 1:** PCV and GCV values of different fodder maize traits




***Abbreviations:** **DTT** = Days to 50 per cent tasseling, **DTS** = Days to 50 per cent silking, **PH** = Plant height(cm), **NLP** = Number of leaves per plant, **LL** = Leaf length (cm), **LW** = Leaf width (cm), **SG** = Stem girth (cm) , **FLWP** = Fresh leaf weight per plant (g), **FSWP** = Fresh stem weight per plant (g), **L:S** = Leaf: stem ratio, **DMYP** = Dry matter yield per plant (g), **GYP**= Grain yield per plant (g), **CP** = Crude protein (%), **NDF** = Neutral detergent fiber (%), **ADF**=Acid detergent fiber (%), **GFYP** = Green fodder yield per plant (g)

**Figure 2:** Heritability and genetic advance values of different fodder maize traits

plant and neutral detergent fiber with green fodder yield in maize; Ali *et al.* (2015) for plant height with green fodder yield in maize; Alawe *et al.* (2020) for dry matter yield per plant with green fodder yield per plant in maize, Rathod *et al.* (2021) for plant height, number of leaves per plant, dry matter percent and crude protein with green fodder yield in maize. These results suggest that taller plants with wider, longer and more number of leaves, thicker stem and higher dry matter yield per plant would be helpful in improvement of green fodder yield per plant.

Correlation gives only the general relation between two variables, whereas path coefficient spits correlation into direct and indirect effects. Based on the data recorded, genotypic correlations were used to estimate path coefficients taking GFYP as a dependent variable (Table 4). The direct positive effect on green fodder yield per plant was exhibited by plant height, stem girth, fresh leaf weight per plant and leaf: stem ratio. Hence, direct selection for these traits could be practised for developing high green fodder yield maize germplasm lines. These results are in consonance with Srivas and Singh (2004); Icoz and Kara (2009); Kapoor and Batra (2015); Alawe *et al.* (2020); Rathod *et al.* (2021) and Borkhatariya *et al.* (2022) in maize.

### *UPGMA Cluster Analysis*

Unweighted pair group method with arithmetic mean (UPGMA) is a type of hierarchical clustering in which a cluster tree (dendrogram) is created to represent data, where each group (or "node") is connected to two or more groups of descendants. Each node in the cluster comprises a collection of similar items; the group of nodes in the chart next to each other is connected. Clusters at one level join clusters at the next level upwards, using a degree of dissimilarity, the cycle continues till altogether nodes are in the tree, providing a pictorial snap of the data in the whole collection. UPGMA was used to divide the forty-eight germplasm lines into four groups, using Euclidean distance as the dissimilarity measure (Figure 3). The germplasm lines were not scattered

**Table 3:** Estimates of genotypic correlation coefficients among yield and quality attributing traits in fodder maize

| *Traits* | *DTT* | *DTS* | *PH* | *NLP* | *LL* | *LW* | *SG* | *FLWP* | *FSWP* | *L:S* | *DMYP* | *GYP* | *CP* | *NDF* | *ADF* | *GFYP* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DTT | 1.00 | 0.99** | 0.21* | 0.19* | 0.09 | 0.08 | 0.16* | 0.14 | 0.17* | -0.00 | 0.12 | -0.07 | -0.03 | 0.08 | -0.04 | 0.17* |
| DTS | | 1.00 | 0.23** | 0.19* | 0.13 | 0.06 | 0.17* | 0.14 | 0.18* | -0.01 | 0.14 | -0.04 | -0.03 | 0.06 | -0.07 | 0.18* |
| PH | | | 1.00 | 0.76** | 0.64** | 0.60** | 0.80** | 0.86** | 0.90** | -0.02 | 0.82** | 0.14 | 0.16 | -0.10 | -0.05 | 0.85** |
| NLP | | | | 1.00 | 0.33** | 0.61** | 0.55** | 0.84** | 0.64** | 0.32** | 0.75** | -0.06 | -0.02 | 0.06 | 0.03 | 0.78** |
| LL | | | | | 1.00 | 0.31** | 0.65** | 0.66** | 0.67** | -0.02 | 0.72** | 0.26** | 0.25** | -0.04 | 0.03 | 0.72** |
| LW | | | | | | 1.00 | 0.29** | 0.83** | 0.39** | 0.62** | 0.61** | -0.02 | 0.12 | -0.05 | 0.01 | 0.63** |
| SG | | | | | | | 1.00 | 0.61** | 0.98** | -0.44* | 0.79** | 0.30** | 0.24** | -0.23* | -0.17* | 0.78** |
| FLWP | | | | | | | | 1.00 | 0.71** | 0.41** | 0.87** | 0.05 | 0.13 | -0.00 | 0.03 | 0.80** |
| FSWP | | | | | | | | | 1.00 | -0.33** | 0.93** | 0.25** | 0.22** | -0.20* | -0.14 | 0.84** |
| L:S | | | | | | | | | | 1.00 | -0.05 | -0.28** | -0.08 | 0.26** | 0.23* | -0.01 |
| DMYP | | | | | | | | | | | 1.00 | 0.25** | 0.21** | -0.11 | -0.06 | 0.98** |
| GYP | | | | | | | | | | | | 1.00 | 0.37** | -0.20* | -0.34** | 0.18* |
| CP | | | | | | | | | | | | | 1.00 | -0.28** | -0.18** | 0.20* |
| NDF | | | | | | | | | | | | | | 1.00 | 0.83** | -0.13 |
| ADF | | | | | | | | | | | | | | | 1.00 | -0.07 |
| GFYP | | | | | | | | | | | | | | | | 1.00 |

