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Genetic Evaluation of Heterosis and Combining Ability of Quality Protein Maize (*Zea mays* L.) Hybrids under Terminal Heat Stress Conditions

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ABSTRACT

Background: The development of quality protein maize (QPM) hybrids tolerant to terminal stress environments has been an essential strategy for reducing the associated loss in grain yield. A study by Badu-Apraku *et al*. (2019) employed line × tester analysis in QPM breeding, highlighting its efficacy in selecting QPM hybrids. While QPM varieties resistant to disease, drought and environmental stresses have been developed conventionally, the adoption of improved QPM genotypes in farmers' field is restricted mainly due to lack of proper team effort among maize breeders, farmers, agricultural extension workers and other relevant stakeholders.

Methods: In line × tester mating design, six lines and three testers were crossed under heat stress environment and 18 F_1s along with parental lines were evaluated along with check varietal during summer season, 2023, P.G research farm, CUTM, Paralakhemudi, Odisha. The objective of the current study was to evaluate parental lines and its crosses based on combining ability and heterosis.

Result: ANOVA revealed significant to revealed significant differences for all the traits between parents, lines, testers and lines vs testers, except for cob height, chlorophyll content and canopy temperature. σ^2GCA/σ^2SCA values for parents/hybrids recorded lower than unity for all the trait studied suggesting preponderance of non-additive gene action. Parental lines CML149, CML143 and CML330 are the best general combiners for early flowering, grain yield per plant and antioxidant status. Among eighteen crosses, two hybrids CML149 × CML330 and CML143 × CML193 recorded significant SCA effects for early flowering, grain yield per plant and antioxidant levels. Hybrids CML149 × CML330 (33.31%) and CML143 × CML193 (28.31%) noted significant standard heterosis for grain yield per plant over commercial check, HQPM-1. Hybrids CML149 × CML330 and CML143 × CML193 were resilient to terminal heat stress as they didn't exhibit signs of leaf firing, tassel blast, root lodging and loss of yield.

Key words: Combining ability, Gene action, Heterosis, Line × Tester design, QPM.

INTRODUCTION

The development of quality protein maize (QPM) hybrids tolerant to terminal stress environments has been an essential strategy for reducing the associated loss in grain yield. A study by Badu-Apraku *et al*. (2019) employed line × tester analysis in QPM breeding, highlighting its efficacy in selecting QPM hybrids. While QPM varieties resistant to disease, drought and environmental stresses have been developed conventionally, the adoption of improved QPM genotypes in farmers' field is restricted mainly due to lack of proper team effort among maize breeders, farmers, agricultural extension workers and other relevant stakeholders (Tandzi *et al*., 2017). In this study attempt was made to develop elite hybrids/segregants of quality protein maize with heat stress tolerance (Edreira *et al.,* 2014).

Combining ability evaluation is a crucial factor in determining the value of inbred lines to get best hybrid combinations (Rajesh *et al.,* 2014). General combining ability (GCA) effects are useful for managing existing diversity, identifying superior parental genotypes with desirable characteristics and establishing linkages between breeding materials. Specific combining ability (SCA) effects, on the other hand, are useful for evaluating recombination frequencies in order to identify potential single crosses between populations or inbred generations. These combined insights provided by GCA and SCA are essential for effective hybrid breeding programs and the development of superior inbred (Thakur *et al.,* 2023);

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(Prasad *et al.,* 2017). Genetic enhancement in tropical maize under terminal heat stress can also be achieved through secondary traits that exhibit strong association with yield such as membrane stability index, tassel blast, leaf firing, root lodging and biochemical parameters like chlorophyll content, catalase and peroxidase Geetha *et al*. (2019). Based on the above findings, a research program was conducted to estimate the nature and magnitude of gene action and variation components under heat stress condition. The goal was to identify potential inbred lines and cross combinations by evaluating their general and specific combining ability, respectively along with the heterotic effects.

MATERIALS AND METHODS

Nine parental QPM lines were subjected to a crossing programme during summer (Mid February to Mid June, 2022) to generate 18 F_1s in a line × tester mating design. Materials used for the present investigation comprises of 18 F_{1s}, parental lines (six lines and three testers) and one standard check (Table 1). The 28 genotypes (18 F1's + 9 Parents + 1 Check) were evaluated at the post graduate research farm, genetics and plant breeding department, School of MSSSoA, Centurion University of Technology and Management, Odisha in a randomized block design (RBD) with three replications during summer 2023. Days to 50% tasseling and days to 50% silking were recorded by counting the number of days from sowing to floral emergence in 50% plants per plot. Five randomly qualified plants were chosen in each replication for recording plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernels row^{-1}, number of kernels row cob^{-1}, 100 grain weight (g), Grain yield plant^{-1} (g), canopy temperature (!), chlorophyll content (%), membrane stability index (%), estimation of protein content (%), estimation of oil content (%), catalase, peroxidase, leaf firing, tassel blast and root lodging. Canopy temperature at midday was measured using an infrared thermometer. Chlorophyll content was assessed using SPAD meter on leaf samples from different parts of the plant. Membrane stability index (MSI) was recorded using electrolyte leakage method, with MSI calculated from electrical conductivity measurements. Catalase activity was determined through an enzymatic assay by monitoring the decrease in absorbance at 240 nm and peroxidase activity was measured by the increase in absorbance at 470 nm in a spectrophotometer.

