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## Genetic Divergence in Maize (*Zea mays* L)

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**Abstract:** Genetic diversity among 25 genotypes of maize were estimated by using Mahalanobis D<sup>2</sup> statistic for eight characters. The genotypes were proposed into seven clusters. The inter-cluster distances were larger than the intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups. The cluster III contained the highest number of genotypes. The cluster III also produced highest grain yield and 1000-grain weight. The highest inter cluster distanced was observed in between cluster III and II and of lowest between cluster IV and V. The highest intra-cluster distance was noticed in cluster IV and lowest for cluster VI.

**Key words:** Genetic divergence, diversity analysis, clustering patterns

### INTRODUCTION

Maize is one of the oldest crop and most important food grain in the world as well as developing countries. It is the highest yielding grain crop having multiple uses. Maize is used in the preparation of nutritious food, animal feed and fodder, in the industrially processed food and also in several non food industrial products. So, maize is not only one of the most important cereal crops in modern agriculture but it was the basic food crops plants in the agriculture systems. In maize it is well known that adequate genetic diversity is necessary in breeding program for development of high yielding varieties. Multi variate analysis is an useful tool for quantifying the degree of divergence between biological population at genotypical level and in assessing relative contribution of different components to the total divergence both intra and inter cluster level (Murty and Arunachalam, 1966; Ram and Panwar, 1970 and Sachan and Sharma, 1971). The present study was therefore undertaken to analyze the genetic divergence of maize genotypes.

### MATERIALS AND METHODS

Twenty-five genotypes of Maize (*Zea mays* L) were grown in randomized complete design with three replication at Regional Agricultural Research Institute, Rhamatpur, Barisal during rabi 1999-2000. The seeds of each entry were sown in two rows of 5 m long with spacing 25 x 20 cm. One plant was kept per hill after thinning. Fertilizers were applied @ 250:120:120:40:5 kg ha<sup>-1</sup> of N, P<sub>2</sub>O<sub>5</sub>, K<sub>2</sub>O, S and Zn, respectively.

The other intercultural operations were done timely to rise the crop uniformly. Observation were recorded from

10 randomly selected plants of the each row for plant height, Ear height, Days to 50% silking, Days to maturity, Number of grains/Ear, 1000 grain weight and Yield (t ha<sup>-1</sup>). The data were then subjected to Mahalanobis D<sup>2</sup> analysis using GENSTAT 5.0 program.

### RESULTS AND DISCUSSION

The analysis of variance on the basis of mean value revealed significant differences among the genotypes for all characters. Diversity analysis for all characters were carried out.

Twenty five genotypes were grouped into seven different clusters using clustering techniques. The clustering patterns and genotype distribution are presented in Table 1. The distribution pattern indicate that maximum number of genotypes were inclined in cluster III (5) and the minimum in cluster I (3) and cluster V (2). Cluster II, IV and VI, VII included to 4 and 3 genotypes respectively. Genetic diversity is generally associated with geographical diversity, but the former is not necessarily directly related with geographic distribution. The genotypes within the same clusters were originated from different geographical regions of the world, which indicated the geographical distribution and genetic divergence did not follow the same trend which might be due to continuous exchange of genetic material among the countries of the world. Similar results was reported by Sheriffa and Shivarhankar (1992) and Shewe *et al.* (1972). The Intra and Intercluster values among the seven cluster are presented in Table 2. The table revealed that the inter cluster distance in most of the cases was larger than the intracluster distance. The highest inter cluster distance was observed between cluster II and III and that of lowest

Table 1: Distribution of 25 genotypes of maize in seven clusters

Cluster No.	No. of Genotypes	Genotypes (Sl. No. Not treatment no)
I	2	G - 11 (Thailand), G - 24 (Local)
II	4	G - 3 (Thailand), G-20 (CIMMYT), G-21 (CIMMYT), G-16 (Pakistan)
III	7	G-1 (Thailand), G-2 (India), G-4 (Thailand), G-10 (Thailand), G-23 (Local), G-16 (Pakistan), G-18 (Vietnam)
IV	4	G-9 (India), G-13 (Vietnam), G-21 (CIMMYT), G-25 (Local)
V	2	G-8 (Thailand), G-15 (Pakistan),
VI	3	G-5 (Thailand), G-14 (Vietnam), G-17 (Thailand)
VII	3	G-6 (Thailand), G-7 (Thailand), G-12 (Thailand)

Table 2: Average Intra and Inter cluster distances (D<sup>2</sup>) for 25 maize genotypes

Cluster	I	II	III	IV	V	VI	VII
I	0.259	8.440	6.390	8.36	5.46	8.30	7.515
II		1.326	14.408	8.736	6.390	7.103	4.957
III			0.264	7.052	10.698	13.165	12.936
IV				1.830	4.895	11.859	7.326
V					1.264	9.639	5.092
VI						0.199	6.951
VII							0.235

Table 3: Cluster Means for 9 characters 25 genotypes in maize

Character	I	II	III	IV	V	VI	VII
DS	82.0	80.1	81.6	83.0	82.2	80.0	8.3
PH	236.0	214.3	208.1	224.6	198.8	213.3	231.0
EH	116.3	114.3	107.9	117.0	99.2	116.4	113.8
EL	16.6	15.5	16.5	14.3	16.0	15.5	14.2
DM	139.6	135.2	142.1	139.6	137.2	140.6	133.9
G/E	468.6	423.3	509.7	499.6	480.8	416.7	451.9
1000 GW	389.8	322.4	403.9	355.5	330.6	376.6	338.2
Y/H	10.0	9.0	9.8	8.8	94.0	10.5	10.2

DS= Days to silking, PH = Plant height, EH = Ear height, EL = Ear length  
DM= Days to maturity, G/E = Grain per year. GW = Grain weight and  
YH= Yield per hectare

Table 4: Relative contribution of eight characters to the total divergence in maize

Character	Vector I	Vector II
Days to 50% silking	0.3638	-0.0171
Plant height (m)	0.0584	0.0239
Ear height (m)	-0.1176	-0.0137
Ear length (m)	-1.1867	-0.5978
Days to maturity	0.3738	0.1133
Number of grains/Ear	-0.0958	-0.0665
1000 grain weight (g)	-0.0687	0.0911
Yield (t/ha)	1.1588	0.0929

between cluster II and VI. The highest intra cluster distance was noticed for cluster II, III IV were far diverged from those of cluster I, VI, VII. Somayagullu *et al.* (1970) reported that the clustering revealed instability due to relatively lesser divergence, where as the widely diverged cluster remained distinct in different environment. This result was also supported by Raut *et al.* (1985). In the cluster II, III and IV were highly diverge. So, they would be more stable. Therefore the genotypes belonging to the distant cluster may be used in hybridization program for obtaining a variation.

The cluster means of eight characters are presented in Table 3. Cluster III showed highest mean values for number of grain/ear and 1000 grain weight. In case of days to 50% silking, cluster IV had higher mean values. In case of days to maturity cluster VII was earlier. High mean values of plant height were recorded in cluster I and lowest in cluster V. Cluster V had lowest mean values for plant height and ear height. Endang *et al.* (1971) stated that clustering pattern could be utilize in choosing parents for cross combination which likely to be generate the highest possible variability for the effective selection of various economic traits.

Contribution of the characters towards divergence are presented in Table 4. The Canonical variate analysis revealed that, the vectors (vector I and II) for plant height and days to maturity were positive. Such results indicated that these two characters contributed maximum towards diversity of the genotypes. So, It is encouraging that the divergence in the present materials due to these two characters will offer a good scope for improvement through rational selection.

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