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Genetic evaluation of quality protein maize hybrids for heterosis and combining ability for grain yield and its component characters

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Abstract

A Diallel mating set of eight newly developed Quality Protein Maize inbreds were utilized to evaluate combining ability and heterosis for yield and its component characters, at Field Experimentation Centre, Department of Genetics and Plant Breeding SHUATS, Prayagraj, during *Kharif* 2018. Analysis of Variance revealed that significant differences among the parents and experimental hybrids for all the characters except for Anthesis Silking Interval. The highest significant positive standard heterosis over standard check HQPM-5 for grain yield per plant was exhibited by LM-13 x HKI-34 (6.03%). The SCA variance component was observed to be higher than the corresponding GCA variance component for all the traits except for Anthesis Silking Interval indicating the preponderance of non-additive gene action for the inheritance of these traits. The parents BHU-N6 and LM-13 were identified as best combiners for grain yield per plant and protein content respectively. On the basis of *per se* performance, heterotic response, SCA estimates for grain yield per plant cross, LM-13 x HKI-34 was found promising and may be exploited commercially after critical evaluation for its superiority and stability across the locations and over years.

Keywords: Diallel, heterosis, combining ability and quality protein maize (*Zea mays* L.)

Introduction

Maize (*Zea mays* L.) plays a significant role in human and livestock nutrition. Over 85% of the maize produced in India is currently used for human consumption, particularly in the economically deprived areas where protein malnutrition and hunger are apparent. However, the normal maize contains high zein fraction, which is practically devoid of lysine and low in tryptophan (Prasanna *et al*. 2001) [12]. A genetic approach to improve the nutritional quality of maize protein yielded the Quality Protein Maize which contains opaque-2, a single gene mutation that alter the protein composition of the endosperm protein and nearly double the essential amino acid concentrations and yielded 10% more grains than traditional maize varieties (Akande and Lamidi, 2006) [1]. Information on heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development.

Maize is a highly cross-pollinated crop and the scope for the exploitation of hybrid vigour depends on the direction and magnitude of heterosis (Reddy *et al.* 2015) [15]. Hybrids are preferred over varieties in maize for their yield potential. The breeding method to be adopted for maize improvement depends on the nature of the gene action involved in the expression of quantitative traits of economic importance, and its strength depends on the genetic variability in the base populations and development of superior inbreds (Rajendran *et al.* 2014) [13]. Development of commercial QPM hybrid usually requires a good knowledge of combining ability of the breeding materials to be used. Selection of parents based on combining ability has been used as an important breeding approach in crop improvement.

The success in commercial production of hybrid maize depends up on the availability of productive diverse Quality Protein Maize inbred lines and clear knowledge of gene action for specific traits. Therefore, the present investigation was undertaken to study the combining ability and estimate the extent of heterosis for grain yield and yield contributing traits.

Materials and Methods

Materials for the present investigation were generated from eight inbred lines of Quality Protein Maize (QPM) *viz*., (BHU-N1, LM-13, HY10RN-10235-462, BHU-N6, CMLK5/ATM CO571, HKI-34, NBPGR 32809 and CML-40, obtained from different sources were utilized to produce twenty eight F_1 hybrids using a half diallel crossing system during *Rabi* 2017-18.

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The 28 hybrids along with their parents and check hybrid (HQPM 5) were raised in Randomized Block Designs with three replications during *Kharif* 2018 at Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P. Each entry was planted in a plot consisting of two rows of 5 m length with a spacing of 60 cm x 20 cm apart. Observations were recorded on plot basis for days to 50% tasseling and days to 50% silking by counting the number of days from sowing to the emergence of tassel and silk in 50% plants. Five randomly selected plants in each replication were used for recording observations on plant height (cm), stem girth (cm), leaf area index (cm^2), cob height (cm), cob length (cm), cob girth (cm), cob weight (g), number of kernel rows per ear, number of kernels per row, 100 seed weight (g) and seed yield per plant (g) for parents and F_1's. Estimation of protein content (%) was done by using Lowry method. The data collected were subjected to Analysis of Variance as suggested by Panse and Sukhatme (1967) [10]**.** The mean data were subjected to combining ability analysis using model-I and method-II as suggested by Griffing (1956) [6] as well as for estimation of per cent heterosis over standard check (Turner, 1953) [17].

