

Research Article

Combining ability analysis for grain yield and its contributing traits in maize (*Zea mays* L.) over environments

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Abstract

Combining ability analysis for grain yield and its contributing traits in maize was performed with 15 inbred line and 3 tester parents and the resulting 45 hybrids using line x tester cross analysis in three environments during *kharif* and *rabi* 2014. The results of combining ability analysis over the environments revealed significant mean squares due to general and specific combining ability indicating that both additive and non-additive gene actions were important in the inheritance of characters studied. The parents L₂ (EIQ -132), L₄(EIQ-134), L₅(EIQ-135), L₆(EIQ-136), L₈(EIQ-138), and L₁₄(EIQ-144) and L₁₅ (EIQ-145) were good general combiners for grain yield and majority of traits over the environments. Hence, these parents can be used in crossing and further exploited for improvement of traits in the population. Six inbred lines *viz.*, L₁(EIQ-131), L₂(EIQ -132), L₃(EIQ-133), L₆(EIQ-136), L₈(EIQ-138) and L₁₄(EIQ-144) were identified good general combiner for maturity related traits. Whereas the crosses L₇ x T₂ (EIQ-137 x EIQ-102), L₁₃ x T₃ (EIQ-143 x EIQ-103), L₁₀ x T₁ (EIQ-140 x EIQ-101), L₁ x T₁(EIQ-131 x EIQ-101) and L₁₁ x T₃ (EIQ-141 x EIQ-103) were identified as potential ones for yield and yield components based on high *sca* effects along with high *per se* performance. These hybrids may be exploited for commercial cultivation by testing them over locations and years for their yield stability.

Key words

Maize, combining ability, grain yield ,line x tester

Introduction

Maize (*Zea mays* L.) is the third largest grain crop in India, after rice and wheat. It is grown during rainy (*kharif*), winter (*rabi*) and spring seasons, but major production is in the rainy season (Yadav *et al.* 2016). Protein of maize is deficient in two essential amino acids, lysine and tryptophan (Bhatia and Rabson 1987). In non-QPM, the endosperm contains a high amount of zein which is completely devoid of lysine and tryptophan. The poor nutritional value of normal maize grain has been well known for a long time (Osborne and Mendel 1914). Maize has protein content with protein quality limited by deficiencies of two essential amino acid like lysine and tryptophan and has excess of leucine and isoleucine, leading to a poor growth in children and pellagra in adults (Mertz *et al.*, 1964).

Line x tester method has been used in various studies Singh *et al.* (2013), Jahan *et al.* (2014), Rastgari *et al.* (2014) and Kumar *et al.* (2015) to determine general combining ability (gca) and specific combining ability (sca) of the lines under study. Line x tester analysis is also helpful in estimating genetic variance components and types of gene effects (Singh and Chaudhary, 1985). Venkatesh *et al.* (2001) using line x tester method found significant differences between lines, testers

and line x tester combinations indicating the contribution of both additive and non-additive (dominance) gene actions in controlling grain yield. The nature of gene action would help in predicting the effectiveness of selection in population. A distinct type of gene action, its magnitude and constitution of genetic architecture are of fundamental importance to plant breeder. The objectives of present study were to estimate gca, sca and gene effects for grain yield and yield contributing traits in maize using hybrids over environments produced by the line x tester mating design.

Materials and methods

The experimental material was generated by making crosses between 15 inbred lines and 3 testers in line x tester mating design. Fifteen parental inbred lines were crossed with three testers during *rabi* 2013 to generate the experimental hybrids for this study. The experimental material, thus, consisting of 45 F₁s (single crosses), 15 inbred lines, 3 testers and 4 checks (HQPM-1, HQPM-5, Pratap QPM-1 and Vivek QPM-9 Table -5) were evaluated during *kharif* and *rabi* 2014 in three environments. Three environments were two locations and two seasons *viz.* E₁ (timely sowing, *kharif* 2014 at Instructional farm Rajasthan college of Agriculture, Udaipur), E₂ (timely sowing, *kharif*

2014 at ARSS, Vallabh Nagar, MPUAT, Udaipur) and E₃ (timely sowing, *rabi* 2014 at Instructional farm Rajasthan college of Agriculture, Udaipur). The experimental material was planted under each environment in randomized block design with three replications in a single row plot of four meter length, maintaining crop geometry of 60 x 25 cm. All the recommended agronomy inputs and practices were applied to the crop during the season, to raise the successful crop. NPK fertilizer were applied at the rate of 120:60:00 kg/ha. The total amount of phosphatic fertilizer and half of the nitrogenous fertilizer were applied as basal dose and rest of the nitrogenous fertilizer were given in two equal doses, one at knee-high stage and another at flowering stage of the crop. The border rows were also planted to neutralize the border effect.

Thirteen quantitative observations were recorded on ten randomly selected competitive plants for each treatment in each replication for plant type traits *viz.* plant height (cm), ear height (cm) for yield and yield contributing traits *viz.*, ear length (cm), ear girth (cm), number of grain rows per ear, 100-grain weight (g), grain yield per plant (g), shelling percentage (%) and harvest index (%). The observations for maturity related traits *viz.* days to 50 per cent tasseling, days to 50 per cent silking, anthesis-silking interval and days to 75 per cent brown husk were recorded on plot basis. The mean values were used for statistical analysis. The observations taken for hybrids and parents were subjected to L x T analysis and combining ability effects of different crosses were worked out. The combining ability variance analysis was based on the method developed by Kempthorne (1957).

Results and discussion

The pooled analysis of variance for combining ability over three environments revealed that the environments, genotypes, parents and crosses exhibited highly significant differences among themselves for all the characters studied (Table -1). The parents *vs* crosses which indicates average heterosis, was also significant for all traits except for anthesis-silking interval, thus considerable amount of average heterosis was reflected in hybrids. This indicates the presence of non-additive gene action (Bello and Olaoye, 2009).

