

## Research Article

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# Combining Ability Studies and Heterotic Groups of White Grain Quality Protein Maize (QPM)

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## ABSTRACT

Information on the combining ability and heterotic patterns of maize germplasm is of great value to maize breeders. The objective of this study was to determine the heterosis and combining ability of seven yellow University Maize inbreds (UMI) as lines and five Quality Protein Maize as testers (QPM) lines in a line x tester fashion to understand the genetic architecture, breeding behavior, recombination potential and prediction of progeny performance. Significant differences among the hybrids were observed for all 18 characters indicating the existence of genetic variability. The line x-tester analysis revealed the importance of dominance gene action for all the characters. Parents CML 144, CML 145 in lines, and UMI 524 in testers have superior *gca* effects and *per se* performance. On the basis of *per se* performance, *sca* effects, and standard heterosis the hybrids CML 145 / UMI 189, CML 146 / UMI 427, CML 147 / UMI 427, and CML 147 / UMI 426 appeared to be best for heterosis breeding. Evaluation of hybrids based on significant *gca* and non-significant *sca* resulted in the identification of CML 143 / UMI 427, CML 144 / UMI 524, CML 145 / UMI 189, CML 145 / UMI 427, CML 145 / UMI 524, CML 146 / UMI 189, CML 147 / UMI 524 as worthy genotypes for commercial exploitation and further utilization in recombination breeding programs. Maximum desirable heterosis over mid-parent was observed for carotene (78.68%) and Tryptophan (62.07 %) followed by single plant grain yield (56.61 %). For heterosis over better parent was observed for protein (54.47%) carotene (78.68%) followed by single plant grain yield (59.99%). Among the hybrids, CML 143 x UMI189 recorded highly significant standard heterosis for carotene (41.66), lysine (13.29), and tryptophan (34.29), and also this hybrid was considered to be the best one for moderate yield (31.25 %) and moderate starch (4.92) and low protein(1.63%), which indicates that heterosis in general, can be commercially exploited especially in maize to improve nutritional qualities along with yield to suit the farmers so the exploitation of heterosis is the best method to increase the qualitative like lysine and tryptophan along with increase in the grain yield in maize.

**Keywords:** Combining ability, heterosis, QPM lines, quality traits UMI lines

## INTRODUCTION

Maize (*Zea mays L.*) is referred to as the “Queen of cereals” as it has got the highest potential among cereal crops. Maize is an important crop after rice and wheat in terms of acreage but ranks second in terms of total production and yield. In India average maize area is 6.93mha, total output is about 13.30 million tones and productivity is 2018 kg/ha. Maize is a potential source of protein for humans and animals. According to the analysis report by FAO (2005)(11), the maize kernel contains approximately 70-75% carbohydrates, 9-31.5% crude protein, 2-3-5 % crude fiber, 3-5% lipids per 100g of kernels. However, like most cereal proteins, maize proteins are

nutritionally poor because of their reduced content of essential amino acids. They contain <35 lysine, but the recommended concentration is 5.5% for human nutrition. The normal maize protein is of very poor quality owing to deficiency in two essential amino acids lysine and tryptophan, high leucine – isoleucine ratio, and low biological value. The discovery of the mutant opaque (2) enhances the nutritional quality of the maize. The lysine value of opaque (2) maize is 3.3 to 4.0 g/ 100g of protein, which is more than twice that of endosperm from the normal maize (1.3g/lysine/100g protein). The decreased level of zein (5-27%) in opaque (2) maize is in contrast to normal endosperm quality. Thus the nutritive value of normal endosperm maize is corrected by a genetically improved and biofortified form known as QPM (Quality protein Maize).

An understanding of the genetic architecture of parents and their mode of inheritance will greatly assist the breeder to formulate appropriate breeding methodologies to incorporate the traits in question into an otherwise desirable variety. The present study was, therefore conducted to estimate *sca* and *gca* for hybrids and parents (QPM lines and normal inbred lines) respectively, for qualitative traits and the extent of heterosis for hybrids combined with yield as well as the nature and magnitude of heterosis.

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## Materials and Methods

The present investigation was carried out at the Agricultural College & Research Institute, Madurai, Tamil Nadu Agricultural University during the year 2002-2005. Seven diverse white color seed and high lysine and tryptophan content QPM maize inbreds were crossed to five UMI (University Maize Lines) maize inbreds testers in a Line x tester mating design to generate experimental hybrid for this study (Table 1).

