



GENETIC DISTANCE, HETEROSIS AND COMBINING ABILITY STUDIES IN MAIZE FOR PREDICTING F₁ HYBRID PERFORMANCE

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SUMMARY

Tools for yield prediction are requisite to any successful heterosis breeding program. With this objective present investigation was designed to work out the relationship between genetic diversity, heterosis and specific combining ability (SCA) and yield for predicting the potential F₁ combinations in maize. A field experiment consisting of 10 inbreds of diverse origin and their 45 crosses was conducted for 3 years. Highly significant genotypic variance was observed by joint analysis of variance. It confirmed the sufficient amount of genetic diversity present in parental inbred lines. The estimates of genetic distance based on Euclidean distance matrix and canonical vector analysis showed that B1-12 and B1-15 and B1-12 and B1-34 are most diverse parent combinations. The correlation coefficient analysis showed that there is strong positive association between yield and heterosis and SCA. Genetic distance between parents was also positively correlated with yield and heterosis but weakly associated with magnitude of $r = 0.1059$ and $r = 0.1104$ respectively. However, association between genetic distance and SCA was significantly positive. The findings of this study revealed that higher SCA genetic diversity is important, whereas heterosis and SCA are effective for predicting the best F₁ combinations in maize.

Keywords: Genetic diversity, heterosis, combining ability, correlation, *Zea mays* L.

Short summary statement: Prediction of heterosis through different breeding tools are important to know the inheritance pattern of morphological traits of hybrids along with their parents. This experiment showed that high heterosis for grain yield and other components traits as well as significant SCA effects were most promising combinations for best F₁ in maize which need to be tested on large scale for commercial exploitation of heterosis.

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INTRODUCTION

Heterosis is a base of breeding program especially for cross pollinated crop like maize. Heterosis depends directly on the existence of dominance and indirectly through interaction involving dominance effect at different loci. According to Falconer and Mackay (1996), the

magnitude of heterosis depends on the magnitude of directional dominance and the magnitude of difference in the gene frequency of two parental lines at all the loci affecting the concerned trait. Whereas, the differences in the gene frequency come from diverse genetic background of the parents. Thus, it is believed that an important part of heterosis is due to specific

combining ability, and the outstanding single cross combination can be identified only by testing the performance of single crosses. The final evaluation of the inbreds, therefore, consists of the evaluation of single crosses produced from them.

On the other hand, genetic diversity is pre requisite for any crop improvement program, as it helps in the development of superior recombinants (Naik *et al.*, 2006). Genetic divergences among the genotypes play an important role in selection of parents having wider variability for different characters. Statistical analysis quantifies the genetically distance among the selected genotype and reflects the relative contribution of specific taints towards the total divergence. The crosses between parents with suitable genetic divergence are generally the most responsive for yielding the most promising segregants, however satisfactory results are obtained only if the germplasm employed in the cross also present high values for the traits of interest (Prasanna, 2012). In most cases, genetic distance is positively correlated with heterosis. Thus, the magnitude of heterosis is generally proportional to the genetic distance between the parents.

The objective of the present study was to evaluate genetic diversity among 10 maize inbred lines to correlate with single cross heterosis, i.e. specific combining ability to the genetic distance of the parental lines for comparison and predicting the most heterotic hybrids.

MATERIALS AND METHODS

Ten maize inbred lines of different origin were selected for these studies (Table 1). All the inbreds were crossed in a diallel fashion without reciprocal crosses. The 45 crosses obtained, together with the 10 parental inbred lines and one local check hybrid (Kanchan 612) were evaluated by randomized block design with 3 replication in 3 environments i.e. summer rainy season of 2010, 2011 and 2012 at Maize Breeding Research Station, SKUAST-J, Poonch (India) located at Latitude 33° 46' 1.7" N and longitude 74° 06' 44.1" E with an altitude of 1002 m.

To obtain the estimates of heretosis, combining ability and genetic divergence of the 45 crosses and 10 parental inbred lines, 5 agronomical traits were assessed during the years; grain yield ($t\ ha^{-1}$), days to 50% flowering, days to maturity, plant height (cm) and shelling percentage. Data were subjected to analysis of variance for each individual environment (Year), and after conformation of significance for sources of variance, joint analysis of variance was performed. Heterosis values were calculated based on average data from 3 environments as mid-parent (MP) heterosis for grain yield. Estimates of specific combining ability (SCA) for grain yield were evaluated according to method 2 of Griffing (1956) Model I by means of a computer program for diallel analysis (Windostat ver. 8.5).

