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GENETIC DIVERGENCE OF EXOTIC INBRED LINES OF MAIZE (*Zea mays.* L)

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Abstract

Sixty exotic inbred lines of maize from CIMMYT were characterized for a few morphological attributes and grain yield at the experimental field of Bangladesh Agricultural Research Institute (BARI) during 2013-14. The inbred lines of the existing investigation were grouped into five distinct non-overlapping clusters based on D^2 analysis. Cluster II was comprised of the highest number of inbreds whilst cluster III and IV included the lowest number of inbreds. The inter cluster distance was higher than intra cluster distance suggesting wider genetic diversity among the genotypes of different groups. The highest inter-cluster distance was exhibited between clusters II and V (D^2 = 15.40) and the lowest inter-cluster distance was observed between clusters I and II (D^2 = 2.82). Cluster II exhibited the highest mean values for cob length and cob diameter, cluster V for number of grain /cob and total grain weight. The lowest mean value for plant height & ear height were found in cluster II and cluster IV for days to pollen shedding and days to silking. Days to silking, plant height, cob length (cm), number of rows /cob, number of grains /cob showed maximum contribution towards total divergence among different characters. The inbred lines were characterized for their morphological traits and kernel yield to achieve more heterotic partners to get higher heterosis.

Keywords: Cluster, genetic diversity, inbred lines, maize.

Introduction

Importance of maize in Asia's cropping systems has grown rapidly in recent years. In rice based cropping system of Bangladesh, it has become an prominent cereal crop. Hybrid is playing an important role in agrarian economy of Bangladesh than synthetic and composite varieties due to its higher yield potentiality. The hybrid varieties which are currently planted throughout the country are imported mostly from India, China, and Thailand. Development of local hybrids will reduce import and farmers would also be able to get quality seeds cheaply and timely. Genetic diversity is one of the useful tools to select appropriate genotypes/lines for hybridization. Diverse parents are expected to yield higher frequency of heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. (Seshu *et al.,* 2014). The

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quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents for hybrid production (Azam *et.al.*, 2013).

For improving the crop plant, knowledge of diversity among elite breeding materials undoubtedly plays an important role. Maize breeders are mainly concerned with the genetic diversity among and within breeding population and elite germplasm, because it largely determines the future prospects of success in breeding programs. In hybrid maize breeding, characterization of genetic diversity of maize germplasm is of great importance. D^2 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 (Seshu *et al.*, 2014). Therefore, the experiment was undertaken to find out suitable inbred lines that could directly be used as parents for hybrid or synthetic variety.

Materials and Methods

Sixty inbred lines were (VL109190, VL109196, VL109198, VL05590, CML254, VL109249, VL109252, VL109262, VL109279, CML162, CML163, CML171, VL109499, CML192, VL109482, CML189, VL1016220, VL1037, VL109579, CML154, VL06679, CML429, CML427, CML473, VL109293, CML465, CML287, CLQRCYQ-70, CML481, CML191, CML164, CML170, CML193, CML172, CML451, CML-181, CML-161, CLQRCYQ-59, CLG-1837, CLRCY-017, CLO-2450, CLO-2720(CML-551), CML-451, CML-165, CLQRCWQ-10, CLQRCWQ-261(CML-555), CML-502, CML-491, CML-287, CML-298, CML-285, CML-429, CML-425, CML-431, CML-430, CML-486, CML-480, T046-1024, CML-511, CLQRCYQ-74) tested from october 2013 to april 2014 at Bangladesh Agricultural Research Institute, Gazipur 1701 to assess their morphological characterization in terms of days to 50% pollen shedding, days to 50% silking, days to maturity, anthesis silking interval (ASI), plant height, ear height, cob length, cob diameter, number of rows/cob, number of grains /cob and for total grain weight.

The geographical location of the experimentations was 24.00"N latitude, and 900.25"E longitude at AEZ 28 with an elevation of 8.4 meter from the sea level (Anon., 1989). The experimental site is situated in the subtropical zone. The soil was sandy loam in texture, with good fertility status and PH of around 6.3. The experimental site belongs to the ‘Shallow red-brown terrace’ soil of Madhupur tract (Haither *et al.*, 1991). This experiment was laid in RCBD design with two replications. Unit plot size was 5 m long maintaining 75 cm and 20 cm spacing between rows and hills, respectively. Fertilizers were applied @ 120,35,70,40,5 and1.5 kg/ha of N, P, K, S, Zn and B, respectively. After proper thinning one healthy plant was kept in each hill. Undesirable and off type plants from each line were rouged out before flowering. Standard agronomic practices were followed to raise a good crop. Genetic diversity was estimated using software of

GENSTAT GENWIN42 version as per Mahalanobis D^2 statistics (Mahalanobis, 1936).

