

HETEROSIS AND GENETIC DIVERGENCE CORRELATION STUDIES FOR YIELD AND ITS RELATED TRAITS IN MAIZE (*ZEA MAYS* L.)

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ABSTRACT

Twenty eight maize hybrids were developed by crossing the eight inbreds in diallel cross excluding reciprocal for studying the magnitude of heterosis in relation to genetic divergence. Genetic diversity was measured using average taxonomic distances as a measure of dissimilarity coefficient and inbreds were grouped into four distinct groups (AI, AII, B, C). The highest (2.2798) inter cluster distance was found between cluster AII and C and the least (1.1968) inter cluster distance was found between cluster AI and AII. Among twenty eight hybrids eleven hybrids were selected that recorded significantly higher mean performance (98.33 to 131.75 g per plant) and as well as significant standard heterosis (11.95 to 30.48%) for grain yield. The cross CM 300 X CML 144 exhibited the lowest (0.4069) dissimilarity coefficient between CM 300 and CML 144 but exhibited the highest (30.48%) heterosis and high mean for yield whereas cross CML 186 X CML 144 recorded the highest (2.0845) dissimilarity coefficient but recorded only 12.31% heterosis and lower mean for yield. The result suggested that genetic divergence were not effecting at predicting the most heterotic crossings, high *per se* performance of specific traits of interest should also become accountable while selecting parents for producing superior hybrid.

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important crops occupying prominent position in the agricultural economy of the world both as food for man and feed for animals. It has yield potential far higher than any other cereal and is sometimes referred to as the miracle crop or "queen of cereals". India's maize production has grown annually by 4.2% from 19.7 million tonnes in 2008-09 to 24.3 million tonnes in 2013-14 (India Maize Summit 2015). Increase in production of maize is due to cultivation of highly productive single cross hybrids owing to availability of superior inbred lines. The single cross hybrids offer better advantage over the other types of hybrids or synthetics because of their uniformity, low cost of seed production. For production of hybrid selection of parents is of paramount importance in a breeding programme. Determination of genetic diversity of any crop species is a suitable precursor for improvement of the crop because it generates baseline data to guide selection of parental lines and design of breeding scheme (Kumar *et al.*, 2015). General view is that genetically diverse parents are likely to produce high heterotic effects and desirable segregants (Kage *et al.*, 2013; Kumar *et al.*, 2015). In this regard, Azad *et al.* (2012) suggested that the crosses involving parental lines from most divergent groups manifested maximum heterosis and generate wide variability in genetic architecture. Positive correlation between genetic divergence and heterosis was also observed in maize by Betran *et al.* (2002). In contrast to general view

Datta *et al.*, (2004) and Oliboni *et al.*, (2012) reported that genetic divergence was necessary for heterosis, however it was not sufficient to ensure heterosis at a high level, mean yield and heterosis should be assessed together in evaluating potential crosses. Thus, it becomes a point of interest to examine as to what extent the genetic diversity shows response in relation to the manifestation of heterosis. Keeping in view the objectives of the present investigation was to measure the genetic divergence among the parental lines of single crosses and ascertain the relationship between heterotic response of hybrids and genetic divergence between their parents.

MATERIALS AND METHODS

The experiment was conducted at the research farm of Tirhut College of Agriculture, Dholi, under Rajendra Agricultural University, Bihar, Pusa. Materials for the present investigation were generated from eight inbred lines, including five quality protein maize (QPM) inbreds (CML 142, CML 144, CML 150, CML 176, CML 186) and three non-QPM inbreds (CM 300, CM 400 and CM 600) obtained from AICRP on maize, Dholi Centre. These parental lines were planted in crossing block in different dates with an interval of three days for synchronization of flowering period in order to facilitate crossing programme. Each plot consisted of three rows of five meter length with row to row and plant to plant spacing of 60 cm and 20 cm respectively. The inbreds were crossed in all possible combinations excluding reciprocals. The 28 crosses obtained

