

GENETIC DIVERSITY ANALYSIS IN MAIZE USING MORPHOLOGICAL CHARACTERS

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Abstract

Genetic divergence among 39 Maize (*Zea mays* L.) inbred lines were estimated using D2 and principal component analysis. All the inbred lines were grouped into five clusters. Cluster V was the largest comprising 11 inbred lines and cluster III was the smallest with 6 inbred lines. Cluster II had the highest intra-cluster distance and Cluster IV had the lowest intra-cluster distance. The inter-cluster distances were larger than the intra-cluster distance suggesting wider genetic diversity among the inbred lines of different groups. Inter-cluster distance was maximum (7.739) between clusters II and III. The results revealed that inbred lines chosen for hybridization from clusters with highest distances would give high heterotic F1 and broad spectrum of variability in segregating generations. The characters- plant height (cm), number of grain rows per cob, grain yield per plant (g) contributed maximum towards divergence among maize inbreds. Considering cluster distance, inter-genotypic distance and other agronomic performances E10 and E26 from cluster I; E11 and E14 from cluster II; E19 and E22 from cluster III; E1 and E33 from cluster IV; E24, E25 and E28 from cluster V may be considered to be better parents for future uses in hybrid program.

Keywords: Maize, Morphological characters and genetic diversity

Introduction

Maize (*Zea mays* L.) plays a significant role in human and livestock nutrition worldwide. It is the world's most widely grown cereal and is the primary staple food in many developing countries (Morris et al., 1999). It is a versatile crop with wider genetic variability and able to grow successfully throughout the world covering tropical, subtropical and temperate agro-climatic conditions. Maize in Bangladesh is becoming an important crop in the rice based

cropping system. It is the third important cereal crop after rice and wheat. In recent years maize is gaining popularity among the farmers mainly due to high yield, more economic return and versatile uses. It is the highest yielding grain crop having multiple uses. The need for demand of maize is increasing gradually. The area and production of maize is increasing day by day in Bangladesh and it continues to expand rapidly at an average rate of 20% year-1 (CIMMYT, 2008).

Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a great heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations. In maize, this information is useful in planning crosses for hybrid and line development, in assigning lines to heterotic groups, and in plant variety protection. Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991) Multivariate analysis is an 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 and Sachan and Sharma, 1971). The present study was therefore undertaken to analyze the genetic divergence in maize inbreds for producing hybrid variety.

Materials and Methods

Thirty nine inbred lines from CIMMYT (India) were grown at the Bangladesh Agricultural Research Institute (BARI), Gazipur during rabi 2010-11. Seeds

were sown on 29 December 2010. The seeds of each inbred line were sown in a single row of 5 m long plot. Spacing adopted was 75 x 20 cm between rows and hills, respectively. One healthy seedling per hill was kept after proper thinning. Fertilizers were applied @ 120,80,80,20, 5 and 1 kg/ha of N, P₂O₅, K₂O, S, Zn and B respectively. Standard agronomic practices were followed (Quayyum, 1993) and plant protection measures were taken when required. Data on days to 50% tasseling and silking were recorded on whole plot basis. Ten randomly selected plants were used for recording observations on plant height (cm), ear height (cm), cob length (cm), cob diameter (cm), number of grain rows/cob, number of grains/row, 1000-grain weight (g), grain yield/plant (g). Genetic diversity was estimated using Mahalanabis (1936) generalized distance (D₂) extended by Rao (1952). Tocher's method was followed to determine the group constellation. Canonical variate analysis was also performed as per Rao (1952) to confirm the results of cluster D₂ analysis. The data were analyzed using GENSTAT 5.0 software program.

Results and Discussion

The analysis of variance showed significant variations among all the inbred lines for all the ten characters

studied. A two-dimensional scatter diagram was constructed using component I in X-axis and component II in Y-axis, reflecting in the relative position (Figure 1). As per scatter diagram the inbred lines were apparently distributed into five clusters. It was also revealed that the inbred lines of cluster III was more diverse from the inbred lines of cluster II.