**Table 4:** Estimates of genotypic path coefficients among yield and quality attributing traits in fodder maize

| *Traits* | *DTT* | *DTS* | *PH* | *NLP* | *LL* | *LW* | *SG* | *FLWP* | *FSWP* | *L:S* | *DMYP* | *CP* | *NDF* | *ADF* | *'GFYP* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DTT | **-0.066** | 0.050 | 0.067 | -0.015 | -0.004 | -0.007 | 0.113 | 0.050 | -0.003 | -0.000 | -0.007 | 0.00034 | -0.0011 | -0.0003 | 0.175* |
| DTS | -0.066 | **0.050** | 0.075 | -0.015 | -0.007 | -0.005 | 0.120 | 0.053 | -0.003 | -0.004 | -0.008 | 0.00036 | -0.0009 | -0.0005 | 0.187* |
| PH | -0.013 | 0.011 | **0.455** | -0.060 | -0.033 | -0.053 | 0.353 | 0.280 | -0.018 | -0.004 | -0.058 | -0.0015 | 0.0015 | -0.0004 | 0.856** |
| NLP | -0.012 | 0.009 | 0.246 | **-0.079** | -0.017 | -0.054 | 0.302 | 0.382 | -0.013 | 0.073 | -0.048 | 0.00027 | -0.0009 | 0.0030 | 0.789** |
| LL | -0.006 | 0.006 | 0.208 | -0.026 | **-0.051** | -0.027 | 0.451 | 0.237 | -0.013 | -0.005 | -0.046 | -0.0023 | 0.0006 | 0.0003 | 0.724** |
| LW | -0.005 | 0.003 | 0.194 | -0.048 | -0.016 | **-0.089** | 0.201 | 0.299 | -0.008 | 0.143 | -0.039 | -0.0011 | 0.0008 | 0.0010 | 0.634** |
| SG | -0.109 | 0.008 | 0.260 | -0.043 | 0.033 | -0.026 | **0.590** | 0.219 | -0.020 | -0.101 | -0.057 | -0.0022 | 0.0034 | -0.0013 | 0.784** |
| FLWP | -0.009 | 0.007 | 0.270 | -0.066 | -0.034 | -0.074 | 0.298 | **0.408** | -0.014 | 0.084 | -0.056 | -0.0012 | 0.00013 | 0.00028 | 0.805** |
| FSWP | -0.011 | 0.009 | 0.260 | -0.051 | -0.035 | -0.035 | 0.677 | 0.257 | **-0.021** | -0.075 | -0.059 | -0.0020 | 0.0030 | -0.0011 | 0.845** |
| L:S | 0.000 | -0.000 | -0.006 | -0.025 | 0.001 | -0.056 | -0.306 | 0.147 | 0.006 | **0.229** | 0.003 | 0.0007 | -0.0038 | 0.0018 | -0.019 |
| DMYP | -0.008 | 0.007 | 0.297 | -0.059 | -0.037 | -0.055 | 0.620 | 0.314 | -0.019 | -0.012 | **-0.064** | -0.0020 | 0.1005 | -0.0005 | 0.983** |
| GYP | 0.005 | -0.002 | 0.045 | 0.005 | -0.013 | 0.002 | 0.208 | 0.020 | -0.005 | -0.064 | -0.015 | -0.0034 | 0.0030 | -0.0027 | 0.181* |
| CP | 0.002 | -0.001 | 0.052 | 0.002 | -0.013 | -0.011 | 0.166 | 0.487 | -0.004 | -0.018 | -0.013 | **-0.0092** | 0.0041 | -0.0014 | 0.202* |
| NDF | -0.005 | 0.003 | -0.033 | -0.005 | 0.002 | 0.005 | -0.163 | -0.003 | 0.004 | 0.061 | 0.007 | 0.0026 | **-0.0144** | 0.0065 | -0.132 |
| ADF | 0.003 | -0.003 | -0.018 | -0.003 | -0.002 | -0.011 | -0.120 | 0.012 | 0.003 | 0.054 | 0.004 | 0.0017 | -0.0120 | **0.008** | -0.074 |