Genetic divergence among 10 parental inbred lines were determined by Euclidean distance matrix, based on Mahalanobis distance (D^2) using Tocher method described by Rao, (1952). Genetic divergence analysis using canonical (Vector) method was also estimated following the method described by Rao, (1952) by the means of computer program (Windostat ver. 8.5). This is a sort of multivariate analysis, where canonical vectors and PCA scores representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively.

To establish an association between yield, heterosis, SCA and genetic distance among parental lines; correlation coefficient analysis was conducted for identification of most effective breeding technique in predicting the effective heterotic hybrids.

RESULTS

The result of joint analysis of variance showed highly significant genotype mean sum square for all the characters under study. Whereas interaction effect was found significant for grain yield and plant height. (Table 1) The mean grain yield of the crosses ranged $5.17\ t\ ha^{-1}$ to $10.34\ t\ ha^{-1}$ and the mean was $7.38\ t\ ha^{-1}$ (Table 2). The highest heterosis value for grain yield was

Table 1. Information of parent lines and estimation of character effect towards divergence and principal component analysis for individual inbred based on canonical vector analysis.

		1 Vector	2 Vector	3 Vector
Eigene Value (Root)		1.974	1.283	0.807
% Var. Exp.		39.487	25.663	16.135
Cum. Var. Exp.		39.487	65.149	81.284
Grain yield kg./ha.		0.151	0.780	0.323
Days to tasselling		0.514	0.453	-0.263
Days to maturity		-0.417	0.264	-0.780
Plant height (cm)		0.515	-0.300	0.011
Shelling %		0.523	-0.164	-0.468
<u>Genotypes</u>				
Inbred Lines	Origin	Vector 1	Vector 2	Vector 3
1. B1-33	Local germplasm	9.880	3.830	-12.184
2. B1-31	CML 150	11.090	2.990	-11.905
3. B1-32	Local germplasm	10.440	4.850	-11.703
4. B1-34	Local germplasm	9.710	3.480	-11.544
5. B1-11	CML 142	11.030	4.120	-11.710
6. B1-10	CML 149	10.450	4.010	-11.808
7. B1-13	CML 271	11.480	4.710	-11.776
8. B1-12	CML 177	11.880	4.870	-12.285
9. B1-15	CML 141	9.940	2.600	-11.930
10. B1-16	CML 158	11.720	4.280	-12.064

observed from the cross B1-31 x B1-32 (451) followed by B1-11 x B1-12 (418), B1-32 x B1-34 (378) and B1-11 x B1-13 (335) (Table 2). Low heterotic values were also observed for few of the crosses like B1-33 x B1-31 (17.5), B1-33 x B1-13 (36.5), B1-33 x B1-16 (57) and B1-33 x B1-11 (61).

The result of combining ability analysis showed that there was high positive and significant SCA effect for the cross B1-31 x B1-32 (1.62), B1-31x B1-13 (1.56), B1-34 x B1-12 (1.26) and B1-31 x B1-12 (1.20). The highest significant negative SCA effect was observed for the cross B1-33 x B1-31 followed by B1-33 x B1-16, B1-34 x B1-10, B1-33 x B1-32 (Table 2).

The estimates of genetic divergence study for genetic distance, ranged from 300.5 for most divergent pair of cross (B1-12 x B1-15) to 45.2 between the least divergent pair (B1-13 x

B1-16) (Table 2). The results obtained from canonical vector method for divergence study revealed that the 3 principal components (Vectors) absorbed 39.487, 25.663 and 16.135 percentage of variability, respectively (Table 1). In Z1, highest element value (0.523) was observed for shelling percentage followed by 0.515 for plant height; in Z2 the maximum element value was found for grain yield (0.780) followed by days to tasselling (0.453) and in Z3 days to maturity with element value -0.780 was the highest.

The correlation coefficient between genetic distance and yield, heterosis and specific combining ability were 0.1059, 0.1104 and 0.3520, respectively (Table 3). Whereas the correlation coefficient between yield and heterosis was 0.8676; between yield and SCA was 0.7002 and between SCA and heterosis was 0.6886.

