

Research Article

Assessment of genetic diversity in newly developed inbred lines of maize (*Zea mays* L.)

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Abstract

An investigation was carried out to assess the genetic diversity of 100 newly developed inbred lines of maize using Mahalanobis D^2 statistics, indicated presence of considerable diversity. The data was recorded on ten quantitative characters. The inbred lines were grouped into 14 clusters based on Mahalanobis D^2 statistic. Among them cluster I accommodated maximum number of inbred lines (31) followed by cluster III (24). Presence of nine solitary clusters indicated larger genetic diversity of inbred lines. The maximum inter cluster distance observed between cluster VI and IX followed by cluster VI and X suggesting greater variability in genetic makeup of inbred lines included in these clusters. The quantitative characters viz., plant height, ear height, shelling percentage and kernels per row contributed maximum towards diversity. Based on cluster distance inbred lines included in cluster VI, IX and X are advisable to used as parents for hybridization programme.

Key words

Maize, inbred lines, genetic diversity, D^2 analysis

Introduction

Maize is known as “Queen of Cereals” because of its highest yield potential and wider adaptability. It is the world’s most widely grown cereal and is the primary staple food in many developing countries (Morris *et al.*, 1999). In India it is grown in 7.5 mha with a production of 23mt and productivity of 2.5 t ha⁻¹. Karnataka state stands first in production in the country with 1.3 mha and production and productivity of 4.4 mt and 3.5 t/ha, respectively (Anon, 2014).

Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for different breeding programmes. In any hybrid breeding program inbred lines are the prerequisite in cross pollinated crop plants. For developing high yielding hybrids in maize, inbred lines need to be evaluated for their genetic diversity. The most limiting factor of maize research is the development, improvement and maintenance of inbred lines. Several studies on maize have shown that inbred lines from genetically diverse parents tend to be more productive than crosses of inbred lines from same source (Vasal, 1998). The manifestation of heterosis in the progeny is usually depends on the genetic divergence of two parents (Saxena *et al.*, 1998). Assessment on genetic diversity among the inbred lines is important for planning an effective hybrid breeding program as the genetically diverged inbred lines are known to produce high heterotic effects. Moll *et al.* (1962) found that the success of heterosis breeding depends on the amount of genetic diversity present in the material. The

greater genetic diversity of the parents is associated with greater heterosis in the F_1 (Moll *et al.*, 1962, Paterniani and Lonquist, 1964; Wellhausen, 1965; Sobrinho and Cordeiro, 1975; Vasal *et al.*, 1992). Therefore, characterization of genetic diversity of maize germplasm or inbred lines is of great importance in hybrid maize breeding (Xia *et al.*, 2005). It has become possible to quantify magnitude of genetic diversity among germplasm with the help of advanced biometrical methods such as multivariate analysis (Rao, 1952) based on Mahalanobis (1936) D^2 statistics. With this view, genetic diversity among 100 newly developed maize inbred lines was studied using multivariate approaches of analysis of variation.

Materials and methods

One hundred new inbred lines of maize developed at experimental plots of College of Agriculture, V. C. Farm, Mandya were evaluated in Randomized Complete Block Design with two replications with a row length of 4m and spacing of 60cm between the rows and 20cm between plants during Kharif 2013. Recommended management practices were followed during crop growth period to raise a healthy crop. The data was recorded on ten morphological characters viz., days to 50 % tasselling, days to 50 % silking, plant height (cm), ear height (cm), ear length (cm), ear circumference (cm), kernel rows per cob, kernels per row, test weight (g) and shelling percentage. Data recorded on mean of five randomly selected plants was used for statistical analysis. Genetic diversity was estimated as per Mahalanobis D^2 statistics (1936). D^2 statistic was used on adjusted mean values for phenotypic diversity analysis.

$$D_p^2 = d^1 S^{-1} d$$

Where, D_p^2 is square of distance considering 'p' traits, D is vector of observed differences of the mean values of 'p' traits, d^1 is transpose of vector of observed differences of the mean value of 'p' traits, X_{i1} is vector of the mean values of all the characters and S^{-1} is inverse of variance and covariance matrix. The computation of D^2 values reduced to simple summation of the squares of the difference between the values of transformed variables of the two populations. This transformation was done by pivotal condensation method. These newly transformed uncorrelated variables were used to calculate the square of distance using the formula

$$D^2 = (Y_{i1} - Y_{i2})^2$$

Where, Y is transformed mean values of 'p' traits. The square root of D^2 provided general distance between two genotypes. The D^2 values were arranged in a matrix form. The significance of D^2 values between any two populations was tested using Hotelling's T^2 statistic.