The interaction of genotypes, parents, crosses, and parents *vs* crosses with environments were significant for all the characters except number of grain rows per ear, 100-grain weight and shelling percentage. While the genotypes x environments for harvest index, parents x environments, for grain yield per plant and harvest index, crosses x environments for ear girth, harvest index and parents *v/s* crosses x environments for ear girth.

Mean squares due to lines, testers and lines x testers were significant for all the characters suggesting significant role of additive and non-additive gene actions like additive x additive, additive x dominance, epistasis and other interaction effects in the expression of these characters. Interaction of lines with environments was significant for all the characters except ear girth, number of grain rows per ear, 100-grain weight, shelling percentage and harvest index. Further, testers x environments interaction was significant for all the characters except ear height, ear length, ear girth, number of grain rows per ear, 100-grain weight, shelling percentage and harvest index. The interaction of lines x testers x environments were significant for all the characters except days to per cent tasseling, number of grain rows per ear, 100-grain weight, shelling percentage and harvest index. This indicated that estimates of *gca* and *sca* effects were highly influenced by environments for large numbers of characters studied. Similar findings reported by Rashmi *et al.* (2013).

Selection of parents with good general combining ability is a prime requisite for any successful breeding programme especially for heterosis breeding. The general combining ability effects of parents (lines and testers) over the environments are presented in Table 2. The estimates of *gca* effects revealed that the good general combiner for yield and majority of yield contributing characters *viz.*, harvest index, ear girth, 100-grain weight, ear length, number of grain rows per ear and shelling percentage were inbred lines L₂ (EIQ -132), L₄ (EIQ-134), L₅ (EIQ-135), L₆(EIQ-136), L₈(EIQ-138), and L₁₄(EIQ-144). Six inbred lines *viz.*, L₁(EIQ-131), L₂(EIQ -132), L₃(EIQ-133), L₆(EIQ-136), L₈ (EIQ-138) and L₁₄(EIQ-144) were identified good general combiner for maturity related traits. These inbred lines possessed favourable genetic architecture for imparting earliness to their progenies. (Jahan *et al.*, 2014) also observed similar phenomenon in their study. For plant type traits two inbred lines L₇(EIQ-137) and L₉ (EIQ-139) were identified good general combiner. Similar finding was reported by (Singh *et al.* 2013) for earliness, dwarfness and yield. In general, inbred lines L₂ (EIQ -132), L₄(EIQ-134), L₅(EIQ-135), L₆(EIQ-136), L₈(EIQ-138), and L₁₄(EIQ-144) and L₁₅ (EIQ-145) have been good general combiner for yield and majority of the characters. This finding is in close agreement with previous reports (Rastgari *et al.*, 2014, Kumar *et al.*, 2015) for yield and most of yield contributing traits.

Among the testers, T₁(EIQ-101) and T₂(EIQ-102) were best general combiner for maturity related traits, whereas, T₁(EIQ-101) and T₂(EIQ-102) also

good general combiner for ear height and plant height respectively. Tester T₃ (EIQ-103) had good general combiner for ear length, ear girth, number of grain rows per ear and harvest index. None of testers exhibited good general combiner for grain yield per plant. The general combining effects observed is due to additive gene effects and additive x additive gene effects (Griffing, 1956).

The estimates of *sca* effects for yield and yield contributing traits on pooled basis are presented in Table 3. Out of 45 crosses only 11 crosses *viz.*, L₁ x T₁ (EIQ-131 x EIQ-101), L₅ x T₁ (EIQ-135 x EIQ-101), L₆ x T₁ (EIQ-136 x EIQ-101), L₁₀ x T₁ (EIQ-140 x EIQ-101), L₇ x T₂ (EIQ-137 x EIQ-102), L₉ x T₂ (EIQ-139 x EIQ-102), L₁₂ x T₂ (EIQ-142 x EIQ-102), L₃ x T₃ (EIQ-133 x EIQ-103), L₁₀ x T₃ (EIQ-140 x EIQ-103), L₁₁ x T₃ (EIQ-141 x EIQ-103) and L₁₃ x T₃ (EIQ-143 x EIQ-103) exhibited significantly positive *sca* for yield per plant. These results are in conformity with findings of Kumar *et al.* (2015). Significant yield performance in specific crosses was due to the combinations on the basis of their *per se* performance and *sca* effects. (Ahmad *et al.*, 2014). None of the hybrid exhibited positive significant *sca* effects for shelling percentage.

Five promising crosses with desirable *sca* effects for various traits *viz.*, days to 50 per cent tasseling, days to 50 per cent silking, anthesis-silking interval, days to 75 per cent brown husk, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of grain rows per ear, 100-grain weight (g), grain yield per plant (g), shelling percentage (%) and harvest index (%) along with mean performance and *gca* effects of parents involved in the crosses on pooled basis are listed in Table 4. The crosses, L₇ x T₂ (EIQ-137 x EIQ-102), L₁₃ x T₃ (EIQ-143 x EIQ-103), L₁₀ x T₁ (EIQ-140 x EIQ-101), L₁ x T₁ (EIQ-131 x EIQ-101) and L₁₁ x T₃ (EIQ-141 x EIQ-103) expressed high significant *sca* effects as well as high *per se* performance for grain yield per plant and other traits. It was also observed that the desirable cross combinations included high x high, high x medium, high x low, medium x high, medium x medium, medium x low, low x high and low x medium and low x low type of general combiners (Table 4). The desirable performance of cross combinations like medium x medium, low x low, medium x low and low x medium general combiners may be ascribed to complementary (dominance x dominance) gene effects.