together with the eight parental inbreds and a QPM check Shaktiman-4 were evaluated in randomized block design (RBD) with three replication under timely and late sown conditions. Entries were grown at a spacing of 60 cm x 20 cm in rows of 5 metre length in plots having three rows per plot. To obtain the estimates of heterosis of 28 crosses and genetic divergence of eight parental lines, ten agro-morphological traits were assessed. Observations were recorded on whole plot basis for days to 50 per cent tassel emergence, days to 50 per cent silk emergence and days to 50% maturity by counting the number of days from sowing to the issuance of tassel, silk and maturity of cob in 50 per cent plants. Five randomly selected plants in each plot were used for recording observations on plant height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, 100 kernel weights (g), and yield per plant (g).

Statistical analysis

Data were subjected to analysis of variance to assess the significance of the components arising due to parents, crosses, crosses including check and parents Vs F₁s for all the ten morph- agronomical traits recorded under two different environments i e, dates of sowing (timely and late sowing) and across the dates of sowing. Numerical taxonomic approach (Sokal and Sneath, 1963 and Sneath and Sokal, 1973) were used for assessing genetic divergence using data on morpho-agronomic characteristics obtained from eight parental inbreds. An average taxonomic distance (Sokal, 1961) was computed as a measure of dissimilarity co-efficient. The genetic distance were subjected to sequential agglomerative hierarchical nested (SAHN) clustering . The dendrograms were constructed provided a relationship among inbred lines by unweighted pair group method using arithmetic average (UPGMA). The level of diversity were identifying using the clusters at appropriate phenon levels. Heterosis was calculated over standard check (SC) as percentage increases or decrease of the performance of the traits over standard check variety in desirable direction by using the following formula:

Standard heterosis (SH); (Meredith and Bridge, 1972)

$$SH = \frac{\bar{F}_1 - \bar{SC}}{\bar{SC}} \times 100$$

Where,

F₁ = Mean performance of F₁ hybrid

SC = Mean performance of standard check

The significance was determined with a t test. However, to make the result more precise and manageable, the result on pooled data basis (across environment) were presented for the study in order to generate generalized information regarding the extent of heterosis, genetic distance and established the relationship between genetic diversity and heterosis.

RESULTS AND DISCUSSION

Partitioning of variance clearly indicated the existence of significant differences among the parents for all the traits recorded in the present study on pooled data basis (across the date of sowing (Table 1). This indicating the existence of exploitable extent of genetic variability among the experimental material. Genetic variability among experimental material was also reported earlier (Azad *et al.*, 2012, Oliboni *et al.*, 2012, Kage *et al.*, 2013, Kumar *et al.*, 2015, Kumar, *et al.*, 2015). The comparison between parents Vs F₁'s were found to be significant for all the characters with the exception of days to 50% tassel emergence and days to 50% silk emergence indicating the performance of hybrids over parents. The environmental effect in the form of variation in the date of sowing was non-significant in most of the cases suggested that relative ranking of the genotypes across the date of sowing was influenced to a considerably greater extent for most of the traits including yield per plant.

The range of mean performance of crosses, heterosis percentage and number of significant crosses is given in Table 2. The value of heterosis for days to 50% tassel and days to 50% silk emergence ranging from -4.30% to 5.34 % and -4.19% to 4.77% respectively indicated the expression of bidirectional dominance deviations for these characters. Crosses recorded negative heterosis for days to 50% tassel and days to 50% silk emergence indicating early maturity of the crosses. Six crosses, CML 176 x CML 150, CM 600 x CML 150, CM 600 x CML 176, CM 600 x CM 400, CM 600 x CML 142, CM 600 x CML 186 recorded significant negative standard heterosis. Under Indian condition early maturing hybrids are

Table 1: Pooled analysis of variance on data obtained for different characters across the date of sowing