All the twelve parents (7 lines and 5 testers), 35 F1's with the check Co 1 were grown in randomized block design with three replications in a single row plot of 5 m length having 60 x 25 cm crop geometry. Border rows were raised all along the field to avoid environmental influence to the experimental material to a certain extent. The yield characters studied were days to 50% tasselling, days to 50% silking, plant height, ear height, cob length, cob breadth, number of grain rows per cob, number of grains per row, ear weight, 100-grain weight and grain yield per plant. The quality characteristics like total sugars content were recorded by the anthrone reagent method (25) in percent followed by total starch content recorded in percentage by the anthrone reagent method (5). The total nitrogen content was estimated by the microkjeldahl method (15) and carotene content as by Rodriquez et al. (1976). The total oil content of dry seed was determined by the Nuclear Magnetic Resonance (NMR) technique (32). The important quality character lysine and tryptophan content were estimated by Rainin Amino HPLC column.

## Results and Discussion

Analysis of variance showed highly significant differences among genotypes for all characters (yield and quality traits) (Table 2). The variance due to parents, hybrids, and parent-hybrid interactions was highly significant for all 19 characters. Mean squares due to females were larger in magnitude than male parents for all the characters.

There was a significant difference among hybrids for all the traits. Mean squares due to parents versus hybrids were also highly significant for all the characters. The relative estimates of variances due to specific combining ability (S2gca) effects were predominant for all the characters studied indicating the predominance of additive components, except for ear weight. The ratio of variances (S2gca/S2gca) due to general and specific combining ability effects ranged from 0.01 to 3.5. These findings, in general, are in conformity with the results reported earlier (29). In the present study, the analysis of GCA and GCA variances showed that yield, yield contributing characters and quality characters were controlled preponderantly by non-additive gene action. These observations suggest that a breeding method that can incorporate both additive and non-additive genetic components would be a useful strategy. The recurrent selection method, which provides a better opportunity for selection, recombination, and accumulation of desired genes, should help to increase fixable as well as non-fixable types of gene action. It could be expected, when parents possessing high gca effects were combined by hybridization, a large proportion of progenies would have high value for the trait concerned, facilitating easy selection for that trait.

The magnitude of genetic variance was given in Table 3 for all the yield characters and quality characters. The magnitude of D2 variances was higher than A2 variances for all the traits

(Figure 1). The ratio between A2 and D2 ranged from 0.014:1 (100 seed weight) to 0.39:1 (days to 50% tasseling). The same fact was reflected in 2gca and 2gca ratio. The magnitude of D2 variance was higher than A2 for all the quality characters. The ratio between D2 and ranged from 0.012: 1 (Total sugar) to 3.5 : 1 (carotene).

The preponderance of specific combining ability variance (SCA) was greater than general combining ability variance (GCA) indicating the non-additive gene action was reported for yield (Bhatnagar et al., 2004). For plant height (8) for ear height (1); for days to 50% silking (35); for cob length (14), for a number of grains per row (20); for cob breadth(14); for 100 seed weight (12); for starch content for carotene (9); for lysine and tryptophan (33); for Protein. In the present study proportional contribution of lines, testers, and hybrids to total genetic variance;

### i) Yield

The contribution of female x male interaction was highest for all the yield contributing characters. The proportional contribution by females and female x male interaction was almost equal for days to 50% tasselling and days to 50% silking. The contribution of lines was higher than the testers for all characters except for ear height, and single plant yield (Table 3). Compare to female and female x male contribution, males contribution was meager.

### ii) Quality

The contribution of females was higher than males for all the quality characters except for protein content. The proportional contribution of females and females x males contribution was almost equal for total sugar and starch content. The contribution of the female x male component was highest for all the characters studied except for oil content (Table 3).

The knowledge of combing ability coupled with per se performance of parents would be of great value in selecting suitable parents for the hybridization program. In the present study, the association between per se performance and gca effects was not evident for all the traits, except days to silking (late silking). A similar result was reported by (23).

Recent development in biometrical genetics has led to the formation of a number of statistical procedures for the genetic analysis of quantitative characters. The Line x Tester method of analysis was developed in order to give information on combining the ability of parents and the genetic mechanism controlling various traits. Experimentally it is a systematic approach to the identification of potential parents and the crosses with the best selection potential in the earliest generation possible (Johnson, 1963). Successful breeding approaches are a direct consequence of the gene action prevalent in the breeding population under consideration. The relative importance of additive or non-additive effects for grain yield is an indication of the type of gene action (1).

The general combining ability effects (gca) of the parents (Tables 4 and 5) indicated that the parents (CML 145 and CML 146) with low mean values and negative gca effects for days to 50% tasseling could be utilized in a breeding program for earliness. The parent's (CML 141 and UMI 524) high mean values combine with high positively significant gca effects for days to tasselling and silking might be used for developing long-duration crops with a higher yield. The parents (CML 142, CML 144, UMI 524 and UMI 814) for plant height, CML 143 and UMI 814 for ear height, CML 144, CML 146 and UMI 524 for cob

length, CML 144 and UMI 524 for cob breadth; CML 144, CML 147 and UMI 524 for a number of kernel rows; CML 145 and UMI 814 for number of kernels per row, CML 144, CML 145 and UMI 524 for ear weight; CML 144 and UMI 524 for 100 seed weight, CML 144 and UMI 524 for single plant yield; CML 144, CML 146 and UMI 524 for total sugar; CML 144 and UMI 524 for starch, CML 144 and UMI 427 for protein, CML 144 and UMI 524 for oil; CML 144 and UMI 427 for carotene, CML 142, CML 145 and UMI 524 for lysine, CML 144, CML 145 and UMI 426 for tryptophan possessed high per se with significant gca effect (Table 5).

