

Original Research Article

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Principal Component and Cluster Analysis in Inbred Lines of Maize (*Zea mays* L.)

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ABSTRACT

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In the present investigation a total of forty seven maize inbred lines were studied to assess the genetic diversity for 10 quantitative traits *viz.*, days to 50% tasseling, days to 50% silking, days to maturity, plant height (cm), ear length (cm), ear height (cm), 100-seed weight (g), kernel rows per ear, number of kernels per row and grain yield per plant (g) using principal component analysis and hierarchical cluster analysis. The PCA identified four principal components (PCs) with Eigen value greater than 1.00 and accounted for 80.35 per cent of total variation. Cluster analysis based on Ward's minimum variance procedure distributed the inbreds into 7 clusters indicating their broad genetic base of which cluster II was the largest containing ten inbreds and maximum inter-cluster distance was recorded between clusters IV and VII (1177.88) suggesting their use in breeding programmes for the exploitation of heterosis for the desirable yield traits.

Introduction

Maize (*Zea mays* L.) is an important cereal crop of the family Poaceae belonging to the tribe Maydeae. The plant is native to South America and has chromosome number of $2n=20$. Maize (*Zea mays* L.) is known as golden crop because every part of this crop is useful to man, animals and the industries. Globally, it is the most important cereal food crop after wheat and rice accounting for 9 per cent of the total food grain production. It has occupied a prominent place in Indian agriculture as it is widely grown in India in

varied climatic situations throughout the year suggesting its wider adaptability.

The major objective of the maize breeding programmes is to develop high yielding hybrids than the existing cultivars as hybrids are popular among the farming community for their yield advantage over the varieties and others. To develop high yielding hybrids in maize, the development and evaluation of inbreds form the major thrust area of the plant breeding programmes. Hence, inbred lines developed through sib mating *etc.* need to be evaluated for their genetic diversity and

performance to plan an effective hybrid breeding programme as genetically diverse parents are known to produce high heterotic effects.

Evaluation, characterization and classification of genotypes based on estimates of genetic diversity will help to identify diverse parental lines which can be used in hybrid breeding to develop potential hybrids or varieties. Several methods have been reported to decipher the pattern and magnitude of variability such as Mahalanobis D^2 analysis, Principal component analysis and hierarchical cluster analysis based on Ward's minimum variance method. PCA and cluster analysis is better utilized for studying the diversity among the genotypes in various crops, In view of the above, 47 inbred lines were investigated to study the nature and magnitude of genetic divergence for grain yield and its component characters to provide a basis for selection of parents in hybridization programme in Maize hybridization programme.

Materials and Methods

Experimental material

The present investigation was carried out during *rabi*, 2016-17 at Agricultural college farm, Bapatla, Guntur district using 47 maize inbred lines obtained from IARI Regional Maize Research Center, Dharwad, Karnataka in a Randomized Block Design with three replications. Each entry was sown in two rows of 3m length maintaining a spacing of 60cmx30cm. Standard agronomic management practices were followed throughout the growing period to maintain proper plant stand and good crop growth. The observations were recorded on ten randomly selected plants for seven quantitative characters *viz.*, plant height, ear length, ear height, 100-seed weight, kernel rows per ear, number of kernels per row and grain yield per

plant. The data on remaining quantitative characters *viz.*, days to 50% tasseling, days to 50% silking and days to maturity were recorded on plot basis. The mean values of the data were used for statistical analysis.

Statistical analysis

The data was analyzed for Principal component analysis (PCA) for dimensional reduction and to know the importance of different traits in explaining multivariate polymorphism. Hierarchical cluster analysis was done following the minimum variance method of Ward (1963) based on squared Euclidean distances.

Results and Discussion

The analysis of variance for 47 inbred lines of Maize for ten quantitative traits showed significant differences between the inbred lines for the characters studied indicating a considerable amount of genetic variability in the studied material and the utility of divergence analysis in the present material for identification of divergent groups.