Sources of Variation	D.F.	Mean sum of Squares									
		Plant height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows per ear	Number of kernels per row	100 Kernel weight (g)	Days to 50% tassel emergence	Days to 50% silk emergence	Days to 50% maturity	Yield per plant (g)
Replication	2	1773.53**	0.05	0.19	0.19	20.03*	2.65	0.15	0.05	0.62	7.13
Environments	1	40174.11**	66.87**	19.78**	17.24**	300.33**	318.55**	5309.54**	5192.13**	14720.04**	4529.37**
Rep. x Env.	2	738.66**	0.01	0.11	0.01	16.05	1.10	0.3873	0.13	0.13	8.86
Parents	7	2740.22**	10.78**	8.35**	7.91**	105.56**	22.48**	47.13**	51.33**	14.43*	554.16**
F ₁	27	652.38**	10.67**	4.74**	4.21**	76.95**	49.05**	34.30**	32.85**	64.30**	1219.27**
F ₁ + Check	28	639.62**	10.34**	4.58**	4.08**	74.29**	49.58**	32.22**	31.81**	62.01**	1179.29**
Parents Vs F ₁	1	34946.77**	564.55**	273.43**	302.16**	3865.39**	3559.04**	1.52	1.11	409.65**	72811.79**
Parents x Env.	7	267.16*	0.07	0.09	0.03	0.55	0.29	11.43	9.81	7.52	7.89
F ₁ x Env.	27	282.31**	0.52	0.23	0.16	1.62	3.28	13.27**	13.85**	34.91**	21.26
F ₁ + Check x Env.	28	274.84**	0.51	0.22	0.15	1.58	3.42	13.20**	13.76**	33.67**	20.55
Parents Vs F ₁ x Env.	1	332.75	0.11	0.00	0.02	3.35	51.88**	2.45	2.92	162.50**	115.72
Error	130	103.60	1.27	0.87	0.90	5.50	5.28	7.13	7.40	6.64	52.24

*, ** Significant at 5% and 1%, respectively.

Table 2: Range of mean performance, significant standard heterosis (%) of hybrid combinations in maize

Traits	Mean performance	SE diff.	Heterosis	Number of significant crosses
Plant height	123.27-160.30	6.01	-16.52% to 10.38%	5
Days to 50% tassel emergence	107.50-118.33	1.54	-4.30% to 5.34%	7
Days to 50% silk emergence	110.50-118.67	1.56	-4.19% to 4.77%	8
Days to 50% maturity	140.00-159.00	1.48	- 5.08% to 7.80%	3
Ear Length	12.96-18.50	0.65	10.32% to 31.65%	13
Ear girth	12.43-16.02	0.54	-12.87% to 12.36%	5
Number of kernels row per ear	12.23-15.25	0.55	11.57% to 15.98%	4
Number of kernels per row	27.43-40.80	1.36	-23.48% to 23.07%	11
100 kernel weight	23.35-34.12	1.32	9.79% to 33.24%	18
Yield per plant	72.75-131.75	4.16	-27.97% to 30.48%	11

Table 3: Standard heterosis for grain yield and other attributes in high yielding hybrid combinations

