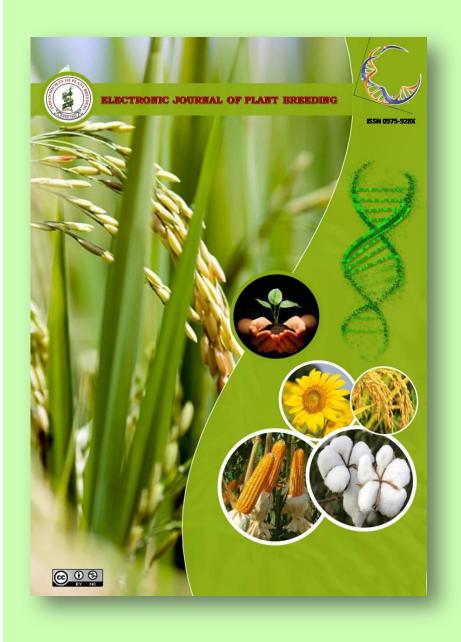
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Research Article

Heterosis and combining ability for grain yield and its component characters in quality protein maize (Zea mays L.) hybrids

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Abstract

A Line X Tester mating set of eight newly developed Quality Protein Maize inbred lines were utilized to evaluate combining ability and heterosis for yield and its components characters, at Field Experimentation Centre, Department of Genetics and Plant Breeding, SHUATS, Allahabad, during *kharif*-2017. Analysis of variance revealed that significant differences among the parents and experimental hybrids for all the characters except anthesis silking interval. Combining ability analysis revealed that estimate of specific combining ability (sca) variances were higher than general combining ability (gca) variances for maximum traits under study, indicating predominance of non-additive gene action of these traits. The parents LM-13 and DMR-N21 were identified as best combiners for yield and its related traits. The best experimental hybrid, on the basis of per se performance, sca effect and standard heterosis for grain yield per plant and its component was LM-13 X IC-32809 was followed by DMR-N21 X IC-32809 and LM-13 X IC-31899. Parents BBB-B2-NBBB, TSK-194and DMR-N21 recorded positive significant GCA for protein content indicating these parents are good combiner for protein content. Further, the study of analysis of variance for combining ability revealed the preponderance of non-additive gene action for all of the traits favouring the exploitation of heterosis breeding.

Key words

Line X Tester, Combining ability, Heterosis and Quality Protein Maize.

Introduction

Maize (*Zea mays* L.) plays a significant role in human and livestock nutrition worldwide. It has great yield potential and attained the leading position among the cereals based on production as well as productivity (Singh *et al.*, 2012).In India maize is grown in an area of 9.2 m ha with an average productivity of 2.5 tonnes/ ha and production of 23.6 million tonnes (Indian Institute of Maize Research- Annual Report, 2016). Where, in Uttar Pradesh maize is grown in an area of 0.9 million ha with an average productivity of 1.70 t/ ha and production of 1.10 million tonnes (Indian Institute of Maize Research - Annual Report, 2016)

However, the nutritional quality of maize protein is considered as poor, In which "Zein" protein of normal maize contain on an average about 2% lysine, which is less than one-half of the concentration recommended for human nutrition by the Food and Agriculture Organization (FAO) of the United Nations.Breeding maize crop with improved nutritional quality led to the discovery of *opaque-2* gene which is found to be associated with higher lysine and tryptophan content. The maize thus produced was called Quality Protein Maize (*opaque-2* maize) containing almost double the quantities of lysine and tryptophan. There is a need at present to evolve new high yielding QPM

hybrids, exceeding the yields of existing best hybrids in terms of quantity and quality.

The effects of general combining abilities (gca) and specific combining abilities (sca) are important indicators of potential value for inbred lines in hybrid combinations. Thus, information on gca effects can aid breeders to exploit existing variability in breeding materials to choose genotypes having desirable attributes and to distinguish relatedness among the breeding materials (Sprague and Tatum, 1942). The sca effects help breeders to determine heterotic patterns among populations or inbred lines to identify promising single crosses and assign them into heterotic groups (Lahane *et al.*, 2014).

Line X Tester analysis, an extension of top cross method in which several testers are used to mate with selected inbred lines is very prominently used for estimation of combining ability of inbred lines and to make the selections easier. This design thus provides information about general and specific combining ability of parents and at the same time it is helpful in estimating various types of gene effects. It is very effective for identification of desired lines, so as to increase the frequency of targeted alleles in hybrids.