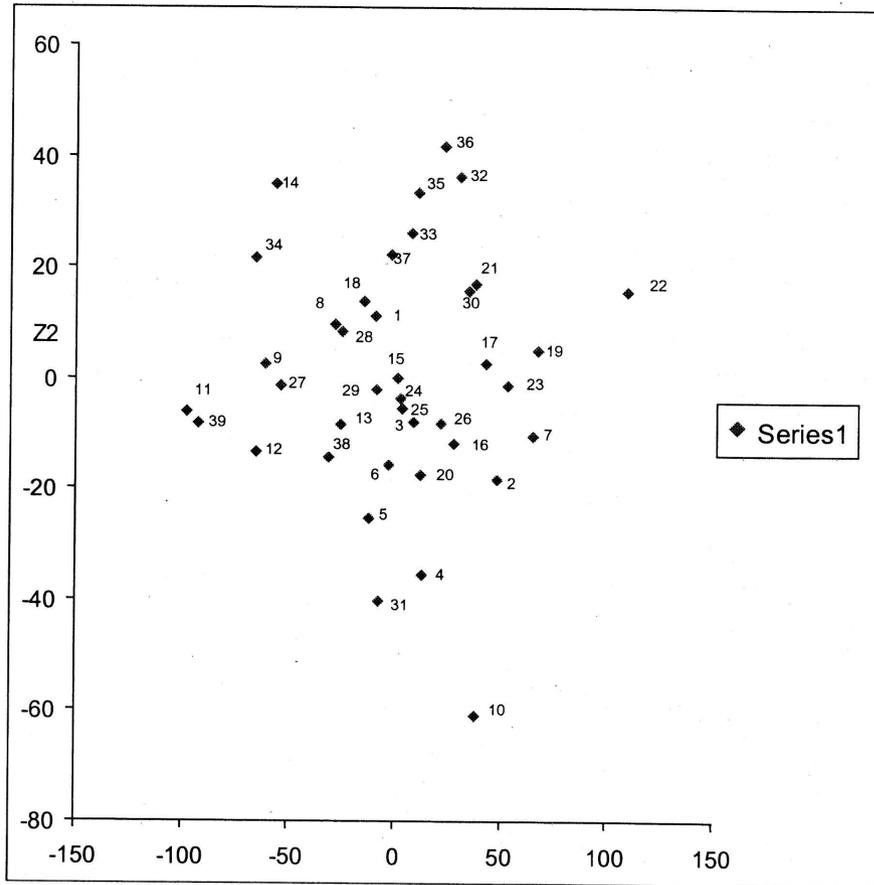


Figure 1: Scatter distribution of 39 Maize (*Zea mays* L) inbred lines based on their principal component scores.

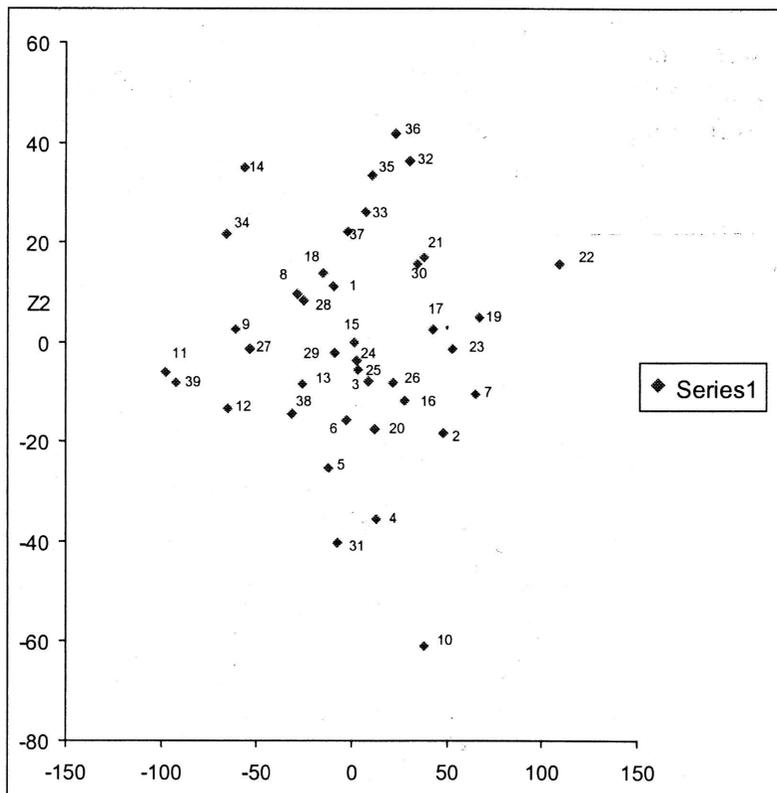


Figure 2: Scatter distribution of 39 Maize (*Zea mays* L) inbred lines based on their principal component scores superimposed with clustering.

After comparing D2 values 39 inbred lines were grouped into five clusters. Cluster V had maximum number of (11) inbred lines followed by II, I, IV and III which had 8, 7, 7 and 6 inbred lines, respectively (Table 2). These results confirmed the clustering pattern of the inbred lines obtained through principal component analysis. Golakiya and Makne (1991) while assessing genetic diversity of 23 genotypes and grouped

them into six clusters. Badignavar et al. (2002), Joel and Mysamy (1998), Islam and Islam (2000) found the same results. The clustering pattern of the genotypes under this study revealed that the genotypes collected from the same location can also group into different clusters. This shows that geographic diversity was not related to genetic diversity of these materials.

