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Genetic analysis of grain yield and endosperm protein quality in the quality protein maize (QPM) lines

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Abstract

To evaluate the performance of Quality Protein Maize (QPM) lines with respect to grain yield and endosperm protein quality, a set of 14 lines developed in India (DMRQPM series) and three exotic testers (from CIMMYT, Mexico) were involved in a Line x Tester mating design. The resultant experimental hybrids along with the parental lines were evaluated at two locations (Delhi and Pantnagar) during *Kharif* 2003, and biochemical analysis for estimation of endosperm protein content and per cent tryptophan in endosperm protein was undertaken on the harvested material (control-pollinated). DMRQPM-65 and CML189 at Delhi and DMRQPM-28-5, CML166 and CML189 at Pantnagar were found to be the best general combiners for grain yield, while DMRQPM-401, DMRQPM-28-5 and DMRQPM-65 exhibited best GCA effects for most of the characters at both the locations. DMRQPM-45 x CML189 and DMRQPM-404 x CML189 displayed highest SCA effects for grain yield at Delhi and Pantnagar, respectively. The study revealed preponderance of variance due to dominance effects over that due to additive effects for most of the characters at both Delhi and Pantnagar. The present investigation identified DMRQPM-404 x CML189 as the best heterotic combination at both locations. DMRQPM-28-5 (0.99%) and CML189 (0.98%) among the inbred lines and DMRQPM-56 x CML189 (1.03%) among the crosses recorded the highest per cent tryptophan content in the endosperm protein. CML189 was found to be the best donor for endosperm quality traits. Taking into account the combining ability effects for grain yield and endosperm protein quality, besides heterosis, DMRQPM65 and CML189 among the inbreds and DMRQPM-45 x CML189 among the crosses were found to be the most promising for utilization in the QPM breeding programmes.

Key words: Maize, QPM, combining ability, grain yield, endosperm protein, tryptophan

Introduction

The discovery of nutritional value of the *opaque2* mutation in maize was a significant breakthrough as it was found to alter the amino acid composition of the endosperm protein, resulting in enhanced concentration of lysine and tryptophan [1]. CIMMYT breeders successfully combined the high lysine potential of *opaque2* with the genetic endosperm modifiers, releasing new maize genotypes that are referred to as "Quality Protein Maize" (QPM) [2]. Several countries in Asia, Africa and Latin America, including India have active QPM breeding programmes.

In view of the growing importance of QPM in India and to hasten the pace of progress of QPM cultivar development, it is important to develop a broad-based QPM germplasm and to identify QPM genotypes, including inbred lines, with high *per se* productivity, combining ability, nutritional quality, through integrated and multidisciplinary research programmes. The present investigation was particularly aimed at identifying promising QPM inbred lines (from India and abroad) and their cross combinations with desirable agronomic performance, combining ability, protein content and quality for potential utilization in QPM cultivar development.

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Materials and methods

A set of 14 QPM inbred lines, of which 13 were developed from high lysine *opaque2* composites, including Shakti 1, under the All India Coordinated Maize Improvement Project (AICMIP) [designated as 'DMRQPM' lines], and one QPM inbred line of Caribbean origin, were used as 'lines', and three genetically diverse, tropical QPM genotypes developed at CIMMYT, Mexico, as 'testers' in a 'line x tester' (L x T) mating design. All the 42 experimental crosses, along with the 17 parents, were evaluated in a randomized complete block design with three replications per entry at two locations: (i) IARI Experimental Farm, New Delhi, and (ii) Crop Research Centre, G.B. Pant University of Agriculture & Technology (GBPUA&T), Pantnagar, during *Kharif* 2003. The materials were planted under a plant-to-plant spacing of 25 cm and a row-to-row spacing of 75 cm, and standard agronomic practices were followed for raising and maintenance of the plants.

Observations on grain yield, days to 50% anthesis and days of 50% silking were recorded on whole plot basis, while for all other characters, i.e., plant height, ear height, ear length, ear diameter, number of kernels per ear row, number of kernel rows and 100-kernel weight, observations were recorded on five randomly selected plants or ears (as applicable) from each plot. For measuring the grain yield per plot, ears from all the plants in each plot were weighed. The moisture content in the ears was determined by 'moisture meter' (Formex Moisture Meter) from a representative sample of the shelled grains. Fresh ear weight per plot at harvest (at 15% moisture) was calculated using the standard procedure. The data generated from the field experiments were analyzed using SPAR1 software for various statistical parameters. Pearson's simple correlation coefficients were worked out among various grain yield components as well as endosperm quality traits, as per the standard procedure.