In principal component (PC) analysis, the number of variables was reduced to linear functions called canonical vectors which accounted for most of the variation produced by the characters under study. The eigen values, per cent variance, per cent cumulative variance and factor loading of different characters studied are presented in Table 1. In this experiment, first four principal components (PC) based on 10 quantitative traits showed eigen values greater than 1. The contribution of these four PCs was 80.35% in the overall variability among the genotypes. The contribution of PC1 was found to be 28.95% in the total divergence of the studied population, in which the major contributing traits were days to 50% tasseling, days to 50% silking, days to maturity, ear height, plant

height, 100-seed weight, ear length, grain yield per plant and number of kernels per row. The second principal component (PC2) was responsible for about 25.16% of the variation and was mainly contributed by days to maturity, days to 50% silking and days to 50% tasseling. The third principal component (PC3) explained 13.96% of variation and was associated mainly with grain yield per plant, kernel rows per ear, days to 50% tasseling, days to 50% silking and days to maturity. The fourth principal component (PC4) explained 12.28% variation and was contributed by number of kernels per row, grain yield per plant, kernel rows per ear, days to maturity, days to 50% tasseling and days to 50% silking.

Cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in desecrating clusters in the two dimensional scattered diagram and the genotypes falling in same cluster were present closer to each other in the scattered diagram.

Two dimensional scatter diagram was shown in Figures 1, and the genotypes numbered 41 and 36 *i.e.*, CDM-306 and CDM-320 scattered away from other genotypes.

These results were in accordance with those of Jinju *et al.*, (2009), Muhammad *et al.*, (2012), Sandeep *et al.*, (2015), Avinash and Mishra (2016) and Shrestha (2016) in maize.

Fig.1 Two dimensional graph showing relative position of 47 maize (*Zea mays* L.) genotypes based on PCA scores

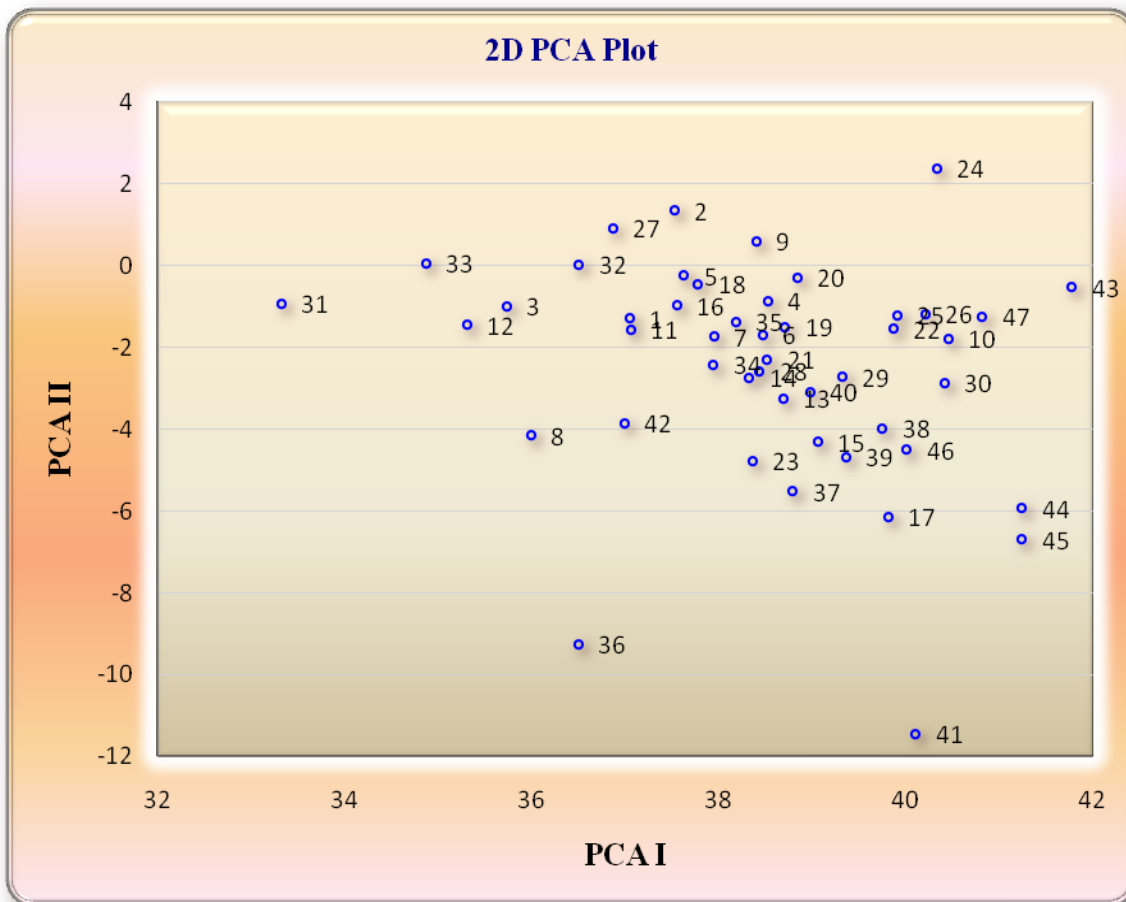


Fig.2 Dendrogram showing relationship of 47 maize (*Zea mays* L.) inbreds in seven clusters based on Euclidean² distance

