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Study of Genetic Diversity in Maize (*Zea mays* L.) Inbreds

Mohammad Quamrul Islam Matin[1, *], Md. Golam Rasul[2], A. K. M. Aminul Islam[2], M. A. Khaleque Mian[2], Nasrin Akter Ivy[2], Jalal Uddin Ahmed[3]

[1]Plant Breeding Division, Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh

[2]Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur, Bangladesh

[3]Department of Crop Botany, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur, Bangladesh

Email address:

quamrul_islam76@yahoo.com (M. Q. I. Matin), mdgolam60@yahoo.com (Md. G. Rasul), aminulgpb@bsmrau.edu.bd (A. K. M. A. Islam), makmian@bsmrau.edu.bd (M. A. K. Mian), ivy.bsmrau@yahoo.com (N. A. Ivy), jahmed06@gmail.com (J. U. Ahmed)

[*]Corresponding author

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Abstract: Genetic diversity among 64 CIMMYT and BARI developed maize inbred lines was conducted at the research farm of Plant Breeding Division, Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur, Bangladesh during Rabi season 2012-13. The genotypes were grouped into six clusters. Cluster III comprised the maximum genotypes (18) which indicated the genetic similarity among them. The minimum genotype (4) was contained in the cluster V. The highest inter-cluster distance was observed between cluster VI and III (9.37) followed by cluster VI and V(8.22) and cluster V and I (7.75) suggesting wider diversity between them and the genotypes in these cluster could be used as donor parents for new maize hybrid development. The highest intra-cluster distance was observed in cluster V (0.846) and the cluster II was had the least intra cluster distance (0.472). The mean values of cluster VI recorded the highest for thousand seed weight (360.80 gm) and yield per hectare (4.72 ton/ha). It appeared that the early maturing genotypes were included in the cluster V (147.75). The positive absolute values of the two vectors revealed that ear height, ear diameter and yield (t/ha) had the greatest contribution to genetic divergence. The negative values for the two vectors for days to 50% tasseling, ear length and thousand seed weight (TSW) indicated the least responsibility of both the primary and secondary differentiations.

Keywords: Genetic Diversity, Maize, Inbred, Cluster Analysis

1. Introduction

Inbred lines are the prerequisite for hybrid variety development in crop plants. For developing high yielding hybrids in maize, inbred lines need to be developed and evaluated for their diverged gene pool. The genetic diversity between the genotypes is important as the genetically diverged parents are able to produce high heterotic effects [1], [2]. Several studies on maize have shown that inbred lines from diverse stocks tend to be more productive than crosses of inbred lines from the same variety [3], [4]. Manifestation of heterosis usually depends on the genetic divergence of the two parental varieties [5]. The quantification of genetic diversity through biometrica1 procedure made it possible to choose genetically diverse parents.

Genetic diversity in maize is a valuable natural resource and plays a key role in hybrid breeding program. Knowledge of germplasm diversity and the relationship among elite breeding materials has a significant impact on the improvement of crop plants [6]. 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 [7].

The importance of genetically diverse genotypes as a source of obtaining transgressive segregants with desirable combinations has been reported by several workers [8]. Genetic resources are, in the sense, the building blocks and

also fundamental not only to a crop improvement program, but also for the very survival of the species in time and space [9]. Moreover, evaluation of genetic diversity is important to know the source of genes for particular trait within the available germplasm [7].

In view of above importance, the present investigation was carried out to identify genetically diverse parents for hybridization.

2. Materials and Methods

The experiment was conducted at the Research farm of Plant Breeding Division, Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur, Bangladesh during Rabi season 2012-13. Sixty four exotic and locally developed maize inbred lines included in the study. Seeds of the sixty four inbreds were sown on 23 November 2012 in Randomized complete block design with three replications. Each entry sown in two rows of 5m long maintaining a spacing of 75cmx25cm. One plant was kept per hill after thinning. Fertilizers were applied at the rate of 120,35,70,40, and 1.5kg/ha of N,P,K, S, and Zn, respectively. The other intercultural operations were done accordingly. Data on plant and ear height, thousand seed weight and field weight were recorded from 10 randomly selected competitive plants for each treatment in each replication. But for days to 50% tasseling, days to 50%silking and maturity, thousand grain weight and yield per hectare, which were recorded on the plot basis and yield was converted to hectare. Statistical analysis was made from the mean of 10 plants. Data were analyzed followingMahalanobis'D^2-statistics. The method proposed by [10] was used for intra-cluster and inter-cluster distance, cluster mean and contribution of each trait towards the divergence.