Results and Discussion

The Analysis of Variance revealed highly significant differences for all the characters studied except for Anthesis Silking Interval. The mean square due to parents differed significantly indicating the parents involved in the study were diverse for all the characters. The variance due to parents vs crosses differed significantly indicating the presence of high heterosis response in the material studied. The variance due to general and specific combining ability was highly significant for all the characters under study except for Anthesis Silking Interval, indicating the influence of both additive and non-additive effects in the expression of these characters. The influence of both types of gene effect was also observed by Patel *et al.* (2016) [11], Ram *et al.* (2017) [14] and Darshan and Marker (2019) [3] in maize. Combining ability analysis revealed that estimates of specific combining ability (SCA) variances were higher than general combining ability (GCA) variances for all the traits under study in all the environments, suggesting preponderance of non-additive gene action for these traits.

GCA effects: The estimates of GCA effects (Table 1) showed that the parents BHU-N1 and HKI-34 were found to be good general combiners for cob length. While the parents BHU-N1, LM-13 and HKI-34 were found to be best combiners for number of kernels per row, parents CML-40 and CML-K5/ATM CO571 were found to be best combiners for 100 seed weight. The parent BHU-N6 was found to be good general combiner for grain yield per plant. The parent LM-13 possess positive significant GCA effect and proved to be a good general combiner for protein content. Thus, the inbred lines which exhibited good general combiner for at least one trait can be used as donor parents for the accumulation of favourable genes.

SCA effects: Specific combining ability effects for grain yield per plant (Table 2) revealed that twenty-two cross combinations showed positive significant SCA effect. Out of which cross, LM-13 x HKI-34 exhibited highest SCA effect for grain yield per plant. Among the 45 crosses, twenty-four cross combinations gave the best performance for protein content in *Kharif* season. Out of which cross, BHU-N1 x HY10RN-10235-462 proved to be good specific combiner for this trait. The number of crosses which depicted significant and positive SCA effects were 16, 15, 12, 27, 19 and 16 for 100 seed weight, number of kernels per row, number of kernel rows per cob, cob weight, cob girth and cob length respectively. Among them LM-13 x NBPGR-32809 for 100 seed weight, BHU-N1 x NBPGR-32809 for number of kernels per row, BHU-N1 x BHU-N6 for number of kernel rows per cob, LM-13 x HKI-34 for cob weight, LM-13 x NBPGR-32809 for cob girth and HY10RN-10235-462 x CML-40 for cob length found good specific combiners. In the present study, the cross which was found to be good for the respective characters had at least one parent with good or average general combiner. Therefore, in diallel analysis one must select hybrids of high specific combining ability in which one of the parents with good general combining ability. Ejigu *et al.* (2017) [5], Mir *et al.* (2017) [9] and Darshan and Marker (2019) [3] were reported similar results for these traits in maize.

Heterosis: The standard heterosis for different traits are presented in Table 3. Considering the higher standard heterosis for grain yield per plant, hybrid LM-13 x HKI-34 exhibited positive significant heterosis. Whereas, cross BHU-N1 x BHU-N6 exhibited positive significant economic heterosis for protein content. The cross BHU-N6 x CML-K5/ATM CO571 for 100 seed weight, BHU-N1 x NBPGR-32809 for number of kernels per row, BHU-N1 x BHU-N6 for number of kernel rows per cob, LM-13 x HKI-34 for cob weight, BHU-N1 x HKI-34 for cob girth and LM-13 x BHU-N6 for cob length recorded positive standard heterosis. Thus, heterosis breeding holds promise for improving quantitative and qualitative traits in maize. In general, it is observed from the heterotic result that the cross which found superior for grain yield and quality traits are different. This indicated that yield and quality have negative relationship i.e. when quality of hybrid increases, the grain yield decreases side by side and vice versa. The results are in agreement with Kumar *et al.* (2008) [7], Dubey *et al.* (2009) [4], Singh *et al.* (2010) [16], Kumar *et al.* (2016) [8], Kumari *et al.* (2018) [7] and Darshan and Marker (2019) [3].

