

Full Length Research Paper

Stability and genetic divergence study of single cross hybrids in maize (*Zea mays* L.)

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A study of stability and genetic divergence was carried out on 22 experimental maize hybrids for 3 years, at the Maize Breeding Research Station, Poonch, India, to evaluate potential crosses particularly for double cross hybrid with a view that well developed single cross hybrids represent an interesting potential base population for double cross hybrid, as they have high and stable yield and desirable agronomic characteristics, with large proportions of favourable loci previously selected. Considering the estimation of stability and genetic diversity together in the present investigation, both directional crosses based on most diverse and stable parents namely PHM 10 x PHM 23, PHM 10 x 35 and PHM 10 x PHM 31 may be recommended which can throw out superior segregants in hybridization.

Key words: Maize hybrid, stability, genetic divergence.

INTRODUCTION

Stability of the genetic divergence genotypes realized in hybrids may be potential parents for greater frequency of partially dominant alleles (Koutsika and Karagounis, 2005). However, the changing environmental conditions affect the performance of maize genotypes which requires a breeding programme that needs to take into account the consequences of environment and genotype interaction in the selection and release of improved varieties. Allard and Bradshaw (1964) suggested that the selection of genotypes should be based on least interactions with environments. Accordingly, well developed single cross hybrids represent an interesting potential base population for double cross hybrid, as they have been previously tested in various environments. Thus, these hybrids generally present high and stable yield and desirable agronomic characteristics, with large proportions

of favourable loci previously selected (Amorim and Souza, 2005).

The study of genetic divergence can assist in the choice of genotypes to be used in breeding programs for the development of new populations (Cruz and Regazzi, 1997). Genetic divergence is related to the degree of distance between populations in the set of genetic characters that differ between the populations. The more genetically diverse parents, the greater the chances of obtaining higher heterotic expression in F₁s and broad spectrum of variability in segregating population (Shekhawat et al., 2001). However, in most cases genetic distance is positively correlated with heterosis (Paterniani et al., 2008). Thus, the magnitude of heterosis is generally proportional to the genetic distance between the parents. According to Cargnelutti et al. (2008), genetic

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Table 1. Pooled analysis of variance over environments for different traits in maize hybrids

Source of variation	df	Grain Yield kg./ha.	Days to Tasselling	Days to Maturity	Plant Height (cm)	Shelling %
Varieties	21.00	4012279.00**	26.63***	24.03***	539.80***	7.86
Environments	2.00	24862880.00***	222.91***	1245.20***	5119.45***	3.81
Var.* Env.	42.00	1505117.25	4.30**	9.08**	213.83	8.13
Pooled Error	126.00	342820.75	1.12	5.11	55.10	2.18

*Significant at P=0.05 **Significant at P=0.01.

divergence (evaluated based on the genetic distance between individuals) is a predictive feature that allows for the identification of crosses with a higher probability of success. Specifically, the evaluation of divergence can identify those crosses that will optimize heterosis while avoiding undesirable features. In the prediction of genetic divergence between genotypes, multivariate methods, such as principal component analysis and canonical variables are very useful tools.

The goal of this study was to evaluate the stability and genetic divergence among 20 experimental hybrids for the choice of suitable parents of new population. We also aimed to strengthen the further research strategies for predicting the high yielding stable and diverse parents (single cross hybrids) for double cross hybrids through estimates of genetic divergence.

MATERIALS AND METHODS

The present experiment was carried out at the Maize Breeding Research Station (MBRS), Poonch (India) situated between 33°-25' to 34°-01' N latitude and 73° -58' to 74° -35' E longitude, at a height of 3300 MSL and bounded by Kashmir valley and line of control with Pakistan. The experimental materials consist of 22 experimental hybrids developed at MBRS, Poonch. The hybrids are moderately resistant to most of the prevailing diseases and insects. The experiment was conducted in randomized block design for three years, that is, 2009, 2010 and 2011 following the recommended agronomical practice for maize and physiological data, which was recorded from mean of five randomly selected plants from each entry. The stability among the hybrids was estimated following the method described by Eberhard and Russell, 1966. To study the genetic divergence among the hybrids used in present experiment and to know the fluctuation in clustering pattern, hybrids were calculated by canonical (Vector) and non-hierarchical Euclidean methods of divergence estimation. The D2 values were calculated by using the method described by Mahalanobis (1936). Genetic divergence analysis using canonical (vector) method is a sort of multivariate analysis where canonical vector and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively, were derived (Rao, 1952). Non-hierarchical Euclidean cluster analysis (Beale, 1969; Kalyal et al., 1985) was conducted using a computer software package (Windostat version 8.5).

