



## Genetic Diversity in Maize (*Zea mays* L.) Inbred Lines

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### Abstract

Thirty yellow inbred lines of normal maize were evaluated for thirteen parameters at the experimental field of Hajee Mohammad Danesh Science and Technology University during 2010-11 to study the genetic divergence using multivariate analysis. The thirty inbreds fell into six distinct clusters. The intra-cluster distances in all the six clusters were more or less low, indicating that the genotypes within the same cluster were closely related. The highest inter-cluster distance was observed between cluster I and cluster IV and the lowest between the cluster II and III. The cluster V and cluster IV contained the highest (9) and lowest (1) number of genotypes, respectively. Cluster VI showed the highest mean values for kernel yield and all the yield contributing traits except days to 50% tasseling and 50% silking. Cluster II had the lowest mean values for ear height and ear length. Days to maturity and ear diameter showed maximum contribution towards total divergence among different characters. Based on medium to high inter-cluster distances, six inbred lines viz. ML06, ML10, ML14, MK19, ML25 and ML26 were selected for hybrid program. Development of hybrids utilizing these genotypes has the chance to obtain higher heterosis with high performing crosses.

**Keywords:** Genetic diversity, cluster analysis, inbred lines, *Zea mays* L.

### 1. Introduction

Maize (*Zea mays* L.) has become an important cereal crop in the rice based cropping system of Bangladesh. Hybrid maize has higher yield potentiality than those of synthetics and composites (Pandey and Gardner, 1992; Vasal *et al.*, 1995). The hybrid varieties which are currently planted throughout the country, are imported from India, China, Thailand etc. The most limiting factor of maize research in Bangladesh is the development, improvement and maintenance of parental/inbred lines. On the other hand, the problem of imported hybrid seed is the involvement of high price and uncontrolled quality. Moreover, the farmers can not get the seeds timely. One important approach to

improve this situation is the development of inbred lines which can produce high yielding hybrid varieties. Before hybrid development, prospective parent (inbred line) selection is a pre-requisite. Several studies on maize have shown that inbred lines from diverse stocks tend to be more productive than crosses of inbred lines from same variety (Vasal, 1998). Saxena *et al.* (1998) also reported that manifestation of heterosis usually depends on the genetic divergence of the two parental lines. The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents for hybrid production. Genetic diversity is one of the useful tools to select appropriate genotypes/lines for

hybridization. The genetic diversity between the genotypes is important as the genetically diverged parents are able to produce high heterotic effects (Falconer, 1960; Arunachalam, 1981; Ghaderi *et al.*, 1984; Mian and Bahl, 1989). Knowledge of germplasm diversity among elite breeding materials have a significant impact on the improvement of crop plant (Hallauer *et al.*, 1988). Maize breeders are consistently emphasizing the importance of diversity among parental genotypes as a significant factor contributing to heterotic hybrids (Ahloowalia and Dhawan, 1963). Characterization of genetic diversity of maize germplasm is of great importance in hybrid maize breeding (Xia *et al.*, 2005). D<sup>2</sup> analysis is a useful tool for quantifying the degree of divergence between biological population at genotypic 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; Sachan and Sharma, 1971). The present investigation was undertaken with a view to estimate the nature and magnitude of genetic diversity in 30 maize inbred lines.

## 2. Materials and Methods

### 2.1. Location of study

The study was conducted during December 2010 to May 2011 at the experimental field of the Dept. of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur.

### 2.2. Plant materials

This study was a part of a long-term maize inbred line development program conducted at the University mentioned above where near-homozygous inbred lines were developed from ten single cross hybrid varieties as source population. The inbred lines were ML-01 to ML-30.

### 2.3. Experimental design, plot arrangement, cultivation practices and data collection

Thirty maize inbred lines were grown in a alpha lattice design with three replications during rabi

season of 2010-2011. The seeds of each entry were sown on 21 December 2010 in 5 m long one row with spacing of 0.75 x 0.20 m between rows and hills, respectively. One plant was kept per hill after proper thinning. Recommended doses of fertilizers were applied. The other intercultural operations were done timely and properly to raise the crop uniformly. Observations were recorded on whole plot basis for days to 50% tasseling (DT), 50% silking (DS) and maturity (DM). Ten randomly selected plants were used for recording observations on plant height (PH), ear height (EH), ear length (EL), ear diameter (ED), ears/plant (EPP), number of kernel rows/ear (KRPE), number of grains/row (GPR), number grains/ear (GPE), 1000-kernel weight (g) (TGW) and kernel yield/plant (g) (YPP). Data were subjected to principal component and Mahalanobis (1936) D<sup>2</sup> analysis extended by Rao (1952) using GENSTAT 5 Computer programme.

## 3. Results and Discussion

Range, mean, standard error and coefficient of variation of 13 different yield contributing characters in 30 maize inbreds are presented in Table 1. The inbred lines were significantly different for all characters studied except ears/plant indicating the presence of notable genetic variability among them. Maximum coefficient of variation was found in grains/ear and yield/plant. Hence there is a scope for selecting high yield potential lines. The D<sup>2</sup> values ranged from 3.49 to 14.98 and principal component scores also indicated a high degree of genetic diversity among the genotypes.