Based on the mean values, line × tester analysis and standard heterosis assessment for yield and its related traits was performed as per the method suggested by Kempthorne (1957). Heterosis was calculated according to the method suggested by Shull (1908). Heterosis expressed as increase or decrease of F_1 hybrid value over the best commercial check HQPM-1 (standard heterosis) for each character was recorded as per the formulas suggested by Hayes *et al.* (1955). *A*nalysis was done using Windostat version 9.2 and graphs were plotted using Minitab v16.0 software.

RESULTS AND DISCUSSION

Analysis of variance

ANOVA for yield and associated traits showed significant variation among parents and crosses (line × tester) for all the traits except chlorophyll content and canopy temperature (Table 2a and 2b). Lines were significant for all traits except cob height, chlorophyll content and canopy temperature. Testers were significant for days to 50% tasseling, days to 50% silking, plant height, cob height, cob length, number of kernel rows cob^{-1}, number of kernels row^{-1}, membrane stability index and peroxidase. Line × tester interaction was significant for most traits except cob height, cob length, chlorophyll content, canopy temperature and oil percentage. The partitioning of variances among the hybrids into components namely, lines and crosses showed significant differences for all the traits except cob height and chlorophyll content (Table 2a and 2b) Subba *et al.* (2022). Genotypes exhibited a predominance of non-additive genetic effects with σ^2GCA/σ^2SCA ratios less than one and the degree of dominance $(\sigma^2A/\sigma^2D)^{1/2}$ greater than 1 for all traits (Table 3). These results suggest further exploitation of non-additive gene effects for traits through heterosis breeding. In our study, traits such as protein content (71.5%) and oil content (85.55%) exhibited high narrow sense heritability. Therefore, hybridization is the

Table 1: List of QPM parental maize inbred lines and testers used as parents for line × tester crosses and standard checks used in the study.

Genotypes	Pedigree	Reaction to heat stress	Sources
CML149	G24QMH159-2-2-2-B-2-B-B-B-#-B	Tolerant	CIMMYT
CML138	XT1055-29-3-1-1-3-B1-B1#B1	Susceptible	CIMMYT
CML334	Pob590C3F374-2-1-2-B-#-3-3-B-#-8	Tolerant	CIMMYT
CML332	89(SUWAN8422)/(P47s3/MP78:518)*183-1-7-3-1-2-B-#-B-B	Susceptible	CIMMYT
CML143	Pob62c6H88-1-1-B-B-B10-B-B	Tolerant	CIMMYT
CML167	G25QSINT-37-3-2-2-B-B	Susceptible	CIMMYT
CML145	Pob63c0HC181-3-2-1-4#-2-B-B-B-B	Resistant	CIMMYT
CML193	CY0192-B-1-1-B	Resistant	CIMMYT
CML330	89(SUWAN8422)/(P473/MP78:518)*-7-1-1-1-1-1-3-4-B-B	Resistant	CIMMYT
HQPM-1(CHECK)	HKI 193-1 X HKI 163	Resistant	CCSHU, RRS

desirable choice for utilizing the presumed heterosis in selective crosses. Sanghera *et al*. (2013) reported high specific heritability for yield related traits.

General combining ability (GCA) effects

The estimates of GCA effects revealed significant differences among the parents suggesting general combining ability for all the traits in preferred direction (Table 4a and 4b). Among the parents, the lines CML149 and CML143 showed highly significant positive GCA effects for grain yield per plant indicating the presence of additive gene action. While line CML149 and tester CML330 exhibited desirable significant GCA effects for 100 grain weight, CML149 for number of kernels row^{-1}, CML143 for number of kernel rows cob^{-1}, CML138 for cob girth. CML138 and CML332 recorded negative and significant GCA effects indicating that they are good general combiners for obtaining hybrids with reduced plant height. The parents CML149, CML334, CML143 and CML145 recorded positive significant GCA effects for protein content, lines CML 149 and CML334 recorded positive significant GCA effects for oil percentage, lines CML149, CML334, CML332 and CML143 recorded positive significant GCA effects for membrane stability index. Parents CML138, CML332 and CML330 recorded positive significant GCA effects for catalase activity. Line CML167 recorded positive significant GCA effects for peroxidase activity (Table 4b). Similarly, for days to 50% tasseling negative GCA effects were recorded by CML149, CML334, CML143, CML167 and CML330 and for days to 50% silking CML149, CML334 and CML167 and CML330 exhibit negative significant GCA effects (Table 4a). Two lines *viz*., CML334 and CML332 recorded negatively significant GCA effects for anthesis silking interval. It is evident that the line CML149 was adjudged as the best combiner for grain yield per plant, number of kernel row^{-1}, protein content, oil content and membrane stability index and thus can be utilized as potential parent due to high *per se* performance with significant GCA effects for the respective traits. Among the nine parents CML149 and CML143 were chosen as the best general combiner for grain yield per plant. Hence these two lines can be utilized in the hybridization programme Barh *et al.* (2015). Good general combiners for earliness were reported by Ahmed *et al*. (2017); Elmyhun *et al*. (2020); Bharti *et al*. (2020); Raihan *et al*. (2023). Similar results were also reported earlier in maize for grain yield per plant Matin *et al.* (2016).

