

GENETIC DIVERGENCE IN MAIZE (*Zea mays* L.)

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ABSTRACT

Genetic divergence of 25 genotypes of maize were estimated using D^2 and Principal Component Analysis. The genotypes under study fell into five clusters. The inter-cluster distances were higher than intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. The intra-cluster value was maximum in cluster V and minimum in cluster I. The inter cluster D^2 values showed the maximum distance between cluster II and III followed by the distance between II and I. The cluster means were higher for days to maturity, plant height and ear height in cluster II; grain yield per plant was higher in cluster IV. Genotypes were much in use having the above mentioned characters in clusters II and IV would offer a good scope for the improvement of this crop through hybridization and rational selection.

Key words: Maize (*Zea mays* L.), divergence, cluster, Bangladesh

INTRODUCTION

Maize is an important cereal crop, which can supply food, feed, fodder, and fuel for domestic use and also raw materials for use in industry. Among food grain crops, globally maize occupies third position in terms of acreage and production. As a versatile crop, it grows successfully throughout the world covering low land, tropical, sub-tropical, and temperate climatic condition (Elias, 1995). Bangladesh is a country with high population density. To feed this ever growing number of people there is a need to increase productivity so that more cereals can be produced from the same area of land. Only maize can yield more than rice and wheat (Elias, 1995).

Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at the intra-cluster and inter-cluster levels (Murty and Arunachalam, 1966; Ram and Panwar, 1970; Sachan and Sharma, 1971; Jatasra and Paroda, 1978). The corn breeders are consistently emphasizing the use of diverse genotypes as a significant factor contributing to high yielding synthetic or hybrid varieties (Ahloowalia *et al.*, 1963). Such a study also permits selection of genetically diverge parents to obtain the desirable recombinant in the segregating generations. Therefore, the experiment

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was undertaken to find out suitable genotypes that could directly be used as a open pollinated variety or parents for hybrid or synthetic variety for this country.

MATERIALS AND METHODS

Twenty-five genotypes of maize (*Zea mays* L.) collected from CIMMYT, Mexico were grown in a randomized block design with 3 replications at Bangladesh Agricultural Research Institute, Gazipur-1701 in the rabi season of 2000. The seeds were sown on November 2000. The unit plot size was 5m long and intra row spacing was 75 cm and 25cm with one plant in each hill. Fertilizers were applied at the rate of 250: 120 :120 : 40: 5 kg N, P₂O₅, K₂O, S and Zn, respectively. The intercultural operations were done timely to raise a good crop. Observations were recorded from 10 randomly selected plants in each plot for days to silking, days to maturity, plant height, ear height, husk cover and grain yield per plant. The data were subjected to Principal Component Analysis and Mahalanobis's D² analysis using Genstat 513 program. The genotypes were grouped into several clusters following the method discussed by Tocher (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance on the basis of plant mean revealed significant differences among the genotypes for all the characters studied indicating a considerable amount of genetic variability for all the characters and, therefore, diversity analysis was carried out.

The distribution pattern in the D² analysis indicated that 25 genotypes fell into five clusters (Table 1). The maximum number of genotypes (11) were grouped in to cluster V followed by cluster I (7), whereas minimum number (1) in to cluster III followed by cluster II. The cluster IV consists of four genotypes. Smith (1990) reported 3 groups in a divergence study of 48 maize cultivars.

Table 1. Distribution of maize genotypes to different clusters in the D² analysis

Clusters	No. of genotypes	Genotypes (Origin)
I	7	MMH9901 (Indian), MMH9856 (India), CTS971004 CA14503XCA03117, CTS971006 CA03113XCA03115, CTS971008 CA031101XCA114502, CTS971012 CA03104XCA03116, CTS971024 CA03115XCA114501
II	1	Ghauri (Pakistan)
III	2	PSC-4212 (India), NSX982023 (Thailand)
IV	4	LVN-25 (Vietnam), CTS971016 CA14504XCA03116, CTS971020 CA03114XCA114505, CTS971022 CA03114XCA14506
V	11	BHM-1, Pasific-700, Yun97Q-19 (China), NSx982029, IRSC706 (Iran), Tongdan 202 (China), DK 999 (Thailand), CTS971002 CA14503XCA14501, CTS971010 CA03101XCA03113, CTS971014 CA14507XCA03116, CTS971018 CA14505XCA03113

The pattern of clustering revealed that the genotypes originated from same country did not form a single cluster. This indicates that geographic diversity is not always related to genetic diversity. Similar results have been reported by Das and Gupta (1984) in black gram and Mian *et al.* (1991) in Pea. Likewise the genotypes of similar origin were grouped in different clusters.

The intra and inter cluster values among the five clusters are presented in Table 2. The inter cluster D^2 values varied from 16.716 to 57.022 indicating high range of diversity present among the genotypes. The highest inter cluster divergence was noted between cluster II and III followed by I and II. It indicated that the genotypes grouped in these clusters were highly divergent from each other. Selection of parents from the highly divergent clusters is expected to manifest high heterosis in crossing and also wide variability in genetic architecture. Murty and Anand (1966) claimed that there is a positive relationship between the specific combining ability and the degree of genetic diversity. The intra cluster D^2 values varied from zero (cluster II) to 9.387 (cluster V). However, cluster II had only one genotype whereas cluster V with eleven entries.

Table 2. Inter and intra (bold) cluster distances in maize obtained by canonical variate analysis

Cluster	I	II	III	IV	V
I	7.949	52.599	21.916	36.600	20.349
II		0.00	57.022	16.716	32.773
III			3.658	44.521	28.184
IV				6.758	17.660
V					9.387

Table 3. Cluster mean values for yield contributing characters of maize

Characters	I	II	III	IV	V
Days to silking	95.00	96.00	90.50	96.59	97.58
Days to maturity	149.48	150.67	148.00	149.00	149.70
Plant height	163.48	209.33	174.00	193.42	182.27
Ear height (cm)	89.29	115.00	70.66	110.25	96.61
Husk cover	2.47	2.00	2.50	2.25	2.27
Grain Yield	4.17	4.51	4.80	5.12	4.83

The cluster mean for five characters is presented in Table 3. Cluster II had maximum number of characters (3) having highest intra cluster means.

Contributions for the characters towards divergence are presented in Table 4. The canonical analysis revealed that, values in both the vectors (Vector I and II) for Plant height (0.0.89 and 0.427), ear height (0.42 and 0.907) and grain yield/plant (0.00 and 0.344) were found positive. Such results indicate that these characters contributed maximum towards divergence of the genotypes. Jagadev and Samal (1991) and Patel *et al.* (1989) reported that plant height and seed yield were higher contributors towards diversity in niger and safflower, respectively. Thiagarjan *et al.* (1988) observed that plant height as higher contributor in cowpea.

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

Characters	Vector I	Vector II
Days to silking	0.878	-0.479
Days to maturity	0.345	-0.272
Plant height	0.089	0.427
Ear height (cm)	0.420	0.907
Husk cover	0.086	-0.243
Grain Yield	0.000	0.344

On the basis of the findings of the present study, it can be recommended that the genotypes from cluster III, IV and V can be selected for hybridization for high yield.

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