Material and Methods

Eight newly developed QPM inbred lines were crossed in a Line X Tester mating design during the rabi season in 2016-2017. The resulting 12 F1's and 8 parents were evaluated along with the check Shaktiman-5 in a randomized block design with three replications during kharif -2017 at Field Experimentation Centre of the Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology Sciences, Allahabad (U.P). The pedigree of the parents used in the crosses was designated as follows: $IC-32809 = T_1$, $IC-31899 = T_2$, CM-600 = L_1 , DMR-N21= L_2 , BBB-B2-NBBB= L_3 , CML-224- $1 = L_4$ TSK-194= L_5 and LM-13 = L_6 . The hybrids were designated as $(L_1 X T_1)$, $(L_1 X T_2)$, $(L_2 X T_1)$, $(L_2 X T_2)$, $(L_3 X T_1)$, $(L_3 X T_2)$, $(L_4 X T_1)$, $(L_4 X T_2)$, $(L_5 X T_1)$, $(L_5 X T_2)$, $(L_6 X T_1)$ and $(L_6 X T_2)$.

Each genotype was grown in three rows of four meters length with 60 x 20 cm² spacing in a randomized block design with three replications. The trial was conducted in a clay loam soils. All the recommended agronomic practices were followed to raise a normal crop. Data were recorded on five randomly selected plants in each treatment for seventeen character viz., days to 50 per cent tasseling, days to 50 per cent silking, anthesis silking interval, days to maturity, plant height, cob height, cob length, tassel length, cob diameter, number of cobs per plant, number of kernel rows per cob, number of kernels per row, 100-seed weight, grain yield per plant, protein content, oil content and starch content. The data collected were subjected to analysis of variance as suggested by Panse and Sukhatme (1985). The combining ability analysis was done according to and estimation of per cent heterosis over standard check.

Results and Discussion

The analysis of variance revealed significant differences among the parents and hybrids for all the traits studied. Analysis of variance revealed significant differences among the parents and experimental hybrids for all the characters except anthesis silking interval (Table-1). Analysis of variance for combining ability revealed the estimate of specific combining ability (sca) variances were higher than the general combining ability (gca) variances for all the traits under study, indicating predominance of non-additive gene action of these traits. Similar results are also recorded by Lahane *et al.* (2014) and Lal *et al.* (2017). Thus they reported the importance of both additive and non-additive gene action in maize.

General combining ability effects (Table-2) revealed that two parents DMR-N21 (-1.75), IC-

32809 (-0.69) and CM-600 (-0.42) exhibited negative significance for days to 50% tasseling. Parents DMR-N21 (-1.75), IC-32809 (-0.64) and CM-600(-0.25) showed negative significance for days to 50% silking. Parents LM-13(-1.22) and DMR-N21 (-1.06) exhibited negative significance gca effects for days to maturity, indicating these parents turned out to be best combiner for earliness. The perusal of sca effects indicated that cross combinations viz., LM-13 X IC-31890 (-1.53), BBB-B2-NBB X IC-32809 (-1.31) and CML-224-1 X IC-32809 (-0.47), showed negative significance sca effects for days to 50% tasseling. Crosses BBB-B2-NBB X IC-32809 (-1.53), LM-13 X IC-31890 (-1.47) and CML-224-1 X IC-32809 (-0.69) showed negative significance sca effects for days to CrossCM-600 X IC-32809(silking. 0.50) showed highest negative significance SCA effect for days to maturity followed by BBB-B2-NBB X IC-31890 (-0.33)and CML-224-1 X IC-32809(-0.17). The ratio of gca/sca variance was less than one, indicates presence of non-additive gene action for controls this trait. This can be exploited for development of early maturing hybrids in Maize. Similar results are also recorded by, Rajesh et al. (2014), Matin et al (2016) and Ejigu et al. (2017).