The results of the present study indicated that it would be desirable to develop multiple crosses to select desirable segregants for yields and favorably associated traits in the advanced generations, as no parents was a good general combiner for all the traits as reported by, (27) and (23). However, CML 144 and UMI 524 might be utilized as potential parents since they possessed high per se with significant gca effects for most of the traits under study. Since maize has enormous variability for all traits; a single genotype with all desirable combinations can recombination breeding through recurrent selection.

The basic idea in any hybridization program is to accumulate favorable genes present in different parents into a single genotype. The hybrids thus obtained are utilized in two ways.

1. Forwarding to further generation and selecting superior individuals in the  
Segregating generations with desirable gene combinations.
2. Directly using the F<sub>0</sub> to exploit hybrid vigor.

The utilization of hybrids in any of the two ways will depend upon the genetic constitution of the parents as well as the hybrids. The hybrids obtained by Line x Tester fashion in the present investigation were evaluated for their performance based on mean, heterosis, and gca effects both individually and in combinations. To exploit the hybrid vigor, the parameters like per se performance of hybrids, gca effects, and standard heterosis of hybrids are to be taken into account (7,19,21,18,,31)

The primary criterion to evaluate a hybrid is its mean performance. (17,21) reported that the per se performance of hybrids appeared to be a useful index for judging the hybrids. (13) suggested that parents with good per se performance would result in good hybrids.

For the formulation of a sound breeding program, it is essential to assess the nature of inheritance of yield and yield contributing characters and the potentialities of parents in hybrid combinations. When the character is unidirectionally controlled by a set of alleles with additives, the choice of parents on the basis of per se may be effective. However, in the case when non-allelic interactions determine the character, selection based on per se performance may vitiate the results and so the combining ability estimates must be considered for parental choice (28).

In the present study, the first top-ranking hybrid that exhibited maximum sca effects is presented in Table 6. The ranking based on sca effects of the hybrids showed reasonable deviation from that based on the magnitude of heterosis for most of the traits. This could be expected since the sca effects are only estimates. The large gca effect need not necessarily result in the exceptional performance of a cross as represented by (3)

The hybrid CML 142 x UMI 426 recorded the maximum sca effect for 17 traits out of the 20 studied. Three reason for the

high sca effect exhibited by this particular hybrid was due to the high or moderate gca effects of one of the parents or both the parents and the per se performance of either one or both the parents were higher. Based on the sca effect and moderate per se performance CML 142 x UMI 426 might be used for a further breeding program.

The sca effects along with the per se performance of hybrids gave an idea about the practical utility of hybrid combinations for heterosis breeding as was reported by (23). Crosses recorded considerably higher per se performance with high sca effects as could be seen in the combination CML 145 x UMI 189 which was late to tasseling, CML 147 x UMI 426 for ear height, CML 146 x UMI 814 for cob length, CML 147 x UMI 189 for single plant yield and CML 146 x UMI 426, CML 142 x UMI 189 for lysine and tryptophan respectively, for the other characters Number of kernel row, ear weight, total sugar, starch, protein oil, and carotene the combinations with high per se values recorded positively significant sca effect.

In the present study CML 147 x UMI 426 for days to 50% tasselling, plant height, CML 147 x UMI 427 for starch and oil, CML 147 x UMI 814 and CML 147 x UMI 524 for tryptophan, one of the parents recorded highly significant gca, while the other recorded highly non- significant gca. Parents with high x high gca effects indicating the presence of additive x additive type of gene action between favorable alleles contributed to be of fixable nature (30). Thus these hybrids would be very much useful for further testing.

Significantly positive gca effects in one of the parents and negative (or) non-significant gca effects on the other parent leading to significantly positive sca effect in the hybrids could be observed for most of the traits. Some of the combinations which fulfill the above condition like CML 145 x UMI 427 for days to 50% silking, CML 146 x UMI 426 for plant height, CML 143 x UMI 427 for starch, and CML 144 x UMI 524 for tryptophan. Parents with low x high or high x low gca effects produced crosses with significant sca effects indicating the presence of additive x dominance type of gene interaction. Therefore, the above crosses could throw desirable transgressive segregants. The additive genetic systems are present in one general combiner and complementary epistatic effects on others act in the same direction to maximize the desirable plant attributes (11). In general, this indicated that a combination of good general combiners was not necessarily the best cross combination nor was a low x low cross always a poor combination. (13) reported similar results.