$$T^2 = \left[\frac{(n_1 + n_2)}{n_1 n_2} \right] \times D^2$$

Using T^2 , the F values were calculated by following F statistic

$$F = \frac{(n_1 + n_2) - P - 1}{(n_1 + n_2 - 2)} \times T^2$$

Where, P is number of traits, n_1 is number of individuals in first population and n_2 is number of individuals in second population. This computed F value was compared with the table F value at five and one per cent level of significance at P and $(n_1 + n_2 - P - 1)$ degrees of freedom. Clustering of genotypes was done according to Tocher's method as described by Rao (1952). Intra and inter-cluster distance, cluster mean and contribution of each trait to the diversity were estimated as suggested by Singh and Chaudhary (1985).

Results and discussion

The mean values of different characters were used in estimating genetic distance between pairs of inbred lines. Estimation of genetic diversity was carried out for 100 inbred lines. All the 100 new inbred lines were grouped in 14 clusters based on the diversity for ten morphological traits. Among the 14 clusters, cluster I was containing maximum number of inbred lines (31) followed by cluster III (24), cluster II (19), cluster V (10) and cluster VI (7) (Table 1 & Figure 1). Whereas clusters IV, VII, VIII, IX, X, XI, XII, XIII and XIV were solitary, the inbred lines in these clusters were distinctly different from others. The findings were supported

by Alam *et al.* (2013) and Mani and Deshpande (2016).

The contribution of 10 characters towards total morphological diversity is presented in Table 2. Out of 10 characters analyzed, plant height (54.89 %) and ear height (34.89 %) contributed major proportion to total genetic diversity followed by shelling percentage (4.12 %), kernels per row (3.41 %) and test weight (1.50 %). The characters such as days to 50 % tasselling (0.69 %) and days to 50 % silking have contributed least to the total genetic diversity. However there was no contribution from ear length, ear circumference and number of kernel rows to the diversity. It was evident that contribution of simply inherited traits which are least affected by environmental factors was more. These results are in agreement with that of Marker and Krupakar (2009) who also identified above said characters as the principal components contributing maximum to the total variation in maize. These characters should be given importance for selecting diverse parents for breeding programmes in maize (Narayan *et al.*, 2015).

Greater range of mean values among the cluster was recorded for different traits. Analysis of cluster means revealed the relative contribution of different traits to the total divergence by the different clusters. Based on range of means, it is possible to know the characters influencing divergence. It helps to identify clusters having different levels of variability for different characters, based on final ranks it is possible to identify clusters having higher and lesser diversity for more number of characteristics. Utilization of low ranked clusters in breeding programme is expected to yield desirable lines in advanced generation of selection. The cluster VI recorded highest mean value for plant height (268.10 cm), ear height (145.83 cm) and test weight (31.94 gm) and solitary cluster X recorded highest mean values for flowering characters. The cluster XII recorded highest mean values for ear length (20.88 cm), cluster IV for ear circumference (14.88 cm), cluster VII for kernel rows (18.50), cluster XIII for kernels per row (38) and cluster VII for shelling percentage (85.87 %). In the present investigation based on morphological traits, it was observed that genotypes grouped under cluster IV ranked first by having majority of characters at desirable direction followed by genotypes under cluster VII and cluster V. Genotypes grouped under cluster X (last rank) recorded many characters in negative direction (Table 3). Therefore selection of genotypes falling in cluster IV, VII and V would be useful to generate desirable genetic resource on crossing between the inbred lines present in the clusters. Based on cluster means Singh and Chaudhari (2001) also reported wide range of variation for grain yield and its components in

maize. Similar results also reported by Ganesan *et al.* (2010). Therefore, it is suggested that most diverse clusters may be used as parents in hybridization programme to develop high yielding hybrids (Lahane *et al.*, 2016).