Thus, it can be concluded that, parents BHU-N6 for grain yield per plant and LM-13 for protein content found good general combiners. The crosses LM-13 x HKI-34 and BHU-N1 x HY10RN-10235-462 were identified as outstanding for grain yield per plant and protein content respectively, due to possessing high SCA and heterotic effects. Therefore, these hybrids and their parents may further utilize in future maize breeding programme.

Acknowledgements

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Table 1: General Combining Ability effects of parents for different parameters in Quality Protein Maize

S. No.	Notation	Genotype name	Days to 50% Tasseling	Days to 50% silking	ASI	Plant height	Plant girth	Leaf area index	Cob height	Cob length	Cob girth	Cob weight	No. of kernel rows per cob	No. of kernels per row	100 seed weight	Grain yield per plant	Protein content
1	P_1	BHU-N1	0.13	0.12	-0.08	-11.72**	-0.32**	0.26**	-3.43**	0.34*	0.30*	0.27	0.04	1.75**	0.05	0.46	-0.05
2	P_2	LM-13	-0.24	-0.28	0.02	-1.68	-0.43**	0.31**	-0.46	-0.67**	-0.06	0.23	0.19	1.47**	-0.23	-0.14	0.32**
3	P_3	HY10RN-10235-462	-0.21	-0.18	-0.05	-2.26	0.27*	-0.06	-0.31	-0.52**	-0.27*	-0.39	-0.02	-1.87**	-1.24**	-0.96**	0.03
4	P_4	BHU-N6	-0.11	0.05	0.08	-1.32	0.05	-0.13**	2.79**	-0.26	-0.19	-0.32	-0.02	-0.99**	-0.33	1.07**	-0.13
5	P_5	CML-K5/ATM CO571	-0.17	-0.08	0.15*	0.7	-0.03	0	-1.60*	0.28	0.16	-0.06	0.04	-0.08	0.75**	-0.25	0.15
6	P_6	HKI-34	0.13	0.22	0.02	14.92**	0.48**	-0.23**	2.82**	0.34*	0.26*	0.1	-0.07	1.13**	-0.96**	-0.18	-0.18
7	P_7	NBPGR-32809	0.26	0.22	-0.05	-2.73	0.22*	0.06	0.58	-0.03	-0.17	-0.35	-0.09	-0.37	0.19	-0.07	-0.06
8	P_8	CML-40	0.23	-0.05	-0.08	4.11	-0.23*	-0.20**	-0.39	0	-0.04	0.51	-0.07	-1.04**	1.78**	0.07	-0.08

**Significant at 1% and *Significant at 5% level

Table 2: Specific Combining Ability effects of crosses for different parameters in Quality Protein Maize