* and ** Significant at 5 and 1 percent respectively

uniformly amongst the clusters. Cluster II was the biggest cluster with 17 germplasm lines followed by cluster IV (16 germplasm lines), cluster I (13 germplasm lines) and cluster III (2 germplasm lines).

There was a wider genetic diversity among genotypes of different clusters as the distances between clusters were greater than the distances within the clusters (Table 5). The intra-cluster distance ranged from 2.54 to 4.43. Cluster I had the greater intra-cluster distance (4.43) followed by cluster III (4.20), cluster II (4.19) and cluster IV (2.54).

The inter-cluster distance ranged from 5.17 to 7.43. cluster II and IV had the greatest inter-cluster distance (7.43) followed by cluster I and IV (6.69), cluster I and III (6.51), cluster II and cluster III (5.80), cluster III and cluster IV (5.24) and cluster I and cluster II (5.17).

**Table 5:** Intra and inter-cluster distances among four clusters

| *Cluster* | *I* | *II* | *III* | *IV* |
|---|---|---|---|---|
| I | 4.43 | 5.17 | 6.51 | 6.69 |
| II | | 4.19 | 5.80 | 7.43 |
| III | | | 4.20 | 5.24 |
| IV | | | | 2.54 |

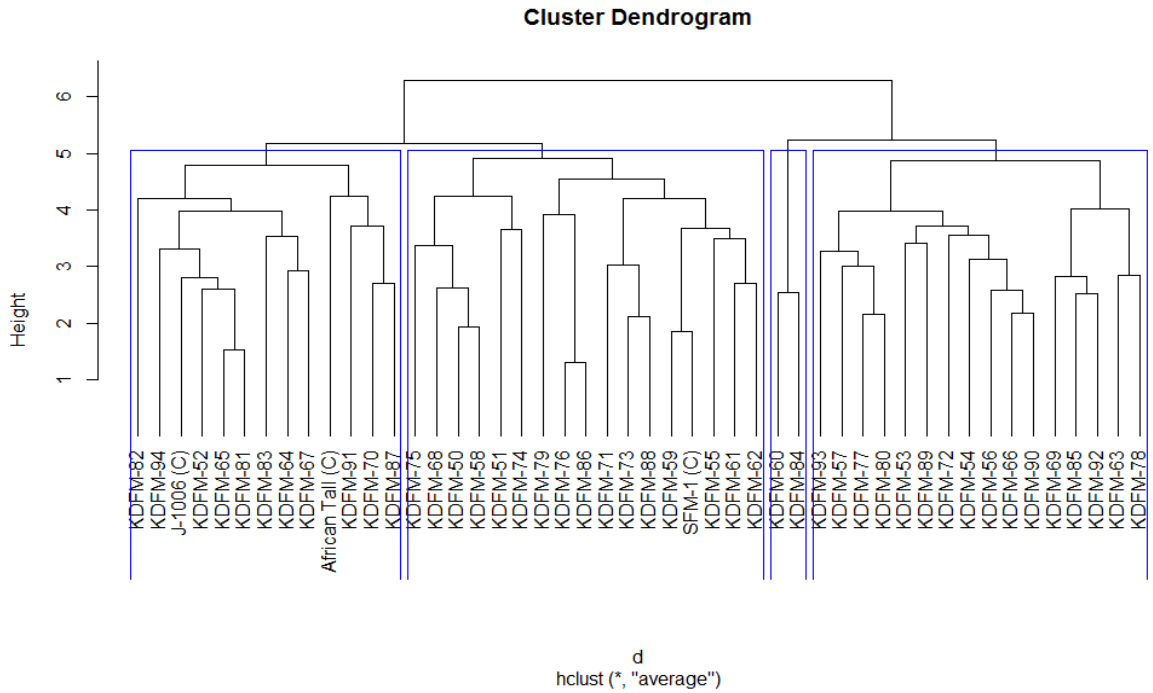



**Figure 3:** UPGMA dendrogram of 48 germplasm lines based on 16 yield and quality attributing traits

### *Principal Component Analysis (PCA)*

Principal component analysis (PCA) is important for elucidating the primary contributor to total variance along each axis of differentiation. It is a data reduction technique used to concurrently describe the interrelationship among set of variables. PCA enables the visualization of distinctions among individuals, the identification of potential groups and finding relationships among individuals and variables. Its main objective is to determine the smallest set of components that can account for the highest proportion of total variability.