All the experimental QPM hybrids involved in the L x T mating design were analyzed for heterosis over two QPM checks (Shaktiman-1 and Shaktiman-2) and three non-QPM checks (PEHM-1, PEHM-2 and PEHM-3). Heterosis of the experimental hybrids over the better parent, mid-parent and the 'checks' for grain yield per plot were calculated using standard procedures.

The endosperm quality traits, namely per cent endosperm protein and per cent tryptophan in the endosperm protein, were analyzed from a separate trial during *Kharif* 2003 at IARI Experimental Farm, New Delhi. The trial, planted in a randomized complete block design with two replications, was control-pollinated by bulk sibbing in each replication. The endosperm protein and tryptophan content were estimated using standard procedure [3]. Cumulative indices for the genotypes were computed using the Least Significant Difference (LSD)-based ranks for the endosperm quality attributes, based on the procedure suggested by Arunachalam and Bandopadhyay [4]. Biochemical analysis of genotypes for estimation of endosperm protein content and per cent tryptophan in endosperm protein was undertaken at Maize Quality Laboratory, Directorate of Maize Research, New Delhi.

Results and discussion

ANOVA for combining ability in the L x T set revealed that the variances due to both lines and testers were significant for most of the characters, indicating that the parental in lines used in this study were significantly different in terms of general combining ability (Table not presented). The study also revealed that for most of the characters, variance due to dominance effects was found to be much higher compared to the variance due to additive effects, signifying the utility of heterosis breeding in the QPM genotypes. However, both additive and non-additive gene action were found to be important for ear diameter and number of kernel rows per ear at both Delhi and Pantnagar, and for number of kernels per row and days to 50% silking at Pantnagar. Pooled analysis revealed significant effects of the environment on majority of the yield-related characters analyzed in the L x T set, reiterating the importance of location-specific identification and utilization of QPM lines in breeding programmes [5].

The GCA effect for grain yield in the QPM genotypes ranged from –0.32 to 0.29 at Delhi and –0.23 to 0.31 at Pantnagar (Table 1). DMRQPM-401 exhibited the highest GCA effect (0.29), followed by DMRQPM-65 (0.27), DMRQPM-404 (0.25) and DMRQPM-28-5 (0.12) at Delhi, while at Pantnagar, DMRQPM-28-5 was found to be the best general combiner (0.31), followed by DMRQPM-401 (0.30), DMRQPM-56 (0.19) and Tuxpeno Carrib. (0.18). Considering grain yield and other related characters (100-kernel weight, ear length, number of kernels per row, plant height, ear height and early maturity), DMRQPM-65 and DMRQPM-28-5 were found to be best general combiners at Delhi and Pantnagar, respectively. When the pooled data set was considered, DMRQPM-401, DMRQPM-28-5 and DMRQPM-65 displayed the best GCA for most of the characters at both locations.