Hybrid Combination	Plant height	Ear length	Ear girth	Kernels row per ear	Kernels per row	100 kernels weight	Days to 50% tassel emergence	Days to 50% silk emergence	Days to 50 % maturity	Yield per plant
1. CM 300 x CML 144	8.56	31.65**	12.36**	15.98**	23.07**	32.30**	-1.19	-1.16	1.02	30.48**
2. CM 300 x CML 142	0.65	27.22**	10.66**	12.87**	15.03**	32.82**	0.45	0.02	0.68	30.20**
3. CM 400 x CML 142	2.12	24.26**	6.16	14.32**	16.49**	21.91**	-1.19	-1.16	-0.79	25.74**
4. CM 142 x CML 186	-4.97	16.48**	4.47	1.95	14.99**	16.13**	1.34	1.30	0.68	18.23**
5. CM 300 X CML 150	-6.55	16.76**	2.30	3.34	13.03**	16.85**	0.59	0.58	-0.11	17.49**
6. CM 400 x CML 186	-13.45**	17.16**	5.92	6.45	13.48**	22.00**	-1.04	-0.58	-1.02	14.93**
7. CM 400 X CML 176	-1.69	15.22**	2.50	11.57**	13.76**	21.36**	-2.23	-1.73	-1.02	13.86**
8. CM 150 X CML 144	2.78	15.23**	-4.28	1.37	14.57**	20.85**	0.30	-0.29	1.24	12.92**
9. CM 300 X CML 176	-10.38**	15.35**	2.17	4.20	12.49**	26.35**	0.45	0.43	-0.34	12.31**
10. CM 186 X CML 144	-7.90	15.44**	-6.52	-2.05	11.43**	15.03**	2.52	2.89*	1.69	12.31**
11. CM 400 X CML 144	-14.00**	12.99**	4.89	7.42	13.03**	27.25**	-0.74	-1.16	0.68	11.95**

Table 4: Composition of cluster based on taxonomic distance in average taxonomic approach in maize on pooled data basis

No. of clusters identified at different phenon* level		Inbreds included in each cluster
60%	50%	
A (6)	AI (4)	CML 142, CML150,CML176,CM 400
	All (2)	CML 144, CM 300
B (1)	B (1)	CML 186
C (1)	C (1)	CM 600

Figures in parenthesis indicate number of inbreds in the respective clusters;*Phenon levels indicates 60 and 50 units of dissimilarity coefficient.

Table 5: Average intra-cluster (diagonal) and inter cluster distances of four clusters in maize on pooled data basis

Clusters	AI	All	B	C
AI	0.8531	1.1968	1.5572	1.4196
All		0.4069	2.1955	2.2798
B			0.0000	1.2369
C				0.0000

of prime importance and negative heterosis for this traits is desirable hence useful materials for breeder in isolating inbred lines for earliness. CM 600 x CML 186 and CM 600 x CM 300 also founded significant standard heterosis for earliness in terms of days to 50% maturity. Premalatha and Kalamani (2009); Bhavana et al.(2011) also observed significant heterosis for earliness in terms of days to 50% tasseling and days to 50% silking in the case of hybrids included in their studies. Existence of heterosis for earliness in terms of days to 50% maturity was also reported by Nigusie and Zelleke (2001). The dwarf stature is widely considered as desirable feature for realizing maximum grain yield per plant in maize. The cross CM 600 x

CML 144 showed the most significant negative heterosis for plant height hence exhibiting dwarfness. It was observed that three crosses CM 400 x CML 186, CM 300 x CML 176, CM 400 x CML 144 recorded significant negative heterosis for height, also exhibited positive significant heterosis for ear length, kernels per row, 100 kernels weight and yield per plant (Table 3). Thus, dwarf hybrid is desirable, used in maximization of higher yield per unit area. Based on the studies conducted earlier, Bhavana et al.(2011); Oliboni et al. (2012) reported significant heterosis for dwarfness.

For exploiting hybrid vigour *per se* performance of hybrids and the extent of heterosis, in addition to specific combining ability effect are important. Selection of parents based on any one of these criteria alone may not be purposefully effective. So, selection must be based on all these parameters. In the present study, the cross combinations were taken into consideration on the basis of their *per se* performance and the magnitude of heterosis in trait(s) of economic importance. The eleven cross combinations, namely, CM 300 x CML 144, CM 300 x CML 142, CM 400 x CML 142, CML 142 x CML 186, CM 300 x CML 150, CM 400 x CML 186, CM 400 x CML 176, CML 150 x CML 144, CM 300 x CML 176, CM 400 x CML 144 and CML 186 x CML 144 were recorded significantly higher mean performance and significantly positive standard heterosis for yield (Table 3). The positive estimates of the greatest value were presented by the crosses CM 300 x CML 142 and CM 300 x CML 144 which demonstrated a desirable increase in ear girth. Increase in heterosis of ear girth was observed to be correlated with the heterosis for number of kernels row per ear. The highest (15.98%) estimates of significant heterosis for number of kernels row per ear was recorded in cross CM 300 x CML 144. Kumar and Satyanarayana (2006), Sofi et al. (2007) and Dubey et al. (2009)

