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Morphological diversity analysis in QPM and non-QPM maize (*Zea mays* L.) genotypes

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ABSTRACT

D^2 statistics used to measure the genetic divergence among the genotypes has been successfully utilized by the breeders to analyze the morphological diversity. Hybridization is one the tools to create variability. One may create more variability through hybridization when parents are diversed. Hence, genetic diversity in the parents is a prerequisite for crop improvement programmes. All the genotypes of maize (Zea mays L.) were grouped into three clusters on the basis of the morphological diversity using Mahalanobis D^2 statistic. Maximum intra-cluster distance was observed in cluster II (15.44) whereas, maximum inter-cluster distance was observed between cluster II and III (25.46). The analysis of divergence indicated significant differences among parental lines for all the agro-morphological characters. On the basis of results obtained in the present investigation, it was concluded that the allelic diversity can be used for future breeding program. The traits under study are also major yield contributing traits and are largely associated with each other. Therefore, these traits should be taken into consideration either simultaneously or alone for selecting a high yielding maize genotype.

Keywords: D^2 analysis, morphological diversity,QPM and non-QPM maize

After wheat and rice, maize or corn is the most important cereal grain in the world *viz-a-viz* India, providing nutrition for humans and animals. Quality of nutrition is an important component which enhances the acceptance of the crop among users. Maize is grown from 58^0 N to 48^0 N in areas with 250 mm to more than 5000 mm of rainfall per year. According to the ASSOCHAM (The Associated Chambers of Commerce and Industry of India), poultry sector forms the largest chunk (51% of total maize consumption in India) followed by human consumption (26%), starch preparation (12%) and livestock feeds (11%) etc. The current level of average yield of maize in the country (21.7 q/ha) is far behind the global average of (50.00 q/ha), and there is a huge scope for improvement in yield potential. A push in maize yields anywhere close to the global average may excalate the maize export as global demand is continuously growing. With the growing demand from feed and starch sector, the overall demand for maize is likely to grow at a brisk pace. Even if we presume that growth in maize consumption is maintained at the average levels of last two decades (5%) in the coming years, it will grow over 30 million tonnes in 2019-20 from about 16 million tonnes in 2008-09 (ASSOCHAM report, May 01, 2009).

Prior to beginning of the twenty first century, India was a net importer of maize, as production growth in the country was not enough to meet the growing demand from the poultry and other sectors. However, adoption of hybrids particularly in non-traditional maize growing states like Karnataka and Andhra Pradesh, and to some extent in some of the traditional maize growing states like Bihar and Maharashtra, pushed the maize yield and production in the country sharply higher, which not only assured its self sufficiency, but also gave some scope on the export front.

Healthy increase in acreage under maize in the recent years also supported the growth in maize production in the country. As diversity is prerequisite for plant improvement, breeders have to study the diversity among the genotypes before starting any breeding programme. We may create more variability through hybridization when parents are diverged. Even, for development of better hybrids we have to use diverse parents.

MATERIALS AND METHODS

The experimental material consisted of 26 genotypes of maize obtained from the All India Coordinated Maize Improvement Project, Department of Genetics and Plant breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during *Rabi* (winter season), 2009-10. The University is situated at $25^018'$ North latitude and $83^003'$ East longitude of South Eastern part of Varanasi city. The altitude is 75.7 m above the mean sea level. The soil of the experimental field was fertile, alluvial loam which is the characteristic of Indo-Gangetic plains and as such, is suitable for sowing the experimental material. This area falls in sub-tropical zone. Analysis of Morphological Diversity involved the inbreds: CML172, CML161, CML173, CML163, CML141, CML162, CML126, CML152, CML 395, CML121, CML140, HKI208, HKI209, HKI235, HKI309, HKI335, HKI409, HKI435, HKI486, HKI586, V25, V348, V351, V358, V372 and V386. These inbreds were obtained from Bajaura (HP), Karnal and Almora (Uttarakhand), were planted in a Randomized Complete Block Design with two replications. Each entry was planted as double row of 2.5 meter length with row-to-row and plant-to-plant distance of 60 cm and 20 cm respectively. Initially two seeds per hill were planted

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and later on one plant was thinned to maintain single plant per hill. Two border rows were also planted to avoid the border effects. All the recommended package of practices was followed to raise a good crop (DMR Report, 2012). Observations on the basis of five plants randomly selected and tagged well in advance in each entry on the following characters were recorded *viz.*, days to 50% tasseling, days to 50% silking, days to 75% brown husk, plant height (cm), ear height (cm), cob length (cm), cob diameter (cm), number of cobs per plant, number of kernels per row, number of rows per ear, cob yield per plant (g) and 100 seed weight (g).

Genetic divergence analysis

The data collected on different characters were analyzed through Mahalanobis's generalized distance D^2 (1936).

Determination of group constellations or clusters

Grouping of the populations into various clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two variables belonging to the same cluster should at least on an average, show a smaller D^2 value than those belonging to different clusters. For this purpose D^2 values of the combinations of each genotype were arranged in ascending order of their magnitudes in a tabular form as described by Singh and Chaudhary (1985). To start with, two populations having the smallest distance from each other were considered, to which a third population having the smaller D^2 value from the first two populations was added. Similarly next, the nearest fourth population was considered and this procedure was continued.