Specific combining ability (SCA) effects

The SCA is a consequence of dominance and epistasis (Sprague and Tatum, 1942). Estimates of specific combining ability for different crosses is presented in Table 4a and 4b. Out of 18 hybrids, nine hybrids, *viz.,* CML149 × CML145, CML149 × CML330, CML138 × CML145, CML138 × CML193, CML334 × CML145, CML332 × CML193, CML143 × CML145, CML143 × CML330 and CML167 × CML330 showed significant and negative SCA for days to 50% tasseling and crosses CML149 × CML145, CML138 ×

Table 2(a): Analysis of variance for important morphological parameters in QPM parents and hybrids.

Source of Variations	Df	Mean sum of square									
		Days to 50% tasseling	Days to 50% silking	Anthesis -silking interval	Plant height (cm)	Cob height (cm)	Cob length (cm)	Number of kernels row^{-1}	Number of kernel rows Cob^{-1}	Cob girth (cm)	Grain yield plant^{-1} (g)	100 grain weight (g)
Replicates	2	4.49**	4.30**	0.82*	2115.74**	99.9	9.85	62.30*	4.59**	2.18*	27974.11**	12.23**
Treatments	26	18.7**	20.88**	1.80**	2614.01**	418.18*	33.61**	142.74**	9.36**	2.66**	31759.59**	33.88**
Parents	8	18**	27.73**	1.78**	545.5**	212.02	67.83**	219.58**	9.91**	2.96**	56248.41**	58.37**
Parents (Line)	5	2.58**	6.98**	1.86**	635.19**	213.78	67.15**	99.95**	8.08**	2.54**	19041.06**	62.58**
Parents (Testers)	2	4.77**	6.33**	0.11	588*	252.86	25.08**	12.11	3.11*	0.77	244	0.33
Parents (L vs T)	1	121.5**	174.2**	4.74**	12.04	121.5	156.7**	1232.6**	32.6**	9.45**	354**	153.3**
Parent vs crosses	1	45.65**	22.96**	3.85**	25287.5**	5916.3**	140.7**	1244.4**	1.38	17.9**	190756.0**	3.85
Crosses	17	17.44**	17.53**	1.69**	2253.69**	191.78	11.21**	41.78**	9.57**	1.61**	10882.71**	24.12**
Line effect	5	33.19	41.08*	3.9*	5525.66*	307.26	19.56	70.46	24.8**	2.04	22234.79	14.52
Tester effect	2	1.91	1.80	0.67	352.07	144.13	7.17	24.57	2.06	0.97	1276.06	4.22
Line * Tester effect	10	12.68**	8.90**	0.8**	998.02**	143.57	7.85	30.88	3.45**	1.53*	7128.01*	32.91**
Error	52	0.24	0.22	0.24	183.15	243.20	4.08	12.39	0.84	0.59	2609.60	1.18
Total	80	6.34	7.04	0.76	1021.49	296.48	13.82	56.00	3.70	1.30	12717.46	12.09

*Significant at p= 0.05% level, **Significant at p= 0.01% level.

CML193, CML334 × CML145, CML332 × CML193, CML143 × CML145 and CML143 × CML330 showed negative significant SCA effects for days to 50% silking (Table 5a). Negative significant SCA effects were exhibited by two hybrids *viz*., CML138 × CML193 and CML332 × CML145 for plant height. The hybrid CML167 × CML145 had positive SCA effect for number kernel rows cob^{-1}. Two hybrids namely, CML149 × CML330 and CML143 × CML193 had positive SCA effect for grain yield per plant and five hybrids had positive SCA effect for 100-grain weight in CML149 × CML330, CML332 × CML145, CML143 × CML145, CML167 × CML193 and CML167 × CML330 (Table 5a). CML149 × CML330 showed positive SCA effect for protein content. Seven hybrids namely, CML149 × CML330, CML138 × CML193, CML334 × CML145, CML332 × CML330, CML143 × CML145, CML167 × CML145 and CML167 × CML193 showed positive significant SCA effects for membrane stability index. CML332 × CML193 and CML143 × CML145

Table 2(b): Analysis of variance for important biochemical parameters in QPM parents and hybrids.

