Original Research Article

Genetic Divergence Studies for Morpho-Agronomical Traits in Maize (*Zea mays* L.) Inbreds

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A B S T R A C T

K e y w o r d s Maize, *Zea mays* L., Genetic divergence, inbred, morpho-agronomical traits	Eight maize inbreds including five quality protein maize (QPM) and three non-QPM were evaluated for obtaining information regarding genetic divergence among these inbreds. ANOVA revealed significant differences among the inbreds for all the ten morpho-agronomical traits. The nature and extent of genetic divergence was measured using average taxonomic distances as a measure of dissimilarity coefficient. Based on dissimilarity coefficient eight inbreds were clustered into five groups (AI, AII(a), AII(b), BI, BII). The highest inter cluster distance was found between cluster AI and cluster BI (2.1189) and the lowest between clusters AI and AII (b) (0.8766). The highest intra cluster distance (0.9964) was recorded in cluster AII b and AII b. Based on inter cluster distances inbreds present in cluster AI and BI were found more diverse, thus advisable to used as parents for producing superior hybrids.

Introduction

Maize is called 'queen of cereal' as it is grown throughout the year due to its photo-thermo insensitive character and highest genetic yield potential among the cereals. It is the most versatile crop with wider adaptability in varied agro-ecologies and has highest genetic yield potential among the food grain crops. The demand for maize is growing globally due to its multiple uses for food, feed and industrial sectors. The trend of genetic gain in favourable environment seems unable to meet the fast growing demand of maize in the country. Thus, to reduce the available yield gaps expansion of area has needed in less favourable environment through genetic enhancement of tolerance to biotic and abiotic stress genotypes and development of improved crop management technology. Cultivation of maize in cold season started in mid 60s in some areas of Bihar and South India. Yield obtained during this season is invariably higher (>6 t/ha) than the *Kharif* season yield (2-2.5 t/ha.) due to long duration of growth and least infestation of pests and diseases. The success and the level of profit from *Rabi* crop depend to a great extent on the choice of maize hybrid/composite to be grown. Farmers should therefore be encouraged to sow only high yielding hybrids suitable for *Rabi* season. The use of F1 hybrid seed is essential for realizing high yield. In order to develop genotypes with desirable traits, the breeder choose

genetically distinct parents because hybrids developed from genetically diverse parents display greater heterosis than those between closely related genotypes. Genetic diversity is considered to be an important criterion for choosing the parents for realizing heterosis and recombination in breeding programmes (Arunachalam, 1981). Hence, a quantitative estimation of genetic distance provides a rational basis for selection of parents. Determination of genetic diversity of any crop species is a suitable precursor for improvement of the crop because it generates base line data to guide selection of parental lines and design of breeding scheme. The objective of the present investigation was to measure the genetic divergence by using taxonomic distance as a measure of dissimilarity among the inbred for morphological and yield components for the development of wide array of single crosses.

Materials and Methods

The experiment was conducted at the research farm of Tirhut College of Agriculture, Dholi, under Rajendra Agricultural University, Bihar, Pusa. Materials for the present investigation were included eight inbred lines (CML 142, CML 144, CML 150, CML 176, CML 186, CM 300, CM 400 and CM 600) obtained from AICRP on maize, Dholi Centre. These inbreds were planted with row to row and plant to plant spacing of 60 cm and 20 cm respectively in plots having three rows per plot in Rabi season. The experimental design for sowing the crops was randomized block design (RBD) with three replication. Recommended package of practices was followed to raise a good crop. Observations were recorded for ten morpho-agronomical traits viz., plant height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, 100 kernel

weight (g), yield per plant (g), days to 50 per cent tassel emergence, days to 50 per cent silk emergence and days to 50% maturity on five plants chosen randomly in each plot.

Assessment of divergence

Numerical taxonomic approach (Sneath and Sokal, 1973) were used for assessing genetic divergence using data on morpho-physiological characters. The adjusted means of genotypes were subjected to linear transformation in order to reduce the effects of different scales of measurement in different metric characters.

