

## Heterosis in relation to genetic divergence in short duration maize (*Zea mays* L.)

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### ABSTRACT

Thirteen lines and three testers were used to produce 39 single cross maize hybrids by line  $\times$  tester mating design. The genetic divergence among thirteen lines and three tester of maize were estimated by using Mahalanobis  $D^2$  statistic for twelve characters. The genotypes were grouped into five clusters. Cluster I comprised 12 parental genotypes ( $L_1, L_2, L_3, L_4, L_5, L_6, L_7, L_8, L_9, L_{11}, L_{12}, L_{13}$ ), while Cluster II ( $T_3$ ), III ( $T_1$ ), IV ( $L_{10}$ ) and V ( $T_2$ ) were mono-genotypic, suggesting more variability in genetic makeup of the genotypes included in these clusters. The correlation coefficients and linear regressions were used to know the effects of parental genetic distance in determining heterosis and *per se* performance of the hybrids. Parental genetic distance exhibited significant negative association and significant linear regression along with very low coefficient of determination with better parent heterosis (BPH) and non-significant with *per se* performance of the hybrids. The present investigation, therefore, the parental genetic distance has significant role in determining heterosis and hybrid performance in kharif maize.

### Introduction

Maize (*Zea mays* L.) is the world's most significant grain crop at present. Maize is India's third most important crop, after rice and wheat. The adaptability of maize grain, as well as its high demand, has resulted in a rapid expansion in global production. Maize kernels contain roughly 60-70 per cent carbohydrates, 9-11 per cent crude protein, 2-3.5 per cent crude fibre, 3-5 percent lipids, and 20 mg of calcium per 100 g of kernels and can be used as direct consumption or processed into food products (Suman *et al.*, 2020). The examination of genetic diversity is a precondition for selecting suitable parents for hybridization in any crop improvement programme. With the development of hybrids, maize acreage and production have

increased because to their great yield potential. As a result, high-yielding hybrid are crucial in maize production. Potential parent selection is required prior to hybrid development. According to Vasal (1998), inbred lines from different stocks likely to be more fruitful than crosses of inbred lines from the same variety. The genetic divergence of the two parental lines usually determines how heterosis manifests (Saxena *et al.*, 1998). The ability to pick genetically diversified parents for hybrid development was made possible by the quantification of genetic diversity using biometrical procedures. Diverse parents should produce a higher frequency of heterotic hybrids as well as a wide range of diversity in segregating generations.

$D^2$  analysis is a valuable method for determining the degree of genetic divergence between biological populations at the genotypic level, as well as determining the relative perspectives of individual components to overall divergence at both the intra- and inter-cluster levels (Suman *et al.*, 2020; Bhadru *et al.*, 2020; Matin *et al.*, 2017).

The goal of this research was to see whether there is a link between the heterotic effect of hybrids and the genetic diversity of parental components in maize.

## Material and Methods

Thirteen phenotypically different inbred lines (used as females) were developed at the International Maize and Wheat Improvement Centre (CIMMYT) in Hyderabad, India and three testers ( $T_1$  from AICRP Ludhiana,  $T_2$  from ANGRAU Hyderabad and  $T_3$  from CIMMYT Hyderabad, used as males) taken for the study. During *rabi* 2019-20, these inbred lines were planted in a single 4-meter-long row and crossed with three testers ( $T_1$ ,  $T_2$ , and  $T_3$ ) utilizing the line  $\times$  tester mating design given by Kempthorne in 1957 to produce 39  $F_1$ s. The 39 hybrids were assessed along with their parents in a randomised block design with three replications at the Irrigation Research Station Farm, Araria, Bihar (India) for the *kharif* 2020 seasons. The experimental plot represent North East Alluvial Plain Zone (BI-2) located at latitude of  $26^{\circ}8'59''$  N, longitude of  $87^{\circ}31'11''$  E and altitude of 47 meters Above MSL.

Seeds from each  $F_1$ s progeny and their parents were planted in two rows of 4 m each, with 0.6 m between rows and 0.2 m between plants within each row. During the crop growing period, the prescribed management methods were followed to ensure a healthy crop. Observations were recorded on twelve quantitative traits from each replication. The traits which were studied include days to 50 % anthesis (days), days to 50% silking (days), anthesis-silking intervals (days), days to 75% brown husk (days), plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), kernel rows per ear, kernels per row, 1000-kernels weight (g) and grain yield ( $\text{kg ha}^{-1}$ ). Out of the twelve quantitative characters, days to 50 % anthesis, days to 50 % silking, anthesis-silking intervals and days to 75% brown husk were recorded on plot basis. Rest of the traits were recorded on the basis of five

randomly chosen plants at appropriate stage. The traits means of the five plants of hybrids and parents were subjected to statistical analysis.