Results and Discussion

Mean, range, standard deviation and co - efficient of variation (cv) of 11 individual characters of the observed inbred lines were quantified in table 1 before diversity analysis. Maximum variation was set up in anthesis silking interval followed by grain weight (gm), ear height (cm) and number of grains /cob, respectively. Similar results have also been reported by Hosen et al. (2014). So, there is plenty of scope for selection of potential inbred lines for effective hybridization.

Table 1. Range, mean, standard deviation and co-efficient of variation among different characters of 60 maize inbred lines at BARI, Joydebpur during rabi 2013-14

Characters	Mean	Range		Standard Deviation	CV%
		Min	max		
Days to pollen shedding	96	84	112	8.48	8.82
Days to silking	99	87	114	8.00	8.11
Anthesis silking intervel	2	-3	5	1.34	55.95
Days to maturity	136	125	149	8.32	6.10
Plant height (cm)	124	84	166	19.85	16.03
Ear height(cm)	54	24	91	15.07	27.87
Cob length(cm)	13	7	19	2.25	17.35
Cob diameter(cm)	12	9	15	1.16	9.42
No. of rows/ cob	12	10	16	1.41	11.71
No of grain /cob	17	10	27	3.84	22.41
Total grain weight (gm)	404	300	800	135.3	33.49

Cluster analysis

According to cluster analysis all the sixty maize inbred lines were grouped into five distinct non-overlapping clusters based on various morphological traits. The discrimination of genotypes into discrete clusters suggested presence of high degree of genetic diversity in the materials evaluated. Earlier workers, Pandey (2013) reported substantial genetic divergence in the pigeon pea materials. The distribution pattern indicated that maximum 20 inbreds were included in cluster II followed by 19 in cluster I. The reminder have been distributed in three clusters: 9 in cluster IV and 6 each in cluster III and V (Table 2). Mustafa *et al.* (2015) grouped forty maize genotypes into 4 clusters.

Table 2. Distribution of 60 inbred lines in five different clusters

Cluster	No of Inbreds	Inbred lines included in different cluster
I	19	VL109196, VL05590, VL109262, VL109482, VL1037, VL109579, CML254, CML162, CML287, CML189, CML191, CML164, CML170, CML491, CML285, CML429, CML425, T0461024, CLQRCWQ10
II	20	VL109190, VL109198, VL109252, VL109249, VL109279, CML163, CML171, CML192, VL109499, VL109293, VL06679, VL1016220, CML154, CML429, CML427, CML473, CML451, CML481, CML193, CML172
III	6	CML465, CLQRCYQ70, CLQRCY017, CML165, CML511, CML181
IV	9	CLQRCYQ74, CML161, CLG1837, CML551, CML502, CML287, CML298, CML431, CML480
V	6	CLQRCYQ59, CLO2450, CML451, CML430, CML486, CML555

Estimates of intra and inter-cluster squared distance (d^2)

The statistical distance represents an index of genetic diversity amongst cluster. Average intra and inter-cluster D2 values among the 60 genotypes revealed that cluster III showed minimum intra cluster value (0.53) indicating that the genotypes within this cluster were similar (Table 3), while cluster I showed maximum intra cluster D2 value (0.76) followed by cluster V (0.61) thereby, revealing the existence of diverse genotypes in two clusters. The inter cluster D2 values ranged from 2.81 to 15.40. The lowest inter-cluster distance was observed between clusters I and II (D^2= 2.82), indicating that inbred lines between these clusters were in genetically close relationship. Crossing of genetically close inbred lines may not produce high yielding hybrids. The highest inter-cluster distance was exhibited between clusters II and V (D^2 = 15.40) followed by clusters III and V (D^2 = 14.49) indicating wider genetic divergence from each other. Hence inter-mating between inbred lines between these may give high heterotic response and thereby better hybrids. These findings are in conformity with the findings of Meena *et al*. (2014), Ganesan *et al*. (2010) and Marker and Krupakar (2009).