3. Results and Discussion

3.1. Cluster Analysis

The analysis of variance revealed highly significant differences among the inbreds for all the ten characters indicated the sufficient genetic variability among the tested inbreds. The sixty four inbreds were grouped into six.

Clusters using the non-hierarchical clustering method by Genstat Version 5.2 software programme in such a way that the genotypes within the cluster had smaller D2 values among themselves than those belonging to different clusters (Table 1). The maximum number of inbreds (18) was comprised into cluster III suggesting overall genetic similarity among them which was followed by cluster IV (14) and II (13) whereas cluster I and VI was consisted of 10 and5 genotypes, respectively. The minimum inbreds (4) comprised into cluster V.

[11] reported five groups in divergence study of maize. [12] identified seven cluster of 39 maize genotypes and [13] grouped 17 maize inbreds into four clusters.

Table 1. *Distribution of 64 inbred lines of maize in five different clusters.*

Cluster	No. of genotypes	Genotypes in different clusters (Entries)
I	10	3, 4, 8, 19,45, 48, 51, 53, 56, 60
II	13	2, 6, 7, 9, 11, 16, 26, 32, 33, 36, 57, 59, 62
III	18	1, 10, 12, 14, 15, 17, 24, 25, 28, 29, 31, 37, 38, 39, 40, 41, 58, 61
IV	14	5, 13, 18, 21, 22, 30, 34, 35, 42, 43, 49, 50, 63, 64
V	4	20, 23, 27, 54
VI	5	44, 46, 47, 52, 55

3.2. Average Intra and Inter Cluster Distance

The intra and inter cluster distance (D^2) values taken from diversity analysis are presented in Table 2. The magnitude of intra cluster distances indicated the extent of genetic diversity among genotypes within the same cluster. The inter cluster distances in all cases were larger than the intra cluster distance which indicated that wider diversity was present among the genotypes of distant group. The genotypes included within a cluster had less diversity among themselves. The highest inter cluster distance of 9.37 was observed between cluster VI and III followed by 8.22 between cluster VI and V, 7.75 between cluster V and I suggesting wide diversity between Them and the genotypes in these cluster could be used as parents for new hybrid development. These findings were supported by [14] and [15]. The minimum inter cluster distance (2.923) observed between cluster III and IV.

The highest intra cluster distance was computed for cluster V (0.841) followed by cluster I (0.721). The cluster II showed the least intra cluster distance (0.472) which indicated that the genotypes in this cluster were more or less homogeneous.

Table 2. *Intra (bold) and inter-cluster distances of 64 inbred lines of maize.*

Clusters	I	II	III	IV	V	VI
I	0.721					
II	3.12	0.472				
III	6.94	4.79	0.523			
IV	4.52	2.97	2.92	0.706		
V	7.75	7.13	4.89	4.63	0.841	
VI	3.98	6.48	9.37	6.66	8.22	0.626

3.3. Principal Coordinate Analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distances were made with E 52 (Table 3). The genotype E 52 made the top two and 4th highest genotypic distance with the genotype E 15(2.412), E16 (2.375) and E 38 (2.343) respectively. The third one was recorded in between genotype E 16 and E 55 (2.350). The lowest distance was found in between E 06 and E 08 (0.137) followed by E 41 and E 42 (0.159), E 34 and E 35 (0.176). The difference between the highest and lowest inter genotypic distance indicated the enormous variability among 64 genotypes of maize studied.