For statistical analysis, the mean of three replications' quantitative attributes was adopted. The data were analysed using the Windowstat 9.2 computer application for divergence analysis (mahalanobis'  $D^2$  analysis). BPH (better parent heterosis) and MPH (mid-parent heterosis) of 39  $F_1$ s hybrids was calculated as follows.

$$BPH = \left( \frac{\bar{F}_1 - \bar{BP}}{\bar{BP}} \right) \times 100$$

Where,  $\bar{F}_1$  = quantitative traits mean of  $F_1$

$\bar{BP}$  = mean of better parent

Genetic divergence between the parents of 39  $F_1$ 's was estimated by Mahalanobis  $D^2$  statistic (Rao, 1952).

## Results and Discussion

Plant height, ear height, days to 50% anthesis, days to 50% silking, anthesis silking intervals, days to 75 per cent brown husk, ear length, ear diameter, kernel rows per ear, kernels per row, 1000 kernels weight, grain yield ( $\text{kg ha}^{-1}$ ) were all used to estimate genetic divergence among thirteen lines and three testers maize genotypes. On the basis of this analysis, all genotypes were divided into five clusters using Tocher's method of clustering based on  $D^2$  values (Table 1.0 and fig. 1). Cluster I comprised 12 parental genotypes ( $L_1$ ,  $L_2$ ,  $L_3$ ,  $L_4$ ,  $L_5$ ;  $L_6$ ,  $L_7$ ,  $L_8$ ,  $L_9$ ,  $L_{11}$ ;  $L_{12}$ ,  $L_{13}$ ), while Cluster II ( $T_3$ ), III ( $T_1$ ), IV ( $L_{10}$ ) and V ( $T_2$ ) 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.*, 2020). Geographic diversity is frequently correlated with genetic diversity, though the latter is not always linked to geographic distribution. The mean values of twelve traits for distinct clusters were compared, and there were significant differences between them (Table 2). Cluster I has the highest mean values for grain yield ( $\text{kg ha}^{-1}$ ), 1000-kernels weight, kernels row per ear, ear diameter, ear length, plant height, ear height, and days to 75% brown husk. Kernels per row and ear length have

minimum mean values in Cluster II, which contains solely T<sub>3</sub>.

Cluster III containing only T<sub>1</sub> have maximum mean value for days to 50 per cent anthesis, days to 50 per cent silking and anthesis- silking intervals while, minimum mean values for grain yield, 1000-kernels weight, ear diameter, plant height, ear height, days to 75 per cent brown husk, kernel rows per year. Cluster IV (L<sub>10</sub>) showed maximum mean for traits namely, kernels per row. These findings are in accordance with (Singh *et al.*, 2005; Marker and Krupakar, 2009; Alam and Alam, 2013; Singh *et al.*, 2019; Sinha *et al.*, 2020).

