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Heterosis and combining ability analysis in quality protein maize inbred lines

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In the present investigation, 42 crosses of quality protein maize (QPM) inbred lines (L1, L2, ….L14) with three testers (T1, T2 and T3) were evaluated against a QPM check , Shakti-1 in a randomized complete block design with 3 replications at G.B. Pant University of Agriculture and Technology, Pantnagar, India during Kharif, 2004. Observations were recorded on days to 50% tasselling and silking, plant height, ear height , ear length, ear diameter, kernel rows per ear, 100-kernel weight, grain yield and incidence of BLSB and BSDM. Protein, lysine and tryptophan contents were also estimated. The characters under study showed highly significant genotypic differences and wide range of variation in mean values. The crosses, L8 x T1, L1 x T3, L8 x T2, L5 x T2, L5 x T1, L2 x T1, L13 x T3, L3 x T1 and L8 x T3 revealed significant positive heterosis for grain yield. The gca effects of the parents showed that among lines, L8 was good for ear length, ear diameter, kernel rows per ear, 100-kernel weight and grain yield. L1, L12 and L13 were the other good general combiners. Based on the sca effects, L3 x T1 and L3 x T2 were good for ear length, ear diameter, kernel rows per ear, 100-kernel weight and grain yield. L14 x T3, L1 x T3, and L4 x T1 were the other specific cross combinations good for different characters. All the inbred lines and their crosses were moderately resistant to both the foliar diseases, BLSB and BSDM. The cross, L13 x T3 superceded the standard check for protein (9.74%), lysine (3.24%) and tryptophan (0.81%).

Key words : QPM, Top cross, GCA, SCA, Grain yield

INTRODUCTION

MAIZE (Zea mays L.), a major cereal crop cultivated all over the world for human food, animal feed as grain and fodder and many other industrial products like starch, oil and glucose etc., has poor quality of protein due to lower contents of two essential amino acids, lysine and tryptophan and an undesirable proportion of leucine and isoleucine.

The opaque-2 gene which is responsible for the enhancement of lysine and tryptophan of maize protein, if incorporated into any population, inbred line or any other germplasm of maize through back cross technique, improves the nutritional status of maize. The modified opaque-2 maize with hard endosperm and vitreous kernels is known as Quality Protein Maize (QPM).Its nutritional superiority over normal maize is well established (Gupta *et al*., 1979). Concerted research efforts have been made on QPM in India and abroad particularly at CIMMYT, Mexico where Drs. S.K. Vasal and E. Villegas were jointly honoured by 'Millennium World Food Prize' during 2000 for their pioneering work on QPM.

In fact, the future is of hybrid cultivars. In QPM also, hybrids are more successful among the farmers as these are always planted with fresh F1 seed every year and thus remain unaffected from contamination through normal maize cultivars. Since the seed of open pollinated maize varieties can be saved and used for next 3-4 years, it gets contaminated if not grown in isolation. If the presently grown maize hybrids and varieties are replaced with QPM hybrids, the latter will provide a definite promise in upgrading the nutritional security of maize-based population. The QPM hybrids like Shaktiman-1, Shaktiman-2, Shaktiman-3, Shaktiman-4, Shaktiman-5, HQPM-1 and a QPM variety, Shakti-1 are under cultivation and catching the area up in eastern U.P., Bihar and some other states.

In a highly cross pollinated crop like maize, exploitation of heterosis can be accomplished through the development and identification of high *per se* performing vigorous parental inbred lines and their subsequent evaluation for combining ability in cross combinations to identify hybrids with high heterotic effects. The magnitude of heterosis shown by the hybrids depends largely on the heterotic pattern and genetic divergence between parental lines. The information about the heterotic patterns and combining ability of parents and crosses both facilitate the breeders in the selection and development of single cross hybrids.

The present study was, therefore, undertaken to assess nature and magnitude of heterosis and combining ability effects for yield and other characters in a line x tester system using 14 QPM inbred lines and 3 testers.

MATERIALS AND METHODS

The experiment was conducted at Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttaranchal during Kharif, 2004. The experimental material comprised 42 top crosses developed by crossing 14 QPM inbred lines of DMR series with 3 broad based testers abbreviated as L1, L2, ….L14 and T1, T2 and T3, repectively. The parental inbred lines and top crosses were evaluated against a QPM check, Shakti-1 in randomized complete block design with 3 replications. The net plot area was 7.5 m2. Observations were recorded on whole plot basis for days to 50% tasselling and silking and fresh ear weight (later converted at 15% grain moisture for grain yield), whereas, the data on other characters like plant height, ear height, ear length, ear diameter, number of kernel rows per ear, 100-kernel weight were taken on 10 randomly selected competitive plants from every plot. The average value of these plants was calculated and used for analysis of variance, heterosis and combing ability. The incidence of two major foliar diseases namely, BLSB and BSDM was also recorded on 1-5 scale. Protein, lysine and tryptophan analysis was done using standardized laboratory procedures.