A breakthrough in maize yield and quality improvement may be possible through hybrid maize breeding programs. Maize being an allogamous crop endowed with the mechanism of protandry and monoecy has lent itself feasible for heterosis breeding and a number of commercial hybrids have been released for cultivation.

The extent of heterosis has been measured as the superiority of hybrids over their mid-parent (relative heterosis) and standard check (Standard heterosis). Among the two heteroses, standard heterosis is given importance for the exploitation of heterotic vigor. The frequency of heterotic combinations is presented in Table 7.

#### **Frequency of positive significant heterotic combinations Over mid parent**

A high percentage of cross combinations was found to have significant positive relative heterosis for the eighteen characters studied (Table 7). The observed number of combinations over

mid-parent was highest in carotene (27) followed by lysine (26), while it was least in plant height (5).

#### Over standard parent

In comparison with the standard parent CO 1, crosses are found to have significant positive standard heterosis for all the characters. The number of combinations over standard parent was highest in 100 seed weight (24) and carotene (24). While it was least in Days to 50% tasselling (5).

Among hybrids CML 143 x UMI 189 (CML 143 x UMI 189) recorded significant standard heterosis for eleven traits it was followed by CML 141 x UMI 427 (CML 141 x UMI 427), CML 146 x UMI 426 (CML 146 x UMI 426) and CML 147 x UMI 189 (CML 147 x UMI 189) which showed significant heterosis for ten different traits. The hybrids CML 141 x UMI 524, CML 141 x UMI 814 recorded early tasselling and silking and the standard heterosis for these cross combinations could serve as a source population for developing early flowering segregants.

Regarding ear height (25.36) and cob length (41.66) the hybrids CML 142 x UMI 427 (CML 142 x UMI 427) had high heterosis. For plant height CML 144 x UMI 189 (42.75) (CML 144 x UMI 189) and CML 146 x UMI 189 (CML 146 x UMI 189) (29.49) had maximum standard heterosis. The number of kernel rows and number of kernels per row had maximum standard heterosis in CML 145 x UMI 524 (24.54) and CML 143 x UMI 524 (54.91)

hybrids respectively. Among the hybrids, CML 141 x UMI 426 (30.08) and CML 144 x UMI 524 (17.52) had significant standard heterosis for ear weight and 100 seed weight. Maximum yield heterosis in the present study, over standard check, was 59.99 percent it was observed in the combination CML 141 x UMI 427. This was followed by CML 141 x UMI 189 with a heterosis of 55.65 percent. These combinations (CML 141 x UMI 427 and (CML 141 x UMI 189) also recorded a high magnitude of heterosis for the single plant yield (55.65) and also yield components viz., number of kernels per row, number of kernel rows and 100 seed weight.

Hybrid CML 146 x UMI 524 recorded highly significant standard heterosis for total sugar (32.11) and starch content (12.49). The hybrid combination CML 146 x UMI 189 recorded significant standard heterosis for protein (36.41) and oil content (40.67)

Among the hybrids CML 143 x UMI 189 recorded highly significant standard heterosis for carotene (41.66) lysine (13.29) and tryptophan (34.29). (33) reported heterosis for carotene, lysine, and tryptophan and also this hybrid was considered to be the best one for moderate yield (31.25 %) and moderate starch (4.92) and low protein (1.63%), which indicates that heterosis, in general, can be commercially exploited especially in maize to improve nutritional qualities along with yield to suit the farmers and industrial needs.

**Table 1: Details of parents**

S.No.	Symbol	Genotype	Parentage	Source
	<b>Lines</b>			
1	L <sub>1</sub>	CML 141	Pob 62C 5HC 24-5-3-2-1-B-B-2-B-B-#	CIMMYT, Mexico
2	L <sub>2</sub>	CML 142	Pob 62 C 5HC 93-5-6-1-3-B-B-B-7-B-B-#	CIMMYT, Mexico
3	L <sub>3</sub>	CML 143	Pob 62C 6HC 88-1-1-B-B-B-10-B-B-#	CIMMYT, Mexico
4	L <sub>4</sub>	CML 144	Pob 62 C 5 HC 182-2-1-2-B-B-B-3-1-#-#	CIMMYT, Mexico
5	L <sub>5</sub>	CML 145	Pob63cOHC181-3-2-14#-2B-B-B-B-#-#	CIMMYT, Mexico
6	L <sub>6</sub>	CML 146	AC 8563 MH 35-3-1-B-2-1-B-B-1-B-B-#	CIMMYT, Mexico
7	L <sub>7</sub>	CML 147	Pob63c2HC53-1-1-B-B-B-9-B-B-#	CIMMYT, Mexico
	<b>Testers</b>			
8	T <sub>1</sub>	UMI 189	2407	MBS, Coimbatore
9	T <sub>2</sub>	UMI 426	(UMI 47) x (UMI 134)	MBS, Coimbatore
10	T <sub>3</sub>	UMI 427	(UMI 25) x (UMI 51)	MBS, Coimbatore
11	T <sub>4</sub>	UMI 524	96123 (Sarhaelx Suwan1)x (Suwan)	MBS, Coimbatore
12	T <sub>5</sub>	UMI 814	Diara Evf-10	MBS, Coimbatore