Table 1. GCA effects for grain yield and related characters in maize

Parents	Delhi			Pantnagar			Pooled		
	GCA effects of grain yield	Mean yield kg/plot	Yield components with significant value in desirable direction	GCA effects of grain yield	Mean yield kg/plot	Yield components with significant value in desirable direction	GCA effects of grain yield	Mean yield kg/plot	Yield components with significant value in desirable direction
L_1	-0.18**	1.07	-	0.19**	0.89	KPR	0.00	0.98	-
L_2	-0.11*	1.17	100KW, PH	-0.01	1.13	-	-0.06	1.15	100KW, PH
L_3	0.29**	1.06	ED, NKR,PH, EH	0.30**	1.20	100KW, NKR, PH, EH	0.29**	1.13	100KW, PH
L_4	-0.32**	1.08	-	0.06	1.24	-	-0.13**	1.16	-
L_5	-0.08	1.23	KPR, EH	-0.07	1.35	EL, KPR	-0.08*	1.29	EL, KPR, EH
L_6	0.25**	0.89	100KW, EL	-0.14*	1.12	-	0.06	1.01	100KW
L_7	0.08	1.08	NKR, KPR	-0.23**	1.34	-	-0.07*	1.21	NKR
L_8	-0.11*	1.10	-	-0.21**	1.09	NKR	-0.16**	1.10	NKR
L_9	0.27**	1.20	100KW, EL, KPR, PH, EH, MFLW, FFLW	0.01	1.07	ED	0.14**	1.13	EL, ED, KPR, EH, MFLW, FFLW
L_{10}	0.01	1.03	-	-0.05	1.22	-	-0.02	1.13	EH
L_{11}	-0.14*	1.34	-	-0.16**	1.29	-	-0.15**	1.31	-
L_{12}	0.12*	1.17	NKR	0.31**	1.06	100KW, EL, KPR, PH, EH,MFLW, FFLW	0.21**	1.11	EL, KPR, PH, EH, FFLW
L_{13}	0.00	1.22	-	-0.17**	1.21	-	-0.09*	1.22	-
L_{14}	-0.08	0.86	-	0.18**	1.10	100KW, NKR, PH	0.05	0.98	-
SE±	0.06			0.06			0.04		
T_1	0.02	0.93	EL, PH	0.03*	1.03	EL, PH, EH	0.02	0.98	EL, PH, EH, MFLW, FFLW
T_2	-0.05	0.97	100KW, NKR	-0.11**	1.25	-	-0.08**	1.11	NKR
T_3	0.03*	1.22	100KW, ED	0.08*	1.19	100KW, ED, KPR	0.05**	1.21	100KW, ED
SE±	0.02			0.02			0.02		

*Significant at P = 0.05; **Significant at P = 0.01

L1 = DMRQPM-56, L2 = DMRQPM-60, L3 = DMRQPM-401, L4 = DMRQPM-28-3, L5 = DMRQPM-403, L6 = DMRQPM-404, L7 = DMRQPM-402, L8 = DMRQPM-58, L9 = DMRQPM-65, L10 = DMRQPM-17-4, L11 = DMRQPM-17-1, L12 = DMRQPM-28-5, L13 = DMRQPM-45, L14 = Tuxpeno Carrib, T1= CML166, T2 = CML167, T3 = CML189; : Yield per plot; 100KW: 100-kernel weight; EL: Ear length; ED: Ear diameter; NKR: No. of kernel rows per ear; KPR: Kernels per ear row; PH: Plant height; EH: Ear height; MFLW: Days to 50% anthesis; FFLW: Days to 50% silking

Among the testers, CML166 and CML189 were observed to be the best general combiners at Pantnagar, while CML189 performed well at Delhi for majority of the yield related characters. Fan *et al.* [6], in a study of QPM germplasm in China, also identified CML166 as the best general combiner.

DMRQPM-45 x CML189 recorded the highest SCA effects for grain yield at Delhi, with positive and significant SCA effects for 100 kernel weight, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, plant height and ear height (Table 2). Other promising QPM crosses identified at Delhi include DMRQPM-402 x CML167, DMRQPM-17-4 x CML166, DMRQPM-28-5 x CML166 and DMRQPM-404 x CML189. However, at Pantnagar, DMRQPM-404 x CML189 exhibited the highest SCA effects for yield with positive and significant SCA effects for several yield components. Other promising crosses with respect to SCA at Pantnagar were DMRQPM-17-1 x CML166, DMRQPM-65 x CML167 and DMRQPM-45 x CML166. Bockholt *et al.* [7] also found significant SCA effects for many yield related traits in QPM germplasm. It is significant to note that DMRQPM-404 x CML189 performed well at both the locations, indicating its adaptability to both the environments.

An analysis of the SCA effects revealed that in most of the cases, the parents involved in experimental crosses having higher SCA had higher GCA. A prominent example was DMRQPM-404 x CML189, where both the parents showed high GCA effects for yield at Delhi and also displayed high SCA effects for grain yield and its components. Although DMRQPM-404 performed poorly at Pantnagar and CML189 showed high GCA, the SCA effects of this cross exhibited positive and significant SCA effects. Similarly, DMRQPM-45 x CML189 showed high SCA effects at Delhi, although DMRQPM-45 had relatively lower GCA and CML189 showed higher GCA effects. These observations clearly suggest that parental interactions, where at least one of the parents had high GCA effects, could also lead to high SCA effects.