Crosses, L₈ x T₁ (EIQ-138 x EIQ-101), for days to 50% tasseling and days to 50% silking, L₃ x T₁ (EIQ-133 x EIQ-101) for days to 50% silking, L₆ x T₁ (EIQ-136 x EIQ-101), for anthesis – silking interval, L₉ x T₂ (EIQ-139 x EIQ-102), for plant

height, L₇ x T₁ (EIQ-137 x EIQ-101) for ear height, L₁₁ x T₃ (EIQ-141 x EIQ-103), L₁₂ x T₃ (EIQ-142 x EIQ-103) and L₁₄ x T₃ (EIQ-144 x EIQ-103) for ear length, L₁₄ x T₃ (EIQ-144 x EIQ-103) and L₃ x T₃ (EIQ-133 x EIQ-103) for number of grain rows per ear had high *sca* performance and high mean values in desirable direction. These desirable cross combinations involved high x high type of general combiners (Rastgari *et al.*, 2014 and Aly, 2013) were reported about interaction between positive and positive alleles in crosses involving high x high combiners which can be fixed in subsequent generations if no repulsion phase linkages are involved. However, those crosses which involved one good combiner and the other medium or poor combiner could produce desirable transgressive segregates if additive genetic system was operating in good combining parent and epistatic effects also act in same direction (additive x dominance).

The crosses, L₁₂ x T₂ (EIQ-142 x EIQ-102), L₂ x T₃ (EIQ-132 x EIQ-103) and L₁₃ x T₁ (EIQ-143 x EIQ-101), showed such combination of *gca* effects for days to 50% tasseling, L₁₂ x T₂ (EIQ-142 x EIQ-102), L₂ x T₃ (EIQ-132 x EIQ-103) and L₁ x T₂ (EIQ-131 x EIQ-102) for days to 50% silking, L₁₄ x T₁ (EIQ-144 x EIQ-101) and L₆ x T₁ (EIQ-136 x EIQ-101) for anthesis – silking interval, L₁ x T₃ (EIQ-131 x EIQ-103), L₂ x T₃ (EIQ-132 x EIQ-103), L₇ x T₃ (EIQ-137 x EIQ-103) and L₉ x T₂ (EIQ-139 x EIQ-102) for days to 75% brown husk. Similarly other crosses were showed such combination of *gca* effects L₁₄ x T₂ (EIQ-144 x EIQ-102) and L₁₀ x T₂ (EIQ-140 x EIQ-102) for plant height, L₉ x T₁ (EIQ-139 x EIQ-101), L₇ x T₂ (EIQ-137 x EIQ-102) and L₁₄ x T₁ (EIQ-144 x EIQ-101) for ear girth, L₁₄ x T₃ (EIQ-144 x EIQ-103), L₈ x T₁ (EIQ-138 x EIQ-101) and L₂ x T₃ (EIQ-132 x EIQ-103) for number of grain rows per ear, L₆ x T₁ (EIQ-136 x EIQ-101), and L₁₄ x T₃ (EIQ-144 x EIQ-103) for 100-grain weight and L₁₀ x T₃ (EIQ-140 x EIQ-103) and L₁₃ x T₃ (EIQ-143 x EIQ-103) for harvest index. None of the crosses exhibited such types of combination for *gca* effect for grain yield and shelling percentage. The preponderance of non-additive gene action for yield contributing traits in most crosses also suggested heterosis breeding as a profitable proposition. The desirable traits can be improved by developing F₁ hybrids from the parents of good general combiners. These results were in agreement with the earlier findings of Jahan *et al.* (2014). For improvement of yield and other desirable traits, a breeding programme which can exploit both the significance of additive and non-additive type of gene action would be useful.

Other desirable performance of cross combinations like medium x medium, low x low, medium x low and low x medium general combiners may be

ascribed to complementary (dominance x dominance) gene effects.

The cross $L_1 \times T_1$ (EIQ-131 x EIQ-101) observed such combination of gca effects for days to 50% tasseling, $L_{11} \times T_2$ (EIQ-141 x EIQ-102), $L_{13} \times T_2$ (EIQ-143 x EIQ-102), and $L_{15} \times T_3$ (EIQ-145 x EIQ-103) for anthesis to silking interval, $L_3 \times T_1$ (EIQ-133 x EIQ-101) for days to 75% brown husk, $L_5 \times T_3$ (EIQ-135 x EIQ-103) and $L_4 \times T_3$ (EIQ-134 x EIQ-103) for plant height, $L_{14} \times T_2$ (EIQ-144 x EIQ-102) and $L_5 \times T_3$ (EIQ-135 x EIQ-103) for ear height, $L_5 \times T_2$ (EIQ-135 x EIQ-102) and $L_{15} \times T_2$ (EIQ-145 x EIQ-102) for ear length, $L_5 \times T_1$ (EIQ-135 x EIQ-101) and $L_{15} \times T_2$ (EIQ-145 x EIQ-102) for ear girth, $L_1 \times T_2$ (EIQ-131 x EIQ-102) for number of grain rows per ear and $L_5 \times T_3$ (EIQ-135 x EIQ-103), $L_{11} \times T_3$ (EIQ-141 x EIQ-103), and $L_2 \times T_2$ (EIQ-132 x EIQ-102) for 100- grain weight.

The crosses $L_7 \times T_2$ (EIQ-137 x EIQ-102), $L_{13} \times T_3$ (EIQ-143 x EIQ-103), $L_{10} \times T_1$ (EIQ-140 x EIQ-101), $L_1 \times T_1$ (EIQ-131 x EIQ-101) and $L_{11} \times T_3$ (EIQ-141 x EIQ-103) exhibited such combination of gca effects for grain yield per plant, $L_{11} \times T_3$ (EIQ-141 x EIQ-103), $L_8 \times T_2$ (EIQ-138 x EIQ-102), $L_9 \times T_1$ (EIQ-139 x EIQ-101), $L_7 \times T_2$ (EIQ-137 x EIQ-102) and $L_{15} \times T_3$ (EIQ-145 x EIQ-103) for shelling percentage and crosses $L_7 \times T_2$ (EIQ-137 x EIQ-102), $L_{10} \times T_1$ (EIQ-140 x EIQ-101) and $L_1 \times T_1$ (EIQ-131 x EIQ-101) for harvest index. Involvement of both combiners with low gca has been attributed to over dominance and epistasis interaction, which has been suggested by Malik *et al.* (2004).