Table 2. Distribution of 39 maize inbred lines in five different clusters

Cluster	No. of inbreds	Inbred lines included in different clusters
I	7	E3,E4, E10, E16, E20, E26, E31
II	8	E9, E11, E12, E13, E14, E27, E34, E39
III	6	E2, E7, E17, E19, E22, E23
IV	7	E1, E21, E30, E32, E33, E35, E36
V	11	E5, E6, E8, E15, E18, E24, E25, E28, E29, E37, E38
Total =		39

Statistical distances represent the index of genetic diversity among the clusters. The intra-cluster distance in all the 5 clusters were more or less low which indicated the close relationship within the inbred lines of same cluster. The intra-and inter-cluster values within and among the clusters are presented in Table 3. Intra-group distances appeared much smaller than the inter-groups, suggesting a lower genetic diversity

among the lines of the same group than those from different groups. Intra-cluster distances varied from 0.514 to 0.800. This is corroborated with the results of Ivy et al. (2007) and Hoque et al. (2008). Comparatively, higher intra-cluster distances were observed in cluster II and I. Clustering revealed instability due to low divergence and widely diverged clusters remain stable in different environment.

Table 3. Inter and intra-cluster (bold) distance (D2) for 39 maize inbred lines

Cluster	I	II	III	IV	V
I	0.711				
II	5.713	0.800			
III	3.547	7.739	0.666		
IV	4.186	5.532	3.630	0.514	
V	3.084	4.310	4.475	3.466	0.610

The highest inter-cluster distance was observed between clusters III and II (7.739), followed by between cluster II and I (5.713), IV and II (5.532), V and III (4.475) (Table 3). The lowest inter-cluster distance was observed between cluster V and I (3.084), followed by V and IV (3.466). The maximum inter-cluster distance was observed between the clusters III and II (7.739) maintaining more distance than other clusters. Genotypes from these two clusters, if involved in hybridization may produce better hybrid and a wide spectrum of segregating population. Similar reports were also made by Singh et al., (1991) who reported that the

greater genetic distances implying higher heterosis than those with similar genetic distances.

Mean values for different clusters are presented in Table 4. The highest mean values for grain yield per plant (g), number of grains per row and cob diameter (cm) were observed in the same cluster IV (Table 4). This means lines included in this group are better for these parameters. Cluster V had the lowest value for ear height. The lowest mean value for plant height was found in cluster I. The mean of cob length was the highest in cluster III. The lowest mean values for days to tasseling and days to silking were found in cluster II.

Table 4. Cluster means for 10 different characters of 39 maize inbred lines

Characters	Clusters				
	I	II	III	IV	V
Days to 50% tasseling	71.86	70.67	70.75	74.57	71.91
Days to 50% silking	76.00	74.83	75.12	78.00	75.45
Plant height (cm)	120.04	139.62	136.90	147.77	120.77
Ear height (cm)	53.86	56.13	67.70	76.16	48.85
Cob length (cm)	12.50	11.88	14.48	13.13	13.15
Cob diameter (cm)	11.79	11.04	13.07	13.30	12.91
Number of grain rows per cob	12.49	12.98	13.73	14.04	14.05
Number of grains per row	18.90	20.55	20.58	23.79	23.35
1000-seed weight	281.43	197.50	321.67	271.43	247.27
Grain yield per plant (g)	50.36	46.39	80.00	87.71	75.44

Contribution of the characters towards divergence is presented in Table 5. Results showed that, Vector I obtained from PCA expressed that the important characters responsible for genetic divergence in the major axis of differentiation were days to silking,

plant height, cob length and grain yield per plant (g). In vector II, which is the second axis of differentiation,

the responsible characters were plant height, ear height and grain yield per plant (g) which played their major role on genetic divergence.

Table 5. Relative contributions of the 10 characters to the total divergence in maize

Characters	Vector I	Vector II
Days to 50% tasseling	-0.26252	0.06796
Days to 50% silking	0.29708	-0.13681
Plant height (cm)	0.01564	0.02427
Ear height (cm)	-0.01213	0.07848
Cob length (cm)	0.06583	-0.03218
Cob diameter (cm)	-0.15007	-0.11426
Number of grain rows per cob	0.06399	0.00572
Number of grains per row	-0.07975	-0.00228
1000 seed weight	-0.06043	-0.01760
Grain yield per plant (g)	0.00656	0.04861

Number of grain rows per cob, plant height and grain yield per plant (g) showed positive values in respect to both the vectors, were the major important traits responsible for genetic divergence in the major axis of differentiation. This means that considerable emphasis should be given on those parameters responsible for genetic divergence.

Considering the magnitude of genetic distance, contribution of character

towards divergence, magnitude of cluster mean and agronomic performance the inbred lines E26 for lower plant height from cluster I; E14 for lower days to 50% tasseling from cluster II; E19 for highest cob length and E22 for highest 1000 grain weight from cluster III; E1 highest number of grains per row and E33 for highest grain yield per plant from cluster IV and E24 highest number of grain rows per cob

and E25 for lowest ear height from cluster V were found promising. Therefore considering group distance and other agronomic performance genotypes E10 and E26 from cluster I; E11 and E14 from cluster II; E19 and E22 from cluster III; E1 and E33 from cluster IV and E24, E25 and E28 from cluster V may be considered to be better parents for future uses in hybrid program.

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