Table 6: Estimates of morpho-agronomical traits based dissimilarity coefficients between parental inbreds and heterosis for grain yield of high yielding hybrid combinations

Hybrid Combination	Dissimilarity coefficient (DC)	Inbred classification ¹ (DC)	Standard heterosis
CM 300 x CML 144	0.4069	All, All	30.48**
CM 300 x CML 142	0.9712	AI, All	30.20**
CM 400 x CML 142	0.8381	AI, AI	25.74**
CML 142 x CML 186	1.7070	AI, B	18.23**
CM 300 x CML 150	1.2477	All, AI	17.49**
CM 400 x CML 186	1.4727	AI, B	14.93**
CM 400 x CML 176	0.9319	AI, AI	13.86**
CML 150 x CML 144	0.9782	AI, All	12.92**
CM 300 x CML 176	1.5643	AI, All	12.31**
CML 186 x CML 144	2.0845	B, All	12.31**
CM 400 x CML 144	1.2898	AI, All	11.95**

¹: Inbred classification represents the clusters in which inbred lines were accommodated; **, ***: Significant at 5 and 1 per cent level, respectively.

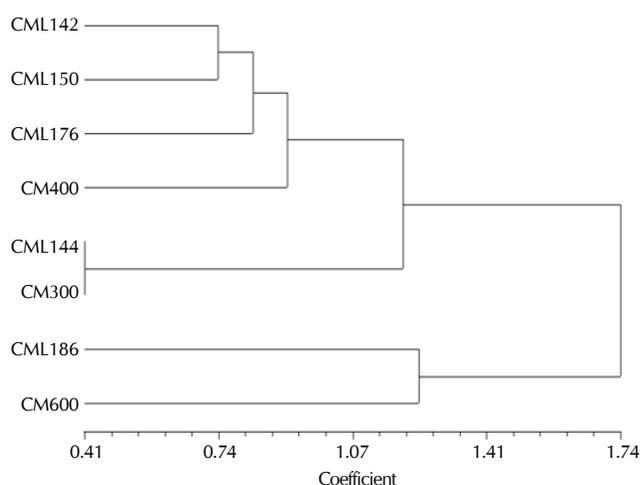


Figure 1: Dendrogram of maize inbreds based on average taxonomic distance for ten characters in over environments

also reported manifestation of significantly positive heterosis in these characters. Maximum significant positive heterosis for number of kernels per row, 100 kernel weight, yield per plant were reported in the cross CM 300 x CML 144. Significant positive heterosis in these characters have been also reported by Kumar and Satyanarayana (2006), Singh *et al.* (2010) and Oliboni *et al.* (2012).

It was observed that heterosis manifestation in respect of grain yield in most of the selected crosses were associated with simultaneous heterosis for ear length, ear girth, kernels row per ear, kernels per row and 100 kernels weight (Table 3). Kumar and Sataynarayana (2006), Premlatha and Kalamani (2009), Sofi *et al.* (2007), Singh *et al.* (2010), and Kumar *et al.* (2013) earlier reported that characters like ear girth, 100 seed weight and number of kernel row per ear are known to exhibit highest correlation with grain yield. The role of yield attributing traits in the improvement of yield were also reported in other crops (Dubey *et al.*, 2014; Gite *et al.*, 2014) The result, therefore, revealed that *per se* performance for yield of hybrids reflected the degree of heterosis manifestation in the hybrids. This is in agreement with the earlier reports made by Singh *et al.* (2010), Oliboni *et al.* (2012), Kumar *et al.* (2015) and Kumar *et al.* (2015).