Table 2. Summary of all 45 cross combinations for mean grain yield, heterosis, specific combining ability and genetic diversity between respective parents.

Cross combination	Yield (t ha ⁻¹)	Heterosis	SCA	Genetic distance* between parents of the cross
B1-33 x B1-31	5.62	17.5	-4.12	145.1
B1-33 x B1-32	6.47	165.5	-2.14	125.4
B1-33 x B1-34	6.41	171.5	-0.78	54.2
B1-33 x B1-11	5.87	61	-0.87	100.9
B1-33 x B1-10	6.06	120.5	-1.13	70.1
B1-33 x B1-13	5.42	36.5	-0.73	178.2
B1-33 x B1-12	6.71	171	0.45	225.4
B1-33 x B1-15	6.73	194	-0.71	107.5
B1-33 x B1-16	5.17	57	-3.41	190.1
B1-31 x B1-32	10.34	451	1.62	206.2
B1-31 x B1-34	8.62	306	1.13	161.1
B1-31 x B1-11	9.06	293.5	0.82	119.3
B1-31 x B1-10	8.76	304	0.61	135.1
B1-31 x B1-13	8.88	296	1.56	183.1
B1-31 x B1-12	7.92	205.5	1.2	200.3
B1-31 x B1-15	8.26	260.5	1.1	121.2
B1-31 x B1-16	8.17	263.5	0.41	145.3
B1-32 x B1-34	8.86	378	0.91	209.1
B1-32 x B1-11	7.29	164.5	-0.44	95.2
B1-32 x B1-10	7.13	189	-1.27	92.6
B1-32 x B1-13	8.66	322	0.47	110.3
B1-32 x B1-12	6.79	140.5	-2.05	129.1
B1-32 x B1-15	7.36	218.5	0.97	210.7
B1-32 x B1-16	7.55	251.5	-0.121	140.4
B1-34 x B1-11	6.44	106.5	-0.36	150.4
B1-34 x B1-10	5.9	93	-2.16	112.1
B1-34 x B1-13	6.17	100	1.11	220.4
B1-34 x B1-12	6.82	170.5	1.26	250.1
B1-34 x B1-15	6.23	132.5	-1.34	90.2
B1-34 x B1-16	5.88	111.5	-0.63	117.4
B1-11 x B1-10	8.69	315.5	0.46	70.2
B1-11 x B1-13	9.09	335.5	0.23	80.6
B1-11 x B1-12	9.86	418	1.06	111.3
B1-11 x B1-15	8.81	334	0.45	188.2
B1-11 x B1-16	8.43	310	0.11	70.8
B1-10 x B1-13	7.02	169	-0.76	120.6
B1-10 x B1-12	7.11	183.5	-2.6	158.4
B1-10 x B1-15	6.87	180.5	-0.18	150.7
B1-10 x B1-16	7.07	214.5	-0.14	130.3
B1-13 x B1-12	6.88	140.5	-1.15	65.4
B1-13 x B1-15	7.54	227.5	0.32	264.2
B1-13 x B1-16	7.16	203.5	-0.33	45.2
B1-12 x B1-15	7.14	193	0.27	300.5
B1-12 x B1-16	6.82	175	-1.92	60.2
B1-15 x B1-16	8.06	320	0.79	242.1

*Genetic distance between respective inbred combinations for 5 morphological characters based on Mahalanobis distance (D^2)

Table 3. Correlation coefficient between grain yield, specific combining ability, heterosis and genetic distance.

	Yield	Heterosis	SCA	Genetic Distance (D ²)
Yield	1.0000			
Heterosis	0.8676**	1.0000		
SCA	0.7002**	0.6886**	1.0000	
Genetic Distance (D ²)	0.1059	0.1104	0.3520**	1.0000

** Significant at the 0.05, i.e. 0.01 probability level.

Table 4. Summary of joint analysis of variance for 5 different morphological characters of all 45 cross combination.

Trait	Genotype	Mean sum square		Mean	CV (%)
		Genotype Environment	x Error		
Grain yield (t ha ⁻¹)	4814.73**	2252.01*	760.07	7.38	15.6
Days to tasselling	31.95**	3.01 ^{ns}	2.29	55.9	4.3
Days to maturity	28.84**	3.62 ^{ns}	7.31	120.7	3.5
Plant height (cm)	647.75**	212.13*	113.73	244.9	6.9
Shelling %	9.43*	5.12 ^{ns}	4.40	85.5	3.9

*, ** Significant at the 0.05, i.e. 0.01 probability level, respectively.