Conclusion

Considering the overall performances, the parents L_2 (EIQ-132), L_4 (EIQ-134), L_5 (EIQ-135), L_6 (EIQ-136), L_8 (EIQ-138), and L_{14} (EIQ-144) and L_{15} (EIQ-145) were the good general combiners and genetically worthy parents, as they contributed favourable genes for grain yield and its components. Hence, these high yielding parents with good attributes for different yield components may be crossed to pool the genes in desirable direction to improve the yield potential. Whereas the crosses $L_7 \times T_2$ (EIQ-137 x EIQ-102), $L_{13} \times T_3$ (EIQ-143 x EIQ-103), $L_{10} \times T_1$ (EIQ-140 x EIQ-101), $L_1 \times T_1$ (EIQ-131 x EIQ-101) and $L_{11} \times T_3$ (EIQ-141 x EIQ-103) were identified as most promising crosses for yield based on *sca* effects, better *per se* also, could be exploited profitably for yield in maize.

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Table - 1 Pooled analysis of variance for combining ability for grain yield and its contributing traits in maize

SI.NO.	Source	d f	Days to 50 % tasselin g	Days to 50% silking	Anthesis-silking interval	Days to 75% brown husk	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of grain rows per ear	100-Grain weight	Grain yield per plant	Shelling percentage	Harvest index (%)
1	Environment	2	2.22E+05*	2.28E+05**	30.03**	3.22E+05**	36627.00**	7248.60**	238.82**	59.06**	123.59**	251.56**	14772.00**	347.23**	468.86**
2	Rep./Env	6	250.67**	231.38**	0.41**	131.25**	164.67**	54.28**	0.75	0.12	2.31**	2.70	26.75	11.04	3.76
3	Genotype	6	86.93**	88.87**	0.77**	39.28**	4459.30**	1442.10**	34.80**	10.88**	24.86**	68.69**	3825.10**	59.89**	318.14**
	Check P vs Chk	3	239.21**	243.33**	0.55**	12.18*	4498.10**	2024.60**	26.04**	3.15**	20.50**	8.51**	3783.60**	126.70**	78.36**
		1	539.78**	572.16**	0.47**	39.88**	23092.00**	7748.30**	647.48**	125.97*	196.85**	472.51**	27550.00**	28.74**	4026.00**
	Parent	1	48.05**	47.58**	0.59**	31.51**	2175.10**	1367.70**	8.46**	8.90**	9.86**	83.03**	1432.50**	68.35**	97.45**
	Tester	2	38.48**	40.15**	0.78**	14.70**	176.33**	230.78**	10.26**	3.14**	11.40**	50.45**	478.88**	24.20**	26.62**
	Line	1	40.97**	40.61**	0.60**	31.74**	2578.00**	1573.20**	7.89**	9.61**	10.24**	92.21**	1209.50**	79.49**	114.42**
	T v/s L	1	166.28**	160.00**	0.06	61.95**	532.90**	764.65**	12.81**	10.50**	1.34**	19.73**	6461.80**	0.70**	1.42**
	P v/s C	1	1252.60**	1234.80**	0.06	38.63**	149340.00**	36831.00**	1153.60**	305.21*	386.63**	2443.50**	1.83E+05**	1554.80*	16793.00**
	Cross	4	33.22**	35.31**	0.88**	43.12**	2143.70**	650.33**	16.38**	5.10**	22.04**	14.43**	769.72**	17.40**	45.24**
	Tester	2	195.09**	225.27**	2.71**	385.81**	5910.80**	983.77**	66.95**	2.95**	59.10**	4.79**	106.69*	22.12**	43.84**
	Line	1	37.55**	39.23**	0.82**	29.17**	2321.00**	867.71**	16.52**	3.71**	33.49**	20.56**	1089.40**	25.35**	54.26**
	L x T	2	19.49**	19.78**	0.78**	25.61**	1785.90**	517.83**	12.70**	5.95**	13.67**	12.06**	657.23**	13.09**	40.83**
4	G x E	1	18.20**	20.61**	0.70**	12.79**	72.49**	51.15**	1.16**	0.23*	0.47	1.64	89.30**	3.03	1.78
	Check x E	6	57.19**	59.67**	0.30**	21.34**	27.69	21.29	0.66	0.01	0.83	0.19	156.94**	0.90	1.01
	Chk x P x E	2	16.02*	17.40*	0.18	0.03	67.85	140.49**	0.91	0.39	0.50	4.45	330.67**	1.07	7.79
	P x E	3	16.21**	17.22**	0.47**	10.32**	48.47*	59.72**	1.53**	0.29*	0.41	1.75	16.88	0.68	0.72
	T x E	4	13.82**	16.04**	0.22*	5.37	12.78	59.11**	0.53	0.73**	1.04*	2.60	5.16	0.26	0.37
	L x E	2	16.76**	17.97**	0.51**	8.73**	27.48**	44.63**	1.76**	0.24	0.30	1.74	18.29	0.70	0.69
	T v/s L x E	2	13.38*	9.18**	0.42**	42.44**	413.67**	272.08**	0.21	0.07	0.66	0.24	20.59	1.24	1.90
	P v/s C x E	2	205.87**	257.33**	2.92**	129.73**	1178.90**	321.49**	1.75**	0.20	0.06	4.49	1704.20**	15.69	20.15**
	Cross x E	8	10.26**	11.76**	0.76**	10.37**	60.83**	43.96**	1.01**	0.22	0.47	1.61	77.46**	3.85	1.82
	T x E	4	37.21**	44.48**	0.68**	29.17**	132.64**	18.85	0.33	0.15	0.59	2.63	302.44**	6.49	1.04
	L x E	2	17.54**	19.29**	0.65**	9.32**	61.28**	30.74**	1.27**	0.17	0.52	1.32	85.16**	4.71	2.71