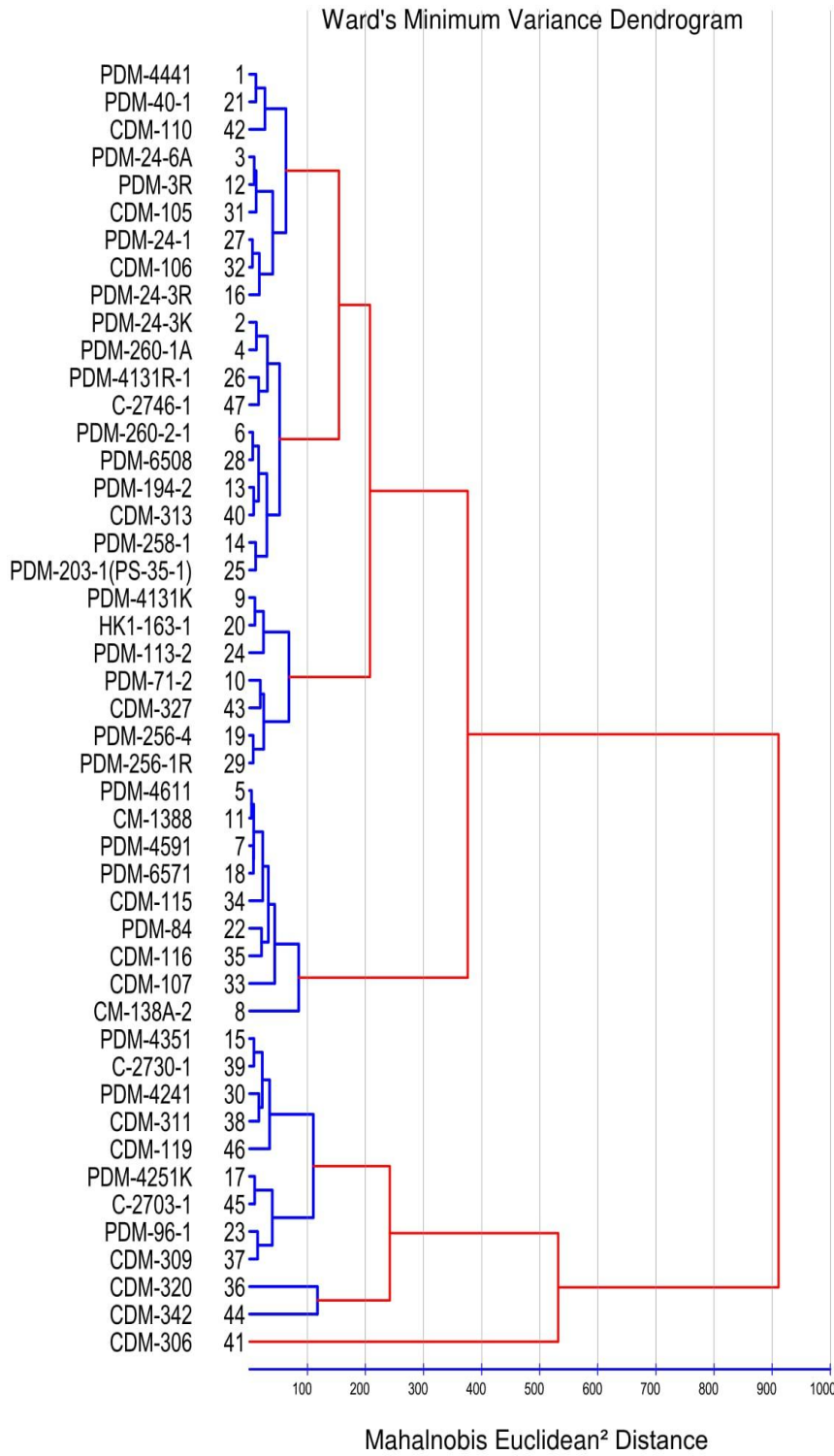


Fig.3 Intra and inter-cluster distance of 47 maize (*Zea mays* L.) inbreds in seven clusters based on Euclidean² values