RESULTS AND DISCUSSION

The combined analysis of variance across locations and years showed highly significant differences among

locations (L) and genotypes (G) and their interaction (G x L). The maximum grain yield variation was observed due to genotypes whereas the environments play highest significant role in variation due to days of tasseling and maturity (Table 1). Genotype environment interaction was highly pronounced in variation for shelling percentage among the genotypes (Dabholkar, 1999). The knowledge about the extent of fluctuations of yield and yield attributes over environments is very important in identifying genotypes, which are widely adapted.

Grain yield is a quantitatively inherited character and there is considerable interaction between genotypes and environments. Some of the crop varieties are widely adapted, whereas others are not. Because of the interactions between genotypes and environments, yield of genotypes tested across years vary and it is a problem for breeders to identify varieties that consistently give high yields in locations with diverse environmental conditions. Kang and Gorman (1989) reported that G x E interactions significantly reduced correlations between phenotypic and genotypic values. The results showed the hybrid PHM 12 was the highest among the others for grain yield, followed by PHM 34, PHM 14, PHM 10 and PHM 31 (Table 2). According to the joint regression model, the most stable hybrid with high mean yield and lowest S2 di value (0.999) was PHM 10 and its regression coefficient (bi) is 1.50, which can be an indication of its responsiveness to favourable environments (Table 2). Whereas the second most stable hybrid is PHM 31 with bi value 1.11, s2di 0.994 and high mean grain yield.

According to the model, the third most stable hybrid was PHM 34 with bi = 0.722, S2 di = -0.993 and mean yield 6.4 t ha⁻¹ followed by PHM 23 and PHM 35 with bi value 1.73 and 0.79 respectively, both the hybrids exhibited high grain yield. Although the mean yield value of PHM 34 is less than PHM 12, the performance of the hybrid under unfavourable environments can be predicted. The evaluation showed that these single cross hybrids have high yield potential and are well suited in the prevailing agro-climatic condition. Further, the hybrids may be used as source material for double cross hybrids as they showed stable yield and desirable agronomic characteristics, with large proportions of favourable loci previously selected. From the point of selecting the hybrids (parents) for hybridization, which are divergent

Table 2. Estimation of stability parameters for grain yield in maize hybrids.

S/N	Variety	Mean (μ)	Regression (bi)	Deviation (S^2di)
1	PHM 10	5440.600	1.508	1.000
2	PHM 11	5146.600	-0.057	0.633
3	PHM 12	6586.500	1.114	0.317
4	PHM 13	4363.700	1.433	0.979
5	PHM 14	5506.700	0.965	0.534
6	PHM 15	5196.300	2.034	0.997
7	PHM 16	3929.000	0.910	0.945
8	PHM 17	4650.200	1.968	0.972
9	PHM 18	3373.900	0.855	0.997
10	PHM 20	2266.400	0.177	0.422
11	PHM 22	5192.400	0.745	0.930
12	PHM 23	4414.300	1.732	0.992
13	PHM 24	4929.200	1.984	0.995
14	PHM 25	2123.200	1.511	0.991
15	PHM 27	3273.500	0.383	0.018
16	PHM 30	3758.300	1.208	0.989
17	PHM 31	5271.500	1.120	0.994
18	PHM 34	6445.000	0.722	0.994
19	PHM 35	5100.900	-0.791	0.960
20	PHM 39	3546.200	-1.105	1.000
21	Check (Kh. 612)	4204.700	1.785	0.894
22	Check (Kh. 517)	4966.000	1.800	0.967

enough for the character of interest, estimation of the genetic distance is most important. The present estimation of genetic divergence gave clear idea about the diverse nature of the population. Wide range of variation was observed in cluster mean performance for most of the characters studied. All the genotypes were grouped into five clusters, indicating the presence of diversity for different traits.