Observations of plant height showed, parent CML-224-1(-16.50), DMR-N21 (-4.88) and IC-32809 (-2.23) exhibited negative significance gca effect. Ratio of gca and sca variance was less than unity revealed predominance of non- additive gene action. The perusal of sca effects indicated that cross combination TSK-194 X IC-31890(-10.73) showed highest negative significance sca effect followed by CML-224-1 X IC-32809 (-9.27) and CM-600 X IC-32809 (-2.84). Bupesh et al. (2015) and Das et al. (2017) were supported the results. Two parents LM-13 (14.56) and DMR-N21 (7.11) exhibited positive significant gca effect for seed yield per plant. Parent DMR-N21 also exhibited positive significance gca effects for various yield and yield components like tassel length, cob girth, number of grain rows per cob, grain yield per plant, starch content and oil content. The perusal of sca effects indicated that crosscombination BBB-B2-NBB X IC-31890(3.30) showed highest positive significance sca effect for seed yield per plant followed by CML-224-1 X IC-31890 (2.83) and LM-13 X IC-32809 (2.69) (Table 3). Similar results are also recorded by Singh (2012) and Ejigu et al. (2017).

Three parents BBB-B2-NBBB (0.42), TSK-194(0.36) and DMR-N21 (0.29) exhibited positive significance gca effects for protein content. Ratio of gca variance to sca variance also recorded less than unity. This suggested the preponderance of



non-additive gene action for this trait. The perusal of sca effects indicated that cross combinationsLM-13 X IC-31890 (0.51),TSK-194 X IC-32809 (0.45)andCML-224-1 X IC-32809(0.39) exhibited significance positive sca effects content.Similar results are also recorded by Lahane et al. (2014), Hyder et.al. (2013) and Mir et al.(2017). Overall perusal estimates of heterosis revealed that crosses LM-13 X IC-32809, DMR-N21 X IC-32809, LM-13 X IC-31899 exhibited Positive significance heterosis for grain yield and other yield attributing characters like 100 seed weight (test weight), number of grains per row, number of grain rows per cob, ear diameter and ear length (Table 4). . Similar findings were also reported in maize by Chahar et al. (2014), Kumar et al. (2016) and Debnath et al. (2016).

Crosses DMR-N21 X IC-32809 and BBB-B2-IC-32809 exhibited negatively significance economic heterosis for traits viz. days to 50% tasselling and days to 50% silking. Cross DMR-N21 X IC-31899 recorded highest negatively significant heterosis for days to 75% maturity. These crosses can be exploited further in breeding program for developing early maturing varieties. Similar findings were also reported in maize by Amiruzzaman et al. (2013) and Mohammad et al. (2017).Crosses TSK-194 X IC-32809 and DMR-N21 X IC-31899 exhibited highest positive significance economic heterosis for protein content. Crosses DMR-N21 X IC-31899,TSK-194 X IC-32809 and CML-224-1 X IC-31899 recorded highest positive significance economic heterosis for starch content. Highest positive significance economic heterosis for oil content was observed in crosses DMR-N21 X IC-31899 and TSK-194 X IC-32809. Hemalatha et al. (2014) and Aminu et al (2017) were reported the similar results for this traits.

The analysis of variance revealed the presence of significant amount variability among of Positive significant experimental materials. heterosis among the hybrids ranged from 4.02 (DMR-N21 X IC-32809) to 5.46 (LM-13 X IC-32809). Therefore, they showed potential to be exploited as single cross hybrids since they are showing more than 5% heterosis over the check (Shaktiman QPM-5). Thus provides an option to include them in multilocation testing. Parents DMR-N21 and LM-13 showed good gca for grain yield and quality traits. Therefore, they can be used as parent for breeding for quality traits. In addition they also offer scope to be used as component line in the development of composite/synthetic maize variety. Positive significant sca effects for qualitative characters were shown by the cross LM-13 X NBPGR-31890 (protein content), TSK-194 X NBPGR-32809 (starch content) and DMR-N21 X NBPGR-31890 (oil content). The genetic worth of cross LM-13 X IC-32809 is also depicted by positive significant sca effect. Further $\sigma^2 gca/\sigma^2 sca$ show the prepondence of non-additive gene action. Thus offer exploitation of heterosis or biparental mating design for yield improvement of maize.

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Table 1.Analysis of variance for important quantitative and qualitative parameters in QPM parents and hybrids.