The intra and inter cluster distance values were worked out from divergence analysis and are presented in Table 4. The intra cluster distance was less than the inter cluster distance, thus genotypes within the cluster had less diversity. Maximum inter cluster distance was recorded between the clusters VI and IX (143.81) followed by cluster VI and X (139.97) suggesting more variability in genetic makeup of the inbred lines included in these clusters. Minimum inter cluster distance was recorded between cluster IX and X (23.07). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. These findings are in conformity with the findings of Ganesan *et al.* (2010) and Marker and Krupakar (2009).

Conclusion

It has been well established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad spectrum variability in segregating generations (Arunachalam, 1981). It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. Based on inter-cluster distances, it is advisable to attempt crossing among the genotypes from cluster VI, IX and X, which may lead to broad spectrum of favorable genetic variability for yield improvement in maize.

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Table 1. cluster wise distribution of newly developed inbred lines of maize

Cluster	No. of genotypes	Cluster composition
I	31	MAI 1-5-2, MAI 1-12-3, MAI 1-36-4, MAI 1-73-5, MAI 1-104-3, MAI 1-35-6, MAI 1-56-5, MAI 1-76-1, MAI 1-39-2, MAI 1-91-3, MAI 1-15-2, MAI 5-3-3-3, MAI 1-6-2, MAI 1-106-1, MAI 1-88-2, MAI 2-4-1-1, MAI 2-16-3-1, MAI 1-9-3, MAI 3-2-4, MAI 1-108-2, MAI 1-31-2, MAI 4-7-3, MAI 1-97-3, MAI 2-11-4, MAI 1-98-3, MAI 1-72-3, MAI 1-17-8, MAI 2-9-1-2, MAI 1-22-3, MAI 1-21-4, MAI 1-18-2
II	19	MAI 1-15-1, MAI 1-19-3, MAI 1-17-2, MAI 1-16-3, MAI 1-37-3, MAI 1-57-3, MAI 1-77-1-1, MAI 1-100-2, MAI 1-38-1, MAI 1-44-2, MAI 3-13-6, MAI 4-5-2, MAI 1-17-12, MAI 1-17-13, MAI 1-43-2, MAI 2-10-3-2, MAI 1-104-2-2, MAI 4-10-3, MAI 1-17-19
III	24	MAI 1-12-1, MAI 1-6-2, MAI 1-48-1, MAI 1-41-3, MAI 1-86-5, MAI 1-87-1, MAI 1-106-3, MAI 2-14-2, MAI 1-59-4, MAI 1-44-1, MAI 1-34-1, MAI 1-7-3, MAI 3-2-5, MAI 3-3-2, MAI 3-7-2, MAI 3-2-4-1, MAI 1-98-4, MAI 2-10-3-1, MAI 2-6-4-2, MAI 2-7-4, MAI 1-41-3, MAI 1-58-3, MAI 1-106-6, MAI 1-104-1
IV	1	MAI 1-20-1
V	10	MAI 1-1-1, MAI 1-4-1, MAI 1-37-4, MAI 1-37-6, MAI 1-42-4, MAI 1-96-1, MAI 1-23-1-1, MAI 1-42-2, MAI 1-66-1, MAI 1-99-1
VI	7	MAI 1-8-3, MAI 1-11-2, MAI 1-65-1, MAI 1-66-1, MAI 1-80-3-1, MAI 1-81-2, MAI 1-85-1
VII	1	MAI 4-4-2-2
VIII	1	MAI 1-35-4
IX	1	MAI 1-96-5-2
X	1	MAI 1-17-11
XI	1	MAI 5-12-1-1
XII	1	MAI 1-38-9
XIII	1	MAI 1-98-1
XIV	1	MAI 1-22-1



Table 2. Contribution of characters towards divergence of inbred lines

Sl. No.	Character	Rank	Times Ranked I	Contribution %
1	Days to 50% tasselling	6	35	0.69
2	Days to 50% silking	7	25	0.50
3	Plant height (cm)	1	2772	54.89
4	Ear height (cm)	2	1762	34.89
5	Ear length(cm)	8	0	0.00
6	Ear circumference(cm)	9	0	0.00
7	Kernel rows per cob	10	0	0.00
8	Kernels per row	4	172	3.41
9	Test weight(g)	5	76	1.50
10	Shelling %	3	208	4.12



Table 3. Cluster wise means values for ten morphological characters in 100 new inbred lines of maize