S. No.	Genotype name	Days to 50% Tasseling	Days to 50% silking	ASI	Plant height	Plant girth	LAI	Cob height	Cob girth	Cob length	Cob weight	No. of kernel rows per cob	No. of kernels per row	100 seed weight	Grain yield per plant	Protein content
1	BHU-N1 x LM-13	-0.67	-0.96	-0.36**	-2.67	-0.52**	0.55**	4.04**	-1.17**	-0.23	-0.95*	0.01	-1.38**	-2.21**	-5.09**	0.65**
2	BHU-N1 x HY10RN-10235-462	-1.70**	-1.40**	0.37**	0.71	0.07	0.30**	1.32	0.83**	1.96**	5.14**	-0.66**	2.19**	2.35**	4.32**	1.27**
3	BHU-N1 x BHU-N6	-2.14**	-2.30**	-0.09	6.54	-0.45**	0.07	12.39**	1.06**	-0.98**	4.49**	1.56**	0.42	0.91**	2.79**	-0.29*
4	BHU-N1 x CML-K5/ATM CO571	0.6	0.84	0.17*	8.96**	0.26	0.66**	12.24**	0.47**	-0.08	3.97**	-0.29	1.17**	1.16**	3.69**	0.61**
5	BHU-N1 x HKI-34	-3.37**	-3.13**	0.31**	10.64**	1.28**	0.78**	-12.51**	1.10**	0.27	1.01*	1.16**	-2.54**	0.69*	0.52	1.22**
6	BHU-N1 x NBPGR-32809	-1.17*	-1.13*	0.04	18.69**	1.32**	0.25**	11.84**	0.93**	2.39**	1.59**	-0.82**	7.97**	5.73**	0.32	0.81**
7	BHU-N1 x CML-40	-0.8	-0.53	0.07	39.65**	-0.13	0.38**	-6.15**	0.50**	0.80**	2.90**	0.50**	3.47**	2.54**	2.15**	0.36*
8	LM-13 x HY10RN-10235-462	-4.00**	-3.66**	0.27**	9.17**	-0.49**	-0.13*	0.32	0.99**	1.30**	2.62**	1.40**	-0.6	0.49	0.73*	1.01**
9	LM-13 x BHU-N6	-2.10**	-1.90**	0.14	10.66**	0.78**	-0.35**	3.89**	0.40*	3.69**	5.09**	-1.70**	5.19**	-1.97**	2.68**	1.22**
10	LM-13 x CML-K5/ATM CO571	0.63	0.9	0.07	5.81	1.12**	-0.34**	-7.27**	0.74**	3.26**	2.94**	1.10**	6.78**	3.45**	1.89**	0.74**
11	LM-13x HKI-34	0.66	0.94	0.21*	4.26	-0.45**	0.06	10.93**	1.06**	-0.79**	6.79**	1.21**	4.40**	4.96**	5.82**	0.66**
12	LM-13x NBPGR-32809	-0.14	-0.4	-0.39**	31.54**	-0.91**	0.13*	5.47**	1.66**	0.98**	2.88**	-0.75**	3.41**	6.51**	1.23**	0.56**
13	LM-13 x CML-40	0.23	-0.46	0.31**	24.44**	0.05	0.17**	11.54**	-0.33*	-1.14**	1.48**	0.56**	-1.59**	3.32**	0.73*	1.20**
14	HY10RN-10235-462 x BHU-N6	0.53	0.67	0.21*	23.74**	0.18	0.04	5.50**	0.84**	2.19**	1.64**	-0.60**	7.71**	-4.46**	0.29	-0.06
15	HY10RN-10235-462 x CML-K5/ATM CO571	0.26	0.14	-0.19*	7.19*	0.50**	-0.52**	2.69**	-0.45**	0.12	2.87**	0.23	-0.32	-1.20**	1.57**	0.69**
16	HY10RN-10235-462 x HKI-34	0.63	0.84	0.27**	-4.23	-0.35*	0.51**	6.35**	-0.48**	0.61**	4.53**	-0.1	2.80**	0.15	2.79**	0.1
17	HY10RN-10235-462 x NBPGR-32809	-0.84	-0.83	0.01	8.92*	0.86**	0.31**	0.62	0.91**	0.36	2.61**	-0.08	-1.25**	2.61**	1.59**	0.88**
18	HY10RN-10235-462 x CML-40	-1.47**	-0.9	0.37	18.98**	-0.47**	0.54**	11.39**	0.44**	3.73**	2.05**	0.56**	6.31**	-0.61	0.83*	1.21**
19	BHU-N6 x CML-K5/ATM CO571	0.16	-0.1	-0.33**	-7.45*	0.33*	-0.25**	-4.96**	0.42**	0.86**	4.47**	0.45*	-0.98*	6.06**	0.27	0.89**
20	BHU-N6 x HKI-34	-0.14	-0.06	0.14	11.83**	-0.48**	-0.24**	3.67**	0.58**	-1.05**	2.77**	0.12	2.36**	-0.48	1.29**	0.97**
21	BHU-N6 x NBPGR-32809	-1.60**	-1.40**	0.21*	12.68**	-0.59**	-0.45**	-1.38	0.17	1.76**	3.89**	0.80**	2.87**	-0.09	1.33**	1.15**
22	BHU-N6 x CML-40	-0.9	-0.46	0.24**	-2.26	-0.54**	0.20**	0.76	0.09	-0.94**	3.15**	-0.33	-4.57**	1.84**	0.84*	1.23**
23	CML-K5/ATM CO571 x HKI-34	-0.07	0.07	0.07	7.02*	0.1	-0.30**	8.32**	-0.05	0.36	4.33**	0.05	-0.66	-1.78**	2.55**	0.82**
24	CML-K5/ATM CO571 x NBPGR-32809	-1.20*	-0.93	0.14	15.37**	0.28	0.58**	10.61**	0.96**	0.49*	3.59**	0.3	-1.38**	1.82**	2.54**	0.82**
25	CML-K5/ATM CO571 x CML-40	1.16*	0.34	0.17*	-14.17**	0.52**	0.28**	3.13**	0.94**	1.04**	4.45**	-1.28**	-0.82	1.30**	2.34**	-0.35*
26	HKI-34 x NBPGR-32809	0.5	0.44	-0.06	-0.15	-0.17	-0.30**	-4.01**	0.60**	-0.08	4.50**	0.18	-1.48**	1.77**	2.02**	0.46**
27	HKI-34 x CML-40	-0.14	0.04	-0.03	-1.29	0.33*	-0.24**	-1.51	-0.62**	1.64**	2.76**	1.49**	2.64**	-3.18**	0.6	0.64**
28	NBPGR-32809 x CML-40	-1.60**	-1.30*	0.04	6.56	0.18	0.10*	6.20**	0.24	1.59**	3.03**	0.85**	2.03**	-0.6	1.62**	1.14**