L x T x E	5	4.70	5.66*	0.82**	9.55**	55.47**	52.37**	0.92**	0.25*	0.44	1.69	57.54**	3.22	1.43
	6													
5 Pooled	3	3.86	3.96	0.08	4.39							27.59		2.78
Error	9					30.85	14.06	0.37	0.18	0.43	2.62		7.10	
	6													

*, ** Significance at 5% and 1% levels of probability respectively

Table -2 Estimate of general combining ability effects (gca) of parents for grain yield and its contributing traits in maize on pooled basis

Parents Lines	Days to 50 % tasseling	Days to 50% silking	Anthesis-silking interval	Days to 75% brown husk	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of grain rows per ear	100-Grain weight	Grain yield per plant	Shelling percentage	Harvest index (%)
L ₁	-0.31	-0.44	-0.13*	-1.03*	2.61*	0.02	-0.08	-0.32**	0.24	-1.35**	-12.20**	-0.38	-3.02**
L ₂	-1.57**	-1.81**	-0.24**	-1.62**	-6.87**	-1.24	-0.88**	0.08	-0.40**	0.37	6.91**	0.37	1.28**
L ₃	-0.64	-0.81*	-0.17**	0.94*	4.83**	3.68**	-0.61**	-0.44**	1.39**	-0.76*	-0.33	-1.16*	-0.96**
L ₄	-0.72	-0.59	0.13*	-0.62	5.28**	-0.02	0.04	0.51**	-0.08	0.75*	3.78**	0.51	-0.20
L ₅	0.65	0.64	-0.02	0.42	0.76	1.02	-0.74**	-0.45**	-0.89**	-0.03	3.71**	-0.06	0.81*
L ₆	-1.20**	-1.40**	-0.20**	-0.06	4.98**	-2.83**	-1.06**	0.09	-1.31**	1.54**	6.25**	-1.08*	0.90**
L ₇	-0.09	0.04	0.13*	-0.84*	-16.28**	-9.69**	-1.14**	0.29**	-0.06	-0.15	-2.85**	0.41	0.03
L ₈	-2.12**	-2.10**	0.02	-1.10**	-6.91**	-0.98	0.56**	-0.51**	1.86**	0.42	3.37**	-0.46	0.49
L ₉	1.62**	1.53**	-0.09	0.71	-12.76**	-6.54**	-0.23	0.42**	-0.88**	-1.26**	-9.97**	0.46	-2.10**
L ₁₀	-0.20	-0.10	0.09	-0.03	-0.35	-6.32**	1.27**	-0.34**	-0.41**	0.70*	-2.15*	-1.82**	-0.98**
L ₁₁	1.80**	1.82**	0.02	1.20**	-13.65**	0.24	0.63**	0.43**	1.44**	-0.96**	-1.72	-0.00	1.06**
L ₁₂	1.02**	1.08**	0.06	0.90*	7.20**	-3.20**	1.00**	-0.12	0.56**	-0.31	1.89	2.12**	0.55
L ₁₃	0.62	0.75	0.13*	2.12**	9.54**	11.68**	0.25*	-0.06	-1.82**	-0.56	-8.75**	-0.05	-0.68*
L ₁₄	1.47**	1.30**	-0.17**	-0.92*	14.98**	7.76**	1.00**	0.55**	1.30**	1.19**	9.34**	1.29*	2.73**
L ₁₅	-0.35	0.08	0.43**	-0.06	6.61**	6.42**	0.00	-0.14	-0.95**	0.41	2.72**	-0.14	0.08
SE (gi)	0.39	0.40	0.06	0.42	1.10	0.75	0.12	0.08	0.13	0.32	1.04	0.53	0.33
Testers													
T ₁	-0.51**	-0.67**	-0.16**	-0.27	3.21**	-2.35**	-0.32**	0.05	-0.53**	0.22	0.76	0.42	-0.09
T ₂	-0.86**	-0.82**	0.04	-1.54**	-7.61**	-0.60	-0.49**	-0.17**	-0.21**	-0.13	-0.98	-0.39	-0.52**
T ₃	1.37**	1.49**	0.12**	1.81**	4.40**	2.95**	0.81**	0.12**	0.74**	-0.08	0.22	-0.03	0.61**



SE (g) 0.20 0.20 0.03 0.21 0.55 0.37 0.06 0.04 0.07 0.16 0.52 0.26 0.17

*, ** Significance at 5% and 1% levels of probability respectively

Table -3 Estimate of specific combining ability effects (sca) of crosses for grain yield and its contributing traits in maize on pooled basis