On the basis of results obtained from the present study, high degree of genetic divergence was observed among the hybrids under study (Liu et al., 2006). It is evident as more number of cluster (five) were formed by 22 hybrids (Figure 1) and high range of inter and intra cluster distance. Singh et al. (2005) also found wide range of variability in maize genotypes in his experiment. The more the diversity of parents, the greater the chances of obtaining high heterosis. (Williams and Hallarver, 2000). More et al. (2006) also reported more number of clusters and genotypes within the clusters in his experiments. Cluster 3 had maximum numbers of hybrids and cluster 2 and 5 had minimum number of hybrids (Figure 1). The maximum inter cluster distance was observed between cluster 1 and 5, and minimum was between cluster 3 and 5 (Table 3). The maximum intra cluster distance was noticed between hybrids of cluster 5 whereas it was minimum in cluster 2 (Table 2). The result indicated that the hybrids in different clusters differ largely and marginally in their genetic architecture as per their

maximum and minimum intra cluster distance, respectively.

Similar experiment was also carried out by Castanon et al. (1999) and Chen et al. (2007) who were of the opinion that geographical and genetic diversity exhibited no correspondence between them as hybrids from one and different origins were grouped together. This might be due to free exchange of genetic material from different regions. These findings were similar to the findings of Yin et al. (2004).

Principal factors were carried out using the principal component (PC) method for factor extraction. Differentiation among populations occurs in stages, or in other words in different axes of differentiation which accounts for total divergence (Cossa, 1990). Theoretically, many axes of differentiation can be envisaged as there are characters contributing to total variation, but it is not absolute. It is possible that most of the variation is accounted for by the first two or more axes of differentiation (Liu et al., 2006).

In the present investigating only the first three principal components showed eigen values more than one and cumulatively they explained 81.28% variability (Table 4). The first principal component explained 39.49% of the total variation and the second and third principal components explained 25.66% and 16.13% variation, respectively. The first principal component (λ_1) absorbed and accounted for maximum (39.49%) proportion of