Genetic divergence based on agro-morphological traits

The mean values for the traits obtained from the joint analysis of variance involving two different environments were used to evaluate genetic divergence amongst the eight parents. Mean sum of squares arising due to interaction of different sources of variation with environments was observed to be non-significant in most of the cases. Average taxonomic distance was used as a measure of dissimilarity for assessing the nature and extent of genetic divergence. When phenon line was drawn at fifty and sixty dissimilarity units as cut off point, four types (AI, All, B, C) and three types (A, B,C) of clustering patterns were obtained respectively (Fig 1 & Table 4). Cluster AI consisted of four inbreds, Viz. CML 142, CML 150, CML 176 and CM 400 whereas cluster All consisted of two inbreds viz. CML 144 and CM 300. This results revealed that QPM and non-QPM was not the basis of divergence amongst the inbreds in the present study. Three non-QPM inbreds were accommodated into three different clusters reflecting relatively wider genetic divergence amongst these inbreds. The highest inter-cluster distance (2.2798) was found between clusters All and C and the least inter-cluster distance (1.1968) was found between clusters AI and All (Table 5). Intra-cluster distances were smaller than the inter cluster distances indicating that the four clusters obtained by cluster analysis were distinct. The highest inter cluster distance between cluster All and C, showing greater divergence between inbreds of these two clusters also showed wider differences in their mean values. Similar results indicating appreciable extent of divergence were also reported by Datta *et al.* (2004), Kumar and Singh, (2005), Kumar *et al.* (2015) and Kumar *et al.* (2015).

Heterosis in relation to genetic divergence

The estimates of heterosis for yield per plant, dissimilarity coefficient and inbreds classification of eleven selected crosses have been presented in Table 6. Amongst the eleven selected high yielding cross combinations the parents of the cross CM 300 x CML 144 exhibited least average taxonomic distance, but the magnitude of standard heterosis in grain yield was recorded to be the highest. Contrarily, the parents of the cross combination CML 186 x CML 144 exhibited remarkably greater average taxonomic distance (2.0845), but the extent of heterosis in grain yield of this hybrid was considerably lower. From these result a lack of linear association between genetic diversity and standard heterosis was observed. This is because

heterosis depends not only on difference in allele frequencies but also on dominance and epistatic interactions of the traits. Furthermore, three cross combinations, CM 300 x CML 144, CM 400 x CML 142 and CM 400 x CML 176, which involved the parental lines of the same group (A) exhibited considerably higher magnitude of heterosis in grain yield per plant (Table 4). These results suggested that greater genetic divergence for higher magnitude of heterosis has its limits. This might be due to the reason that crosses between extremely divergent parents create a situation where the harmonious functioning of alleles is rather disturbed and consequently the physiological functions are not as efficient as in a situation where the alleles had evolved under more or less similar selection pressure. A lack of clear relation between parental genetic divergence in maize and magnitude of heterosis in the hybrids was also reported earlier by many researchers (Zheng and Wang, 1995; Melo *et al.*, 2001). Out of eleven crosses showing significant standard heterosis for grain yield, only three crosses involved the parental lines belonging to the same group. Rest of the eight crosses involved the parental lines belonging to diverse group. Thus, the results showed that heterotic hybrids was considerably greater when parental lines from genetically diverse groups were involved in the cross combinations. Further, the heterosis was found to be higher with moderate or intermediate genetic diversity than with extreme ones (Moll *et al.*, 1965) which was also observed in the present study. Based on the above finding it was concluded that the genetic diversity are not always sufficient to reveal which combinations should used for hybridization. Instead, data on high *per se* performance with respect to specific trait of interest and heterosis should be assessed together in evaluating potential crosses. Similar finding have been reported earlier by Datta *et al.* (2004), Singh *et al.* (2005) and Oliboni *et al.* (2012).

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