### 3.1. Cluster analysis

By application of non-hierarchical clustering using co-variance matrix, 30 inbred lines of maize were grouped into six different clusters (Table 2). It was revealed that cluster V comprised maximum number (nine) of genotypes, followed by cluster III and cluster I comprising 7 and 6 genotypes, respectively. The lowest single genotype was included in cluster IV.

**Table 1.** Minimum, maximum, mean, std. error and co-efficient of variation (CV%) of yield and other yield contributing characters of 30 maize inbreds

Characters	Minimum	Maximum	Mean	Std. error	CV (%)	F- test
1. Days to 50% tasseling	79.00	91.00	83.00	0.51	3.36	**
2. Days to 50% silking	81.00	94.00	85.93	0.549	3.50	**
3. Days to maturity	119.0	137.0	126.27	0.719	3.12	**
4. Plant height	114.2	219.8	171.53	3.478	11.11	**
5. Ear height	46.83	67.13	57.18	1.09	10.44	**
6. Ear length	13.50	19.53	16.31	0.263	8.85	**
7. Ear diameter	11.52	15.87	13.56	0.215	8.66	**
8. Number of ears/plant	1.000	1.300	1.09	0.024	12.04	NS
9. Number of kernel	10.73	17.13	13.92	0.319	12.53	**
10. Number of grains/row	19.80	34.47	25.72	0.732	15.59	**
11. Number of grains/ear	213.0	543.0	369.54	14.849	30.17	**
12. 1000 grain weight	150.8	427.8	293.14	10.081	18.84	**
13. Yield/plant	47.93	131.21	84.30	3.879	25.21	**

\*\* Significant at 1% level of probability, NS = not significant.

**Table 2.** Distribution of 30 maize inbred lines among six clusters

Cluster	No. of Genotypes	Genotypes
I	6	ML05,ML08,ML14,ML28,ML29,ML30
II	5	ML02,ML07,ML16,ML17,ML23
III	7	ML09,ML10,ML11,ML20,ML22,ML26,ML27
IV	1	ML15
V	9	ML03,ML04,ML06,ML12,ML13,ML18,ML19,ML21,ML24
VI	2	ML01,ML25

Clustering pattern of inbred lines under this study reveals that the inbred lines showed considerable genetic diversity among themselves by occupying six different clusters. Similar results were reported by Singh *et al.* (2005) and

Liu YuAi *et al.* (2006) in maize and by Masud *et al.* (1995) in pumpkin. Another study was carried out by Chen FaBo *et al.* (2007) who reported that 186 maize genotypes could be classified into ten clusters.

**Table 3.** Average intra (bold face) and inter-cluster distance ( $D^2$ ) of 30 maize inbred lines

Clusters	I	II	III	IV	V	VI
I	<b>0.952</b>					
II	6.100	<b>0.651</b>				
III	7.160	3.838	<b>0.500</b>			
IV	14.984	10.069	7.852	<b>0.000</b>		
V	10.654	6.353	3.494	4.387	<b>0.630</b>	
VI	8.518	8.179	4.668	9.645	5.926	<b>0.725</b>

The maximum inter-cluster divergence (Table 3) was observed between the clusters I and IV and it was minimum between clusters III and V. The maximum intra-cluster distance was observed in cluster I and minimum in cluster IV. Cluster IV had only a single genotype. The crosses involving parents from most divergent clusters are expected to manifest maximum heterosis and generate wide variability in genetic architecture. Intra cluster distance was much lower than the inter cluster one, suggesting, heterogeneous and homogeneous nature between and within groups, respectively. This was further supported by an appreciable variation observed for cluster means (Table 4).

Mean values of DM, PH, ED,EL, EPP, GPR, GPE, TGW and YPP were the highest in cluster VI; DT, DS, and EH in cluster I and KRPE in cluster V. A wide range of variations for several characters among single as well as multigenotypic cluster was observed. However, the difference was clear for PH, EL, ED, GPE, TGW and YPP, which has contributed largely to the total divergence. Similar results have also been reported by Singh *et al.* (2005) and Chen FaBo *et al.* (2007). Hence, for the improvement of different characters viz. EL, GPR, GPE, TGW, ED, KRPE and YPP under the present study, inbred lines should be selected from cluster I, V and VI.