S.	Mean Sum of	Characters											
No	Squares	df	Days to 50%	Days to 50%	Plant height	Cob height	Days to	Grain	Test	Grain yield/	Protien	Oil	Starch
			tasselling	silking			maturity	rows/cob	weight	Plant	content	content	content
1	Replicates	2	0.60	0.52	57.42	25.02	0.42	0.07	0.12	1.04	0.02	0.01	0.20
2	Treatments	19	41.49**	43.98**	5046.10**	1861.44**	8.42**	3.54**	4.00**	298.41**	0.68**	0.54**	25.96**
3	Parents	7	9.85**	9.28**	553.85**	292.07**	11.05**	2.45**	1.37**	112.35**	0.32**	0.24**	21.31**
4	Parents(Line)	5	9.07**	9.82**	654.63**	324.67**	10.99**	3.27**	1.49*	115.12**	0.42**	0.34**	19.04**
5	Parents(Tester)	1	13.50**	13.50*	450.67**	416.67**	0.17*	0.24	1.93*	123.31**	0.09**	0.00	1.67
6	Parents(LvsT)	1	10.13*	2.35*	153.13**	4.50**	22.22**	0.57	0.18	87.56**	0.02	0.00	52.28**
7	Parents vs Crosses	1	648.03**	697.22**	87696.9**	31546.9**	45.51**	18.32**	11.38**	1409.76**	0.88**	1.03**	125.9**
8	Crosses	11	6.49**	6.67**	391.09**	161.44**	3.38**	2.89**	5.00**	315.77**	0.90**	0.69**	19.83**
9	Line Effect	5	5.58*	5.12*	568.56*	153.64*	6.91**	2.03*	10.11**	649.42**	1.12	1.12	13.57
10	Tester Effect	1	17.36*	14.69*	178.22*	373.78*	0.00	1.36	1.07	26.87	0.00	0.52	3.30
11	L x T Effect	5	5.23*	6.63**	256.20**	126.78**	0.53*	4.04**	0.69	39.90**	0.85**	0.29**	29.39**
12	Error	38	1.55	1.85	41.39	18.84	0.52	0.24	0.43	4.55	0.01	0.02	0.75
13	Total	59	14.38	15.37	1653.62	612.43	3.06	1.30	1.57	99.07	0.23	0.19	8.85

^{**}Significance at 1% and *Significance at 5% level

Table 2. General Combing ability effects of parents for important quantitative and qualitative parameters in Quality protein Maize

S.No	Genotypes	Days to	Days to	Plant	Cob	Days to	Grain	Test	Grain yield/	Protein	Oil	Starch
		50%	50%	height	height	maturity	rows/cob	weight	plant	content	content	content
		tasseling	silking									
1	CM-600	-0.42	-0.25	6.27*	-4.72*	1.11**	0.61**	1.54**	-9.49**	-0.27**	-0.40**	-0.40
2	DMR-N21	-1.75**	-1.75**	-4.88	-0.22	-1.06**	-0.06	-0.69*	7.11**	0.29**	0.63**	1.75**
3	BBB-B2-NBBB	0.42	0.42	-0.66	-5.72**	0.61	-0.26	-1.99**	-13.69**	0.42**	-0.41**	0.40
4	CML-224-1	0.25	0.25	-16.50**	-1.06	1.11**	0.71**	-0.51	0.91	-0.67**	-0.24**	0.24
5	TSK-194	0.58	0.58	10.50**	7.11**	-0.56	-0.13	0.88**	0.58	0.36**	0.38**	0.72
6	LM-13	0.92	0.75	5.27	4.61*	-1.22**	-0.86**	0.76**	14.56**	-0.12**	0.04	-2.71**
7	IC-32809	-0.69*	-0.64	-2.23	-3.22**	0.00	0.19	0.17	0.86	0.01	0.12**	-0.30
8	IC-31899	0.694*	0.639	-2.23	3.22	0.00	-0.19	-0.17	-0.86	-0.01	-0.12**	0.30

^{**}Significance at 1% and *Significance at 5% level

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Table 3. Specific Combining ability effects for important quantitative and qualitative characters in Quality Protein Maize hybrids.