**Significant at 1% and *Significant at 5% level

Table 3: Economic heterosis (Hc) for Quantitative and Qualitative traits in Quality Protein Maize

S. No.	Genotype name	Days to 50% Tasseling	Days to 50% silking	ASI	Plant height	Plant girth	LAI	Cob height	Cob girth	Cob length	Cob weight	No. of kernel rows per cob	No. of kernels per row	100 seed weight	Grain yield per plant	Protein content
1	BHU-N1 x LM-13	-9.43**	-8.48**	16.67	-10.94	-19.28*	56.12**	-16.63**	-5.54	-11.87*	-3.27	5.69	-6.93	7.03	-13.35**	0.12
2	BHU-N1 x HY10RN-10235-462	-11.32**	-9.09**	50.00**	-9.43	1.16	34.13**	-20.53**	10.71	4.97	5.14*	-1.87	6.12	25.98**	2.84	3.05
3	BHU-N1 x BHU-N6	-11.95**	-10.30**	33.33*	-5.79	-10.54	23.31**	0.96	-4.36	7.81	4.26	16.98**	-9.38	23.15**	3.80	12.66**
4	BHU-N1 x CML-K5/ATM CO571	-6.92*	-4.85	50.00**	-3.40	-0.58	48.87**	-5.92	2.04	5.56	3.85	1.78	-3.28	30.24**	2.99	-1.86
5	BHU-N1 x HKI-34	-13.84**	-11.52**	50.00**	5.18	23.81**	45.42**	-36.77**	4.94	12.47*	-0.46	13.25*	-12.45*	18.58**	-2.84	0.76
6	BHU-N1 x NBPGR-32809	-9.43**	-7.88*	33.33*	0.00	20.23*	36.39**	-3.24	17.11**	6.78	-0.25	-3.76	20.62**	51.68**	-3.01	-1.98
7	BHU-N1 x CML-40	-8.81*	-7.27*	33.33*	14.99*	-9.96	32.10**	-31.99**	6.28	4.00	3.07	7.59	1.63	43.07**	0.70	-6.16
8	LM-13 x HY10RN-10235-462	-16.35**	-13.94**	50.00**	0.54	-9.48	20.10**	-17.54**	-0.88	3.09	1.22	16.90**	-17.35**	14.56*	-5.05*	4.03
9	LM-13 x BHU-N6	-12.58**	-10.30**	50.00**	1.85	7.17	9.75	-7.43	21.22**	-1.69	5.12*	-9.40	7.14	6.26	2.46	4.58
10	LM-13 x CML-K5/ATM CO571	-7.55*	-5.45	50.00**	0.32	11.33	14.98*	-31.01**	18.25**	4.69	2.21	14.92*	16.33**	41.02**	-1.53	2.75
11	LM-13 x HKI-34	-6.92*	-4.85	50.00**	7.15	-5.37	21.05**	3.29	-9.51	8.72	8.39**	14.92*	12.04*	39.90**	6.03**	-1.01
12	LM-13 x NBPGR-32809	-8.18*	-7.27*	16.67	12.35	-16.91*	33.77**	-8.39	0.28	10.22	1.68	-1.90	2.85	54.35**	-2.42	-0.82
13	LM-13 x CML-40	-7.55*	-7.88*	50.00**	12.20	-8.85	25.92**	-0.66	-14.24*	-7.19	0.85	9.43	-17.97**	45.79**	-3.09	4.85
