

D² STATISTICAL ANALYSIS OF YIELD CONTRIBUTING TRAITS IN MAIZE (*ZEA MAYS* L.) INBREDS

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Abstract

Investigation was carried out to determine the genetic divergence in the 25 maize inbred lines. Analysis of variance revealed highly significant differences among all the inbreds. Inbreds were grouped into five clusters, indicating the presence of genetic diversity. The clusters I, IV and V had the highest number of inbreds (6). The maximum inter-cluster distance was observed between clusters I and III (19.279) and the highest intra-cluster distance was recorded in cluster III (0.243) and also wide range of variation was observed in cluster mean performance for the characters studied. Intercrossing among the inbreds belonging to clusters II and III was suggested to develop high yielding inbreds with desirable characters.

Introduction

Maize (*Zea mays* L.) is the third most important cereal crop in the world after rice and wheat. It has become an important cereal crop in rice cropping system of Bangladesh. It is cultivated in a wider range of environments than wheat and rice because of its greater adaptability (Kage *et al.* 2013).

The cultivated area and production of maize is increasing day by day due to its yield potentiality (Uddin *et al.* 2008). Maize is a unique crop because of its versatile use and low cost per unit production (Banik *et al.* 2009). Due to its wide utilization, the main goal of maize breeding programs is to develop new inbreds and hybrids that will out yield the existing hybrids with respect to a number of characters (Sreckov *et al.* 2010). High yield potentiality and its multipurpose use as food can be reduced the wheat production area and maize imports. Maize is also the most demandable cereal food of the poultry industry in Bangladesh (Zaman and Alam 2013).

One important approach to improve this research situation is the development of inbred lines which can produce high yielding hybrid varieties. Before hybrid development, prospective inbred line selection is a pre-requisite. For developing high yielding hybrids in maize, inbreds need to be evaluated for their diverged gene pool (Alam *et al.* 2013). In crop improvement programme, genetic diversity is an essential prerequisite for hybridization. Inclusion of diverse parents helps in isolation of superior recombinants. Several methods for multivariate analysis such as D² analysis and cluster analysis have also been reported. An assessment of the nature and magnitude of diversity between lines will help to choose better parents for hybridization. Intercrossing between genetically divergent inbreds is expected to produce superior hybrids and desirable recombinants. Mahalanobis' D² statistic of multivariate analysis is recognized as a powerful tool in quantifying the degree of genetic divergence among the inbreds (Hemavathy *et al.* 2006).

It also helps to identify the suitable inbreds for hybridization programme on the basis of their clustering pattern. The present investigation was undertaken with a view to estimating the nature and magnitude of D² statistical analysis among 25 maize inbred lines.

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Materials and Methods

The study was conducted during November, 2009 to April, 2010 at the experimental field of the Department of Botany, University of Rajshahi, Bangladesh. 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 seven-generation single cross hybrid varieties as source population. The inbred lines were IL-1 to IL-25.

Twenty five maize inbred lines were grown in a randomized block design with three replications during the growing season of 2009 - 2010. The seeds of each entry were sown on 25 November, 2009 in 5 m long one row with spacing of 0.1×0.3 m between rows and hills, respectively. One plant was kept per hill after proper thinning. Recommended doses of fertilizers were applied. Necessary intercultural operations and irrigation were done during the crop period to ensure normal growth, development of the plants and properly to raise the crop uniformly. Bamboo stick support was given to the growing plants and allowed them to creep on a rope nets. Observations were recorded on whole plot basis for days to tasseling (DT), silking (DS) and maturity (DM). Ten randomly selected plants were used for recording observations on plant height (PH), ear height (EH), cob length (CL), cob diameter (CD), number of rows/cob (NRC), number of kernels/row (NKR), number of grains/cob (NGC) and grain yield/plant (GYP).

The analysis was carried out by applying standard statistical techniques for analysis of variance to establish significance level among the inbreds as described by Singh and Choudhary (1985) and Steel and Torrie (1980). Data were subjected to principal component and Mahalanobis (1936) D^2 statistical analysis extended by Rao (1952) using GENSTAT-5 computing soft wares.

Results and Discussion

Mean and coefficient of variation of 11 yield contributing characters in 25 maize inbred lines are presented in Table 1. Analysis of variance exhibited significant differences among the inbreds for all the characters under this investigation. Thus, it indicated considerable amount of genetic divergence among 25 inbreds. Maximum CV% was found in ear height. Hence there is a scope for selecting high yield potential lines. IL-15 took longest period for days to tasseling and the selection of line from a cross took the shortest period for first tasseling. The results showed that IL-4 had the highest number of kernels/row and the lowest in IL-15. IL-24 had the longest cob and IL-2 had the shortest. In case of number of grains/cob, the highest value was obtained in IL-18 and the lowest value in IL-8. For grain yield/plant, IL-1 had the highest yield and IL-4 the lowest (Table 1). Genetic parameters, such as GCV, PCV, $h^2b\%$, GA and GA% were estimated for all the characters under study (Table 1). All the characters showed marked differences between GCV and PCV estimates indicating that substantial variation for these characters was contributed by environmental components. Higher values of GCV for ear height, days to silking, cob diameter, days to tasseling and grain yield indicated higher degree of genetic variability in these traits. Similar results have also been observed by Wannows *et al.* (2010) and Zaman and Alam (2013) in maize inbred lines.