**Table 2: Analysis of variance for grain yield and qualitative traits QPM lines and**

S.No.	Characters	Crosses (df=34)	Females (df= 6)	Males (df=4)	Female x male (df=24)	Error (df=92)	S <sup>2</sup> gca	S <sup>2</sup> sca	S <sup>2</sup> gca/sca
1.	Days to 50% tasseling	125.96**	295.46**	173.99**	96.96**	0.622	9.18	24.23	0.39
2.	Days to 50% silking	105.08**	209.70**	109.22**	84.78**	0.42	5.24	24.69	0.21
3.	Plant height (cm)	4562.4**	14441.13**	1069.41**	3766.06**	12.48	0.34	13.91	0.02
4.	Ear height (cm)	409.37**	1692.31**	270.93**	427.81**	2.28	0.37	3.36	0.11
5.	Cob length (cm)	44.48**	91.65**	1.62**	45.75**	0.02	0.016	0.088	0.18
6.	Cob breadth (cm)	13.37**	6.92**	3.56**	5.43**	0.03	5.4	123.82	0.04
7.	No. of kernel rows	12.06**	13.77**	16.45**	6.91**	0.05	0.92	52.02	0.01
8.	No. of kernels per row	152.68**	453.18**	159.66**	80.83**	0.79	14.27	53.05	0.26
9.	Ear weight (g)	24.21**	2044.74**	386.36**	91.71**	5.54	10.16	7.94	0.02
10.	100 seed weight (g)	26.65**	65.09**	22.96**	21.00**	0.63	4.82	328.02	0.014
11.	Single plant yield (g)	1204.6**	19015.70**	317.44**	623.24**	0.75	39.40	142.97	0.27
12.	Total sugar	1.84**	8.79**	2.37**	1.10**	0.16	0.001	0.033	0.03
13.	Starch	59.42**	318.48**	28.98**	53.19**	0.43	0.934	10.54	0.08
14.	Protein	14.22**	20.85**	17.31**	15.08**	0.23	0.032	2.31	0.012
15.	Oil	1.18**	4.93**	0.52**	1.01**	0.08	0.081	0.405	0.197
16.	Carotene	0.008**	0.009**	0.014**	0.003**	0.005	0.006	0.0017	3.5
17.	Lysine	2.56**	3.96**	0.34**	1.46**	0.035	0.614	14.28	0.043
18.	Tryptophan	0.128**	0.007**	0.013**	0.023**	0.004	0.061	3.68	0.016

**Table 3: Estimates of components of variance of yield and quality traits in QPM and normal maize lines**

Characters	$\sigma^2 gca$	$\sigma^2 sca$	$\sigma^2 gca / \sigma^2 sca$	$\sigma_A^2$	$\sigma_D^2$	$\sigma_A^2 / \sigma_D^2$	Contribution (%)		
							Lines	Testers	Line x Tester
Days to 50% tasseling	9.18	24.23	0.39	36.72	96.92	0.39	36.96	14.51	49.53
Days to 50% silking	5.24	24.69	0.21	20.96	98.76	0.21	36.82	11.71	48.47
Plant height (cm)	0.34	13.91	0.02	1.36	55.64	0.024	33.23	12.83	54.94
Cob length (cm)	0.016	0.088	0.18	0.064	0.35	0.18	31.09	11.41	57.52
Cob breadth (cm)	5.4	123.82	0.04	21.63	495.28	0.04	36.51	16.28	47.21
Ear height (cm)	0.37	3.36	0.11	1.48	13.44	0.11	20.93	26.29	52.76
No. of kernel rows	0.92	52.02	0.01	3.68	208.08	0.017	32.35	12.05	55.82
No. of kernels per row	14.27	53.05	0.26	57.08	212.2	0.26	36.21	32.13	42.51
Ear weight (g)	10.16	7.94	0.02	0.64	31.76	0.02	29.58	9.30	38.29
100 seed weight (g)	4.82	328.02	0.014	19.28	1312.08	0.014	38.54	20.23	41.23
Single plant yield (g)	39.40	142.97	0.27	157.6	571.88	0.27	19.65	29.04	51.31
Total sugar	0.001	0.033	0.03	0.004	0.132	0.030	39.39	10.68	59.93
Starch	0.934	10.54	0.08	3.73	42.16	0.08	37.84	3.50	58.64
Protein	0.032	2.31	0.012	0.12	9.24	0.012	22.48	12.45	65.05
Oil	0.081	0.405	0.197	0.32	1.62	0.197	52.93	3.73	43.33
Carotene	0.006	0.0017	3.5	0.024	0.0068	3.5	21.16	25.46	53.38
Lysine	0.614	14.28	0.043	2.45	57.12	0.042	32.04	12.08	55.83
Tryptophan	0.061	3.68	0.016	2.45	14.72	0.166	41.08	11.12	47.80