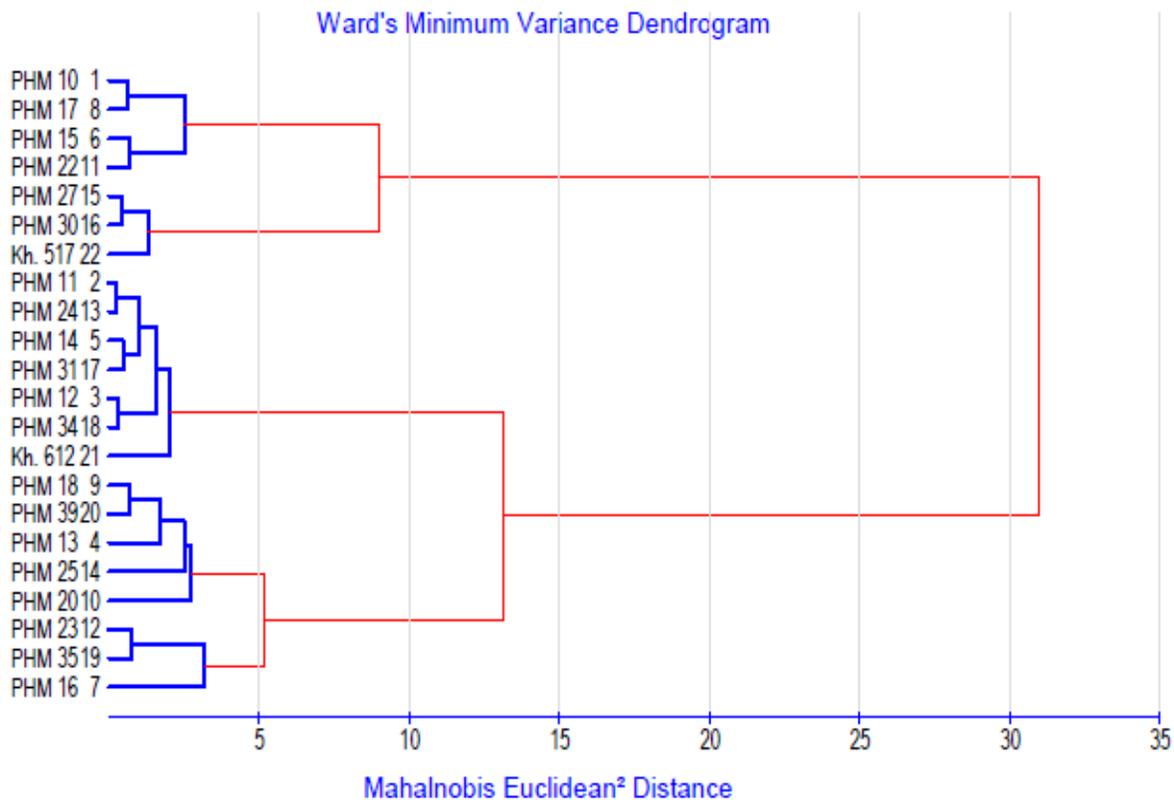


Figure 1. Clustering pattern of maize hybrids by Euclidean method.

Table 3. Mean inter and intra cluster distance among five clusters in hybrid maize by Euclidean method.

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster
1 Cluster	2.497	6.783	7.61	15.616	18.370
2 Cluster		1.752	8.062	7.413	13.540
3 Cluster			1.907	7.066	5.373
4 Cluster				3.817	5.590
5 Cluster					3.911

variability and the remainder accounted for progressively lesser amount of variation (25.66 and 16.13) for λ_2 , λ_3 and λ_4 , respectively. The study through canonical analysis revealed that on the basis of two axes, the cumulative percentage of variation absorbed by $\lambda_1 + \lambda_2$ was 65.15% whereas there are three effective axes Z1, Z2 and Z3 where $\lambda_1 + \lambda_2 + \lambda_3 = 81.28\%$.

In Vector 1 shelling percent with element value 0.523; in Vector 2 grain yield with element value 0.780 and in Vector 3 days to maturity with element value -0.780, contributed maximum to the total divergence at primary, secondary and tertiary axes of differentiation based on canonical vectors Z1, Z2 and Z3, respectively. Liu et al. (2006) also reported the similar types of findings in his

experiment. The character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. Genetic divergence between genotypes was measured in terms of spatial distance and resulted in formation of three dimensions (3D) based on three PCA scores (λ_1 , λ_2 and λ_3 graphs) as depicted in Figure 2. Three principal factor scores were used to plot all the 22 hybrids using PCA1, PCA2 and PCA3, that is, 3D plot which accounted for most important component traits namely: shelling percent, grain yield and days to maturity. A similar type of study was also carried out by More et al. (2006), who reported that leaf area per plant, plant height

Table 4. Canonical vectors which supply best linear function of variates, value of canonical roots and percentage of variation absorbed by respective roots.

Parameter	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
Genotype	Vector 1	Vector 2	Vector 3
1PHM 10	10.620	3.399	-12.184
2PHM 11	9.927	3.049	-11.905
3PHM 12	9.925	3.386	-11.703
4PHM 13	9.931	2.504	-11.544
5PHM 14	9.813	3.079	-11.710
6PHM 15	10.435	3.142	-11.808
7PHM 16	9.440	2.866	-11.776
8PHM 17	10.535	3.187	-12.285
9PHM 18	9.808	2.443	-11.930
10PHM 20	9.487	2.245	-12.064
11PHM 22	10.440	3.018	-11.995
12PHM 23	9.363	2.727	-11.730
13PHM 24	9.757	2.985	-12.018
14PHM 25	9.435	2.208	-11.849
15PHM 27	10.314	2.437	-12.086
16PHM 30	10.477	2.549	-12.055
17PHM 31	9.514	3.041	-11.769
18PHM 34	9.912	3.307	-11.889
19PHM 35	9.453	2.769	-11.707
20PHM 39	9.721	2.693	-12.098
21Kh. 612	9.848	3.031	-11.937
22Kh. 517	10.422	2.670	-11.715