Source of variations	Df	Mean sum of square						
		Chlorophyll content (%)	Canopy temperature (°C)	Protein (%)	Oil (%)	Membrane stability index (%)	Catalase (Unit mg^{-1})	Peroxidase (Unit mg^{-1})
Replicates	2	419.16**	19.33	10.70**	0.99	89.67**	0.005	0.004
Treatments	26	104.77	32.12	4.31**	3.11**	270.85**	0.01**	0.27**
Parents	8	90.83	14.3	4.54**	4.36**	397.25**	0.01**	0.16**
Parents (Line)	5	93.4	13.21	3.97**	2.95**	75.38**	0.01**	0.13**
Parents (Testers)	2	53.28	0.68	0.03	0.08	33.17**	0.003	0.12**
Parents (L vs T)	1	153.01	47.02	16.42**	19.99**	2734.79**	0.04**	0.34**
Parent vs Crosses	1	40.3	48.22	7.26**	1.70*	22.28**	0.10**	0.18**
Crosses	17	115.13	39.56*	4.04**	2.60**	225.99**	0.01**	0.33**
Line effect	5	66.87	81.35	11.22**	8.21**	476.73*	0.02	0.64
Tester effect	2	290.05	3.09	1.51	0.16	145.80	0.02	0.02
Line * Tester effect	10	104.28	25.96	0.95*	0.29	116.65**	0.007**	0.24**
Error	52	79.17	21.35	0.28	0.36	2.63	0.00	0.01
Total	80	95.99	24.80	1.86	1.27	91.98	0.01	0.09

*Significant at p= 0.05% level, **Significant at p= 0.01% level.

Table 3: Estimates of genetic components of variance and degree of dominance and heritability for morphological and biochemical parameters in QPM.

Trait	σ^2 lines	σ^2 testers	σ^2 gca	σ^2 sca (lines × testers)	σ^2 E	σ^2 gca/ σ^2 sca	Degree of dominance	Heritability (NS) %
Days to 50% tasseling	2.27	-0.59	0.36	4.19 **	0.02	0.830	3.41	14.55
Days to 50% silking	3.57 *	-0.39	0.92	2.94**	0.02	0.883	1.25	38.47
Anthesis-silking interval	0.34	-0.0074	0.109	0.19 **	0.07	0.347	1.57 **	45.17
plant height	503.07 *	-35.88	143.76 **	263.69 **	68.97	0.896	1.35 **	46.36
Ear height (cm)	18.18 **	0.03	6.08	-38.81	86.66	0.446	2.52 **	20.26
ear length (cm)	1.3	-0.03	0.4	0.98	1.63	0.230	1.55	23.75
Number of kernels row^{-1}	4.39	-0.35	1.23	4.87	5.42	0.523	1.98	19.3100
No of kernals rows cob^{-1}	2.37 **	-0.07	0.73 *	0.86 **	0.28	0.012	1.08	56.23
Ear girth (cm)	0.05	-0.03	0	0.30 *	0.20	0.591	11.3	-0.94
Grain yield plant^{-1} (g)	1678.53	-325.10	342.77	1335.69 *	1040.30	0.203	1.9700	22.3900
100 grain weight (g)	-2.04	-1.59	-1.74	10.64 **	0.32	0.181	2.47	-46.6
Protein %	1.14**	0.03	0.4	0.20 *	0.1100	0.332	0.7200	71.5
Oil%	0.88 **	-0.0071	0.28	-0.04	0.14	0.037	0.39	85.55
Canopy temperature ©	6.15	-1.27	1.2	-1.65	10.3	0.309	1.17	21.7746
Membrane stability (%)	40.008 *	1.6200	14.41	38.48 **	0.39	0.310	1.6300	42.57
Chlorophyll content %	-4.15	10.31	5.49	1.38	33.38	0.106	0.5	24.01
Catalase	0.0015	0.0007	0.0010	0.0017 **	0.0006	0.408	1.31	46.05
Perioxides	0.043	-0.012	0.0058	0.0806 **	0.0027	0.049	3.71	12.29

*Significant at p= 0.05% level, **Significant at p= 0.01% level.

showed positive significant SCA effects for catalase activity. Six hybrids *viz*., CML149 × CML145, CML138 × CML145, CML334 × CML193, CML332 × CML193, CML143 × CML145 and CML167 × CML330 showed positive significant SCA effects for peroxidase activity. Based on SCA effect (Table 5a), hybrids, CML149 × CML330 and CML143 × CML193 were identified as promising specific combiners for grain yield per plant, indicating their potential in heterosis breeding for increased grain yield (Table 8) Barh *et al.* (2015); Lane *et al.* (2015). Besides yield, CML149 × CML330 possessed significant negative SCA effect for days to 50% tasseling and significant positive SCA effects for 100 grain weight, protein content and membrane stability index. In the present study it was observed that the grain yield was predominantly controlled by non-additive gene action (dominance and epistasis). Two hybrids, CML138 × CML193 and CML332 × CML145 showed negative SCA effects for plant height and were considered appropriate for development medium tall, non-lodging hybrids. Bharti *et al*. (2020) reported elite specific combiners for earliness and grain yield. Similar results were reported by Raihan *et al*. (2023) for grain yield; Ahmed *et al*. (2017) for grain yield, 100 grain weight and early flowering.