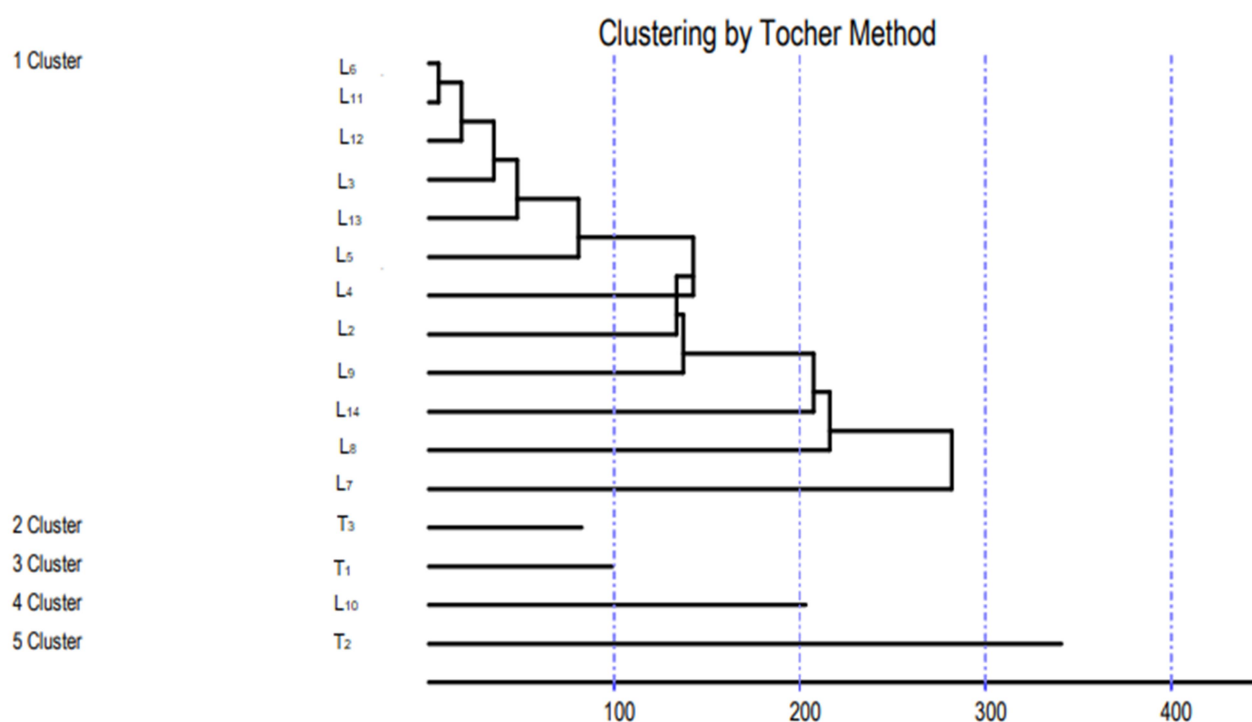
The highest inter cluster distance (Table 2.0) was recorded between cluster II and IV (1585.35) followed by cluster II and V (1423.23). The lowest inter cluster distance was observed between cluster III and IV (353.93). The intra-cluster distance for cluster I was found 182.71 while intra-cluster distance of cluster II, III, IV and V were found zero.

**Table 1: Grouping of parents based on  $D^2$  statistics and Tocher's method of clustering**

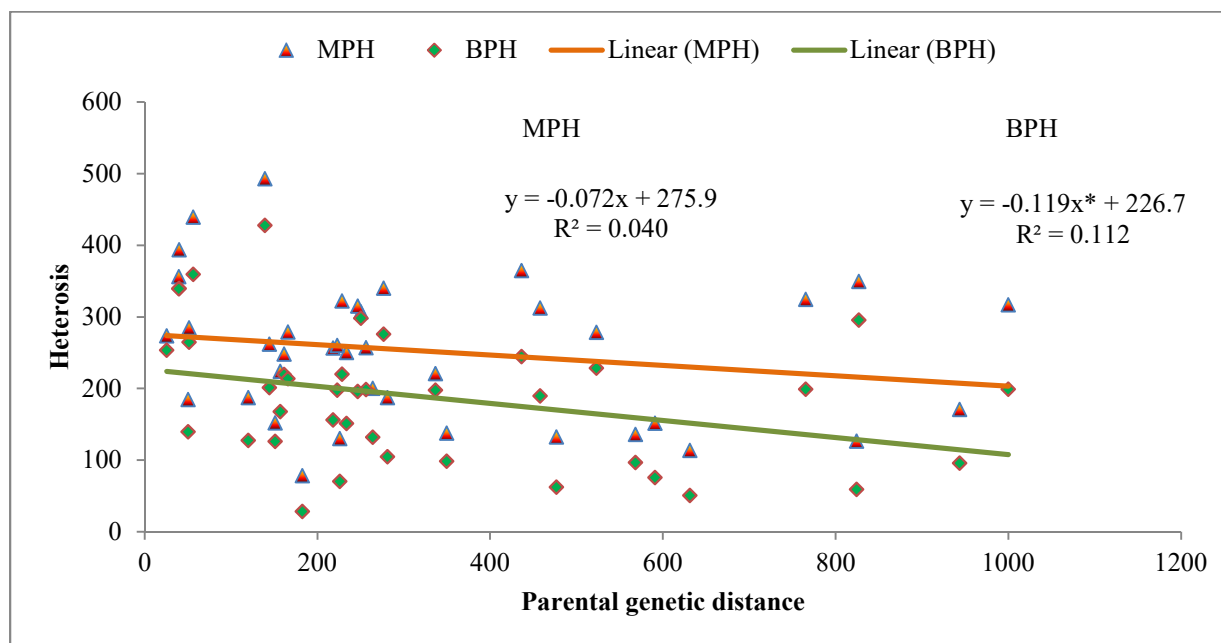
Cluster	Number of genotypes	Cluster composition
I.	12	L <sub>1</sub> , L <sub>2</sub> , L <sub>3</sub> , L <sub>4</sub> , L <sub>5</sub> ; L <sub>6</sub> , L <sub>7</sub> , L <sub>8</sub> , L <sub>9</sub> , L <sub>11</sub> ; L <sub>12</sub> , L <sub>13</sub>
II.	1	T <sub>3</sub>
III.	1	T <sub>1</sub>
IV.	1	L <sub>10</sub>
V.	1	T <sub>2</sub>