and days to 50 percent flowering were the major contributor towards divergence, while studying forage maize. Amongst 22 maize hybrids, studied in the present study PHM 10 exhibited great extent of genetic diversity on the basis of 3D diagram based on PCA scores and Euclidian distance matrix, which reflected it as most diverse genotype for PHM 20 followed by PHM 25, PHM 23, PHM 35, PHM 31 etc. Whereas, the minimum genetic was observed between PHM 14 and K 612 (Figure 2). The hybrids, PHM 10, PHM 23, PHM 35 and PHM 31 showed significantly high stability and divergence for grain yield. Expectations for different combinations of quality characters along with yield and yield attributes should be considered as selection criteria for desired improvement. The similar type of work have also been done by Mishra and Dash (1997) who had found similar response of breeding material towards stability and

divergence.

Conclusion

Estimation of combining ability of parents is not always sufficient to reveal which combination should be used in breeding crosses. Instead analysis related to stability and genetic divergence of hybrids should be assessed together in evaluating potential crosses particularly for double cross hybrid. Considering the estimation of stability and genetic diversity together in the present investigation, both directional crosses namely PHM 10 x PHM 23, PHM 10 x 35 and PHM 10 x PHM 31 may be recommended which can throw out superior segregants in hybridization.

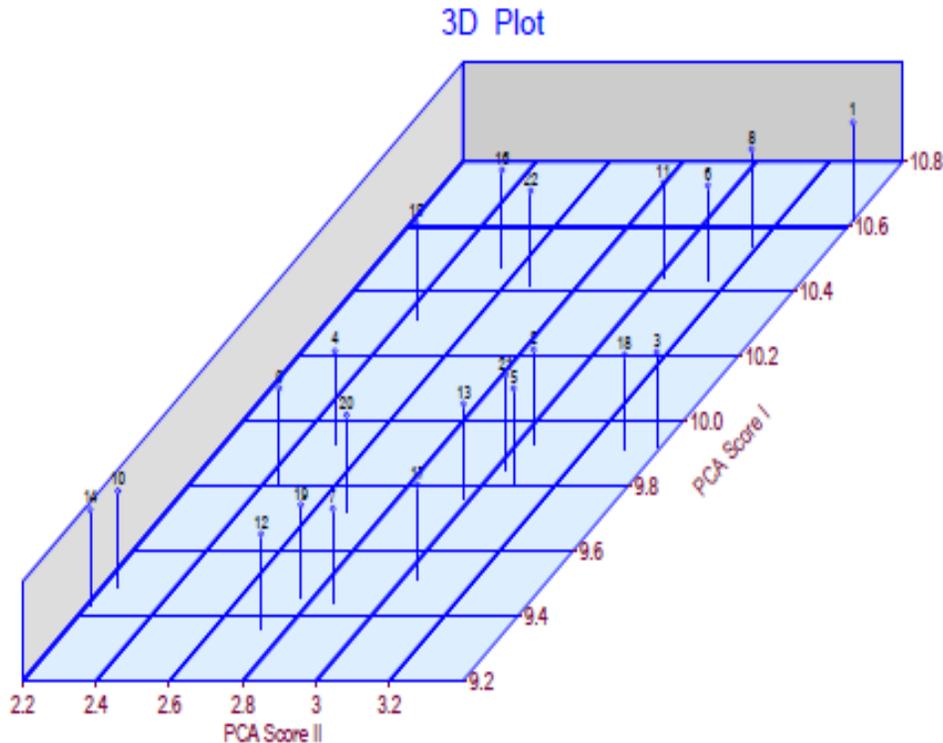


Figure 2. Three- dimensional representation of hybrids using 3 principal components based on canonical variates

Conflict of Interest

The authors have not declared any conflict of interest.

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