RESULTS AND DISCUSSION

QPM may make its greatest contribution in improving the protein quality of the diet of maize-based population. In past few years, many developing countries have released new QPM hybrids and varieties for the farmers and several others including India

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have launched major QPM promotion programmes. In an effort to generate new material and subsequently to draw the inferences, the present investigation was executed using line x tester analysis for studying the performance of 14 QPM inbred lines and their crosses with 3 testers for yield and its component characters. Information on heterosis and combining ability were obtained using standard statistical techniques.

The analysis of variance revealed that all genotypes differed significantly for the characters studied. This indicated that there was significant inherent variability among the genotypes for these characters. In this study, the extent of heterosis was measured over the mid-parental value (average heterosis), better parent (heterobeltiosis) and standard check (standard heterosis) for all the characters. Most of the crosses had positive average heterosis for grain yield (Table 1). It was maximum for the cross, L8 x T1 followed by L1 x T3, L8 x T2, L5 x T2, L5 x T1, L2 x T1, L13 x T3, L3 x T1 and L8 x T3. Similar trend was observed for heterobeltiosis and standard heterosis. Same pattern of positive

Table 1 : Mid parent (MP) better parent (BP) and standard parent (SP) heterosis (%) for grain yield

Cross	Grain yield		
	MP	BP	SP
L_1 x T_1	11.40	-12.20	30.18
L_1 x T_2	5.862	-22.48*	42.59*
L_1 x T_3	77.15**	54.11**	135.543**
L_2 x T_1	45.19**	24.27	84.25**
L_2 x T_2	0.089	-21.24	44.87*
L_2 x T_3	-26.59	-37.95**	-5.17
L_3 x T_1	34.60*	0.476	48.97*
L_3 x T_2	19.88	-16.24	54.071**
L_3 x T_3	-44.37**	58.88**	-37.163
L_4 x T_1	-4.70	-23.26	13.782
L_4 x T_2	-2.79	-27.47*	33.413
L_4 x T_3	11.94	-10.87	36.216
L_5 x T_1	47.68**	3.017	52.74*
L_5 x T_2	51.03**	-0.436	83.157**
L_5 x T_3	10.76	-23.39	17.08
L_6 x T_1	-11.035	-30.77*	2.64
L_6 x T_2	-23.79	-44.786**	1.57
L_6 x T_3	23.38	-4.95	45.25*
L_7 x T_1	-12.28	-33.93*	-2.051
L_7 x T_2	-8.38	-35.50**	18.65
L_7 x T_3	12.51	-16.11	28.75**
L_8 x T_1	88.40**	30.004	92.75**
L_8 x T_2	61.41**	5.42	93.94**
L_8 x T_3	34.13*	-8.2	40.08*
L_9 x T_1	21.846	-7.25	37.51
L_9 x T_2	-41.52**	-58.47**	-23.60
L_9 x T_3	28.19	-3.416	47.61*
L_{10} x T_1	-4.70	-23.26	13.78
L_{10} x T_2	10.76	-23.391	17.08
L_{10} x T_3	19.812	5.901	57.019**
L_{11} x T_1	-3.832	-15.35	26.02
L_{11} x T_2	14.40	-12.30	38.18
L_{11} x T_3	2.08	-22.24	44.8*
L_{12} x T_1	19.82	59.01**	57.019**
L_{12} x T_2	10.10	-10.31	63.94**
L_{12} x T_3	22.05	6.48	62.740**
L_{13} x T_1	-3.73	16.35	22.022
L_{13} x T_2	20.99	-3.53	77.465**
L_{13} x T_3	35.58**	16.31	77.77**
L_{14} x T_1	13.13	-19.48	19.37
L_{14} x T_2	-22.09	-47.75**	-3.89
L_{14} x T_3	25.09	11.77	34.84

*, ** significant at 5% and 1% level of probability.

heterosis was also reported by Debnath (1984), Lamkey (1986), Beck *et al*. (1990), Tomar and Do-Ngo-min (1990), Ganguli *et al.* (1989) and Ghosh (1994) also reported same pattern of positive heterosis. The results obtained thus suggested that there was sufficient heterosis available in the experimental material for grain yield and its components.