**Table 4: General combining ability effects of parents for yield traits**

Parents	Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob breadth (cm)	No. of kernel rows	No. of kernels/row	Ear weight (g)	100 seed weight (g)	Single plant yield (g)
CML 141	2.73**	1.77**	-4.18**	-11.75**	-3.87**	-0.49**	-1.33**	-0.66**	-17.42**	-4.10**	6.47**
CML 142	-0.73**	-1.92**	2.28*	-16.28**	-1.17**	-0.12**	-0.25**	-0.26	-9.34**	-0.45*	-15.04**
CML 143	-1.71**	-1.06**	-12.39**	2.13**	-0.08**	0.03	-0.26**	0.42**	-3.57**	0.40*	5.27*
CML 144	3.26**	0.22*	14.27**	14.43**	4.34**	0.25**	1.49**	-0.49**	12.87**	2.23**	10.70**
CML 145	-2.45**	2.30**	12.05**	1.33**	0.68**	0.15**	-0.62**	0.82**	12.63**	0.10	-1.59
CML 146	-2.56**	0.50*	-10.88*	3.15**	0.72**	0.02	-0.01	0.16	-3.78**	1.73**	4.30*
CML 147	1.46**	-1.81**	9.07**	6.97**	-0.62**	0.14**	0.99**	0.01	8.62**	0.90**	-16.63**
<b>SE</b>	<b>0.20</b>	<b>0.28</b>	<b>1.23</b>	<b>0.39</b>	<b>0.03</b>	<b>0.05</b>	<b>-0.06</b>	<b>0.20</b>	<b>0.61</b>	<b>0.20</b>	<b>2.02</b>
UMI 189	-1.98**	-2.02**	-3.32**	-4.47**	-0.12**	0.05	-0.27**	-2.63**	-3.42**	-1.20**	-5.73**
UMI 426	1.87**	1.37	0.77	3.51**	0.22**	0.10**	-0.73**	0.07	-5.11**	0.41*	3.62**
UMI 427	-0.31*	0.56	-10.17**	-1.76**	-0.31**	-0.25**	0.75**	1.96**	1.41**	0.37*	4.81**
UMI 524	3.36**	2.56**	8.31**	3.84**	0.34**	0.13**	1.10**	-1.43**	5.59**	1.34**	5.55**
UMI 814	3.78**	-0.65*	4.41**	-1.12**	0.13**	-0.03	-0.85**	2.03**	1.54**	-0.91**	4.05**
<b>SE</b>	<b>0.17</b>	<b>0.32</b>	<b>1.16</b>	<b>0.33</b>	<b>0.03</b>	<b>0.04</b>	<b>0.05</b>	<b>0.32</b>	<b>0.51</b>	<b>0.17</b>	<b>1.64</b>

\*Significant at 5% level

\*\*Significant at 5% level

**Table 5. General combining ability effects of parents for quality traits**

Parents	Total sugar (%)	Starch (%)	Protein (%)	Oil (%)	Carotene (%)	Lysine (%)	Tryptophan (%)
CML 141	0.05	1.83**	0.31*	-0.75**	0.014*	0.38**	-0.20**
CML 142	-0.62**	2.11**	-1.78**	-0.27**	-0.019**	0.50**	0.11**
CML 143	-0.86**	-2.83**	-0.14	-0.72**	0.016*	-0.69**	-0.30**
CML 144	1.00**	2.12**	1.84**	0.64**	0.023**	0.27**	0.23**
CML 145	-0.79**	-1.89**	0.77**	0.30**	0.008	0.42**	0.27**
CML 146	0.68**	0.25	-1.02**	0.42**	0.045**	0.31**	-0.15**
CML 147	0.53**	-1.59**	0.01	0.37**	0.041**	0.35**	0.23**
<b>SE</b>	<b>0.05</b>	<b>0.43</b>	<b>0.13</b>	<b>0.07</b>	<b>0.0068</b>	<b>0.10</b>	<b>0.04</b>
UMI 189	-0.34**	-1.45**	-0.73**	-0.13*	-0.009	0.15	-0.15*
UMI 426	-0.07**	1.38**	-0.92**	0.15*	0.016**	-0.28**	0.29**
UMI 427	0.19**	0.73	0.98**	0.03	0.018**	-0.19*	-0.20**
UMI 524	0.48**	2.08**	-0.27*	0.24**	-0.023**	0.21*	0.07
UMI 814	-0.26**	1.42**	0.95**	-0.01	0.001	0.11	0.13*
<b>SE</b>	<b>0.04</b>	<b>0.41</b>	<b>0.11</b>	<b>0.06</b>	<b>0.0056</b>	<b>0.09</b>	<b>0.06</b>