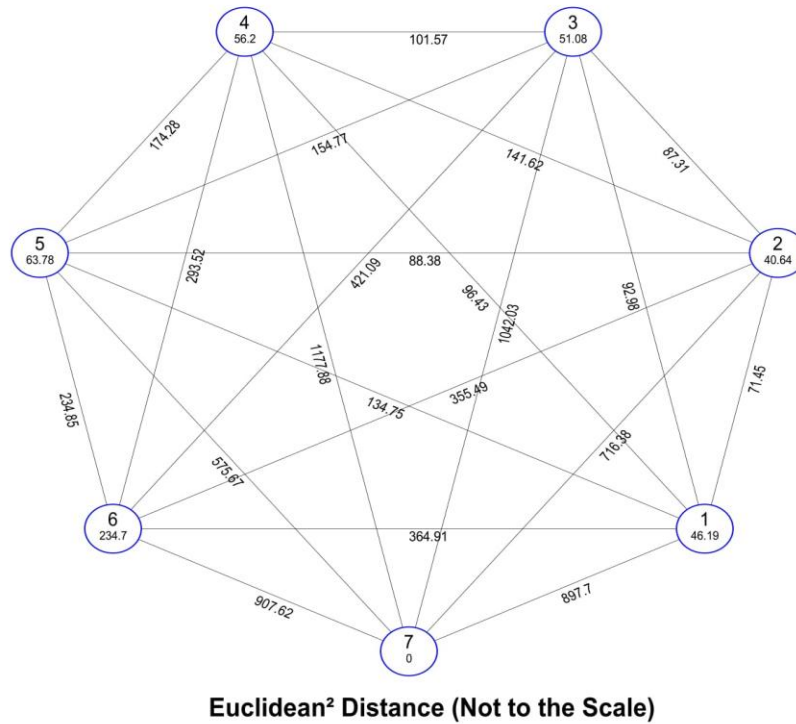


Table.1 Eigen values, proportion of the total variance represented by first four Principal components, cumulative per cent variance and component loading of different characters in maize (*Zea mays* L.)

	PCA ₁	PCA ₂	PCA ₃	PCA ₄
Eigen Value (Root)	2.89	2.52	1.40	1.23
% Var. Exp.	28.95	25.16	13.96	12.28
Cum. Var. Exp.	28.95	54.10	68.07	80.35
Days to 50% tasseling	0.55	0.11	0.04	0.09
Days to 50% silking	0.55	0.13	0.03	0.07
Days to maturity	0.52	0.16	0.13	0.13
Plant height	0.21	-0.40	-0.29	-0.37
Ear length	0.07	-0.17	-0.13	-0.27
Ear height	0.22	-0.43	-0.37	-0.27
100-seed weight	0.08	-0.19	-0.71	-0.30
Kernel rows per ear	-0.10	-0.44	0.21	0.16
Number of kernels per row	0.04	-0.28	-0.27	0.70
Grain yield per plant	0.07	-0.51	0.36	0.28
PC = Principal component				

Table.2 Clustering pattern of 47 maize (*Zea mays* L.) inbreds by Ward's minimum variance method

Cluster No	No. of inbreds	Names of inbreds
I	9	PDM-4441, PDM-40-1, CDM-110, PDM-24-6A, PDM-3R, CDM-105, PDM-24-1, CDM-106, PDM-24-3R
II	10	PDM-24-3K, PDM-260-1A, PDM-4131R-1, C-2746-1, PDM-260-2-1, PDM-6508, PDM-194-2, CDM-313, PDM-258-1, PDM-203-1(PS-35-1)
III	7	PDM-4131K, HK1-163-1, PDM-113-2, PDM-71-2, CDM-327, PDM-256-4, PDM-256-1R
IV	9	PDM-4611, CM-1388, PDM-4591, PDM-6571, CDM-115, PDM-84, CDM-116, CDM-107, CM-138A-2
V	9	PDM-4351, C-2730-1, PDM-4241, CDM-311, CDM-119, PDM-4251K, C-2703-1, PDM-96-1, CDM-309
VI	2	CDM-320, CDM-342
VII	1	CDM-306

Table.3 Average intra and inter-cluster Euclidean² values among seven clusters in 47 maize (*Zea mays* L.) inbreds

Cluster No.	I	II	III	IV	V	VI	VII
I	46.19	71.45	92.98	96.43	134.75	364.91	897.70
II		40.64	87.31	141.62	88.34	355.49	716.38
III			51.08	101.57	154.78	421.09	1042.03
IV				56.20	174.28	293.51	1177.88
V					174.28	293.85	575.70
VI						234.70	907.62
VII							0.00

Note: Diagonal values are intra-cluster distances. Off-diagonal values are inter-cluster distances

Table.4 The nearest and the farthest cluster from each cluster using Ward's Minimum Variance method in 47 inbreds of maize (*Zea mays* L.)