Table 3. *Ten highest and ten lowest inter genotypic distances among the 64 genotypes of maize.*

Inter genotypic distance					
SI. No.	**Genotypic combination**	**Highest distance**	**SI. No**	**Genotypic combination**	**Lowest distance**
1.	E15 and E52	2.412	1.	E06 and E08	0.137
2.	E16 and E52	2.375	2.	E41 and E42	0.159
3.	E16 and E55	2.350	3.	E34 and E35	0.176
4.	E38 and E52	2.343	4.	E51 and E53	0.192
5.	E15 and E55	2.322	5.	E07 and E13	0.195
6.	E16 and E54	2.305	6.	E54 and E55	0.202
7.	E15 and E46	2.258	7.	E11 and E40	0.210
8.	E15 and E54	2.256	8.	E06 and E13	0.212
9.	E39 and E52	2.254	9.	E33 and E42	0.214
10.	E38 and E55	2.212	10.	E07 and E28	0.214

4. Construction of Scatter Diagram

Based on these values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1.Z_2) using component scores 1 as X axis and component scores 2 as Y axis was constructed which has been presented in Figure 1. The positions of the genotypes in the scatter diagram were apparently distributed into six groups which indicated the existence of considerable diversity among the genotypes. Significant genetic diversity in maize was also investigated by [12], [13].

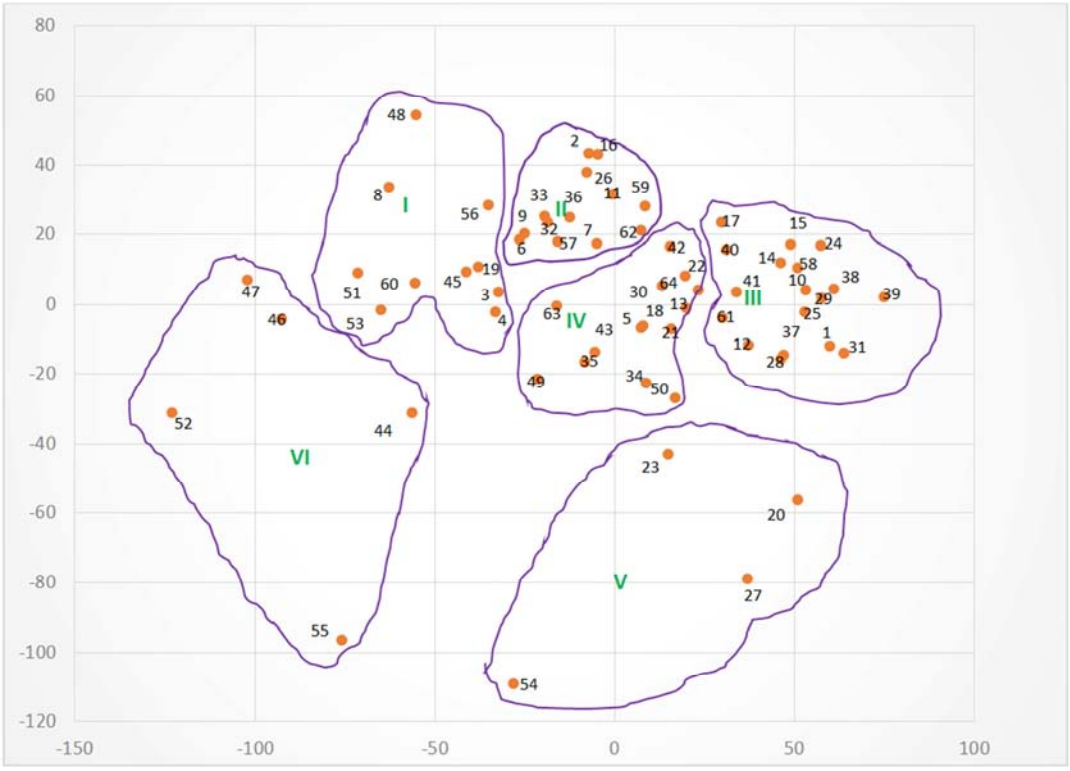

Figure 1. *Scatter distribution of 64 maize inbreds based on their principal component scores superimposed with clustering (1….. 64= serial no. of maize inbred lines).*

4.1. Cluster Mean

Mean values of cluster for yield and its different contributing characters were presented in the Table 4. It appeared that the early maturing genotypes were included in the cluster V (147.75) followed by cluster VI(149). The highest days to maturity was recorded in cluster II (153.80) followed by cluster IV (153.29). The dwarf genotypes were included in the cluster II (85.38) followed by cluster III (88.08) and the tallest genotypes included in the cluster V (156 cm) followed by cluster IV(106.71). The highest ear height identified in cluster VI (23.97 cm) followed by cluster I (16.47cm). The lowest ear height were included in cluster III (26.22 cm) and the highest in cluster VI (77.92 cm). The bold grain size was found in cluster VI (360.80 g) followed by cluster I (338.80g) and the smallest in cluster III (244.11g).