**Table 2: Intra and inter-cluster distances pooled over environments**

Cluster	I.	II.	III.	IV.	V.
I.	182.71				
II.	378.09	0.00			
III.	401.75	1018.40	0.00		
IV.	628.36	1585.35	353.93	0.00	
V.	619.98	1423.23	822.40	401.80	0.0



**Figure 1: Clustering of parents based on  $D^2$  statistic and Tocher's methods**



**Fig. 2** Relation of parental genetic distance with heterosis in maize

\*: level of significance at 5 %

### Parental genetic diversity and its relationship with heterosis (Grain yield)

It is believed that genetically divergent parental pairings create hybrids with strong heterotic response, yet this may not be the only criterion in deciding which parents to use in a hybridization programme for any crop. Furthermore, a few parents over a series of cross combinations may generate stronger  $F_1$ s, whereas particular combinations perform better or worse than predicted based on the average performance of the genotypes involved. The person's correlation coefficients were computed parental genetic distance with better parent heterosis and *per se* performance of  $F_1$ s for grain yields. The parental genetic distance between pair of parents of crosses had significant negative correlation with better parent heterosis (BPH) value (-0.34\*) (Table: 3). The linear regressions of parental genetic distance on BPH were significant with  $R^2$  value of 0.112 (Fig. 2). The *per se* performance of  $F_1$ s was little influenced by parental genetic distance as evidenced from non-significant negative correlation and regression, and also very low coefficient of determination (Fig. 3). This indicated that meager variation attributable to BPH and *per se* performance  $F_1$ s could be explained due to parental

genetic distance between pair of parents of crosses (Balestre *et al.*, 2008; Dhliwayo *et al.*, 2009). The relation of *per se* performance of parents on *per se* performance of  $F_1$ s indicates that it were positively correlated (0.30) (Table-3 & Fig. 4). The high yield was due to the high *per se* performance of parents rather than the high parental diversity. As a result, while choosing parents for hybridization, both genetic diversity and high *per se* performance of parents for the desired character should be considered in order to produce a superior varietal hybrid. The diversity of the parents should not be the exclusive criterion for selection. This result is confirmatory with Prasad and Singh (1986), Betran *et al.* (2003), Srdic *et al.* (2007), and Devi and Singh (2011).

**Table 3: Person's correlation coefficient among different parameters in maize**

	$D^2$	MP	BP	$F_1$	Parents
$D^2$	1				
MP	-0.20	1.00			
BP	-0.34*	0.95**	1.00		
$F_1$	-0.06	0.71**	0.59**	1.00	
Parents	0.20	0.44**	0.52**	0.30*	1.00

