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## Assessment of genetic diversity in inbred lines of maize (*Zea mays* L.) and its relationship with heterosis

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### Abstract

The genetic divergence among thirteen genotypes of maize were estimated by using Mahalanobis  $D^2$  statistic for ten characters. The genotypes were grouped into three clusters. Cluster I comprised 11 parental genotypes (CLQR, VL111, R4093, R6429, S8481, S8200, CML490, HK1, WLS, CLQRC and G18), while Cluster II (CLQ25) and III (CG18) were mono-genotypic. The highest inter cluster distance was recorded between cluster II and III (4.88) followed by cluster I and III (4.67). Maximum genetic distance was observed between the parents WLS and G18, whereas minimum distance was observed between the parents VL111 and S8481 suggesting more variability in genetic makeup of the genotypes included in these clusters. Cluster I comprising of 11 genotypes have maximum mean values for number of kernels per row and number of kernels row per cob while minimum mean values for plant height and ear height. Cluster II containing only CLQ25 have maximum mean values for ear girth and grain yield per plant. The highest contribution in the manifestation of total genetic divergence was exhibited by grain yield per plant (28.63%) followed by ear girth (28.47%), ear length (19.23%), number of kernel per row (11.50), number of kernels row per cob (10.04). Out of 30 crosses, 11 crosses showed positive significant heterobeltiosis for grain yield per plant. The crosses CLQ25 × CLQR and WLS × R4093 belongs to high divergent class. It could be concluded that genetic diversity can be utilized as a reliable parameter for predicting heterosis in hybrids.

**Keywords:** genetic diversity, mahalanobis  $d^2$ , genetic distance, heterobeltiosis

### 1. Introduction

Maize (*Zea mays* L.) is one of the oldest crop and most important food grain in the world as well as in developing countries. It is the highest yielding grain crop having multiple uses. It occupies a prominent position in global agriculture after wheat and rice. In India, maize ranks third next to rice and wheat. The nutritional qualities of maize are on par with other cereals in most of the aspects. The maize kernel contains approximately 60-70 % carbohydrates, 9-11 % crude protein, 2-3.5 % crude fiber, 3-5 % lipids and 20 mg of Ca/100g of kernels. In any crop improvement programme, assessment of genetic diversity is an essential prerequisite for identifying potential parents for hybridization. Maize acreage and production have shown an increasing trend with the introduction of hybrids due to their high yield potential. Before hybrid development, prospective parent (inbred line) selection is a pre-requisite. Several studies on maize have shown that inbred lines from diverse stocks tend to be more productive than crosses of inbred lines from same variety (Vasal, 1998) [23]. Manifestation of heterosis usually depends on the genetic divergence of the two parental lines (Saxena *et al.*, 1998) [19]. The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents for hybrid production. Diverse parents are expected to yield higher frequency of heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations.  $D^2$  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 in intra and inter-cluster level (Murty and Arunachalam, 1966; Ram and Panwar, 1970; and Sachan and Sharma, 1971) [13, 15, 18]. The present study was therefore undertaken to analyze the genetic divergence of maize genotypes.

## 2. Materials method

Thirteen genotypes of maize (*Zea mays* L.) were grown in Randomized Block Design with three replications at TCA, Dholi, Centre, Muzaffarpur, India, during *rabi*, 2017-2018. Each entry was sown in a two row of 4m length. The spacing between row to row was 75 cm and plant to plant was 25 cm. Observations were recorded on five randomly selected plants in each entry and in each replication for days to 50 per cent tasseling, days to 50 per cent silking, days to 50 per cent brown husk, plant height (cm), ear height (cm), cob girth (cm), cob length (cm), number of kernel rows per cob, number of kernels per row, yield per plant. The data were subjected to Mahalanobis D<sup>2</sup> analysis. Genetic diversity was estimated as per Mahalanobis D<sup>2</sup> statistics (Mahalanobis, 1936) [10] and clustering of genotypes was done according to Tocher's method as described by (Rao, 1952) [16].

## 3. Results and discussion

The genetic divergence among 13 maize genotypes was estimated for 10 characters, viz., Plant height, Ear height, days to 50 % tasseling, days to 50 % silking, days to 50 % brown husk, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, grain yield per plant. Based on this analysis, all the genotypes were grouped into three clusters on the basis of Tocher's method of clustering utilizing D<sup>2</sup> values (Table 1.0). Cluster I comprised 11 parental genotypes (CLQR, VL111, R4093, R6429, S8481, S8200, CML490, HK1, WLS, CLQRC, G18), while Cluster II (CLQ25) and III (CG18) were monogenotypic. Similar approach was adopted earlier by various researchers (Singh and Chaudhary, 2001; More *et al.*, 2006; Bhoite and Dumbre, 2007; Farzana *et al.*, 2007; Alam and Alam, 2013; Singh *et al.*, 2019) [21, 12, 5, 7, 1, 22]. Genetic diversity is generally associated with geographical diversity, but the former is not necessarily directly related with geographical distribution. A comparison of the mean values of ten traits for different clusters showed considerable differences among them (Table 2.0). Cluster I comprising of 11 genotypes have maximum mean values for number of kernels per row and number of kernels row per cob while minimum mean values for plant height and ear height. Cluster II containing only CLQ25 have maximum mean values for ear girth and grain yield per plant. Cluster III containing only CG18 have minimum mean values for days to 50% tasseling, days to 50% silking, days to 50% brown husk while, maximum mean values for ear length. These findings are in accordance with (Singh *et al.*, 2005; Marker and Krupakar, 2009; Alam and Alam, 2013; Singh *et al.*, 2019; Kushwaha *et al.*, 2020) [20, 11, 1, 22, 9]. The highest inter cluster distance (Table 3.0) was recorded between cluster II and III (4.88) followed by cluster I and III (4.67). The lowest inter cluster distance was observed between cluster I and II (4.62). The intra-cluster distance for cluster I was found 4.37 while intra-cluster distance of cluster II and