Table 2a : Summary of parents showing high general combining ability (gca) effects for grain yield and other characters

S.No.	Character		Number	Parents
1.	Days to 50% tasselling	Early	1	L_2
		Late	1	L_4
2.	Days to 50% silking	Early	1	L_2
		Late	-	-
3.	Plant height	High	3	L_2, L_{13}, Tester 3
		Low	1	Tester 2
4.	Ear height	High	2	L_2, L_{13}
		Low	2	L_4, Tester 2
5.	Ear length		5	L_1, L_6, L_8, L_{13}, Tester 3
6.	Ear diameter		4	L_8, L_{11}, L_{12}, L_{13}
7.	Kernel rows per ear		5	L_1, L_6, L_8, L_{10}, Tester 1
8.	100-Kernel weight		2	L_1, L_8
9.	Grain yield		4	L_1, L_8, L_{12}, L_{13}

Table 2b : Summary of the crosses showing high specific combining ability (sca) effects for grain yield and other characters

Sl. No.	Character		Number	Cross
1.	Days to 50% tasselling		1	L_2 x T_1
2.	Days to 50% silking		1	L_1 x T_3
3.	Plant height	High	3	L_1 x T_3, L_3 x T_3, L_{12} x T_2
		Low	4	L_4 x T_3, L_6 x T_3, L_{12} x T_1, L_{14} x T_2
4.	Ear height	High	5	L_1 x T_3, L_3 x T_3, L_4 x T_1, L_5 x T_1, L_{12} x T_2
		Low	4	L_4 x T_3, L_5 x T_3, L_6 x T_3, L_{12} x T_1
5.	Ear length		8	L_2 x T_2, L_2 x T_3, L_3 x T_1, L_3 x T_1, L_3 x T_2, L_4 x T_2, L_7 x T_1, L_{14} x T_1, L_{14} x T_3
6.	Ear diameter		9	L_2 x T_2, L_2 x T_3, L_3 x T_2, L_4 x T_2, L_7 x T_1, L_8 x T_1, L_{10} x T_2, L_{14} x T_1, L_{14} x T_3
7.	Kernel rows per ear		13	L_1 x T_1, L_2 x T_2, L_2 x T_3, L_3 x T_1, L_3 x T_2, L_5 x T_2, L_6 x T_2, L_7 x T_1, L_7 x T_3, L_9 x T_1, L_{13} x T_2, L_{14} x T_1, L_{14} x T_3
8.	100-Kernel weight		6	L_3 x T_1, L_3 x T_2, L_6 x T_2, L_7 x T_3, L_8 x T_1, L_{14} x T_3
9.	Grain yield		12	L_1 x T_3, L_2 x T_1, L_3 x T_1, L_3 x T_2, L_5 x T_2, L_6 x T_3, L_8 x T_1, L_8 x T_2, L_9 x T_1, L_9 x T_3, L_{10} x T_3, L_{13} x T_2

The combining ability analysis was performed through line x tester technique (Kempthorne, 1957) in order to sort out promising QPM inbred lines which may have good potential for yield and may be utilized for commercial production of hybrids. Variance due to sca was considerably higher than variance due to gca for all the characters except plant and ear heights which indicated prevalence of non-additive gene action for these characters. Larger contribution of line x tester interaction to the total sum of squares due to hybrids than the lines and testers separately for all the characters except days to tasselling and silking indicated that the variability among the crosses for these characters was mainly due to interaction of lines and testers. The estimates of gca effects of the parents showed that among the lines, L8 was found good for ear length, ear diameter, kernel rows per ear, 100-kernel weight and grain yield. L12 and L13 were the other good general combiners (Table 2a). These results were in accordance with El-Hosary (1985), Coomin *et al.* (1991) and Singh (1994). Based on sca results, different crosses showed good sca effects for one or more characters (Table 2b). The crosses, L3 x T1 and L3 x T2 showed good positive sca for ear length, ear diameter, 100-kernel weight and grain yield. L14 x T3, L1 x T3 and L4 x T1 were the other specific cross combinations good for one or the other characters. The crosses showing good sca for most of the characters have been used as single cross hybrids. Similar results were reported by Beck *et al*. (1990), Ordas *et al.* (1991) and Singh (1994).

All the inbred lines and their crosses were moderately resistant to both the foliar diseases, BLSB and BSDM. The lines, L10, L13 and L14 (1.0, 1.0) and crosses L1 x T2, L9 x T3, L10 x T1, L10 x T2, L10 x T3, L13 x T1 and L13 x T2 showed better resistance (1.0, 1.0) to these diseases as compared to standard check (1.5, 2.0). The cross, L3 x T2 had highest protein (11.5%), whereas, maximum lysine (3.92%) and tryptophan (0.95%) contents were shown by the cross, L4 x T3 and L11 x T1, respectively. The cross L13 x T3 superceded the standard check for protein (9.74%), lysine (3.24%) and tryptophan (0.81%).

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