Heritability estimates in broad sense were relatively high for all the characters except cob length. Cob length had low h^2b with low GCV and GA. The GCV alone is not enough in determining the extent of variation, which is heritable. High estimates of $h^2b\%$ along with high GA% for days to silking, ear height and number of kernels/row suggested that improvement of these characters would be effective through phenotypic selection due to additive gene action. High $h^2b\%$ estimates for plant height, cob height, number of rows/cob and number of kernels/row were also reported in maize by Sattar (2003) and Wannows *et al.* (2010).

Table 1. Estimation of mean performance and genetic parameters for grain yields and yield components in maize inbred.

Characters	Mean	CV%	F-test	PCV%	GCV%	h ² b%	GA	GA(% of mean)
Days to tasseling	89.683	5.530	**	21.779	20.201	86.032	29.206	38.599
Days to silking	67.450	7.297	**	28.961	27.990	93.406	37.588	55.727
Days to maturity	104.786	5.263	**	9.738	8.212	71.114	14.949	14.226
Plant height (cm)	104.016	7.450	**	16.148	14.610	81.858	28.325	27.231
Ear height (cm)	47.675	15.328	**	32.055	28.273	77.795	24.491	51.371
Cob length (cm)	11.925	12.622	*	20.03	18.146	57.649	2.764	23.180
Cob diameter (cm)	12.636	12.984	**	24.636	21.142	73.646	4.723	37.376
No. of rows/cob	12.064	12.705	*	21.94	17.956	66.980	3.652	30.273
No. of kernels/row	13.336	13.429	**	19.343	14.524	77.183	8.264	40.189
No. of kernels/cob	155.133	13.661	**	14.718	6.648	66.082	47.624	30.691
Grain yield/plant (g)	71.126	8.466	**	21.477	18.281	72.449	18.588	32.054

*, ** Significant at 5% and 1% level of probability, respectively.

Table 2. Distribution of 25 maize inbred lines in 5 different clusters.

Group/cluster no.	No. of inbred lines	Name of inbred lines present in a cluster
I	6	IL1, IL3, IL5, IL7, IL8, IL12
II	4	IL6, IL9, IL17, IL21
III	3	IL2, IL4, IL22
IV	6	IL10, IL13, IL14, IL15, IL16, IL20
V	6	IL11, IL18, IL19, IL23, IL24, IL25
Total = 25		

Twenty five maize inbred lines were grouped into 5 different clusters by using clustering techniques. The inbred lines distribution is presented in Table 2. The maximum number of inbreds (6) is in clusters I, IV and V which were followed by cluster II (4). The cluster III contained three lines and occupied least position.

The D² analysis carried out involving 25 inbred lines for 11 characters revealed that altogether 5 clusters have been formed (Table 3). The clustering pattern of the lines revealed that the lines collected from the same place did not form a single cluster. Inter and intra-cluster distance ($D = \sqrt{D^2}$) values were worked out from divergence analysis and are presented in Table 3. From the table it was revealed that the inter-cluster distance was larger than the intra-cluster distance indicating wide diversity among the inbred lines of different groups. The maximum intra-cluster distance ($D = 0.243$) was observed in cluster III followed by cluster I ($D = 0.223$) and II ($D = 0.683$). The cluster II contained four inbred and hence, its intra-cluster distance was 0.169. The highest inter-cluster distance ($D = 19.279$) was observed between clusters I and II followed by clusters I and V ($D = 18.844$), clusters I and IV and III and V contained approximately same values, suggesting more variability in genetic makeup of the inbred lines included in these

clusters. These findings were supported by Singh *et al.* (2005), Azad *et al.* (2012) and Zaman and Alam (2013).

The inbred lines belonging to the clusters separated by high statistical distance could be used in hybridization programmes for obtaining a wide spectrum of variation among the segregates. In this context, inbred lines from cluster I and II should be selected as parents in hybridization programmes for yield improvement in maize inbred lines. The distance between clusters III and IV was minimum (3.766) followed by the distance between the clusters II and V (3.986) indicating that the inbred lines belonging to these clusters were comparatively less diverse. These relationships were also reflected in the scatter diagram (Fig. 1). Marker and Krupakar (2009), Azad *et al.* (2012) and Zaman and Alam (2013) reported that the clustering revealed instability due to relatively lesser divergence, where the widely divergent cluster remains distinct in different environments. It is expected that the crosses between the lines of clusters I and II would exhibit high heterosis and also likely to produce new recombinants with desired characters.

Table 3. Average intra- (bold) and inter-cluster distance (D^2) for 25 maize inbred lines obtained on the basis of 11 morphological characters.