Analysis of phenotypic correlations revealed that grain yield in QPM genotypes was positively correlated, as expected, with 100 kernel weight, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, plant height and ear height at both the locations (Table 3). However, days to 50% anthesis and days to 50% silking were found to be negatively associated with grain yield, as was also reported by Sadek *et al.* [8]. This suggests that the selection for the early maturity could result in some reduction in the grain yield potential. The correlations between grain yield and endosperm quality traits (percent endosperm protein and percent tryptophan in endosperm protein) were found to be non-significant in the present set of QPM genotypes, although Pixley and Bjarnason [9] reported negative correlation between grain yield and percent endosperm protein as well as and grain yield and percent tryptophan in endosperm protein, in QPM germplasm developed at CIMMYT, Mexico. Negative association between percent endosperm protein and percent tryptophan in endosperm protein is undesirable, and it is important for the QPM breeders to break this linkage for simultaneous improvement of these traits [9].

Analysis of heterosis in the QPM crosses analyzed in this study revealed that the 'better-parent heterosis' ranged from –17.21% to 77.92% at Delhi; DMRQPM-401 x CML166 emerged as the highest yielder with 77.92% heterosis, followed by DMRQPM-17-4 x CML166 and DMRQPM-402 x CML167 (Table 4). At Pantnagar, DMRQPM-28-5 x CML166 recorded the best performance with 100.95% heterosis for grain yield. Analysis of standard heterosis over the non-QPM check (PEHM-1) revealed DMRQPM-45 x CML189 as the best performer for yield with 9.90% heterosis at Delhi, while at Pantnagar, Tuxpeno Caribb. x CML189 was the highest yielder (14.28% heterosis), followed by DMRQPM-28-5 x CML166 (12.17%) and DMRQPM-401 x CML189 (11.11%). DMRQPM-404 x CML189 performed consistently well at both the locations with 6.25% heterosis at Delhi and 9.52% heterosis at Pantnagar. The present study also revealed DMRQPM-45 x CML189 as the best hybrid at Delhi with highest heterosis (12.23%), followed by DMRQPM-404 x CML189 (8.51%) and DMRQPM-65 x CML166 (2.66%) over the best QPM check (Shaktiman-1). The Pantnagar trial revealed Tuxpeno Caribb. x CML189 as the best performer with 10.20% heterosis (Table 4). However, the present investigation also identified an experimental hybrid DMRQPM-404 x CML189 that exhibited heterotic performance at both the locations, signifying its utility across environments. Overall, observations on heterosis reaffirms the earlier observations [5, 10] that the QPM hybrids could not only have nutritional superiority but also yield potential comparable to or sometimes better than those of the non-QPM hybrids. Nevertheless, the extent of standard heterosis shown by the QPM hybrids emphasizes the need for further widening of QPM germplasm base for the better exploitation of heterosis.

A high positive correlation was observed between the heterosis estimates and the SCA effects of the

Table 2. SCA effects for grain yield and related characters in selected experimental crosses of maize