14	HY10RN-10235-462 x BHU-N6	-7.55*	-5.45	50.00**	8.59	8.85	10.58	-4.75	11.76*	0.44	-1.15	-1.87	4.09	-12.40*	-3.61	-9.85*
15	HY10RN-10235-462 x CML-K5/ATM CO571	-8.18*	-6.97*	33.33*	0.75	12.64	-4.76	-15.67**	-2.55	-8.34	1.15	5.66	-22.04**	10.78	-3.68	-0.46
16	HY10RN-10235-462 x HKI-34	-6.92*	-4.85	50.00**	2.26	7.22	23.90**	-3.43	1.30	-7.69	3.95	1.92	-6.13	8.84	-1.24	-8.88
17	HY10RN-10235-462 x NBPGR-32809	-9.43**	-7.88*	33.33*	-0.16	22.23**	26.87**	-15.52	-2.97	1.31	0.30	1.90	-26.52**	28.14**	-3.30	-0.61
18	HY10RN-10235-462 x CML-40	-10.69**	-8.48**	50.00**	8.95	-6.06	26.16**	-0.66	20.64**	-1.84	0.76	7.59	-1.22	19.38**	-4.48*	2.29
19	BHU-N6 x CML-K5/ATM CO571	-8.18*	-6.67*	33.33*	-6.43	6.48	2.26	-22.57**	8.05	0.53	3.72	7.59	-21.23**	54.40**	-2.30	-0.06
20	BHU-N6 x HKI-34	-8.18*	-6.06	50.00**	11.43	1.79	-5.23	-2.78	-4.82	2.97	1.34	3.79	-4.51	10.36	-0.25	-2.35
21	BHU-N6 x NBPGR-32809	-10.69**	-8.48**	50.00**	2.37	-4.21	-2.85	-13.85*	12.15*	-4.94	2.38	9.45	-8.17	18.56**	0.04	0.37
22	BHU-N6 x CML-40	-9.43**	-7.27*	50.00**	-1.99	-10.48	11.53	-12.06*	-6.45	-4.41	2.57	0.00	-37.96**	37.32**	-0.62	0.98
23	CML-K5/ATM CO571 x HKI-34	-8.18*	-6.06	50.00**	9.92	9.64	-2.62	-2.39	5.15	0.34	4.15	3.79	-12.24*	9.18	-0.36	-1.16
24	CML-K5/ATM CO571 x NBPGR-32809	-10.06**	-7.88*	50.00**	4.91	8.27	38.64**	-2.33	3.43	5.75	2.31	5.66	-20.42**	34.54**	-0.17	-0.06
25	CML-K5/ATM CO571 x CML-40	-5.66	-6.36*	50.00**	-7.33	4.95	19.02**	-15.13**	7.47	6.78	4.96*	-7.53	-20.82**	40.26**	-0.28	-10.89*
26	HKI-34 x NBPGR-32809	-6.29	-5.15	33.33*	4.20	9.27	-0.83	-17.80**	-0.05	3.38	3.97	3.79	-16.33*	25.13**	-1.01	-6.38
27	HKI-34 x CML-40	-7.55*	-6.36*	33.33*	7.28	10.06	-7.73	-15.47**	12.10*	-6.78	2.61	15.11**	-3.67	7.15	-3.43	-4.85
28	NBPGR-32809 x CML-40	-10.06**	-8.48**	33.33*	1.99	3.58	14.74*	-7.18	9.20	-2.87	2.33	9.45	-11.44*	27.12**	-1.29	0.82

**Significant at 1% and *Significant at 5% level

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