Cluster	Plant height (cm)	Ear height (cm)	Days to 50% tasselling	Days to 50% silking	Ear length (cm)	Ear circumference (cm)	Kernel rows per cob	Kernels per row	Test weight (g)	Shelling %	Score	Rank
I	206.87 (8)	93.16 (6)	55.84 (8)	57.58 (8)	13.27 (9)	12.33 (9)	13.96 (7)	26.36 (6)	26.30 (8)	78.08 (7)	76	9
II	180.06 (11)	72.44 (9)	55.00 (7)	57.11 (7)	12.13 (12)	12.21 (10)	13.39 (10)	22.21 (11)	24.23 (11)	77.24 (9)	97	11
III	236.40 (2)	112.79 (4)	54.76 (6)	56.60 (6)	14.25 (7)	11.97 (11)	13.45 (9)	27.33 (5)	23.69 (12)	79.62 (5)	67	5
IV	225.60 (4)	81.20 (7)	48.00 (3)	50.00 (3)	12.75 (10)	14.88 (1)	16.00 (2)	24.50 (9)	27.38 (6)	80.64 (3)	48	1
V	182.16 (10)	102.68 (5)	56.80 (10)	58.40 (10)	14.19 (8)	11.56 (12)	12.68 (11)	23.93 (10)	25.69 (9)	64.66 (12)	97	12
VI	268.10 (1)	145.83 (1)	56.57 (9)	58.29 (9)	15.20 (4)	12.88 (7)	14.04 (5)	26.11 (7)	31.94 (1)	77.53 (8)	52	3
VII	204.00 (9)	69.00 (11)	46.00 (2)	48.00 (2)	15.25 (3)	14.00 (2)	18.50 (1)	31.75 (3)	16.26 (14)	85.87 (1)	48	2
VIII	215.00 (6)	130.00 (3)	58.00 (11)	60.00 (11)	14.75 (5)	12.88 (8)	14.00 (6)	31.25 (4)	29.80 (2)	56.23 (13)	69	7
IX	154.00 (13)	62.00 (12)	50.00 (4)	52.00 (4)	9.63 (14)	10.00 (14)	10.25 (13)	20.50 (12)	25.34 (10)	81.93 (2)	98	13
X	152.20 (14)	71.30 (10)	60.00 (14)	62.00 (14)	14.75 (5)	10.75 (13)	9.75 (14)	19.50 (13)	28.90 (4)	67.73 (11)	113	14
XI	175.00 (12)	50.00 (14)	44.00 (1)	45.00 (1)	12.75 (11)	13.13 (6)	15.00 (3)	24.75 (8)	26.98 (7)	79.87 (4)	67	6
XII	210.00 (7)	140.00 (2)	59.00 (12)	61.00 (12)	20.88 (1)	13.75 (4)	13.50 (8)	34.50 (2)	28.68 (5)	78.19 (6)	59	4
XIII	229.00 (3)	57.00 (13)	59.00 (13)	61.00 (13)	18.75 (2)	13.25 (5)	12.50 (12)	38.00 (1)	22.88 (13)	76.35 (10)	85	10
XIV	220.10 (5)	75.80 (8)	50.00 (5)	52.00 (5)	11.88 (13)	14.00 (3)	14.25 (4)	14.75 (14)	29.37 (3)	51.10 (14)	74	8



Table 4. Intra and inter-cluster distances for newly developed inbred lines of maize

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	23.33	41.92	43.87	29.97	39.35	85.02	35.52	47.04	64.64	62.85	58.73	51.20	47.59	41.01
II		26.00	74.50	51.10	42.49	118.12	36.57	73.71	34.73	35.89	33.79	77.87	57.29	52.49
III			28.51	40.42	63.83	54.54	60.44	42.04	99.47	97.48	91.52	44.61	61.18	55.52
IV				0.00	56.32	81.10	28.99	57.91	74.78	77.64	59.83	64.22	33.33	32.31
V					29.53	101.29	53.57	48.65	57.15	48.44	61.69	54.09	71.07	54.20
VI						30.77	104.90	62.97	143.81	139.97	136.49	62.80	100.39	92.43
VII							0.00	72.21	54.05	61.70	37.87	75.45	36.46	45.13
VIII								0.00	96.53	87.70	95.05	25.68	77.74	58.31
IX									0.00	23.07	27.15	98.76	79.08	74.81
X										0.00	41.65	91.97	81.16	71.90
XI											0.00	99.88	60.77	60.99
XII												0.00	85.47	74.78
XIII													0.00	43.19
XIV														0.00