S.	Genotypes	Days to	Days to	Plant	Cob	Days to	Grain	Test	Grain	Protein	Oil	Starch
No		50%	50% silking	height	height	maturity	rows/cob	weight	yield/	content	Content	content
		tasseling							plant			
1	CM-600 X IC-32809	-0.14**	-0.19*	-2.84*	-2.78**	-0.50*	-0.13	-0.09**	0.30	0.05	0.05	0.75
2	CM-600 X IC-31890	0.14	0.19	2.84*	2.78	0.50*	0.13	0.09	-0.30**	-0.05	-0.05	-0.75
3	DMR-N21 X IC-32809	0.19	0.64	1.34	-3.61	0.00	-1.19**	0.08	2.60*	-0.30**	-0.27**	-3.19**
4	DMR-N21 X IC-31890	-0.19	-0.64	-1.34*	3.61	0.00	1.19**	-0.08**	-2.60*	0.30**	0.27**	3.19**
5	BBB-B2-NBB X IC-32809	-1.31**	-1.53**	-1.11*	5.22*	0.33	0.87**	0.28	-3.30*	-0.09	-0.26**	1.26*
6	BBB-B2-NBB X IC-31890	1.31	1.53	1.11	-5.22*	-0.33**	-0.87**	-0.28*	3.30*	0.09	0.26**	-1.26*
7	CML-224-1 X IC-32809	-0.47	-0.69*	-9.27*	-2.44**	-0.17	-0.29	-0.31**	-2.83*	0.39**	0.25**	-1.03
8	CML-224-1 X IC-31890	0.47	0.69*	9.27*	2.44**	0.17	0.29	0.31	2.83*	-0.39**	-0.25**	1.03
9	TSK-194 X IC-32809	0.19	0.31	10.73**	-2.94	0.17	1.01**	-0.42**	0.54	0.45**	0.18*	3.19**
10	TSK-194 X IC-31890	-0.19	-0.31**	-10.73**	2.94	-0.17**	-1.01**	0.42	-0.54	-0.45**	-0.18*	-3.19**
11	LM-13 X IC-32809	1.53*	1.47	1.16	6.56*	0.17**	-0.26	0.46	2.69*	-0.51*	0.06	-0.98
12	LM-13 X IC-31890	-1.53*	-1.47**	-1.16	-6.56*	-0.17**	0.26	-0.46	-2.69*	0.51**	-0.06	0.98

^{**}Significance at 1% and *Significance at 5% level

Table4. Estimates of economic heterosisfor important quantitative and qualitative characters in Quality Protein Maize hybrids.

S.	Genotypes	Days to	Days to 50%	Plant	Cob	Days to	Grain	Test weight	Grain	Protein	Oil	Starch
No		50%	silking	height	height	maturity	rows/cob		yield/ plant	content	Content	content
		tasseling										
1	CM-600 X IC-32809	-13.55**	-13.04**	4.19	-20.55**	-6.05**	-6.09*	-3.45	-27.78**	-8.04**	-17.92**	0.18
2	CM-600 X IC-31890	-10.32**	-9.94**	9.04**	-9.51**	-4.84**	-7.00*	-4.13	-30.72**	-9.36**	-24.63**	-1.01
3	DMR-N21 X IC-32809	-15.48**	-14.29**	0.86	-17.18**	-8.06**	-17.83**	-11.96**	-4.02	-5.61**	-3.42	-2.22*
4	DMR-N21 X IC-31890	-13.55**	-14.29**	1.71	-4.60	-8.06**	-4.29	-14.02**	-12.73**	0.95	2.48	7.14**
5	BBB-B2-NBB X IC-32809	-14.19**	-14.29**	1.71	-14.11**	-5.65**	-5.19	-16.49**	-37.59**	-1.74	-24.43**	1.93
6	BBB-B2-NBB X IC-31890	-6.45**	-6.21**	4.89	-17.79**	-6.45**	-19.64**	-20.20**	-31.47**	0.19	-18.66**	-0.64
7	CML-224-1 X IC-32809	-12.90**	-13.04**	-9.77**	-16.87**	-5.65**	-6.55*	-12.79**	-18.64**	-8.64**	-10.67**	-1.34
8	CML-224-1 X IC-31890	-8.39**	-8.07**	1.23	-6.44	-5.24**	-5.19	-11.69**	-13.70**	-17.78**	-25.50**	2.22*
9	TSK-194 X IC-32809	-10.97**	-10.56**	12.71**	-9.82**	-7.26**	-3.39	-7.57**	-14.83**	3.75**	0.34	4.95**
10	TSK-194 X IC-31890	-9.03**	-9.32**	4.58	1.53	-7.66**	-19.64**	-5.51*	-18.35**	-6.63**	-11.54**	-2.78**
11	LM-13 X IC-32809	-7.74**	-8.07**	5.63*	-3.37	-8.06**	-16.93**	-4.41	5.46*	-12.66**	-8.72**	-5.24**
12	LM-13 X IC-31890	-10.97**	-11.18**	6.65*	-9.51**	-8.47**	-16.03**	-9.63**	-3.47	-1.33	-15.91**	-1.80

^{**}Significance at 1% and *Significance at 5% level