Parents	Delhi			Pantnagar			Pooled		
	GCA effects of grain yield	Mean yield kg/plot	Yield components with significant value in desirable direction	GCA effects of grain yield	Mean yield kg/plot	Yield components with significant value in desirable direction	GCA effects of grain yield	Mean yield kg/plot	Yield components with significant value in desirable direction
L_2 x T_1	0.15*	1.52	100KW, ED	0.23**	1.96	-	0.19**	1.74	100KW
L_4 x T_1	-0.09	1.07	100KW	0.22**	2.01	PH	0.06	1.54	100KW, PH
L_9 x T_1	0.18*	1.93	100KW, ED	-0.42**	1.33	ED	-0.12*	1.63	ED
L_{10} x T_1	0.31**	1.80	100KW, EL, ED, PH	-0.30**	1.39	EH	0.01	1.60	100KW
L_{11} x T_1	0.07	1.40	NKR, KPR, EH	0.41**	1.99	100KW, KPR, PH	0.24**	1.70	100KW, NKR, KPR, PH, EH, MFLW, FFLW
L_{12} x T_1	0.30**	1.89	100KW, ED, NKR, MFLW, FFLW	0.08	2.12	-	0.19**	2.01	100KW, ED, EH
L_{13} x T_1	-0.34**	1.13	-	0.15*	1.72	PH, EH, MFLW, FFLW	-0.09	1.43	PH, EH, MFLW, FFLW
L_4 x T_2	0.25**	1.35	EL, KPR, EH	0.18*	1.84	-	0.22**	1.59	EL, KPR, EH
L_5 x T_2	0.21**	1.54	100KW, EL, ED	0.09	1.62	-	0.15**	1.58	ED, PH, EH
L_7 x T_2	0.39**	1.89	100KW, ED, MFLW, FFLW	-0.18*	1.20	-	0.11	1.54	MFLW, FFLW
L_8 x T_2	-0.10	1.19	-	0.17*	1.57	PH, EH	0.03	1.38	100KW, PH, EH
L_9 x T_2	0.12	1.80	KPR, MFLW	0.31**	1.92	EL, KPR, PH, EH, FFLW	0.21**	1.86	EL, KPR, PH, EH, MFLW, FFLW
L_{10} x T_2	-0.08	1.34	-	0.16*	1.71	PH, EH	0.04	1.52	KPR
L_6 x T_3	0.30**	2.04	EL, KPR, PH, EH, MFLW	0.42**	2.07	100KW, EL, KPR, PH, EH, MFLW, FFLW	0.36**	2.06	EL, KPR, PH, EH, MFLW, FFLW
L_8 x T_3	0.25**	1.62	EL, KPR, PH, MFLW, FFLW	0.16*	1.74	100KW	0.20**	1.68	100KW, EL
L_{13} x T_3	0.63**	2.11	100KW, EL, ED, NKR, KPR, PH, EH	-0.12	1.49	-	0.25**	1.80	EL, KPR
L_{14} x T_3	0.22**	1.63	ED	0.19*	2.16	-	0.21**	1.89	EL, ED, PH
SE±	**0.08**			**0.08**			**0.06**		

*Significant at P = 0.05; **Significant at P = 0.01

L1 = DMRQPM-56, L2 = DMRQPM-60, L3 = DMRQPM-401, L4 = DMRQPM-28-3, L5 = DMRQPM-403, L6 = DMRQPM-404, L7 = DMRQPM-402, L8 = DMRQPM-58, L9 = DMRQPM-65, L10 = DMRQPM-17-4, L11 = DMRQPM-17-1, L12 = DMRQPM-28-5, L13 = DMRQPM-45, L14 = Tuxpeno Carrib, T1= CML166, T2 = CML167, T3 = CML189; : Yield per plot; 100KW: 100-kernel weight; EL: Ear length; ED: Ear diameter; NKR: No. of kernel rows per ear; KPR: Kernels per ear row; PH: Plant height; EH: Ear height; MFLW: Days to 50% anthesis; FFLW: Days to 50% silking

Table 3. Phenotypic correlation coefficients among grain yield and its components in maize

Traits	YLD	100KW	EL	ED	NKR	KPR	PH	EH	MFLW	FFLW	PROT$^{\$}$	TRYP$^{\$}$
YLD	-	0.492**	0.715**	0.490**	0.492**	0.671**	0.764**	0.707**	-0.487**	-0.398**	0.091	-0.029
100KW	0.758**	-	0.009	0.588**	-0.121	-0.088	0.327*	0.129	-0.215	-0.194	-0.070	0.084
EL	0.806**	0.456**	-	0.024	0.320*	0.883**	0.688**	0.708**	-0.407**	-0.280*	0.274*	-0.127
ED	0.438**	0.391**	0.313*	-	0.227	0.087	0.246	0.163	-0.281*	-0.254*	-0.109	0.182
NKR	0.399**	0.272*	0.253	0.271*	-	0.413**	0.370**	0.520**	-0.236	-0.231	-0.025	0.014
KPR	0.815**	0.427**	0.893**	0.354**	0.224	-	0.653**	0.746**	-0.474**	-0.371**	0.162	-0.088
PH	0.840**	0.615**	0.748**	0.403**	0.309*	0.742**	-	0.817**	-0.411**	-0.351**	0.284*	-0.246
EH	0.726**	0.462**	0.743**	0.388**	0.325*	0.714**	0.811**	-	-0.469**	-0.409**	0.274*	-0.176
MFLW	-0.433**	-0.270*	-0.436**	-0.301*	-0.014	-0.390**	-0.373**	-0.372**	-	0.950**	-0.021	0.156
FFLW	-0.454**	-0.285*	-0.480**	-0.304	-0.043	-0.411**	-0.361**	-0.362**	0.966**	-	0.030	0.188
PROT$^{\$}$	-0.005	-0.199	0.088	-0.062	-0.061	0.083	0.027	0.084	0.157	0.141	-	-0.736**
TRYP$^{\$}$	0.140	0.257	0.057	0.054	0.178	-0.002	0.111	0.106	-0.001	-0.022	-0.736**	-