Table 3. Inter and intra (bold) cluster distance for 60 maize inbred lines

Cluster	I	II	III	IV	V
I	**0.760**				
II	2.818	**0.589**			
III	3.131	3.716	**0.531**		
IV	5.938	8.375	7.308	**0.587**	
V	12.932	15.402	14.486	7.379	**0.613**

Singh and Chowdhury (1985) suggested that three points should be considered while selecting genotypes for breeding program: i) choice of particular cluster from which genotypes are to be used as parents, ii) selection of particular genotypes from the selected clusters and iii) relative contribution of characters to total divergence. The cluster mean values of all characters for 60 maize inbred lines are presented in Table 4 which indicated the comparison of cluster means for eleven different characters. Cluster II exhibited the highest mean values for maximum number of characters viz. days to pollen shedding, days to silking , days to maturity, cob length and for cob diameter. Cluster III exposed the highest means for plant height and number of rows /cob. Under cluster V the highest mean value appeared in characters of anthesis silking interval, ear height, no of grains /cob and grain weight. Concomitant result has also been reported by Marker and Krupakar (2009), Meena *et al*. (2014) in maize. Cluster II had the lowest mean value for plant height and ear height and cluster IV for days to pollen shedding and days to silking.

Table 4. Cluster mean value of 60 maize inbred lines of maize

Characters	Cluster				
	I	II	III	IV	V
Days to pollen shedding	99.47	101.30	91.00	87.22	87.67
Days to silking	101.2	103.55	94.00	90.33	90.83
Anthesis silking intervel	1.79	2.25	3.00	3.11	3.17
Days to maturity	138.89	142.60	130.00	126.89	128.17
Plant height (cm)	121.26	110.30	152.17	131.11	138.17
Ear height(cm)	53.11	40.75	70.83	63.11	71.17
Cob length(cm)	12.84	13.45	12.67	12.78	12.83
Cob diameter(cm)	12.32	12.45	12.17	12.33	12.17
No. of rows/ cob	12.53	11.90	13.33	12.89	13.00
No of grains /cob	17.89	15.75	16.50	17.22	19.83
Total grain weight (gm)	372.42	311.30	306.67	522.22	733.33

Table 5 represents contributions of eleven characters of 60 inbred lines towards divergence. The canonical variate analysis disclosed that the foremost characters were days to pollen shedding, days to silking, anthesis silking interval, days to maturity, plant height, cob length (cm), number of rows/ cob and number of grains /cob for major vector I. Similar results have also been reported by Azad et *al. (*2012) for days to maturity, cob length (cm), cob diameter (cm) and grains / ear. These were the salient characters in the major axis of differentiation for genetic divergence. The prime characters in vector II which was the second axis of differentiation were days to silking, plant height (cm), ear height(cm), cob length(cm), number of rows /cob, and number of grains /cob . The role of days to silking, plant height, cob length (cm), number of rows /cob, number of grains /cob for both the vectors were positive across two axis which is the indication of the important components of genetic divergence in this materials. Similar results have also been reported by Hosen *et al.* (2014) and Azad *et al.* (2012).The greater divergence in the present material due to those characters will offer a good scope for improvement of yield through rational selection of parents for producing heterotic hybrids.

Table 5. Relative contribution of the 11 characters to the total divergence in maize

Characters	Vector I	Vector II
Days to pollen shedding	0.00219	-0.01783
Days to silking	0.00249	0.02115
Anthesis silking intervel	0.00319	-0.04692
Days to maturity	0.02578	-0.07417
Plant height (cm)	0.00160	0.01103
Ear height(cm)	-0.04893	0.04759
Cob length(cm)	0.00369	0.04630
Cob diameter(cm)	-0.14683	-0.09538
No. of rows/ cob	0.18096	0.16798
No. of grains /cob	0.03949	0.01353
Total grain weight (gm)	-0.03297	-0.00809

Conclusion

The main intention of maintenance and characterization of new exotic inbreed line was to select deviant inbred lines for significant hybridization schedule. Sixty inbred lines were grouped into five different clusters. Maximum heterosis can be achieved by crossing the parents selected from most divergent clusters. So, crosses between the inbreds of cluster V with those of cluster II would be expected to exhibit high heterosis with recombinants of desired characters in maize

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