While transforming the variables, mean of each variable was subtracted and the difference was divided by standard deviation. Using numerical taxonomic approach (Sokal and Sneath 1963; Sneath and Sokal, 1973) for assessing genetic divergence, an average taxonomic distance (Sokal, 1961) was computed as a measure of dissimilarity. The standardized data were utilized for the computation of taxonomic distance (d) as follows:

$$d_{jk} = \sqrt{\{\Sigma 1/n(X_{ij} - X_{ik})^2\}}$$

Where,

X_{ij} = Mean value of jth entry for the ith character

X_{ik} = Mean value of kth entry for the ith character

$\overset{n}{\underset{}{\Sigma}}$ = Sum over n characters

D = Distance in a phenetic space divided by $\sqrt{n}$

While computing average taxonomic distance for a pair of objects, only those values for i were used for which both X_{ik} and X_{ij} were present. For multistate data recorded on qualitative variables, similarity coefficients were computed on the basis of simple matching. The method for tree building involved sequential agglomerative hierarchical nested (SAHN) clustering based on distance matrices and similarity coefficients. The dendrograms were constructed on the axis of dissimilarity between genotypes and group of genotypes by unweighted pair group method using arithmetic average (UPGMA). Considering forty fifty and sixty dissimilarity units as cut of point for minimum dissimilarity, the clusters were identified at this phenon level.

Results and Discussion

The analysis of variance revealed significant differences among genotypes for all the traits (Table1). This indicating the existence of exploitable extent of genetic variability among the experimental material. Genetic variability among experimental material was also reported earlier (Azad *et al.,*. 2012, Oliboni *et al.,* 2012, Kage *et al.,* 2013, Kumar *et al.,* 2015, Kumar, *et al.,* 2015). The monthly meteorological average data recorded from cropping season of rabi maize has presented in table 2.

The mean values of the traits obtained was used to evaluate genetic divergence. Average taxonomic distance were used as a measure of dissimilarity for assessing the nature and extent of genetic divergence. Taking into consideration broad classification of entries (at sixty dissimilarity units as cut-off points) as indicated by dendrogram (Fig. 1 and Table 3) of the eight inbreds were divided into two groups. Group A consisted of six inbreds, namely, CML 142, CML 144, CML 150,

CML 176, CM 300 and CM400. The other group B comprised only two inbreds, namely, CML 186 and CM 600. The clustering pattern revealed that genotype originated from different geographical regions had been grouped in cluster A which indicated that there was no association between genetic diversity and geographical diversity. Similar results were reporte by Sridhar *et al.,* (2002) and Singh *et al.,* (2009). At different phenon levels the inbreds could be differentiated into different clusters (Table 3) suggesting adequate scope for selecting superior and diverse parents to be exploited for any breeding programme.

But, at fifty dissimilarity units as cut off point, clusters A and B were further divided into two sub clusters in each (AI, AII & BI, BII). Sub-cluster AI and consisted of three inbreds in each namely CML 142, CML 144, CM 300 and CML 150, CML 176 and CM 400 respectively. Sub-cluster B I and B II was mono genotypic consisted of inbred CML 186 and CM 600 respectively.

This increased the number of genotypic constellations from two to four. Similar results were reported by Zheng and Wang (1995) and Singh *et al.,* (2009).

Average taxonomic distance revealed considerable genetic differences between the inbreds (Table 4). The least average taxonomic distance (0.3567) was observed between CM 300 and CML 144 and the highest average taxonomic distance (2.4038) was observed between CM 600 and CM 300 (Table 4). At phenon level forty dissimilarity units as cut off point, only sub-cluster AII was further sub-divided into two sub-clusters AII (a) and AII (b). Sub-cluster AII (a) was monogenotypic, consisted of inbred CML 150. Sub-cluster AII (b) consisted of two inbreds, namely, CML 176 and CM 400.

Fig.1 Dendrogram of maize inbreds based on average taxonomic distance for ten traits
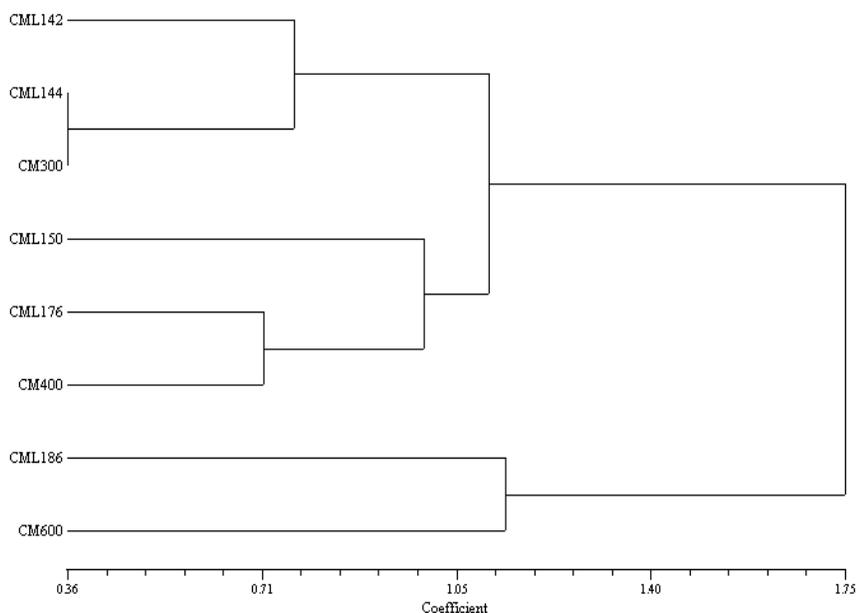