Principal component analysis was performed using yield and quality attributing traits in fodder maize germplasm lines including three checks. The analysis revealed that the number of principal components formed were equal to number of characters studied. The criteria followed for selecting the principal components to be included in further analysis was based on Eigen values of principal components. Out of 16, only 5 principal components (PCs) exhibited more than 1 Eigen value and showed 88.33% variability among the traits studied which was also reported by Muhammad *et al.* (2015); Jain and Patel (2016); Shazia *et al.* (2017); Mounika *et al.* (2018); Poonia *et al.* (2021) and Kifayat *et al.* (2022). The results showed that the first principal component, i.e., PC1 accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively lesser and lesser amount of variation. PC1 accounted for 43.5% of total variability, whereas, PC2, PC3, PC4 and PC5 exhibited 15.4, 12.4, 9.5 and 6.7% respectively, for the traits under study (Table 6 and Figure 4).

**Table 6:** Eigen values, percent variability and cumulative percent variability for 16 principal components in fodder maize

| *Principal component* | *Eigen value* | *Percentage of variance* | *Cumulative percentage (%)* |
|---|---|---|---|
| PC1 | 6.966 | 43.5 | 43.5 |
| PC2 | 2.468 | 15.4 | 59.0 |
| PC3 | 1.981 | 12.4 | 71.3 |
| PC4 | 1.516 | 9.5 | 80.8 |
| PC5 | 1.073 | 6.7 | 87.5 |
| PC6 | 0.793 | 5.0 | 92.5 |
| PC7 | 0.549 | 3.4 | 95.9 |
| PC8 | 0.330 | 2.1 | 98.0 |
| PC9 | 0.148 | 0.9 | 98.9 |
| PC 10 | 0.110 | 0.7 | 99.6 |
| PC11 | 0.043 | 0.3 | 99.9 |
| PC12 | 0.011 | 0.1 | 99.9 |
| PC13 | 0.007 | 0.0 | 100.0 |
| PC14 | 0.003 | 0.0 | 100.0 |
| PC15 | 0.001 | 0.0 | 100.0 |
| PC16 | 0.000 | 0.0 | 100.0 |

Eigen loadings of $\pm$0.3 were considered as major contributory factors to the variations that were observed. The higher the loadings, regardless of sign, the more they will be discriminating between the accessions. PC1 accounted for the highest variation which was mainly due to the high positive vector loadings of plant height, number of leaves per plant, stem girth, fresh leaf weight per plant, fresh stem