III were found zero. The genetic distance between parents (Table 4.0) varied from 2.38 to 4.89. Maximum genetic distance was observed between the parents WLS and G18, whereas minimum distance was observed between the parents VL111 and S8481. Similar findings were reported by (Farzana Jabeen *et al.*, 2007; Nehvi *et al.*, 2008; Singh *et al.*, 2019; Kushwaha *et al.*, 2020) [7, 14, 22, 9] in case of maize. The contribution of traits under study towards divergence is summarized in Table 5.0. The highest contribution in the manifestation of total genetic divergence was exhibited by grain yield per plant (28.63%) followed by ear girth (28.47%), ear length (19.23%), number of kernel per row (11.50), number of kernels row per cob (10.04). The contribution of remaining traits in manifestation of genetic divergence was low or zero. Similar observation was recorded by (Anderson, 1957; Rao, 1952; Nehvi *et al.*, 2008; Rigon *et al.*, 2015; Ganesan *et al.*, 2010; Singh *et al.*, 2019; Kushwaha *et al.*, 2020) [2, 16, 14, 17, 8, 22, 9].

### Parental genetic diversity and its relationship with heterosis

For choice of parents to be utilized in hybridization programme of any crop, it is believed that genetically divergent parental combinations produce hybrids of high heterotic response, though it may not be the sole factor. Besides, a few parents over a series of cross combinations may produce better F<sub>1</sub>'s, while certain combinations do relatively better or worse than would be expected on the basis of average performance of genotypes involved. Study of Table 6.0 indicated that majority of crosses belong to moderate divergence class. The cross CLQ25 × R4093, CML490 × VL111 and HK1 × VL111 exhibited significant better parent heterosis for maximum number of traits including plant height, days to 50% brown husk, ear length, number of kernels per row and grain yield per plant by CLQ25 × R4093 while, days to 50% brown husk, ear length, ear girth, number of kernels per row and grain yield per plant by CML490 × VL111 and HK1 × VL111. CLQ25 × R4093 and CML490 × VL111 belongs to moderate divergence class while, HK1 × VL111 belongs to low divergence class. This suggests the accumulation of favorable alleles in parents and when they came in hybrid combination given superior performance even in low divergence.

Study of Table 7.0 showed that out of 30 crosses, 11 crosses showed positive significant heterobeltiosis for grain yield per plant. The crosses CLQ25 × CLQR and WLS × R4093 belongs to high divergent class, CLQ25 × R4093, CG18 × R4093, CML490 × CLQR and CML490 × VL111 belongs to moderate divergence class while, R6429 × R4093, S8481 × CLQR, S8200 × CLQR, HK1 × VL111, and CLQRC × VL111 belongs to low divergence class. Similar approach was adopted earlier (Arunachalam *et al.* (1983); Banu *et al.*, (2006); Fan *et al.*, (2004); [3, 4, 6].

**Table 1:** Clustering pattern of 13 inbred lines on the basis of D<sup>2</sup> statistics

Cluster	Number of Genotypes within cluster	Genotypes in cluster
I	11	CLQR, VL111, R4093, R6429, S8481, S8200, CML490, HK1, WLS, CLQRC, G18
II	1	CLQ25
III	1	CG18

**Table 2:** Cluster mean for various traits:

	PH	EH	DFT	DFS	DFBH	EL	EG	NKPR	NKRPC	GY
Cluster I	123.5576	61.6545	81.9091	85.4545	118.0909	9.9697	13.0364	15.4848	11.7576	4.6479
Cluster II	147.6000	73.3667	84.0000	86.3333	123.3333	10.2333	15.2333	14.6667	10.6667	5.4933
Cluster III	124.5000	61.8333	81.6667	85.3333	115.6667	11.2000	14.3333	14.6667	10.0000	5.2633

**Table 3:** Mean intra and inter cluster distance ( $D^2$ ) among three clusters:

	Cluster I	Cluster II	Cluster III
Cluster I	4.37		
Cluster II	4.62	0.00	
Cluster III	6.67	4.88	0.00