At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered for in that cluster. The groups of the first cluster were then omitted and the rest were treated in a similar way. This process was continued till all the populations were included into one or the other cluster. After the formation of the clusters, the averages inter and intra cluster divergence (distances) was calculated. The square root of the D^2 values obtained from the above, represent the distance (D) between and within clusters.

Average intra-cluster distance

For the measurement of intra-cluster distances, the formula used was $\Sigma_i D_i^2/n$ where, $\Sigma_i D_i^2$ was the sum of distances between all possible combinations (n) of the populations included in a cluster.

Average inter-cluster distance

Clusters are taken one by one and their distances from other clusters were calculated. The distance between two clusters was the sum of the D^2 values between the members of the other cluster divided by the product of number of genotypes in both the clusters under consideration.

Contribution of individual character towards divergence

In all the combinations each cluster was ranked on the basis of its combination towards divergence between two entries ($di = Yt^i - Yt^j$). Rank one is given to the highest mean difference and rank 'p' to the lowest difference where 'p' is the total number of characters. Percentage contribution of each character (X) towards genetic divergence was calculated using the formula:

$$X = \frac{N \times 100}{M}$$

where, N = Number of genotype combinations where the character was ranked first.

M= All possible combinations of number of genotypes

RESULTS AND DISCUSSION

The genetic divergence among 26 maize genotypes was estimated for 12 characters, *viz.*, days to 50 % tasseling, days to 50 % silking, plant height, ear height, days to maturity, cob length, number of cobs per plant, number of rows per ear, number of kernels per row, 100 seed weight, yield per plant and ear diameter. Based on this analysis, all the genotypes were grouped into three different clusters. The clustering pattern of genotypes is presented in table 1. Twenty two genotypes fell into cluster I, which was the biggest cluster and accommodated maximum number of genotypes. It was followed by cluster II that accommodated three genotypes. Cluster III consisted of only one genotype.

Table 1: Clustering pattern of 26 maize genotypes on the basis of D^2 analysis for 12 characters

Cluster No.	No of genotypes	Genotypes
Cluster-1	22	CML121, CML140, V348, KHI209, KHI 586, CML152, CML 395, V372, KHI309, KHI335, CML172, CML161, KHI486, CML162, V386, V351, V358, V25, , CML126, KHI435, CML173, CML163
Cluster-2	3	KHI235, KHI409, KHI208,
Cluster-3	1	CML141.

D^2 analysis is an important method for the evaluation of genetic diversity amongst the genotypes and selection of parents for the breeding programme (Arunachalam, 1981). Without the selection of suitable parents in conventional methods of hybridization, generally results in the wastage of resources. Greater success can be achieved through correct choice of parents based on genetic divergence. Crosses between genetically diverse parent's results in

The D^2 analysis has been a more precise and reliable test in the quantitative estimation of genetic diversity. Twenty two genotypes were grouped into cluster I, three genotypes into cluster II, and one genotype into cluster III. This wide diversity observed in elite genotypes was due to the involvement of diverse parental lines in the hybridization programme at different research centers and selection under different environmental situations. Cluster I with three genotypes, exhibited intra-cluster D^2 value (12.67) as well as within group average distance (3.55). Genotypes from this cluster could be utilized as parental lines for hybrid breeding programme or recombination breeding programme owing to their wider within group distance. Thus the cluster I was most divergent group among the clusters.

Maximum D^2 value (25.46) and average distance (5.04) was observed between cluster II and III. Thus, these two clusters were most divergent among the clusters. The other clusters showing high inter-cluster D^2 values were cluster I and III (24.84), II and I (20.85). Parental lines selected from these individual groups showing high inter-cluster distance are likely to produce superior progenies and hybrids. Khumkar *et al.* (2002) and Singh *et al.* (2009) have also reported that selection of parents for hybridization should be done from two clusters having wide inter-cluster distances to get maximum variability in the segregating generation.

The average intra and inter-cluster D^2 values and respective average genetic distances between and within clusters are presented in Table 2. Cluster II with three genotypes exhibited maximum intra-cluster D^2 value (15.44) along with maximum within group average distance (3.92). It was followed by cluster I (D^2 = 12.67) with twenty two genotypes and cluster III (D^2 = 0.00) with one genotype. Considering inter-cluster distance, cluster II and III were found to be highly divergent as indicated by maximum D^2 value (25.46) and average distance (5.04) between them. This followed by cluster me and III, cluster II and me, showed average inter-cluster D^2 value of 24.84 and 20.85 respectively. Cluster I and II exhibited minimum genetic distance (4.56) between them, which showed that genotypes in these two clusters were somewhat similar in genetic constitution and a greater heterosis than those between closely related ones (Moll and Stuber, 1971).