*Significant at P = 0.05; ** Significant at P = 0.01; $: Data from the separate controlled pollinated trial at IARI Experimental Farm, New Delhi; Upper diagonal represents correlation coefficients at Delhi and lower diagonal from Pantnagar; P'ngr: Pantnagar, YLD: Yield per plot; 100KW: 100-kernel weight; EL: Ear length; ED: Ear diameter; NKR: No. of kernel rows per ear; KPR: Kernels per ear row; PH: Plant height; EH: Ear height; MFLW: Days to 50% anthesis; FFLW: Days to 50% silking; PROT: Percent Protein in Endosperm; TRYP: Percent Tryptophan in Endosperm Protein

experimental hybrids, suggesting that the hybrid vigour is maize could be strongly influenced by non-additive gene action [10]. However, it must be kept in view that high SCA effects may not always translate into heterosis, as was observed in some of the experimental hybrids in the present study, indicating that additive and epistatic gene actions also play important role in heterosis.

It is important to develop broad-based QPM germplasm and identify genotypes (inbreds as well as hybrids) with high per se productivity, combining ability along with the nutritional quality (% protein in the endosperm and % tryptophan in the endosperm protein). The present study revealed significant genetic variability among the QPM genotypes for grain yield and its components as well as protein quality parameters. The average per cent endosperm protein contents among the inbred lines and hybrids were 9.97 and 9.79 (Table not presented), respectively. The overall range of per cent endosperm protein content across the QPM genotypes was 7.05 to 11.40. A similar range was earlier reported in the QPM genotypes [11]. Although the mean values of per cent endosperm protein content in Shakti-1 (QPM check) and Surya (non-QPM check) were comparable with those of the QPM genotypes under study, confirming a similar trend observed in earlier study [3], a few of the QPM genotypes, such as DMRQPM-17-1 and DMRQPM-58, were found superior to Shakti-1. Other promising inbred lines in terms of endosperm protein content include CML167 (10.85%), CML166 (10.65%) and CML189 (10.45%). Among the crosses, DMRQPM-17-4 x CML167 recorded the highest per cent endosperm protein content, followed by DMRQPM-402 x CML167 and DMRQPM-403 x CML167. It must be kept in view that per cent endosperm protein content assumes importance in QPM breeding, since higher per cent protein in the endosperm would lead to higher concentrations of lysine and tryptophan.

In the present study, the percent tryptophan in endosperm protein was found to be in the range of 0.74 to 1.03 (as compared to 0.36 in non-QPM check), implying the presence of genetic variability for enhanced tryptophan content in the QPM genotypes. All the QPM genotypes recorded almost 2-2.5-fold higher per cent tryptophan content in endosperm flour as compared to the non-QPM check (Surya), confirming the nutritional superiority of QPM.

Table 4. Better-parent, mid-parent and standard heterosis for grain yield of the selected QPM experimental crosses