The highest yield was produced by the cluster VI (4.72 t/ha) followed by cluster I (3.77 t/ha) and that of the lowest yield was recorded in the genotypes of the cluster II (2.66

t/ha) followed by cluster III (2.77 t/ha). Considering all the characters it appeared that the genotypes in the cluster VI had good performance. The genotypes in this cluster had relatively shorter growth duration, lower days to 50% female flowering, bold grain size and the maximum yielding ability. Cluster I also showed intermediate grain size and reasonable yielding capacity. These findings were in accordance with [16] and [12].

Table 4. *Cluster means for 10 different characters of 64 inbred lines.*

Characters	Clusters					
	I	II	III	IV	V	VI
Days to 50% tasseling	100.20	99.38	96.94	93.21	89.75	91.00
Days to 50% pollen shedding	102.10	102.31	100.44	96.43	93.50	93.60
Days to 50% silking	104.70	105.15	102.44	98.29	95.25	95.80
Plant height (cm)	101.26	85.38	88.08	106.71	156	149.16
Ear height (cm)	49.56	27.31	26.22	38.06	66.25	77.92
Days to maturity	153.80	156.62	152.56	153.29	147.75	149
Cob length (cm)	16.47	9.71	9.00	12.17	12.54	23.97
Cob diameter (cm)	2.68	1.77	1.72	2.08	2.19	3.43
TSW (g)	338.80	308	244.11	280.71	246.25	360.80
Yield (t/ha)	3.77	2.66	2.77	3.09	3.03	4.72

4.2. Contributions of Characters Towards Divergence

Contributions of characters towards divergence were estimated through canonical variate analysis. In this method, vectors of canonical roots were calculated to represent the genotypes in the graphical form [17]. The coefficients pertaining to the different characters in the first two canonical roots are presentedinTable 5. The positive absolute values of the two vectors revealed that ear height, ear diameter and yield (t/ha) had the greatest contribution to genetic divergence. The negative values for the two vectors for days to 50% tasseling, ear length and thousand seed weight (TSW) indicated the least responsibility of both the primary and secondary differentiations. However, the positive absolute values of vector-1and negative absolute value for vector-2 for the characters like days to pollen shedding, days to maturity indicated the responsibility of primary differentiation. It was supported by [13]. Responsibilities of secondary differentiation were noticed in days to 50% silking and plant height.

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

Sl. N0.	Characters	Vector I	Vector II
I	Days to 50% tasseling	- 0.3656	- 0.0337
II	Days to 50% pollen shedding	0.3481	- 0.0031
III	Days to 50% silking	- 0.0126	0.0088
IV	Plant height (cm)	- 0.0204	0.0390
V	Ear height (cm)	0.0145	0.0352
VI	Days to maturity	0.0693	- 0.0582
VII	Ear length (cm)	- 0.1244	- 0.0658
VIII	Ear diameter (cm)	0.6630	0.4803
IX	TSW (g)	- 0.0684	- 0.0190
X	Yield (t/ha)	0.3620	0.3744

According to [1], [18], [19] genetically distant parents usually able to produce higher heterosis. [20] reported that the clustering pattern could be utilized in choosing parents for cross combinations which likely to generate the highest possible variability for effective selection of various economic traits. The positive absolute values of the two vectors revealed that ear height, ear diameter and yield (t/ha) had the greatest contribution to genetic divergence. From the above findings, the present study indicated that the cluster VI, I, IV and V showed higher distance between them. Parental material selection from those clusters would provide manifestation of heterosis as well as wide range of variation during hybridization.

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