DISCUSSION

The combined analysis of variance across environments showed maximum grain yield variation due to genotypes, confirming the presence of high degree of genetic diversity in breeding material. Whereas, environment also played significant role in variation for grain yield, reflected in significant interaction effect (Table 4). Eighteen F₁ hybrids showed highest result for grain yield. The grain yield has become the main focus of breeding as it is connected to other characters (Rahman *et al.*, 2007).

The values of heterosis for grain yield were high positive for most of the crosses indicating the absence of bidirectional dominance derivatives. The parents of highly heterotic cross (B1-31 x B1-32) had different genetical background i.e. local germplasm and CIMMYT breeding line. Hallauer and Miranda (1981) explained that in addition to the existence of genes with some degree of dominance controlling the character, the expression of heterosis also depends on the divergence between genotypes, as differences in allele frequencies are required at loci involved in the expression of desirable characteristics. Whereas

low heterotic effect is likely due to low genetic complementarity of loci with non-additive effects, possibly because these crosses displayed some degree of parental relationship (Aliu *et al.*, 2008).

Estimates of specific combining ability for predicting the yielding capacities of the crosses produced, indicated the presence of positive and negative cross compatible parents in the population of study with high and low magnitude of interaction effects (Table 2). Sundarajan and Kumar (2011) and Makumbi *et al.*, (2012) also observed the different level of SCA effects in his experiments. The high positive and significant SCA effect highlighted the importance of non-additive (dominance and/or epistatic) gene action expressed in F₁ cross that performed better than the mean of their parents. However, there were crosses with highly negative SCA values like. B1-33 x B1-31. The influence of SCA could bring about both positive and negative values. Positive value meant that F₁ hybrid was better than F₁ hybrid that having negative value (on the equivalent character) (Muraya *et al.*, 2006; Gowda *et al.*, 2013). The cross with high positive SCA effect (B1-31 x B1-32) also showed the high heterotic effect in the present study. These data agree with

the findings of Devi and Singh (2011) who stated that SCA and heterosis are highly related parameters.

Genetic divergence study of parental lines through Euclidean distance matrix based on Mahalanobis D^2 revealed that there was wide range of genetic diversity from 300.5 to 45.2. These data are supported by the findings of Li *et al.* (2004) and Rodrigo *et al.* (2012). Showemimo (2004) reported that estimates of the generalized Mahalanobis distance (D_2) clearly indicated that the pairs of genotypes are more divergent and more similar genetically.

With the aim of more critical prediction of genetic divergence between genotypes, multivariate methods, such as principal component analysis and canonical variables were applied in the present study. The result showed that the first principal component (vector I) absorbed and accounted for maximum (39.48%) proportion of variability and remaining once accounted for progressively lesser and lesser amount of variation (25.63% and 16.13%)

for vector II and vector III, respectively (Table 1). The highest element value (0.523) was observed for shelling % in vector I (PCA I), whereas, the maximum element value (0.780) was recorded for grain yield in vector II (PCAII). As the first 2 vectors showed eigen values more than one and cumulatively they expressed 65.15% variability (Table 1). Genetic divergence between genotypes measured in terms of spatial distance and resulted in formation of 2 dimensional (2D) representation based on 2 PCA scores (vector I and vector II) for each individual genotypes (Figure 1). The figure reflected highest diversity between B1-34 and B1-12 followed by between B1-12 and B1-15. Whereas, minimum diversity were observed between B1-33 and B1-34 followed by between B1-13 and B1-16. The estimates of genetic divergence based on PCA score method was slightly differ from Euclidean distance matrix. These findings are in general agreement with the findings of Dauda and Olakojo (2007) and Alam *et al.* (2012).