\*, \*\*: level of significance at 5 % and 1 %, respectively

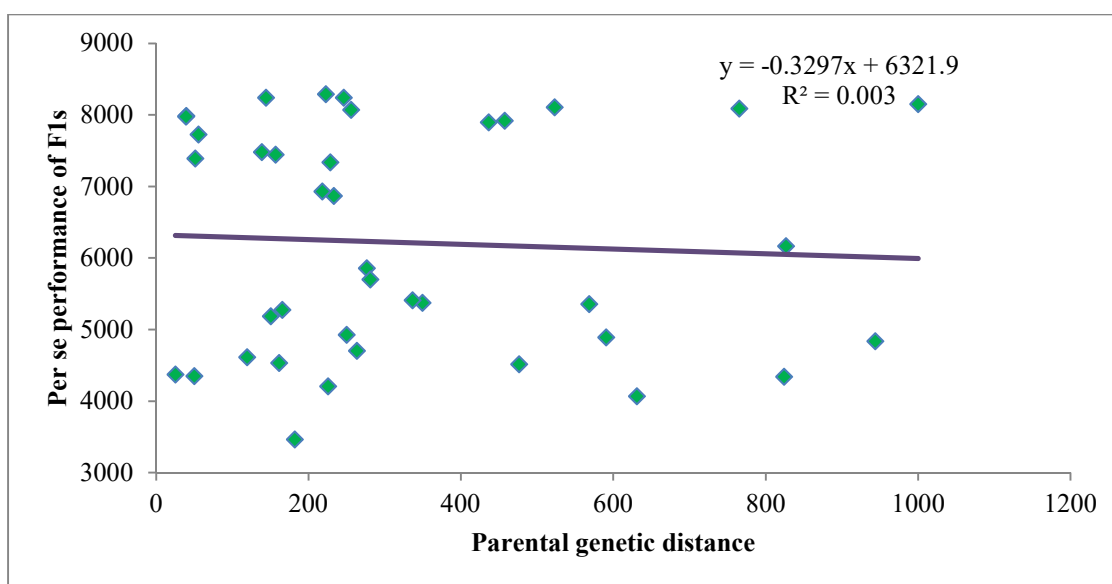
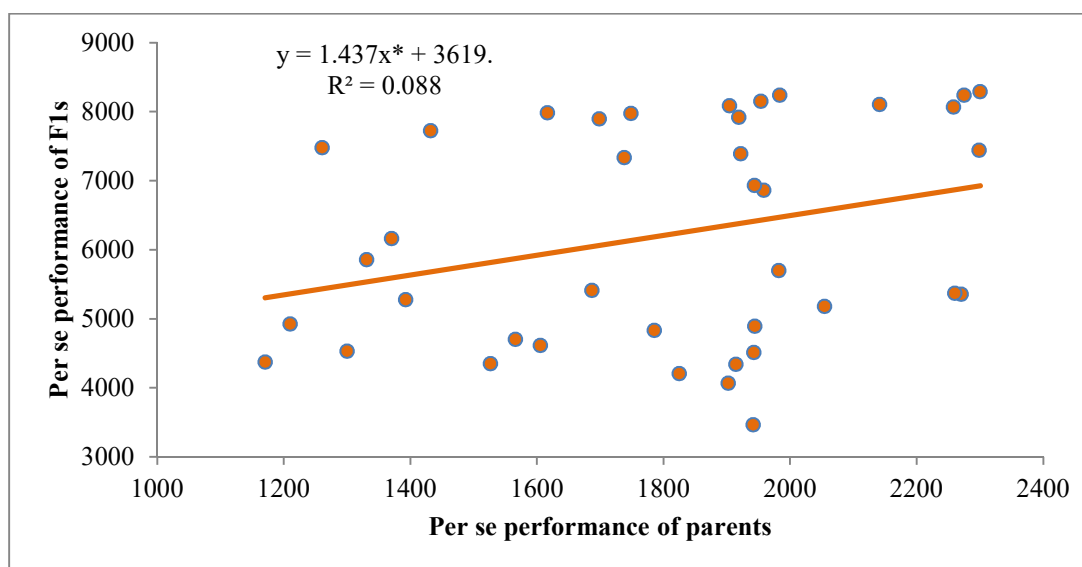


Fig. 3 Relation of parental genetic distance with *per se* performance of F<sub>1</sub>s in maize



\*: level of significance at 5 %

Fig. 4 Relation of *per se* performance of parents with *per se* performance of F<sub>1</sub>s in maize

## Conclusion

The mahalanobis  $D^2$  methods was used in order to identify diverse parents in maize and genetically diverse parents might be used in breeding programmes to produce heterotic individuals. There were sixteen maize lines grouped into five clusters. Crosses involving parents/inbred lines from the most divergent clusters are predicted to have the

most heterosis and produce the most genetic variability. Based on the findings of this study, we believe that parental diversity should not be used as the sole criterion for selection. Parents with moderate genetic diversity but high *per se* performance may be more valuable than parents with high parental diversity alone in *kharif* maize.

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