**Table 4:** Genetic distance between parents

	CLQR	CLQ25	VL111	CG18	R4093	R6429	S8481	S8200	CML490	HK1	WLS	CLQRC
CLQ25	4.87											
VL111	4.66	4.62										
CG18	4.83	4.88	4.48									
R4093	4.48	4.67	4.13	4.74								
R6429	4.52	4.52	3.55	4.59	4.20							
S8481	3.76	4.05	2.38	4.29	4.54	4.30						
S8200	4.08	4.37	3.87	4.47	4.83	3.56	4.35					
CML490	4.54	4.67	4.61	4.65	4.73	3.68	3.77	4.70				
HK1	4.85	4.81	4.37	4.81	4.41	4.76	4.00	3.91	4.28			
WLS	4.50	4.68	4.29	4.73	4.88	4.04	4.36	4.84	4.81	4.37		
CLQRC	4.77	4.81	4.19	4.86	4.65	4.78	4.43	4.28	4.40	4.84	4.59	
G18	4.57	4.73	4.45	4.75	4.85	4.02	4.20	4.79	4.86	4.42	4.89	4.58

**Table 5:** Contribution percentage of different traits towards total divergence:

S. No.	Source	Contribution %
1	Plant height (cm)	0.03
2	Ear height (cm)	0.01
3	Days to 50% Tasseling	0.24
4	Days to 50% Silking	1.07
5	Days to 50% brown husk (days)	0.78
6	Ear length (cm)	19.23
7	Ear girth (cm)	28.47
8	Number of kernel per row	11.50
9	Number of kernels row per cob	10.04
10	Grain Yield per plant	28.63

**Table 6:** Relationship between parental diversity and heterosis in  $F_1$  crosses

S No	Crosses	Number of characters for which the $F_1$ was heterotic	Cluster to which parents belong		$D^2$ -value	Divergence class
			Line	Tester		
	CLQ25 × CLQR	4	II	I	4.87	High
	CLQ25 × VL111	3	II	I	4.62	Moderate
	CLQ25 × R4093	5	II	I	4.67	Moderate
	CG18 × CLQR	2	III	I	4.83	Moderate
	CG18 × VL111	2	III	I	4.48	Moderate
	CG18 × R4093	2	III	I	4.74	Moderate
	R6429 × CLQR	2	I	I	4.52	Moderate
	R6429 × VL111	4	I	I	3.55	Low
	R6429 × R4093	3	I	I	4.20	Low
	S8481 × CLQR	4	I	I	3.76	Low
	S8481 × VL111	4	I	I	2.38	Low
	S8481 × R4093	4	I	I	4.54	Moderate
	S8200 × CLQR	4	I	I	4.08	Low
	S8200 × VL111	4	I	I	3.87	Low
	S8200 × R4093	4	I	I	4.83	Moderate
	CML490 × CLQR	3	I	I	4.54	Moderate
	CML490 × VL111	5	I	I	4.61	Moderate
	CML490 × R4093	3	I	I	4.73	Moderate
	HK1 × CLQR	4	I	I	4.85	High
	HK1 × VL111	5	I	I	4.37	Low
	HK1 × R4093	4	I	I	4.41	Low
	WLS × CLQR	3	I	I	4.50	Moderate
	WLS × VL111	4	I	I	4.29	Low
	WLS × R4093	3	I	I	4.88	High
	CLQRC × CLQR	3	I	I	4.77	Moderate
	CLQRC × VL111	4	I	I	4.19	Low
	CLQRC × R4093	3	I	I	4.65	Moderate
	G18 × CLQR	3	I	I	4.57	Moderate
	G18 × VL111	3	I	I	4.45	Moderate
	G18 × R4093	3	I	I	4.85	High

**Table 7:** Divergence classes of crosses exhibiting positive significant heterobeltiosis for grain yield per plant

Sl. No.	Crosses	Heterobeltiosis	Divergence class
1	CLQ25 × CLQR	182.38**	High
2	CLQ25 × R4093	176.60**	Moderate
3	CG18 × R4093	175.59**	Moderate
4	R6429 × R4093	204.74**	Low
5	S8481 × CLQR	167.18**	Low
6	S8200 × CLQR	118.27*	Low
7	CML490 × CLQR	186.06**	Moderate
8	CML490 × VL111	215.89**	Moderate
9	HK1 × VL111	176.19**	Low
10	WLS × R4093	179.83**	High
11	CLQRC × VL111	155.74**	Low

#### 4. Conclusion

Genetic diversity analysis was done to find out diverse inbred lines in maize, Genetically diverse parents might be utilized in breeding programme to get heterotic individuals. Thirteen maize inbred lines were clustered into three clusters. The crosses involving parents/inbred lines from most divergent clusters are expected to manifest maximum heterosis and generate wide variability in genetic architecture. Based on the quantitative data, the inbred lines were clustered into three cluster A, B and C. Cluster A accommodated 11 inbred lines namely CLQR, VL111, R4093, R6429, S8481, S8200, CML490, HK1, WLS, CLQRC, G18, while cluster B and C consisted of single inbred lines CLQ25 and CG18, respectively. Majority of crosses belong to moderate divergence class. The cross CLQ25x R4093, CML490 x VL111 and HK1 x VL111 showed heterosis for maximum number of five characters, having  $D^2$  value 4.67, 4.61 and 4.37, respectively.

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