Table.1 Analysis of variance on data obtained for different traits in maize inbreds

Sources of Variation	D. F.	Mean sum of Squares									
		Plant height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows per ear	Number of kernels per row	100 Kernels weight (g)	Days to 50% tassel emergence	Days to 50% silk emergence	Days to 50% maturity	Yield per plant (g)
Replication	2	171.05	0.04	0.01	0.07	32.36	0.59	0.49	0.02	0.49	15.06**
Parents	7	973.87**	5.81**	4.51**	4.03**	53.17**	12.79*	38.04**	42.67**	12.76**	325.88**

*, ** significant at 5% and 1% respectively

Table.2 Composition of clusters based on taxonomic distance in average taxonomic approach for cluster analysis using data on ten traits of maize

No. of clusters identified at different phenon level*			Inbreds included in each cluster
60%	50%	40%	
A(6)	AI(3)	AI(3)	CML 142, CML 144, CM 300
	AII (3)	AII (a) (1)	CML 150
		AII (b)(2)	CML 176, CM 400
B(2)	BI(1)	BI(1)	CML 186
	BII (1)	BII (1)	CM 600

Figures in parenthesis indicate number of inbreds in the respective clusters.
* Phenon levels indicates 60, 50 and 40 units of dissimilarity coefficient.

Table.3 Average taxonomic distance for ten traits of maize

CML142 CML144 CML150 CML176 CML186 CM300 CM400 CM600

CML142 | 0.0000

CML144 | 0.7046 0.0000

CML150 | 0.7825 0.9732 0.0000

CML176 | 0.7278 1.2132 0.8224 0.0000

CML186 | 1.7521 2.2627 1.6900 1.3408 0.0000

CM300 | 0.8213 0.3567 1.2473 1.3547 2.3419 0.0000

CM400 | 0.8004 1.4297 1.1703 0.7081 1.3545 1.4872 0.0000

CM600 | 1.6478 2.2290 1.4919 1.2703 1.1413 2.4038 1.2408 0.0000

Table.4 Average intra cluster (diagonal) and inter cluster distances of five clusters of maize in E_2

Clusters	AI	AII(a)	AII (b)	BI	BII
AI	0.6275	1.001	0.8766	2.1189	2.0935
AII (a)		0.000	0.9964	1.6900	1.4919
AII (b)			0.7081	1.3477	1.2556
BI				0.000	1.1413
BII					0.000

It was observed that the genotypes that originated in one region had been distributed into different clusters indicating that genotypes with same geographic origin could have undergone change for different characters under selection. This could be due selection pressure, genetic drift and environment, which created greater diversity rather than genetic distance (Singh *et al.,* 2009).

Average distance between and within the clusters was computed in Table 5. The highest inter cluster distance (2.1189) was found between cluster AI and cluster BI followed by that between clusters AI and BII, clusters AII (a) and BI, clusters AII (a) and BII, clusters AII (b) and BI, cluster AII(b) and BII, clusters

BI and BII, the clusters AII (a) and AII (b) and clusters AI and AII (a). The inter-cluster distance between clusters AI and AII (b) was found to be the smallest (0.8766).The highest intra cluster distance (0.9964) was recorded in cluster AII b and AII b. The intra-cluster distances were smaller than the inter-cluster distances indicating the distinctness of the different clusters. Clusters AII (a), BI and BII were monogenotypic. Among multigenotypic clusters AI and AII (b), cluster AI had less intra-cluster distance than the intra-cluster distance in cluster AII (b). The highest inter cluster distance between cluster AI and BI, showing greater divergence between inbreds of these two clusters also showed wider differences in their mean values. Similar results indicating appreciable extent of

divergence were also reported by earlier workers (Datta *et al.,* 2004; Kumar and Singh, 2005).

The data on inter cluster distance and *per se* performance of the genotypes were used for selecting genetically diverse and agronomically superior genotypes. Based on the result it might be concluded that genotypes of divergent inter cluster groups would be used in crossing programme for the development of high heterotic crosses.

Acknowledgement

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