Cluster No.	Nearest cluster with D ² values	Farthest cluster with D ² values
I	II (71.45)	VII (897.70)
II	I (71.45)	VII (716.38)
III	II (87.31)	VII (1042.03)
IV	I (96.43)	VII (1177.88)
V	II (88.34)	VII (575.70)
VI	IV (293.51)	VII (907.62)
VII	V (575.70)	IV (1177.88)

Table.5 Mean values of seven clusters estimated by Ward’s minimum variance method from 47 maize (*Zea mays* L.) inbreds

Cluster No.	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear length (cm)	Ear height (cm)	100 seed weight (g)	Kernel rows per ear	No. of kernels per row	Grain yield per plant (g)
I	53.63	59.96	90.96	141.75	17.71	50.01	18.32	12.74	19.71	58.28
II	56.87	63.50	99.47	140.27	20.80	47.65	20.58	13.45	21.46	71.57
III	58.14	64.67	100.43	168.55	20.20	61.09	18.36	13.18	17.66	50.20
IV	55.15	61.33	94.33	156.56	20.02	59.13	14.17	13.42	22.76	56.21
V	57.00	63.63	97.49	173.99	21.22	64.31	20.85	14.69	25.82	94.93
VI	55.17	61.33	94.50	184.37	21.38	74.63	16.30	14.27	45.21	103.61
VII	56.33	61.33	96.00	182.27	17.13	66.40	34.78	17.87	27.27	170.96

Note: Bold figures indicate minimum and maximum values in each character

The principal component scores of genotypes were used as input for cluster analysis using Euclidean² distances in order to group the genotypes into various clusters and to confirm the results of principal component analysis. Forty seven genotypes were grouped into seven clusters using the Ward's minimum variance procedure (Anderberg, 1993) and the distributions of the genotypes into different clusters are depicted in Table 2 and Figure 3. Among all the clusters, cluster II was the largest containing ten genotypes followed by clusters I, IV, and V containing nine genotypes in each cluster, cluster III with seven genotypes, cluster VI with two genotypes and cluster VII was monogenotypic having only one genotype. The mutual relationship between clusters is represented diagrammatically in Figure 4 by taking average intra and inter-cluster Euclidean² distances. The average intra and inter-cluster Euclidean² distance were estimated based on Ward's minimum variance and are presented in the Table 3. Similar results of clustering were reported by Mehrnaz *et al.*, (2014), Hafiz *et al.*, (2015), Muhammad *et al.*, (2015) and Sandeep *et al.*, (2015).

The nearest and farthest cluster for each of the seven clusters are presented in Table 4. The cluster VII was solitary with intra-cluster distance zero. Cluster II had minimum intra-cluster Euclidean² distance value of 40.64 followed by cluster I (46.19), cluster III (51.08), cluster IV (56.20), cluster V (174.28) and maximum was recorded in the cluster VI (234.70). The maximum inter-cluster distance was observed between clusters IV and VII (1177.88) followed by clusters III and VII (1042.03) and clusters VI and VII (907.62) suggesting wide genetic diversity between these clusters and can be exploited for traits improvement in the breeding programmes.

Cluster means were computed for the 10 characters studied by Ward's minimum

variance method and are presented in Table 5. Out of all the clusters, cluster VI showed higher mean values for most of the yield contributing traits like plant height, ear length, ear height and number of kernels per row indicating the importance of this cluster genotypes in maize yield improvement programmes.

Based on inter-cluster distances and *per se* performance of the genotypes included in the farthest clusters, genotypes *viz.*, CDM-306, CDM-320, CDM-342 AND CM-138A-2 are showing maximum inter cluster distance and good *per se* performance. Hence, they can be included in crossing programmes for generating heterotic hybrids for various yield traits in maize.

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