Standard heterosis

The per cent of standard heterosis expressed by different F_1 hybrids over the commercial check varieties HQPM-1 for yield and yield contributing characters are presented in (Table 6a and 6b). The extent of heterosis in F_1 hybrids varied within the spectrum of characters and among the crosses. Negative heterosis is considered desirable for days to 50% tasseling and days to 50% silking in the development of hybrids with earliness whereas, for plant height in developing medium tall, non-lodging hybrids.

The magnitude of heterosis depends on the degree of non-additive gene action and broad genetic diversity among parents. All characters studied in eighteen hybrids were compared with standard check HQPM-1. Eleven hybrids showed negative significant standard heterosis for days to 50% tassel emergence ranging from -4.15% to 8.29% and the hybrid CML332 × CML193 exhibited maximum negative significant standard heterosis. Seven hybrids registered negative significant standard heterosis for days to 50% silking ranging from -3.55% to 8.63% and the hybrid CML334 × CML145 displayed maximum negative significant standard heterosis for days to 50% silking (Table 6a). The cross CML138 × CML193 recorded most negative significant standard heterosis and can be used to produce

Table 4(a): General combing ability effects of parents for important morphological parameters in quality protein maize.

Genotypes	Days to 50% tasseling	Days to 50% silking	Anthesis-silking interval	Plant height (cm)	Cob height (cm)	Cob length (cm)	Number of kernels row^{-1}	Number of kernel rows Cob^{-1}	Cob girth (cm)	Grain yield plant^{-1}(g)	100 grain weight (g)
CML149	-1.519**	-1.241**	0.278	20.241**	7.093	1.667	3.796*	-0.167	0.502	44.833*	1.944**
CML138	3.259**	3.870**	0.611**	-33.981**	-0.574	0.778	2.019	-2.278**	0.61*	-47.27*	1.056*
CML334	-1.519**	-2.352**	-0.833**	34.352**	3.759	-0.556	0.019	0.5	0.038	15.611	-1.056*
CML332	1.370**	0.537**	-0.83**	-14.759*	2.426	1	-0.093	-0.944*	-0.238	-27.167	-0.833*
CML143	-0.630**	-0.13	0.500*	-9.648	-3.241	-0.444	-1.426	2.722**	-0.547	66.278*	0.056
CML167	-0.963**	-0.685**	0.278	3.796	-9.463	-2.444*	-4.315*	0.167	-0.374	-52.27*	-1.16**
CML145	0.370**	0.259**	-0.111	-3.037	-3.241	0.444	-1.204	0.222	-0.232	-9.772	-0.222
CML193	-1.3	0.093	0.222	-2.037	1.259	0.278	1.13	-0.389	0.001	4.833	-0.333
CML330	-0.241*	-0.352**	-0.111	5.074	1.981	-0.722	0.074	0.167	0.231	4.889	0.556*

*****Significant at p= 0.05% level, **Significant at p= 0.01% level.

Table 4(b): General Combing ability effects of parents for important biochemical parameters in quality protein maize.

Genotypes	Chlorophyll content (%)	Canopy temperature (°C)	Protein (%)	Oil (%)	Membrane stability index (%)	Catalase (Unit mg^{-1})	Peroxidase (Unit mg^{-1})	Chlorophyll content (%)
CML149	4.848	3.071	1.579**	0.952**	6.996**	-0.039*	-0.108**	4.848
CML138	-2.652	-2.418	-0.447	-0.349	0.479	0.043*	-0.082*	-2.652
CML334	0.748	1.351	0.510*	1.054**	1.46**	-0.016	-0.256**	0.748
CML332	0.47	1.106	-1.583**	-0.654*	8.514**	0.069**	0.014	0.47
CML143	-1.719	-4.874*	0.591*	0.363	8.816**	-0.001	-0.081*	-1.719
CML167	-1.696	1.765	-0.651*	-1.366**	-88.606**	-0.057**	0.513**	-1.696
CML145	3.765	0.244	0.334*	0.051	2.443	-0.036**	0.025	3.765
CML193	0.459	0.234	-0.166	-0.11	-3.125	0.006	0.014	0.459
CML330	-4.224	-0.478	-0.168	0.06	0.682	0.031*	-0.039	-4.224

*Significant at p= 0.05% level, **Significant at p= 0.01% level.

short stature hybrids for lodging resistance. Out of three hybrids registered positive significant standard heterosis for cob length, the cross CML149 × CML145 displayed maximum positive significant standard heterosis (47.37%).