**Table 7:** Contribution of various characters in different principal components

| *PCs* | *DTT* | *DTS* | *PH* | *NLP* | *LL* | *LW* | *SG* | *FLWP* | *FSWP* | *L:S* | *GFYP* | *DMYP* | *GYP* | *CP* | *NDF* | *ADF (%)* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PC1 | 0.081 | 0.084 | 0.356 | 0.302 | 0.272 | 0.263 | 0.313 | 0.349 | 0.343 | 0.051 | 0.376 | 0.366 | -0.062 | 0.046 | -0.047 | -0.034 |
| PC2 | 0.027 | 0.016 | 0.008 | 0.193 | 0.007 | 0.258 | -0.261 | 0.203 | -0.197 | 0.484 | -0.020 | -0.032 | -0.331 | -0.114 | 0.438 | 0.443 |
| PC3 | -0.679 | -0.678 | -0.005 | -0.003 | 0.065 | 0.127 | -0.034 | 0.091 | -0.025 | 0.130 | 0.029 | 0.057 | 0.102 | -0.030 | -0.125 | -0.025 |
| PC4 | 0.138 | 0.132 | -0.038 | 0.050 | -0.066 | 0.313 | -0.260 | 0.133 | -0.207 | 0.460 | -0.061 | -0.088 | 0.030 | 0.192 | -0.469 | -0.499 |
| PC5 | 0.022 | 0.014 | -0.062 | -0.197 | 0.309 | -0.023 | -0.057 | 0.014 | -0.065 | 0.098 | -0.032 | -0.003 | 0.414 | 0.762 | 0.191 | 0.233 |

*Abbreviations: DTT = Days to 50 per cent tasseling, DTS = Days to 50 per cent silking, PH = Plant height(cm), NLP = Number of leaves per plant, LL = Leaf length (cm), LW = Leaf width (cm), SG = Stem girth (cm) , FLWP = Fresh leaf weight per plant (g), FSWP = Fresh stem weight per plant (g), L:S = Leaf: stem ratio, GFYP = Green fodder yield per plant (g), DMYP = Dry matter yield per plant (g), GYP = Grain yield per plant (g), CP = Crude protein (%), NDF = Neutral detergent fiber (%), ADF = Acid detergent fibre (%)

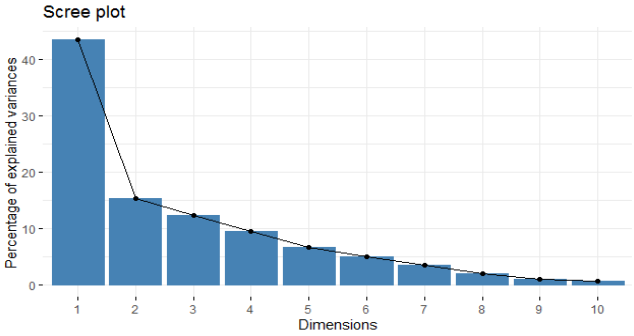



**Figure 4:** Scree plot

weight per plant, green fodder yield per plant and dry matter yield per plant. Hafiz *et al.* (2015) and Chikuta *et al.* (2015) reported a significant contribution from the first principal component towards overall variability while analyzing different traits.

The diversity in PC2 was due to positive loadings from leaf: stem ratio, neutral detergent fiber and acid detergent fiber. The diversity in PC3 was due to negative vector loadings from days to 50 per cent tasseling and days to 50 per cent silking. PC4 had positive vector loadings from leaf: stem ratio, leaf width and negative vector loadings from neutral detergent fiber and acid detergent fiber. PC5 had positive loadings from leaf length, grain yield per plant and crude protein. Similar results were reported by Avinash *et al.* (2016), Sinha *et al.* (2019) and Pavithra *et al.* (2022).

From this study, it was clear that the key yield-related traits are primarily represented in PC1 (Table 7). Consequently, germplasm lines falling within this principal component and having high PC scores should be targeted for the cultivation of high-yield varieties. Germplasm lines with the highest PC scores (KDFM-86, KDFM-79, KDFM-76, KDFM-55) in PC 1 are poised to serve as donors for the transfer of desired traits, as indicated by their trait contributions. Following hybridization, the careful selection of optimal recombinants in subsequent segregating generations might be fruitful for the development of high-yielding fodder maize lines.

The PCA biplot effectively reveals the inter-relationship among maize traits (Figure 5). The first two PC's were used to generate a biplot. Based on PC1 and PC2 green fodder yield per plant, dry matter yield per plant, plant height, fresh leaf weight per plant, fresh stem weight per plant, stem girth, number of leaves per plant, leaf: stem ratio, neutral detergent fiber and acid detergent fiber displayed notably extended vectors, suggesting the presence of substantial variation among germplasm lines. In simpler terms, these traits exhibit pronounced variation across the 48 germplasm lines investigated, suggesting their role as the most prominent discriminators within the studied data.