Hybrids	Days to 50 % tasseling	Days to 50% silking	Anthesis-silking interval	Days to 75% brown husk	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of grain rows per ear	100-Grain weight	Grain yield per plant	Shelling percentage	Harvest index (%)
L ₁ x T ₁	0.69	0.78	0.08	2.90**	1.86	3.35*	-0.36	-0.60**	-1.24**	0.92	10.15**	1.02	2.36**
L ₂ x T ₁	0.51	0.48	-0.03	0.27	5.90**	1.83	-0.53*	0.49**	0.59*	-1.07	-5.05*	-0.66	-1.58*
L ₃ x T ₁	-1.53	-1.63*	-0.10	-3.62**	-15.14**	-5.21**	-0.45	-0.18	-1.11**	-0.05	-3.96	0.12	0.10
L ₄ x T ₁	0.21	0.26	0.05	-1.51	11.75**	-2.84	1.15**	-0.30	-0.18	0.96	0.30	-0.74	0.85
L ₅ x T ₁	0.51	0.81	0.31**	0.68	8.71**	1.35	-0.38	1.36**	0.63*	-0.79	6.24**	-0.39	0.49
L ₆ x T ₁	-0.31	-0.70	-0.40**	-1.51	-7.06**	-4.80**	1.26**	-0.23	-0.02	1.76**	4.15*	0.26	0.46
L ₇ x T ₁	-0.08	-0.04	0.05	0.49	-10.14**	-9.17**	-0.02	-0.42*	0.29	-0.93	-10.80**	-0.83	-0.93
L ₈ x T ₁	-2.94**	-3.00**	-0.06	-0.58	-2.95	-6.54**	0.84**	-0.18	1.79**	0.73	-2.42	-0.97	-1.39*
L ₉ x T ₁	0.66	0.48	-0.18	2.16*	5.79**	2.57	0.35	1.20**	0.31	-0.17	0.43	1.53	-0.79
L ₁₀ x T ₁	0.92	0.67	-0.25*	-1.21	6.94**	7.23**	0.84**	-0.10	-0.20	0.07	10.24**	1.04	3.10**
L ₁₁ x T ₁	-0.53	-0.15	0.38**	-0.43	-4.55*	-1.32	-0.18	-1.16**	0.35	-0.18	1.84	-1.06	0.74
L ₁₂ x T ₁	2.36**	2.48**	0.12	0.86	-6.51**	-2.10	-1.51**	0.33	-0.42	0.44	-5.67**	-0.58	-0.93
L ₁₃ x T ₁	-1.57*	-1.19	0.38**	0.53	-8.62**	-2.43	-0.84**	-0.61**	-0.16	-0.22	-9.36**	0.53	-1.02
L ₁₄ x T ₁	-0.08	-0.63	-0.55**	0.46	24.38**	18.72**	-0.16	1.10**	-0.80**	-2.18**	3.97	0.78	-1.43*
L ₁₅ x T ₁	1.18	1.37	0.20	0.49	-10.36**	-0.62	0.01	-0.72**	0.16	0.72	-0.04	-0.04	-0.02
L ₁ x T ₂	-1.62*	-1.62*	-0.00	-0.94	-7.09**	0.83	0.83**	0.38*	1.85**	-0.49	-4.12*	-0.58	1.61*
L ₂ x T ₂	1.09	1.19	0.11	1.43	-6.95**	4.20**	0.58*	-0.32	-2.00**	1.48*	2.66	0.30	-0.20
L ₃ x T ₂	1.38	1.30	-0.08	0.87	7.46**	-2.95*	-0.32	-0.40*	-0.72**	0.25	-0.61	-1.26	-0.91
L ₄ x T ₂	-0.32	-0.36	-0.04	0.20	5.68*	2.98*	0.08	-0.13	0.74**	-1.10	0.86	1.46	-0.14
L ₅ x T ₂	0.53	0.41	-0.12	-0.61	16.31**	8.38**	1.42**	-0.54**	0.09	-1.10	-4.60*	0.54	-1.11
L ₆ x T ₂	0.49	0.56	0.07	2.54**	-4.02	-3.54*	-0.44	-0.30	1.13**	-0.33	2.93	-0.68	1.82**
L ₇ x T ₂	-0.40	-0.33	0.07	1.20	-3.43	8.53**	0.86**	1.13**	0.73**	1.29*	19.88**	1.49	3.44**
L ₈ x T ₂	-0.02	0.16	0.18	-0.65	18.42**	4.16**	0.13	-0.12	-0.26	-0.31	1.20	1.59	0.26
L ₉ x T ₂	-0.77	-0.81	-0.04	-1.68*	-17.39**	-6.40**	0.24	-0.10	0.74**	0.89	6.48**	0.66	1.41*
L ₁₀ x T ₂	0.27	0.71	0.44**	0.28	-16.69**	-7.95**	-0.79**	-0.04	0.01	-0.24	-16.69**	0.06	-5.38**
L ₁₁ x T ₂	1.38	0.90	-0.49**	0.39	-2.72	-0.17	-1.79**	0.30	-1.12**	-1.52*	-10.29**	-0.75	-1.09
L ₁₂ x T ₂	-2.62**	-2.47**	0.14	-1.65*	12.65**	7.16**	-0.23	-0.43*	0.46	0.48	4.60*	-0.15	-0.62
L ₁₃ x T ₂	1.68*	1.30	-0.38**	0.35	11.31**	-2.06	-0.33	0.52**	-0.49	-0.14	-3.65	0.23	-0.84
L ₁₄ x T ₂	-0.95	-0.92	0.03	-1.28	-17.13**	-15.69**	-1.55**	-1.29**	-1.57**	0.84	-2.22	-1.81	1.11
L ₁₅ x T ₂	-0.14	-0.03	0.11	-0.46	3.57	2.53	1.30**	1.33**	0.42	0.00	3.56	-1.10	0.62
L ₁ x T ₃	0.92	0.84	-0.08	-1.96*	5.23*	-4.17**	-0.48	0.22	-0.61*	-0.43	-6.03**	-0.44	-3.98**
L ₂ x T ₃	-1.60*	-1.67*	-0.08	-1.70*	1.05	-6.02**	-0.05	-0.17	1.41**	-0.41	2.39	0.35	1.78**
L ₃ x T ₃	0.15	0.33	0.18	2.75**	7.68**	8.16**	0.77**	0.59**	1.84**	-0.20	4.57*	1.14	0.81