For number of kernels row^{-1} cross CML149 × CML330 displayed most positive significant standard heterosis. For grain yield per plant standard heterosis value ranged from -29.82% to 33.31% and the cross CML149 × CML330

Table 5(a): Specific combining ability effects for important morphological characters in quality protein maize hybrid.

Genotypes	Days to 50% tasseling	Days to 50% silking	Anthesis-silking interval	Plant height (cm)	Cob height (cm)	Cob length (cm)	Number of kernels row^{-1}	Number of kernel rows cob^{-1}	Cob girth (cm)	Grain yield plant^{-1}(g)	100 grain weight (g)
CML149 × CML145	-0.81**	-0.815**	0.11	16.926	0.130	2.667	-3.907	0.000	0.510	-48.056	-0.222
CML149 × CML193	1.35**	0.019**	-0.333	-4.741	-0.704	-2.167	0.426	-1.056	-0.390	-32.611	-3.111**
CML149 × CML330	-0.53*	-0.204	0.333	-12.185	0.547	-0.500	3.481	1.056	-0.120	80.667*	3.333**
CML138 × CML145	-0.593*	-0.259	0.333	-7.852	2.463	-1.778	-0.130	-0.222	-0.590	-5.944	0.667
CML138 × CML193	-0.75**	-1.093**	0.11	-20.51*	-7.370	1.056	-2.463	0.056	0.493	-30.167	0.444
CML138 × CML330	1.35**	1.352**	0.22	28.370*	4.907	0.722	2.593	0.167	0.097	36.111	-1.111
CML334 × CML145	-0.8**	-1.037**	-0.222	10.815	-4.537	0.556	4.537	-1.66*	-0.342	7.167	0.111
CML334 × CML193	0.68**	0.796**	0.111	7.148	1.630	-1.611	-2.130	0.611	0.608	-6.389	0.889
CML334 × CML330	0.130	0.241	0.111	-17.963	2.907	1.056	-2.407	1.056	-0.266	-0.778	-1.000
CML332 × CML145	3.63**	3.074**	-0.556	-24.07*	-10.87	-1.000	-0.352	0.444	1.083*	12.611	1.556*
CML332 × CML193	-3.87**	-2.759**	1.11**	20.593*	8.963	1.167	1.981	-0.278	-0.317	12.056	-0.333
CML 332 × CML330	0.241	-0.315	-0.556	3.481	1.907	-0.167	-1.630	-0.167	-0.767	-24.667	-1.222
CML143 × CML145	-1.37**	-1.259**	0.111	5.148	8.13	-0.222	1.315	0.111	-0.304	20.500	4.000**
CML143 × CML193	2.13**	1.907**	-0.222	0.148	-0.370	0.278	2.315	0.722	-0.661	78.278*	-0.1556*
CML143 × CML330	-0.75**	-0.648**	0.111	-5.296	-7.759	0.056	-3.630	-0.833	0.966	-79.77*	-2.444**
CML167 × CML145	-0.037	0.296	0.333	-0.963	4.685	-0.222	-1.463	1.333*	-0.357	13.722	-6.111**
CML167 × CML193	0.463*	0.130	-0.333	-2.630	-2.148	1.278	-0.130	-0.056	0.267	-2.167	3.667**
CML 167 × CML330	-0.426*	-0.426	0.11	3.593	-2.537	-1.056	1.593	-1.27*	0.090	-11.56	2.444**

*Significant at p= 0.05% level, **Significant at p= 0.01% level.

Table 5(b): Specific combining ability effects for important biochemical characters in quality protein maize hybrid.

Genotypes	Chlorophyll content (%)	Canopy temperature (°C)	Protein (%)	Oil (%)	Membrane stability index (%)	Catalase (Unit mg^{-1})	Peroxidase (Unit mg^{-1})
CML149 × CML145	-1.809	1.001	-0.833*	-0.022	-6.098**	0.021	0.303**
CML149 × CML193	-1.137	-0.323	-0.106	-0.204	-4.099**	-0.014	-0.376**
CML149 × CML330	2.946	-0.667	0.939*	0.226	10.197**	-0.006	0.073
CML138 × CML145	-0.176	-0.411	0.047	-0.097	-1.474	-0.025	0.226**
CML138 × CML193	0.896	-1.034	0.174	-0.053	4.914**	0.027	-0.316**
CML138 × CML330	-0.720	1.445	-0.221	0.150	-3.439**	-0.002	0.09
CML334 × CML145	-5.176	-3.446	0.159	0.443	4.741**	0.004	-0.146*
CML334 × CML193	3.230	4.063	-0.150	-0.093	-5.124**	-0.038	0.242**
CML334 × CML330	1.946	-0.617	-0.009	-0.340	0.383	0.034	-0.096
CML332 × CML145	11.802	4.938	-0.184	-0.316	-4.254**	-0.081*	-0.329**
CML332 × CML193	-4.293	-3.426	-0.124	0.195	0.344	0.071*	0.295**
CML 332 × CML330	-7.509	-1.513	0.308	0.121	3.911**	0.009	0.034
CML143 × CML145	-4.943	0.145	0.188	0.100	4.986**	0.066**	0.158*
CML143 × CML193	5.130	-1.546	-0.071	-0.259	-0.326	-0.026	0.069
CML143 × CML330	-0.187	1.401	-0.116	0.158	-4.659**	-0.041	-0.228**
CML167 × CML145	0.302	-2.227	0.624	-0.097	2.100*	0.015	-0.212**
CML167 × CML193	-3.826	2.266	0.277	0.414	4.292**	-0.02	0.086
CML 167 × CML330	3.524	-0.038	-0.901*	-0.316	-6.392**	0.005	0.126*