The PCA analysis organized the lines into groups that spread across all four quadrants, indicating significant variability in traits. The right top quadrant consisted of the germplasm lines KDFM-65, KDFM- 81, KDFM- 83, KDFM-84, KDFM-82, KDFM-71, KDFM-91, KDFM-87, KDFM-70, KDFM-76, J-1006 and African tall and were related to plant height, leaf length, fresh leaf weight per plant, number of leaves per plant, leaf: stem ratio, days to 50% tasseling and days to 50% silking. The right bottom comprised of germplasm lines KDFM-88, KDFM-73, KDFM-75, KDFM-62, KDFM-58, KDFM-50, KDFM-68, KDFM-61, KDFM-55, KDFM-59, KDFM-79, KDFM-86 and SFM-1 related to green fodder yield per plant, dry matter yield per plant, fresh stem weight per plant, stem girth, crude protein and grain yield per plant. The germplasm lines KDFM-67, KDFM-94, KDFM-52, KDFM-80, KDFM-77, KDFM-63, KDFM-72, KDFM-89, KDFM-78, KDFM-66, KDFM-93, KDFM-53 and KDFM-57 in left top quadrant were

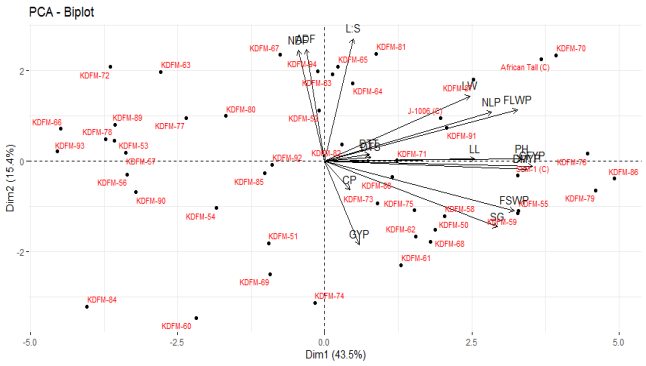



**Figure 5:** PCA Biplot

closely related to acid detergent fiber and neutral detergent fiber. The germplasm lines KDFM-56, KDFM-90, KDFM-92, KDFM-85, KDFM-54, KDFM-51, KDFM-69, KDFM-74, KDFM-84 and KDFM-60 showed no significant improvement for any trait as indicated by their positions on the axes devoid of trait arrows.

The biplot demarcated the germplasm lines with different traits explained by the first two dimensions. As a result, a breeder can easily estimate the genetic distance between genotypes, facilitating informed decisions for genotype selection. This is made possible by condensing multiple variables into the two primary principal components, analyzed simultaneously. Germplasm lines close to each other on the score plot are similar, while lines near the origin are distinctive, and those farther away are particularly extreme.

The cosine of the angle between the vectors of the two traits measures the degree of correlation similarity between them, considering their variation across different germplasm lines. The traits pair plant height and leaf length had an angle of zero, indicating a perfect correlation of +1. Traits of each group had acute ($<90^0$) angles between them, indicating they were positively correlated and their variation was similar, so each trait within a particular group can substitute for the other trait in the same group. The traits like leaf: stem ratio had a near-right angle with fresh stem weight per plant, indicating that variation of one trait was more or less independent of the other trait (near zero correlation). On the contrary, NDF and ADF had obtuse angle ($>90^0$) with green fodder yield per plant, indicating that their variation was in the opposite direction (negative correlation).

The biplot formed by the first two PC's grouped the 48 germplasm lines in a manner akin to UPGMA cluster analysis, utilizing the entire data from all the traits. This demonstrated that PCA is a dependable approach for pinpointing key traits that account for the most significant variations and serves as a reliable means to predict crucial traits that influence the clustering of distinct line. In this context, traits possessing substantial absolute values near unity within the first PC exert a more pronounced influence on clustering compared to those with lower absolute values nearer to zero. Hence, in the current study, the differentiation of genotypes into distinct clusters arose from the relatively substantial contributions of a few select traits, rather than minor contributions from each trait.

## Conclusion

Analysis of diverse multivariate parameters revealed that the existing germplasm lines exhibit substantial variability across various yield components and quality traits. The strategic selection of these germplasm lines in future breeding programs holds promise for the development and release of cultivars with improved yield and quality characteristics.

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