**Table 4.** Cluster mean for thirteen characters in 30 genotypes of maize inbred line

Characters	Clusters					
	I	II	III	IV	V	VI
1. Days to 50% tasseling	87.3	83.2	81.9	79	81.4	82.5
2. Days to 50% silking	90.3	86.4	84.9	83	83.9	86
3. Days to maturity	129.5	126.8	124.7	122	124.7	130
4. Plant height	162.3	170.1	181	175	166.6	190.1
5. Ear height	62.7	54.8	57.5	61.6	53.5	60.2
6. Ear length	16.3	15.5	17.1	16.3	15.8	17.9
7. Ear diameter	13	13.2	13.8	11.8	13.8	15
8. Number of ears/plant	1.1	1.1	1	1	1	1.2
9. Number of kernel	12.1	13.7	13.8	10.7	15.4	15.2
10. Number of grains/row	22.3	23.3	25.2	33	27.3	32.9
11. Number of grains/ear	266.5	306.8	368.7	406.6	441.6	495.5
12. 1000 grain weight	356.3	253.2	294.4	150.8	270.4	372.6
13. Yield/plant	74	73.9	93.9	57.9	83.8	122.7

**Table 5.** Latent vectors for 13 principal component characters of 30 maize inbred lines

Characters	Vectors 1	Vectors 2
1. Days to 50% tasseling	-0.1039	-0.1682
2. Days to 50% silking	-0.4969	-0.0883
3. Days to maturity	0.1146	0.1203
4. Plant height	-0.0468	-0.0268
5. Ear height	-0.0180	0.0101
6. Ear length	0.3102	-0.3955
7. Ear diameter	0.3081	0.1288
8. Number of ears/plant	-3.0817	-0.8830
9. Number of kernel	-1.0115	0.5906
10. Number of grains/row	-0.3285	0.0371
11. Number of grains/ear	0.0549	-0.0311
12. 1000 grain weight	-0.0297	-0.0291
13. Yield/plant	-0.0133	0.0195

The principal component analysis revealed that in major vector I, the important characters responsible for genetic divergence in the major axis of differentiation were DM, EL, ED and GPE (Table 5). In vector II, which was the second axis of differentiation, the characters, DM, EH, ED, KRPE, GPR and YPP were important. The role of DM, ED for both the vectors was positive across two axis which is the indication of the important components of genetic divergence in this materials.

Group constellation was also independently derived by principal component analysis to verify grouping obtained through  $D^2$  statistic in a two dimensional chart (Z1-Z2). Therefore, scores obtained for the first two components were plotted against two main axis and then superimposed with clustering (Fig. 1). This clustering pattern confirmed the results obtained by  $D^2$  analysis.

The crosses involving parents belonging to the maximum divergent clusters were expected to manifest maximum heterosis and also wide

variability in genetic architecture. Thus, crosses among the genotypes of clusters I, III, V and VI would exhibit high heterosis and is also likely to produce new recombinants with desired characters in maize.

#### 4. Conclusions

Genetic diversity was studied to find out the more diverse inbred lines in maize which might be used in hybridization programme. Thirty maize inbred lines were grouped into six different clusters. The crosses involving parents/inbred lines from most divergent clusters are expected to manifest maximum heterosis and generate wide variability in genetic architecture.

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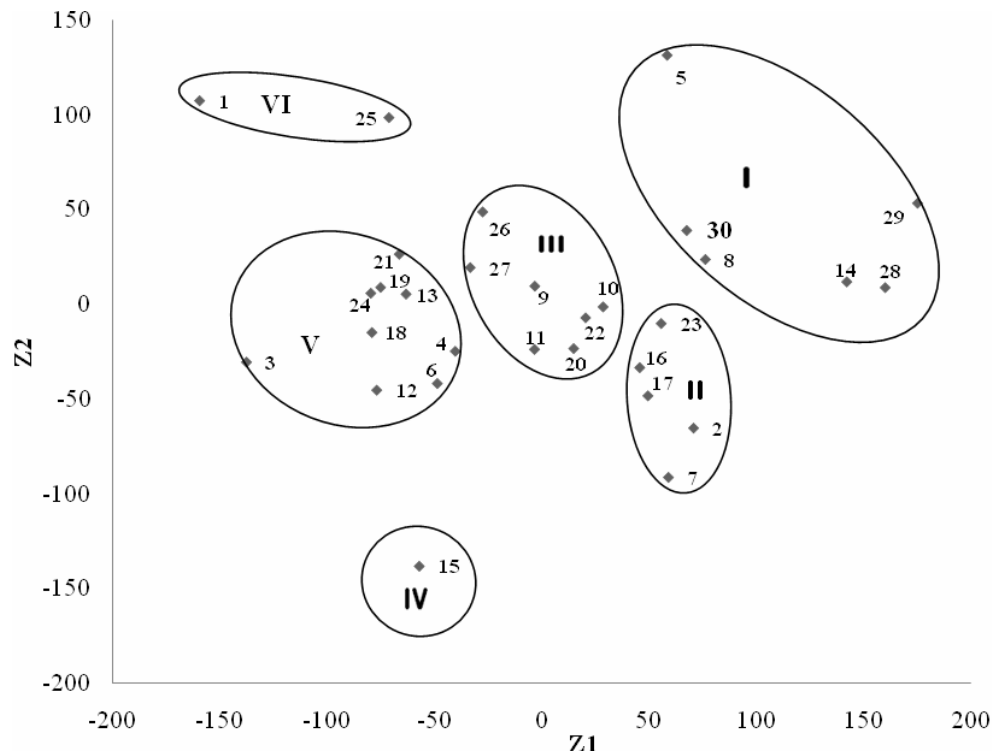


Fig. 1. Scatter diagram of 30 genotypes of maize inbred lines.

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