Table 2: Average inter and intra-cluster D^2 and D values (parenthsis)

Cluster distances	Group 1	Group 2	Group 3
Group. 1	12.67(3.55)	20.85 (4.56)	24.84(4.98)
Group. 2	20.85(4.56)	15.44(3.92)	25.46(5.04)
Group. 3	24.84(4.98)	25.46(5.04)	0.00(0.00)

hybridization between these groups may not generate sufficient variability.

The cluster means of various traits are presented in Table 3. High cluster mean for days to 50 % tasseling were recorded for cluster I (99.73) whereas it was low (93.50) for Cluster III; Similarly, days to 50 % silking was recorded highest for Cluster I (105.27) and lowest (100.00) for Cluster III, plant height was recorded highest for Cluster III (160.80), followed by Clusters II and I. The cluster with lowest cluster means could be used for development of plants with reduced height. Ear height was recorded highest for Cluster II (76.62) followed by I (59.10) and III (21.70). Days to maturity was recorded highest for Cluster III (138.00) followed by Cluster I and II. The cluster with lowest mean values for days to maturity could be used for breeding of early flowering cultivars. High Cluster mean recorded for plant height in cluster III (160.80 cm) which also showed highest days to maturity (138.00), cobs per plant (1.09), number of kernels per row and low value of ear diameter (3.01), days to 50% tasseling (93.50), days to 50% silking (100.00), and ear height (21.70). Cluster II comprising of three genotypes have highest mean for yield per plant (101.50), ear height (76.62), cob length (17.22), 100 seed weight (29.83) and this cluster showed lowest mean for number of kernels row per ear (05.83), number of kernels per row (22.17), days to maturity (136.83 cm); Cluster I contained only one genotype with higher mean for days to tasseling (99.50), days to 50% silking (105.27), number of kernels per row 28.07 and lowest mean for plant height (113.47), cob length (13.35) cobs per plant (1.43), 100 weight seed (24.09) and yield per plant (38.84).

The genetic divergence among clusters was well reflected in cluster means. For earliness, cluster II (136.83) was found to be good. High cluster mean were recorded for days to maturity, plant height (160.80), number of kernels per row (13.50) in cluster III. High mean values of ear height (141.72), yield per plant (101.50), 100 seed weight (29.83) were found in cluster II. Cluster I gave high mean values for days to 50% tasseling (99.73), days to 50% silking (105.27) and number of kernels per row (28.07).

Table 3: Cluster mean for 12 quantitative characters in maize

Cluster means	Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Ear height (cm)	Days to maturity	Cob length (cm)	Cob plant^{-1}	Ear diameter (cm)	No. of row ear^{-1}	No. of kernel row^{-1}	100 seed Weight (g)	Yield plant^{-1} (g)
Cluster 1	99.73	105.27	113.47	59.10	136.86	13.35	1.43	3.16	13.45	28.07	24.09	38.84
Cluster 2	95.83	101.83	141.72	76.62	136.83	17.22	1.90	4.10	05.83	22.17	29.83	101.50
Cluster 3	93.50	100.00	160.80	21.70	138.00	13.50	1.90	3.01	13.50	24.50	27.50	54.50

These observations suggested that none of the clusters contained genotypes with all the desirable traits, which could be directly selected and utilized. The hybridization between genotypes of different clusters would be rewarding for the development of desirable genotypes. Recombination breeding between genotypes of different clusters has also been suggested by Alom *et al*. (2003), Datta *et al*. (2004), Beyene (2005), Datta and Mukherjee (2005) and Sharma *et al*. (2012). Maximum percent contribution to divergence was by ear diameter (4.10) followed by 100 seed weight (29.83) and grain yield per plant (19.38). Other clusters contributed less than 5% towards variability.

A critical examination of the nature of clusters revealed that the genotypes together in a cluster were related by pedigree or originated in same ecological region as in cluster I or similarities in their morphological characters as seen in cluster II. Different clusters could be regarded as useful sources of genes for yield and quality components and the genotypes from these clusters may, therefore, be used as parents in crossing program to incorporate the characters for which they have better values over others.

On the basis of results obtained in the present investigation, it was concluded that the allelic diversity can be used for future breeding program. The traits under study are also major yield contributing traits and are largely associated with each other. Therefore, these traits should be taken into consideration either simultaneously or alone for selecting a high yielding maize genotype. Nine genotypes were grouped in one cluster and one genotype i.e. CM141 in another cluster in D^2 analysis. It suggests that the hybrid combinations using CM141 as one of the parents with all other genotypes many result in higher heterotic combinations. The other superior combination may be obtained by using parents of cluster I and cluster II.

Table 4: Percentage contribution of different characters in genetic variability

SL. No.	Traits	Times ranked 1st	Contribution (%)
1.	Ear diameter (cm)	91	28.00
2.	Ear height (cm)	70	21.54
3.	Plant height (cm)	69	21.23
4.	Yield per plant (g)	63	19.38
5.	Days to 50% tasseling	18	5.54
6.	No. of kernel per row	7	2.15
7.	Cob length (cm)	3	0.92
8.	No. of row per ear	2	0.62
9.	100 seed weight (g)	2	0.62
10.	Days to 50% silking	0	0.00
11.	Days to maturity	0	0.00
12.	Cobs per plant	0	0.00

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