L ₄ x T ₃	0.11	0.10	-0.00	1.30	-17.43**	-0.14	-1.23**	0.43*	-0.56*	0.14	-1.16	-0.72	-0.71
L ₅ x T ₃	-1.04	-1.23	-0.19	-0.07	-25.03**	-9.73**	-1.03**	-0.83**	-0.72**	1.89**	-1.65	-0.14	0.61
L ₆ x T ₃	-0.19	0.14	0.33**	-1.03	11.08**	8.35**	-0.82**	0.53**	-1.11**	-1.43*	-7.07**	0.42	-2.29**
L ₇ x T ₃	0.48	0.36	-0.12	-1.70*	13.57**	0.64	-0.84**	-0.71**	-1.02**	-0.36	-9.08**	-0.66	-2.51**
L ₈ x T ₃	2.96**	2.84**	-0.12	1.23	-15.47**	2.38	-0.97**	0.29	-1.53**	-0.42	1.22	-0.62	1.14
L ₉ x T ₃	0.11	0.33	0.22	-0.48	11.60**	3.83*	-0.59*	-1.10**	-1.05**	-0.72	-6.90**	-2.19*	-0.62
L ₁₀ x T ₃	-1.19	-1.38	-0.19	0.93	9.75**	0.72	-0.05	0.15	0.19	0.17	6.46**	-1.09	2.29**
L ₁₁ x T ₃	-0.85	-0.75	0.11	0.04	7.27**	1.49	1.98**	0.86**	0.77**	1.70**	8.44**	1.81	0.35
L ₁₂ x T ₃	0.26	-0.01	-0.26*	0.78	-6.14**	-5.06**	1.74**	0.10	-0.04	-0.91	1.07	0.73	1.55*
L ₁₃ x T ₃	-0.11	-0.12	-0.00	-0.88	-2.69	4.49**	1.17**	0.09	0.65*	0.36	13.01**	-0.76	1.86**
L ₁₄ x T ₃	1.03	1.55	0.51**	0.82	-7.25**	-3.02*	1.71**	0.19	2.37**	1.34*	-1.75	1.03	0.32
L ₁₅ x T ₃	-1.04	-1.34	-0.30**	-0.03	6.79**	-1.91	-1.31**	-0.61**	-0.58*	-0.72	-3.53	1.14	-0.60
SE (Sij)	0.78	0.79	0.12	0.83	2.21	1.49	0.24	0.17	0.26	0.64	2.09	1.06	0.66

*, ** Significance at 5% and 1% levels of probability respectively

Table -4 Top five promising crosses of maize for grain yield and its component traits on pooled basis

Characters	Crosses	SCA effects	CV (%)	Per se performance of crosses	GCA effects		GCA status of parent
					Female parent	Male parent	
Days to 50 % tasseling	L ₈ x T ₁	-2.94**	2.75	64.44	-2.12**	-0.51**	H x H
	L ₁₂ x T ₂	-2.62**		67.56	1.02**	-0.86**	L x H
	L ₁ x T ₂	-1.62*		67.22	-0.31	0.86**	M x L
	L ₂ x T ₃	-1.60*		68.22	-1.57**	1.37**	H x L
	L ₁₃ x T ₁	-1.57*		68.56	0.62	-0.51**	M x H
Days to 50 % silking	L ₈ x T ₁	-3.00**	2.70	66.67	-2.10**	-0.67**	H x H
	L ₁₂ x T ₂	-2.47**		70.22	1.08**	-0.82**	L x H
	L ₂ x T ₃	-1.67*		70.44	-1.81**	1.49**	H x L
	L ₃ x T ₁	-1.63*		69.30	-0.81*	-0.67**	H x H
	L ₁ x T ₂	-1.62*		69.56	-0.44	-0.82**	M x H
Anthesis- silking interval	L ₁₄ x T ₁	-0.55**	12.00	1.56	1.30**	-0.16**	L x H
	L ₁₁ x T ₂	-0.49**		2.00	0.02	0.04	M x M
	L ₆ x T ₁	-0.40**		1.67	-0.20**	-0.16**	H x H
	L ₁₃ x T ₂	-0.38**		2.22	0.13*	0.04	L x M
	L ₁₅ x T ₃	-0.30**		2.67	0.43**	0.12**	L x L
Days to 75 % brown husk	L ₃ x T ₁	-3.62**	1.95	104.56	0.94*	-0.27	L x M
	L ₁ x T ₃	-1.96*		106.33	-1.03*	1.81**	H x L
	L ₂ x T ₃	-1.70*		106.00	-1.62**	1.81**	H x L
	L ₇ x T ₃	-1.70*		106.78	-0.84*	1.81**	H x L
	L ₉ x T ₂	-1.68*		105.00	0.71	-1.54**	M x H