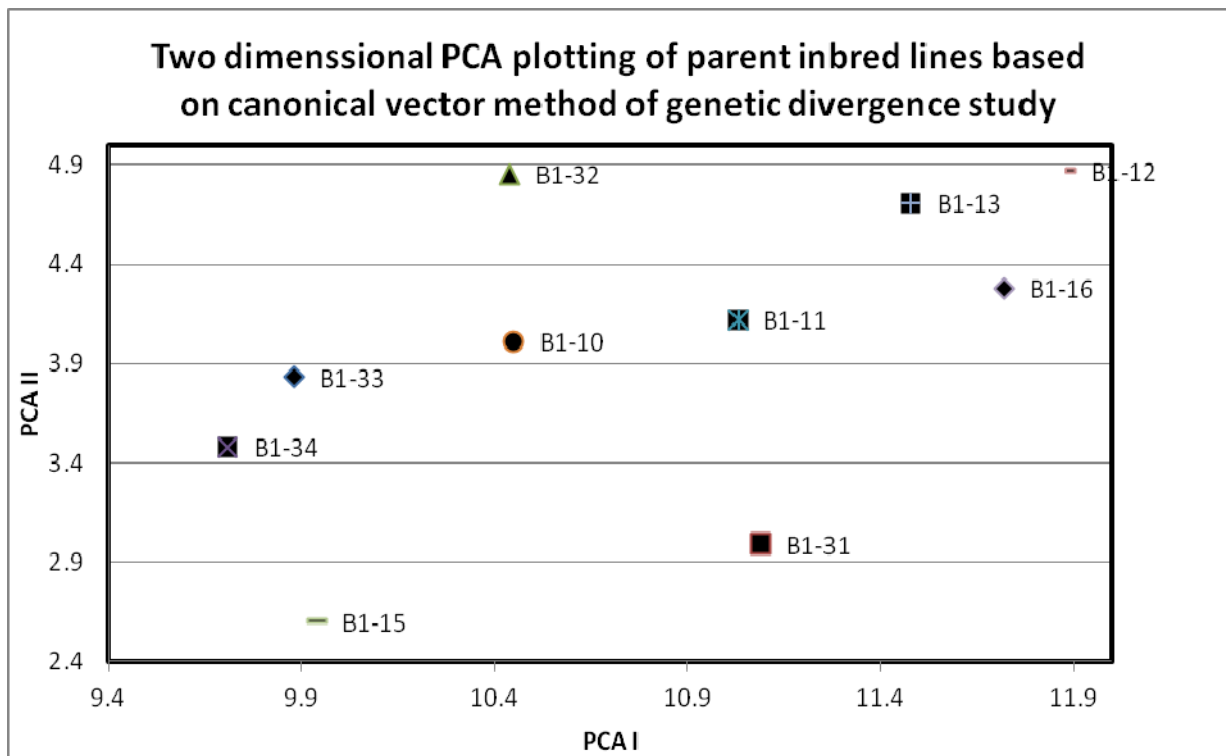


Figure 1. 2D representation of inbred lines for their genetic divergence.

Results presented in Table 3 are demonstrating positive correlation between parental genetic distance and F₁ yield, specific combining ability and heterosis. The correlation coefficient between genetic distance and grain yield for hybrids is positive but weak ($r = 0.1059$). The correlation coefficient of genetic distance and specific combining ability (SCA) were positive and significant ($r = 0.3520$). The result also indicated that the correlation between genetic distance of parents and heterosis for yield of hybrids is positive but weak ($r = 0.1104$) (Wegary *et al.*, 2013). This is supported by the findings of Drinic *et al.* (2002), Marsan *et al.* (1998) and Betran *et al.* (2003). The cross between the most divergent inbreds (B1-12 x B1-15) (Table 2) showed heterosis of 193. Moreover, the cross between least divergent parents (B1-11 x B1-13) represented heterosis of 335.5. These data indicated that estimate of genetic diversity alone may not be enough to reveal the best combination of genotypes for successful breeding program.

On the other hand, strong positive and significant correlation was observed between yield and heterosis and SCA i.e. $r = 0.8676$ and $r = 0.7002$, respectively. The correlation between heterosis and SCA of crosses were also found to be strong, positive and significant (Drinic *et al.*, 2002 and Betran, *et al.*, 2003). The relationship between grain yield and heterosis and specific combining ability could be used to predict F₁ hybrid appearance (Devi and Singh, 2011).

Genetic diversity is necessary for heterosis as it is positively related with yield. However, it is not sufficient to predict the performance of F₁ combinations. Hence, estimation of heterosis and combining ability together provide effective breeding tool to predict the yield potential of maize F₁ hybrids.

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