\*Significant at 5% level

\*\*Significant at 5% level

**Table 6. Three top ranking hybrids in the basis of gca effects along with their respective gca status and per se performance for grain yield and qualitative traits QPM lines and hybrids**

S.No.	Characters	Crosses	sca effect	gca effect of parents	per se performance of F <sub>1</sub> 's
1	Days to 50% tasseling (Early)	CML 143 x UMI 524	0.13 <sup>88</sup>	A x H	51.66
		CML 145 x UMI 189	1.15 <sup>88</sup>	H x A	52.00
		CML 143 x UMI 427	1.81 <sup>88</sup>	A x L	53.00
2	Days to 50% tasseling (late)	CML 142 x UMI 427	-2.44 <sup>**</sup>	A x L	68.00
		CML 142 x UMI 814	0.68 <sup>88</sup>	A x H	67.00
		CML 143 x UMI 426	-2.05 <sup>**</sup>	A x A	66.00
3	Days to 50% silking (Early)	CML 143 x UMI 427	1.85 <sup>88</sup>	A x L	54.66
		CML 146 x UMI 524	1.92 <sup>88</sup>	H x H	54.66
		CML 143 x UMI 524	-0.59 <sup>88</sup>	A x H	55.33
4	Days to 50% silking (Late)	CML 143 x UMI 426	-1.85 <sup>**</sup>	A x A	68.33
		CML 142 x UMI 426	-2.72 <sup>**</sup>	A x H	67.66
		CML 146 x UMI 814	-2.67 <sup>**</sup>	H x H	65.33
5	Plant height (cm)	CML 142 x UMI 426	-5.24 <sup>**</sup>	A x H	224.53
		CML 143 x UMI 426	-16.66 <sup>**</sup>	A x A	223.13
		CML 147 x UMI 189	24.38 <sup>**</sup>	L x L	209.36
6	Ear height (cm)	CML 146 x UMI 426	8.90 <sup>88</sup>	H x L	146.33
		CML 142 x UMI 426	-9.36 <sup>**</sup>	L x L	138.53
		CML 145 x UMI 426	-2.10 <sup>88</sup>	H x L	138.70
7	Cob length (cm)	CML 146 x UMI 814	1.26 <sup>**</sup>	L x H	24.55
		CML 142 x UMI 426	0.58 <sup>*</sup>	A x L	23.52
		CML 147 x UMI 189	1.58 <sup>**</sup>	L x L	23.54
8	Cob breadth (cm)	CML 145 x UMI 189	0.32 <sup>**</sup>	A x L	5.39
		CML 142 x UMI 426	0.46 <sup>**</sup>	H x L	5.24
		CML 146 x UMI 814	0.11 <sup>88</sup>	A x H	5.07
9	No. of kernel rows	CML 145 x UMI 524	0.45 <sup>88</sup>	A x H	17.59
		CML 145 x UMI 814	1.59 <sup>**</sup>	A x L	17.10
		CML 147 x UMI 189	1.04 <sup>*8</sup>	L x L	16.67
10	No. of kernels per row	CML 146 x UMI 189	2.03 <sup>88</sup>	H x L	45.67
		CML 142 x UMI 426	-0.53 <sup>88</sup>	A x L	44.36
		CML 144 x UMI 189	5.58 <sup>88</sup>	L x L	43.66
11	Ear weight (g)	CML 146 x UMI 524	5.21 <sup>*</sup>	A x H	89.50
		CML 146 x UMI 814	-5.01 <sup>*</sup>	A x H	85.60
		CML 142 x UMI 426	-8.15 <sup>**</sup>	A x L	80.90
10.	100 seed weight (g)	CML 147 x UMI 189	4.78 <sup>**</sup>	L x L	31.55
		CML 142 x UMI 426	5.44 <sup>**</sup>	A x L	30.45
		CML 144 x UMI 814	3.89 <sup>**</sup>	H x H	29.35
13	Single plant yield (g)	CML 147 x UMI 189	14.97 <sup>*</sup>	L x L	164.70
		CML 142 x UMI 426	15.25 <sup>*</sup>	A x L	163.73
		CML 146 x UMI 814	15.56 <sup>**</sup>	A x H	160.96
14	Total sugar	CML 146 x UMI 524	-0.33 <sup>**</sup>	A x H	6.03
		CML 142 x UMI 426	0.24 <sup>*</sup>	A x L	5.63
		CML 146 x UMI 814	0.71 <sup>**</sup>	A x H	5.30
15	Starch	CML 145 x UMI 426	2.59 <sup>**</sup>	A x L	72.21
		CML 142 x UMI 426	2.61 <sup>**</sup>	L x L	71.55
		CML 145 x UMI 189	2.13 <sup>**</sup>	A x L	71.20
16	Protein	CML 146 x UMI 524	2.10 <sup>**</sup>	A x H	9.82
		CML 144 x UMI 189	-1.15 <sup>**</sup>	H x L	9.83
		CML 142 x UMI 426	0.64 <sup>*</sup>	A x L	9.68
17	Oil	CML 142 x UMI 426	0.57 <sup>**</sup>	L x L	5.51
		CML 143 x UMI 814	0.33 <sup>**</sup>	L x H	5.53
		CML 147 x UMI 189	0.64 <sup>**</sup>	L x L	5.01
18	Carotene	CML 146 x UMI 524	0.035 <sup>*</sup>	A x H	0.41
		CML 142 x UMI 426	-0.034 <sup>*</sup>	A x L	0.38
		CML 147 x UMI 426	0.068 <sup>**</sup>	L x L	0.37
19	Lysine	CML 142 x UMI 426	1.98 <sup>**</sup>	A x L	4.12
		CML 146 x UMI 427	0.43 <sup>**</sup>	A x L	4.08
		CML 146 x UMI 189	2.48 <sup>**</sup>	A x L	4.01