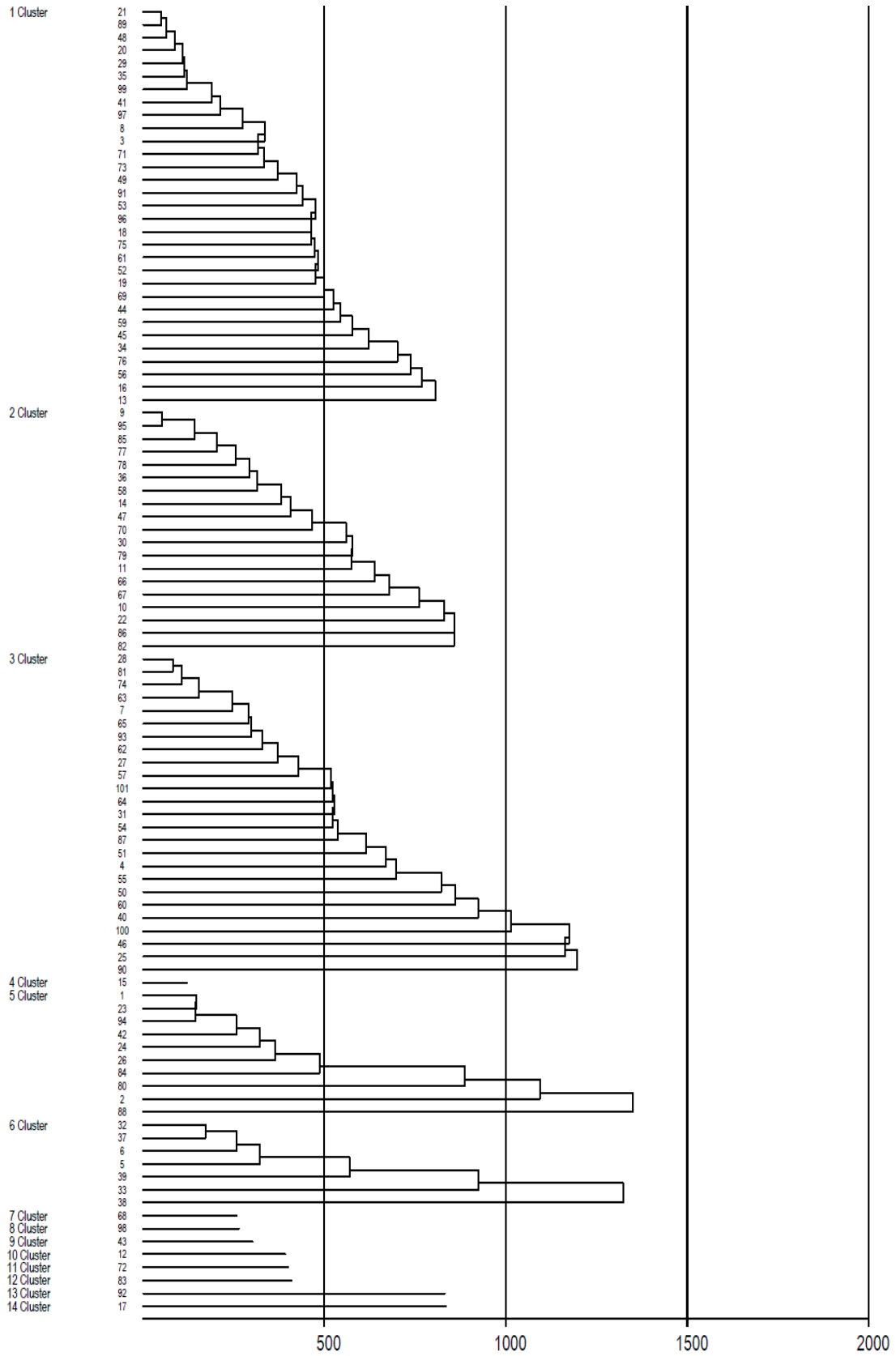


Fig. 1. Dendrogram depicting genetic diversity in 100 newly developed inbred lines of maize