*Significant at p= 0.05% level, **Significant at p= 0.01% level.

Table 6(a): Estimates of standard heterosis for important morphological characters in quality protein maize hybrids.

Genotypes	Days to 50% tasseling	Days to 50% silking	Anthesis-silking interval	Plant height (cm)	Cob height (cm)	Cob length (cm)	Number of kernels row^{-1}	Number of kernel rows cob^{-1}	Cob girth (cm)	Grain yield plant^{-1} (g)	100 grain weight (g)
CML149 × CML145	-3.11**	-1.52**	75.00*	30.89**	23.36	47.37**	-2.17	-15.22*	-10.61	-17.14	-7.61*
CML149 × CML193	-0.52	1.02*	75.00*	19.21*	29.13	15.79	19.57	-26.09**	-16.67*	-10.76	-17.39**
CML149 × CML330	-3.63**	-1.52**	100.00*	19.02*	32.28	20	26.09*	-8.7	-12.12	33.31*	6.52*
CML138 × CML145	4.66**	7.11**	125.00**	-13.75	14.96	13.68	4.35	-30.43**	-19.55*	-27.76*	-7.61*
CML138 × CML193	3.63**	5.58**	100.00*	-20.34*	6.56	30.53*	4.35	-32.61**	-7.58	-29.82*	-8.70*
CML138 × CML330	6.74**	8.63**	100.00*	11.3	27.03	22.11	17.39	-28.26**	-9.09	-15.72	-10.87**
CML334 × CML145	-3.11**	-3.55**	-25	35.40**	10.76	20	13.04	-21.74**	-22.58**	-11.61	-16.30**
CML334 × CML193	-1.55**	-1.02*	25	33.90**	27.56	5.26	-1.09	-10.87	-11.82	-11.4	-14.13**
CML334 × CML330	-2.59**	-2.54**	0	23.73**	30.71	15.79	-5.43	-4.35	-17.67*	-10.2	-17.39**
CML332 × CML145	8.29**	7.11**	-50	-12.05	-1.31	20	-3.26	-17.39**	-12.12	-19.55	-10.87**
CML332 × CML193	-4.15**	-2.03**	100.00*	13.75	37.01	32.63*	11.96	-26.09**	-22.73**	-16.57	-17.39**
CML 332 × CML330	2.07**	1.02*	-50	8.1	27.03	17.89	-3.26	-21.74**	-24.73**	-24.36*	-17.39**
CML143 × CML145	-2.59**	-0.51	100.00*	7.34	19.69	15.79	-2.17	4.35	-27.55**	1.98	0
CML143 × CML193	2.07**	4.06**	100.00*	5.08	13.39	17.89	8.7	4.35	-28.67**	28.31*	-18.48**
CML143 × CML330	-2.59**	-0.51	100.00*	6.03	2.89	9.47	-14.13	-2.17	-11.79	-16.22	-18.48**
CML167 × CML145	-1.04*	1.02*	100.00*	11.49	4.46	3.16	-20.65	-4.35	-26.45**	-24.65*	-36.96**
CML167 × CML193	-1.04*	0.51	75.00*	11.11	0.79	11.58	-8.7	-17.39**	-18.67*	-24.93*	-5.43
CML 167 × CML330	-2.59**	-1.02*	75.00*	18.64*	1.31	-9.47	-6.52	-21.74**	-18.18*	-26.91*	-6.52*

*Significant at p= 0.05% level, **Significant at p= 0.01% level.

Table 6(b): Estimates of standard heterosis for important biochemical characters in quality protein maize hybrids.