Cross	Grain yield/plot							
	% Better parent heterosis		% Mid-parent heterosis		% Standard heterosis (over QPM check: Shaktiman-1)		% Standard heterosis (over Non-QPM check: PEHM-1)	
	Delhi	P'ngr	Delhi	P'ngr	Delhi	P'ngr	Delhi	P'ngr
L_1 x T_1	29.19	83.82**	38.21**	96.88**	-26.06**	-3.57	-27.60**	0.00
L_2 x T_1	30.00*	73.24**	44.44**	81.51**	-19.15*	0.00	-20.83*	3.70
L_3 x T_1	77.92**	71.87**	88.94**	84.73**	0.00	5.10	-2.08	8.99
L_4 x T_1	-1.54	62.82**	5.79	77.65**	-43.09**	2.55	-44.27**	6.35
L_9 x T_1	61.00**	23.99	80.91**	26.35	2.66	-32.14**	0.52	-29.63**
L_{10} x T_1	74.76**	13.90	83.36**	23.67	-4.26	-29.08**	-6.25	-26.46**
L_{11} x T_1	4.47	54.92**	23.28	72.09**	-25.53**	1.53	-27.08**	5.29
L_{12} x T_1	62.29**	100.95**	80.32**	103.51**	0.53	8.16	-1.56	12.17
L_{14} x T_1	37.14*	79.15**	42.75**	85.31**	-31.91**	1.02	-33.33**	4.76
L_7 x T_2	74.15**	-10.45	83.47**	-7.34	0.53	-38.78**	-1.56	-36.51**
L_9 x T_2	50.70**	53.60**	66.21**	65.52**	-4.26	-2.04	-6.25	1.59
L_{12} x T_2	26.29	54.93**	37.69**	67.92**	-21.81*	-1.02	-23.44**	2.65
L_1 x T_3	-9.02	68.63**	-3.20	92.64**	-40.96**	2.55	-42.19**	6.35
L_3 x T_3	54.10**	75.49**	65.15**	75.98**	0.00	7.14	-2.08	11.11
L_6 x T_3	67.21**	73.95**	93.06**	79.22**	8.51	5.61	6.25	9.52
L_9 x T_3	19.67	60.50**	20.83	69.03**	-22.34*	-2.55	-23.96**	1.06
L_{12} x T_3	11.48	67.51**	13.97	77.45**	-27.66**	1.53	-29.17**	5.29
L_{13} x T_3	73.22**	22.80	73.22**	23.99*	12.23	-23.98**	9.90	-21.16*
L_{14} x T_3	33.33*	81.51**	56.41**	88.37**	-13.30	10.20	-15.10	14.28
SE±	0.17	0.17	0.14	0.15	0.17	0.17	0.17	0.17

*Significant at P = 0.05; **Significant at P = 0.01

L1 = DMRQPM-56, L2 = DMRQPM-60, L3 = DMRQPM-401, L4 = DMRQPM-28-3, L5 = DMRQPM-403, L6 = DMRQPM-404, L7 = DMRQPM-402, L8 = DMRQPM-58, L9 = DMRQPM-65, L10 = DMRQPM-17-4, L11 = DMRQPM-17-1, L12 = DMRQPM-28-5, L13 = DMRQPM-45, L14 = Tuxpeno Carrib, T1= CML166, T2 = CML167, T3 = CML189

DMRQPM-28-5 (0.99) among the inbred lines, and DMRQPM-56 x CML189 (1.03) among the experimental hybrids, were found to be superior for per cent tryptophan content in endosperm protein. Among the testers, CML189 was found to be the best donor for tryptophan content as compared to CML166 and CML167, indicating the presence of favourable alleles in CML189 for this specific trait. Similarly, among the L x T set, DMRQPM-65 x CML189 showed the best overall performance for endosperm protein content and quality.

'Cumulative Indices' for each genotype were computed, taking into account both endosperm protein content and per cent tryptophan content in endosperm protein. On this basis, DMRQPM-65 x CML189 (1.47) was identified as the best QPM entry, followed by

DMRQPM-17-1 x CML167 (1.40), DMRQPM -28-5 x CML166 (1.34), DMRQPM -28-5 x CML167 (1.26) and DMRQPM-45 x CML189 (1.25) (Table not presented). The study also revealed CML189 (1.48) as the best among the QPM inbred lines, followed by DMRQPM-402 (1.41) and DMRQPM-28-5 (1.29). Incidentally, both DMRQPM-28-5 and CML189 were found to be the excellent general combiner at both Delhi and Pantnagar for grain yield and majority of the yield-related traits. In contrast, DMRQPM-401, a good general combiner at both the locations for grain yield and its components, recorded high per cent tryptophan in protein (0.97), but low per cent endosperm protein content (7.90). Similar trend was observed in DMRQPM-404 x CML189.

In conclusion, the present study based on multi-location evaluation was successful in identifying some highly promising QPM inbred lines and experimental hybrids with respect to grain yield as well as endosperm protein quality attributes. Such genotypes could be valuable in enhancing the genetic base of QPM germplasm and cultivars in India.

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