Clusters	I	II	III	IV	V
I	0.223				
II	19.279	0.169			
III	8.097	11.205	0.243		
IV	11.627	7.741	3.766	0.164	
V	18.844	3.986	11.232	7.468	0.167

A two dimensional scattered diagram was constructed using principal component score-I (PCA score-I) as “X” axis and principal component II (PCA score-II) “Y” axis, reflecting the relative position (Fig. 1). As per scattered diagram, the inbreds were apparently distributed into five clusters; it was also revealed that the inbreds of cluster IV were more diverse from the inbreds of cluster V and II.

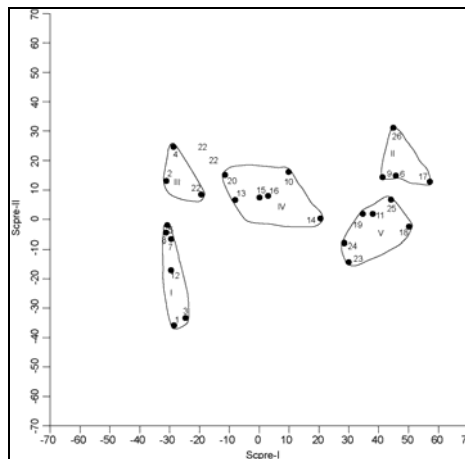


Fig. 1. Two dimensional scattered diagram representing distribution of 25 maize inbreds based on PCA scores superimposed with clustering from D^2 analysis.

The genetic differences between clusters were reflected in their cluster means. Cluster mean values for 11 yield related characters are presented in Table 4. The highest mean values for days to tasseling, silking and maturity, ear length and grain yield/plant were observed in the cluster V. Number of rows/cob, number of kernels/row and number of kernels/cob were found maximum in cluster I and minimum in cluster V. Required minimum days to tasseling, silking, maturity, plant and ear height were observed in cluster II indicating the early and short inbreds in this group. The highest yield was produced by the cluster V and that of lowest yield was produced by the inbreds of the cluster II followed by cluster IV. Considering all the characters it appears that the inbreds in the cluster III had good performance.

The inbreds in this cluster had shorter growth duration, short statured plant, shortest ear height, intermediate grain performance and reasonable yielding ability. Similar results have also been reported by Azad *et al.* (2012) and Zaman and Alam (2013). Hence, for the improvement of different characters *viz.* DT, DS, DM, EL and GYP under the present study, inbred lines should be selected from clusters V, II and III. Contribution of characters towards divergence was obtained from canonical variate analysis (CVA) and is presented in Table 5. In this method, vectors of canonical roots were calculated to represent the inbreds in the graphical form (Rao 1952).

Table 4. Cluster means and relative contributions of 11 characters to the total divergence in maize inbreds.

Characters	Clusters					Vector I	Vector II
	I	II	III	IV	V		
Days to tasseling	64.75	65.55	64.67	65.41	65.88	0.249	0.032
Days to silking	66.73	65.80	64.89	66.21	66.18	0.156	-0.448
Days to maturity	102.40	105.55	101.89	102.31	103.51	0.146	0.512
Plant height	114.40	119.15	105.85	109.55	102.25	-0.148	0.099
Ear height	45.39	49.91	43.84	47.96	49.75	0.365	0.485
Cob length	12.08	13.50	10.93	13.70	11.76	-0.262	0.126
Cob diameter	11.20	10.85	12.10	11.50	11.25	0.295	-0.028
No. of rows/cob	13.75	12.85	12.15	11.90	12.25	-0.400	-0.173
No. of kernels/row	23.55	21.85	23.31	20.50	19.90	0.273	-0.320
No. of kernels/cob	261.56	193.25	230.00	275.70	198.65	-0.439	-0.275
Grain yield/plant (g)	73.23	70.08	71.51	75.14	80.62	0.390	-0.253

The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 4. The values of vector 1 and vector II revealed that both the vectors had positive values for days to tasseling, days to maturity and ear height. These results indicated that these three characters had highest contribution towards divergence among the 11 characters for 25 maize inbred lines. In vector I, other important characters responsible for genetic diversity in the major axis of differentiation were days to silking, days to maturity, cob diameter, number of kernels/row and grain yield/plant while in vector II (the second axis of differentiation) days to tasseling, days to maturity, plant and ear height and cob length contributed positive impact on divergence. Negative values in both the vectors were for number of rows/cob and number of kernels/cob indicated these two characters had lowest contribution to the total divergence. So, the greater divergence in the present materials due to these three characters will offer a good scope for improvement of yield through selection of parents. These results get sufficient validation from the findings of Azad *et al.* (2012) and Zaman and Alam (2013).

High variability existed among the studied maize inbreds. The selection of parents for further breeding programme to the maximum divergent cluster such as cluster I and cluster II, cluster I and cluster V, cluster I and cluster IV in the present study, which would exert high heterosis and wide variability in genetic architecture in subsequent generations. From this study it is evident that the clusters I and II were highly diverged. So, clusters I and II would be more suitable. The lines belonging to the distant clusters could be used in hybridization program for obtaining a wide spectrum of variation among the segregants.

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