Plant height (cm)	L ₅ x T ₃	-25.03**	3.57	145.78	0.76	4.40**	M x L
	L ₄ x T ₃	-17.43**		157.89	5.28**	4.40**	L x L
	L ₉ x T ₂	-17.39**		129.89	-12.76**	-7.61**	H x H
	L ₁₄ x T ₂	-17.13**		155.89	14.98**	-7.61**	L x H
	L ₁₀ x T ₂	-16.69**		141.00	-0.35	-7.61**	M x H
Ear height (cm)	L ₁₄ x T ₂	-15.69**	5.23	68.00	7.76**	-0.60	L x M
	L ₅ x T ₃	-9.73**		70.78	1.02	2.95**	M x L
	L ₇ x T ₁	-9.17**		55.33	-9.69**	-2.35**	H x H
	L ₁₀ x T ₂	-7.95**		61.67	-6.32**	-0.60	H x M
	L ₈ x T ₁	-6.54**		66.67	-0.98	-2.35**	M x H
Ear length (cm)	L ₁₁ x T ₃	1.98**	4.12	18.90	0.63**	0.81**	H x H
	L ₁₂ x T ₃	1.74**		19.04	1.00**	0.81**	H x H
	L ₁₄ x T ₃	1.71**		19.01	1.00**	0.81**	H x H
	L ₅ x T ₂	1.42**		15.68	-0.74**	-0.49**	L x L
	L ₁₅ x T ₂	1.30**		16.31	0.00	-0.49**	M x L
Ear girth (cm)	L ₅ x T ₁	1.36**	3.22	14.54	-0.45**	0.05	L x M
	L ₁₅ x T ₂	1.33**		14.60	-0.14	-0.17**	M x L
	L ₉ x T ₁	1.20**		15.25	0.42**	0.05	H x M
	L ₇ x T ₂	1.13**		14.83	0.29**	-0.17**	H x L
	L ₁₄ x T ₁	1.10**		15.27	0.55**	0.05	H x M
Number of grain rows per ear	L ₁₄ x T ₃	2.37**	4.85	18.44	1.30**	0.74**	H x H
	L ₁ x T ₂	1.85**		15.91	0.24	-0.21**	M x L
	L ₃ x T ₃	1.84**		18.00	1.39**	0.74**	H x H
	L ₈ x T ₁	1.79**		17.16	1.86**	-0.53**	H x L
	L ₂ x T ₃	1.41**		15.78	-0.40**	0.74**	L x H
100-grain weight (g)	L ₅ x T ₃	1.89**	6.00	30.00	-0.03	-0.08	M x M
	L ₆ x T ₁	1.76**		31.73	1.54**	0.22	H x M
	L ₁₁ x T ₃	1.70**		28.87	-0.96**	-0.08	L x M
	L ₂ x T ₂	1.48*		29.93	0.37	-0.13	M x M
	L ₁₄ x T ₃	1.34*		30.67	1.19**	-0.08	H x L
Grain yield per plant (g)	L ₇ x T ₂	19.88**	7.04	101.86	-2.85**	-0.98	L x M
	L ₁₃ x T ₃	13.01**		90.29	-8.75**	0.22	L x M
	L ₁₀ x T ₁	10.24**		94.64	-2.15*	0.76	L x M
	L ₁ x T ₁	10.15**		84.51	-12.20**	0.76	L x M
	L ₁₁ x T ₃	8.44**		92.76	-1.72	0.22	L x L
Shelling percentage	L ₁₁ x T ₃	1.81	3.44	80.26	-0.00	-0.03	M x M
	L ₈ x T ₂	1.59		79.23	-0.46	-0.39	M x M
	L ₉ x T ₁	1.53		80.89	0.46	0.42	M x M
	L ₇ x T ₂	1.49		79.99	0.41	-0.39	M x M
	L ₁₅ x T ₃	1.14		79.46	-0.14	-0.03	M x M
Harvest index (%)	L ₇ x T ₂	3.44**	4.68	41.77	0.03	-0.52**	M x L
	L ₁₀ x T ₁	3.10**		40.85	-0.98**	-0.09	L x M
	L ₁ x T ₁	2.36**		38.08	-3.02**	-0.09	L x M
	L ₁₀ x T ₃	2.29**		40.74	-0.98**	0.61**	L x H
	L ₁₃ x T ₃	1.86**		40.62	-0.68*	0.61**	L x H



*, ** Significance at 5% and 1% levels of probability respectively,
H = Desirable significant (+ or -) gca effects, M = Desirable non-significant (+ or -) gca effects and L = Undesirable significant (+ or -) gca effects

Table 5 Details of Inbred lines used as Parents

Sl.NO.	Symbol/Name	Pedigree	Origin
1	L ₁ (EIQ-131)	NP-06-07R-58-3-2-1-2-1	AICRP on maize, Udaipur
2	L ₂ (EIQ -132)	NP-06-07R-74-2-1-6-1-1-1	AICRP on maize, Udaipur
3	L ₃ (EIQ-133)	NP-06-07R-58-3-2-1-9-1	AICRP on maize, Udaipur
4	L ₄ (EIQ-134)	NP-06-07R-16-13	AICRP on maize, Udaipur
5	L ₅ (EIQ-135)	NP-06-07R-77-11-1-2-2-2	AICRP on maize, Udaipur
6	L ₆ (EIQ-136)	NP-06-07R-77-2-1-1-2-1	AICRP on maize, Udaipur
7	L ₇ (EIQ-137)	NP-06-07R-77-89-12-1-1	AICRP on maize, Udaipur
8	L ₈ (EIQ-138)	NP-06-07R-80-16-1-1-2-1	AICRP on maize, Udaipur
9	L ₉ (EIQ-139)	NP-06-07R-76-8-3-1-3-1	AICRP on maize, Udaipur
10	L ₁₀ (EIQ-140)	NP-06-07R-76-8-3-4-2	AICRP on maize, Udaipur
11	L ₁₁ (EIQ-141)	NP-06-07R-76-8-3-1-5	AICRP on maize, Udaipur
12	L ₁₂ (EIQ-142)	NP-06-07R-80-12-1-1	AICRP on maize, Udaipur
13	L ₁₃ (EIQ-143)	NP-06-07R-80-5-1-2-1-2-1	AICRP on maize, Udaipur
14	L ₁₄ (EIQ-144)	H06-R-6136-64-1-2-1-1	CIMMYT
15	L ₁₅ (EIQ-145)	H06-R-64-1-4-1-2-1	CIMMYT
16	T ₁ (EIQ-101)	NP-77-1	AICRP on maize, Udaipur
17	T ₂ (EIQ-102)	NP-76-11-3	AICRP on maize, Udaipur
18	T ₃ (EIQ-103)	H06R-68-1- 16	CIMMYT
19	HQPM-1	HKI193-1 x HKI163	CCS, HAU
20	HQPM-5	HKI163 x HKI 161	CCS, HAU
21	Pratap-QPM-1	DMRQPM-106 x HKI-193-1	AICRP on maize, Udaipur
22	Vivek QPM-9	VQL1 x VQL2	VPKAS, Almora



Where, AICRP - All India Coordinated Research Project
CCS, HAU - Chaudhary Charan Singh Haryana Agricultural University, Hissar
CIMMYT - International Wheat and Maize Improvement Centre, Mexico
VPKAS - Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora (U.K.)