20	Tryptophan	CML 142 x UMI 189	1.39**	L x L	1.24
		CML 142 x UMI 426	-1.84**	A x L	1.18
		CML 146 x UMI 427	0.64**	A x L	1.08

Table 7 : Sumup of per cent heterosis or grain yield and other qualitative traits in QPM maize lines

S.NO	Characters	No. of crosses significantly superior to mid-parent	Range	No of crosses significantly superior to better parent	Range	Cross combination showing highest heterosis in desired directions over	
						Mid parent	Better parent
1	Days to 50% tasseling	7	0.88 to 13.48	5	0.62 to 13.98	CML 145 x UMI 426	CML 145 X UMI 426
2	Days to 50% silking	7	0.39 to 14.81	10	0.78 to -14.73	CML 147 x UMI 426	CML 141 x UMI 814
3	Plant height (cm)	5	4.39 to 49.40	12	0.41 to -42.75	CML 146 x UMI 427	CML 144 x UMI 189
4	Ear height (cm)	20	1.22 to 23.05	16	0.04 to 28.38	CML 141 x UMI 814	CML 142 x UMI 189
5	Cob length (cm)	21	1.93 to 41.66	13	1.23 to -52.47	CML 142 X UMI 427	CML 146 x UMI 189
6	Cob breadth (cm)	12	0.11 to 28.89	13	1.12 to -29.47	CML 145 X UMI 426	CML 144 x UMI 524
7	No. of kernel rows	12	1.72 to 27.17	18	0.45 to 53.33	CML 141 x UMI 189	CML 141 x UMI 427
8	No. of kernels per row	20	0.06 to 55.10	17	1.30 to 57.97	CML 142 x UMI 427	CML 143 X UMI 814
9	Ear weight (g)	18	0.64 to 32.42	12	-0.39 to 46.56	CML 142 x UMI 427	CML 141 x UMI 426
10	100 seed weight (g)	24	0.16 to 24.47	24	0.88 to -39.61	CML 146 X UMI 427	CML 143 x UMI 524
11	Single plant yield (g)	22	-2.08 to 56.61	22	4.02 to 59.99	CML 141 X UMI 427	CML 141 x UMI 427
12	Total sugar	18	0.62 to -43.75	15	-0.80 to -40.87	CML 143 x UMI 426	CML 144 x UMI 189
13	Starch	15	0.12 to 22.86	15	-0.12 to -24.91	CML 141 x UMI 427	CML 145 x UMI 814
14	Protein	25	0.16 to -47.84	12	0.97 to -54.47	CML 145 x UMI 427	CML 146 x UMI 189
15	Oil	23	0.35 to 37.65	21	0.84 to -44.91	CML 146 x UMI 189	CML 144 x UMI 427
16	Carotene	27	1.84 to 78.68	24	3.38 to -47.46	CML 146 x UMI 427	CML 146 x UMI 189
17	Lysine	26	0.78 to 14.01	23	0.48 to -12.48	CML 141 x UMI 427	CML 146 x UMI 189
18	Tryptophan	15	0.83 to 62.07	18	2.99 to -35.96	CML 143 x UMI 189	CML 145 x UMI 524

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