Genotypes	Chlorophyll content (%)	Canopy temperature (°C)	Protein (%)	Oil (%)	Membrane stability index (%)	Catalase (Unit mg^{-1})	Peroxidase (Unit mg^{-1})
CML149 × CML145	27.53	11.74	-8.07	4.95	-29.01**	-84.29**	196.10**
CML149 × CML193	18.93	7.83	-5.64	-3.02	-35.56**	-81.43**	-72.73*
CML149 × CML330	16.97	4.7	25.54*	10.9	-2.33	-67.14**	81.82*
CML138 × CML145	8.38	-8.51	-20.36**	-26.99	-32.48**	-68.57**	176.62**
CML138 × CML193	1.09	-10.37	-24.36**	-29.70*	-30.98**	-28.57	-38.96
CML138 × CML330	-19.48	-5.19	-28.61**	-21.04	-39.32**	-30	98.70*
CML334 × CML145	3.16	-6.36	-8.89	17.87	-19.27**	-81.43**	-36.36
CML334 × CML193	19.8	15.66	-17.57*	1.93	-47.60**	-81.43**	110.39**
CML334 × CML330	0.33	-0.18	-16.07*	0.15	-30.51**	-40.00*	-41.56
CML332 × CML145	57.67	17.53	-35.00**	-39.13*	-54.10**	-81.43**	-2.6
CML332 × CML193	-5.66	-7.05	-39.71**	-31.01*	-55.88**	1.43	236.36**
CML 332 × CML330	-31.45	-3.52	-35.11**	-28.77	-42.34**	-14.29	114.29**
CML143 × CML145	-4.13	-14.09	-7.71	-5.88	-6.47**	-48.57*	150.65**
CML143 × CML193	17.95	-19.08	-15.86*	-17.94	-26.45**	-70.00**	111.69**
CML143 × CML330	-14.69	-12.52	-16.36*	-4.33	-27.42**	-65.71**	-24.68
CML167 × CML145	13.06	-1.57	-16.36*	-50.58**	-42.60**	-94.29**	237.66**
CML167 × CML193	-11.21	11.59	-25.43**	-42.46*	-48.80**	-91.43**	349.35**
CML 167 × CML330	-2.5	2.74	-38.07**	-55.45**	-61.42**	-70.00**	344.16**

*Significant at p= 0.05% level, **Significant at p= 0.01% level.

Table 7: Best crosses selected on the basis of per se performance and heterosis (%) for yield.

Hybrid combinations	Per se performance of grain yield plant^{-1} (g)	HQPM^{-1} (check)	Standard heterosis (%)
CML149 × CML 330	533.3	524.6667	33.31*
CML143 × CML 193	530.4	524.6667	28.31*

Table 8: Best two QPM hybrids identified on the basis of per se performance of grain yield per plant and heat stress characters.

Crosses	Grain yield plant^{-1} (g)	100 seed weight (g)	Leaf firing	Tassel blast	Root lodging	Catalase (Unit mg^{-1})	Peroxidase (Unit mg^{-1})
CML 149 × CML 330	533.3	32.7	0	0	0	0.0767	0.4667
CML 143 × CML 193	530.4	25.1	0	0	0	0.07	0.5433

showed most positive significant standard heterosis (Table 7). For 100 grain weight the standard heterosis of hybrids ranged from -36.96% to 6.52% and hybrid CML149 × CML330 exhibited maximum positive significant standard heterosis (6.52%). Standard heterosis for protein content ranged from -39.71% to 25.54% and hybrid CML149 × CML330 showed maximum positive significant standard heterosis (Table 8).

Twelve hybrids registered positive significant standard heterosis for peroxidase activity ranging from -72.73% to 349.35% and hybrid CML167 × CML193 recorded most significant standard heterosis. Similar findings were reported by Mohammad *et al*. (2017) for protein content along with grain yield per plant in QPM maize. Aswin *et al*. (2020); Singh *et al*. (2022) also reported similar results in grain yield per plant.

CONCLUSION

The evaluation of parents based on *per se* performance and general combining ability (GCA) effects revealed that lines CML149, CML143 and tester CML330 were selected as potential contributors for future breeding programs. The importance of considering both mean performance and GCA effects in parent selection was emphasized. Crosses involving good GCA parents namely, CML149 × CML330 and CML143 × CML193 where shown to have high SCA effects for grain yield, terminal heat stress tolerance and high mean performance. These crosses could be exploited for development of high performing QPM hybrids due to non additive gene action for yield and its associated traits. Hybrids CML149 × CML330 and CML143 × CML193 exhibited significant per se performance, favourable SCA effects and standard heterosis for grain yield and other important traits making them promising candidates for further evaluation and utilization in breeding programs.

The assessment of hybrids based on *per se* performance, specific combining ability (SCA) effects and standard heterosis provided a comprehensive understanding of their potential. None of the crosses, exhibiting tolerance to terminal heat stress, displayed symptoms of leaf firing, tassel blast, root lodging and yield reduction. Crosses exhibiting high SCA were derived from parents that are generally good combiners for grain yield per plant. Such crosses deliver good segregants provided additive genetic system in a good combiner and epistatic effects in the crosses play in same direction for maximal character expression under consideration. Ample scope exists for QPM hybrid development under high temperature conditions and the need to expedite by following appropriate breeding procedures.

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Conflict of interests

The authors declare that there is no conflict of interest regarding the publication of this paper.

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