RESEARCH ARTICLE Agricultural Science Digest, Volume 42 Issue 2: 159-164 (April 2022)

Study of Combining Ability and Heterosis in Quality Protein Maize using Line × Tester Mating Design

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10.18805/ag.D-5460

ABSTRACT

Background: High protein content with good quality maize is likely to gain wider acceptance if hybrids are produced that have agronomic performance similar to normal hybrids and retain an enhanced nutritional quality. Thus, an attempt was made to develop quality protein maize hybrids for the benefit of different sections of society depending on maize.

Methods: During the *Rabi* season of 2016-17 (hybrids were obtained crossing ten inbred lines and four testers following line × tester mating design) and 2017-18 (evaluation of hybrids and parents involved along with two commercial checks based on different agro-morphological traits).

Result: Highly significant differences were observed among lines, testers and crosses. Combining ability revealed SCA variances was higher indicating preponderance of non-additive gene action. The contribution of line × tester interaction was higher suggesting parents used in this study can provide high heterotic cross combinations. The parents CML 508, CML 163-D and CML 169 were superior general combiners, indicating their efficacy as parents in future maize breeding programs. Heterosis identified superior yield advantage of the crosses namely, CML508 × CML154-2, CML170 × CML169 and CML163-D × DMRQPM103 over the standard commercial checks HQPM1 and 900 M Gold.

Key words: General combining ability, Heterosis, Line × Tester, Quality protein maize, Specific combining ability.

INTRODUCTION

Maize also commonly known as corn is one of the world's most widely grown cereals and is one of the staple food crops and in the world; it ranks third in production next to wheat and rice. It has expansive adaptability under diverse agro-climatic conditions. The suitability of maize to diverse environments is unparalleled by any other crop. Single cross hybrids are adopted for commercial cultivation in advanced countries. Various quality protein maize (QPM) hybrids have been produced in Africa and Latin America as well as in India, yet it is increasingly being felt to develop urgently more QPM hybrids in India which can yield at par with conventional hybrids. The relative ability of a genotype to transmit its desirable performances to its crosses is termed combining ability (Kanagarasu, 2010). Combining ability analysis is not only the quickest method of understanding the genetic mechanisms controlling the inheritance of quantitative traits but also gives essential information about the selection of parents and enable the breeders to select suitable parents for use in hybrid improvement.

The performance of a hybrid is related to the two types of combining ability recognized in quantitative genetics *i.e.*, general (GCA) and specific (SCA) combining abilities of the inbred lines involved in the cross. GCA is a measure of the additive effects of gene and refers to the standard performance of the genotype in a series of hybrid combinations and whereas; SCA is related to the non-additive effects of the genes (dominance, epistatic and G×E interaction) and refers to the performance of a parent in a particular cross concerning GCA (Sprague and Tatum, 1942; Rojas and Sprague, 1952). Thus, the selection of hybrids for the breeding programmes is based on their *per se* performance, GCA effects of their parents and SCA effects of hybrids. The high GCA effects are due to additive gene action as well as additive × additive type of epistatic gene action (Griffing, 1956). The recent trend even in the developing and underdeveloped countries is to go for single crosses as these are the high yielders under most favorable environments and also show higher uniformity than the double and three way crosses (Atanaw *et al.* 2003). The line × tester design has been widely used in maize breeding by several workers and continues to be applied in quantitative genetic studies in maize due to its significance (Sharma *et al.* 2004). The current investigation was undertaken to estimate the combining ability of parents and hybrids, nature and proportion of gene action and

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How to cite this article: Subba, V., Nath, A., Kundagrami, S., Ghosh, A. (2022). Study of Combining Ability and Heterosis in Quality Protein Maize using Line × Tester Mating Design. Agricultural Science Digest. 42(2): 159-164. DOI: 10.18805/ag.D-5460.

Submitted: 22-07-2021 **Accepted:** 09-11-2021 **Online:** 09-12-2021

understand the extent of heterosis for yield and yield-related traits in quality protein maize by adopting one of the powerful tools *i.e.*, Line × Tester analysis (Kempthorne, 1957).

MATERIALS AND METHODS

Ten female inbred lines were hybridized with four inbred testers (used as the male pollinator) following a line × tester mating design (Kempthorne, 1957) at the University of Calcutta Experimental Farm, Baruipur, West Bengal, India (Latitude 22°52′N, Longitude 88° 52′E), during the *Rabi* season of the year 2016-17. All the inbred lines used for the experiment were Quality Protein Maize; CML 508, CML 510 and CML 511 were obtained from CIMMYT, Centre (Hyderabad, India) and the rest were from the Indian Institute of Maize Research (Ludhiana, India).

For hybridization, the female parents were detasseled and ear shoots were covered with butter paper bags to avoid unwanted pollination. On the male parent, before anthesis, the tassels were covered with butter paper bags and following anthesis pollen grains collected in the bags were acquired and dusted over the emerging silk of the female cobs. Following physiological maturity, the F_1 seeds were collected and stored for evaluation in the following season.

During the following *Rabi* season of the year 2017-18, forty single-cross hybrids, lines and the testers were cultivated in three replications following randomized complete block design (RCBD) at the same location mentioned above. Furthermore, two commercial hybrids, namely 900M Gold and HQPM1 were also planted as standard checks. The plants were sown at a row to row spacing of 60 cm and a plant to plant spacing of 20 cm. All necessary package and practices suited to the given location were thoroughly followed.

The observations related to eight morphological traits were conducted from five randomly selected plants from each block. Data related to important traits, namely days to tasseling (50%), days to silking (50%), plant height (cm), cob length (cm), cob diameter (cm), number of grains per cob,100 grain weight (gm), grain yield per plant (g) were recorded and analysed using SPAR 3.0. Further more, heterosis over the midparent, better parent and standard checks were calculated for the forty single cross hybrids.

RESULTS AND DISCUSSION

The study revealed significant differences among the lines, testers as well as crosses. The significantly high variability observed among the parents indicate that sufficient heterosis can be expected among the single cross hybrids (Table 1a). Such expectations can be further validated from the parameter parent vs crosses, which showed significant variance for all the traits, thus suggesting that the crosses obtained differed significantly from the parents. Earlier studies conducted (Singh *et al.* 2012; Kambe *et al.* 2013) also showed similar observations in the case of maize. The genetic components of variance calculated for the eight traits revealed that non-additive gene action was predominant, as evinced from the higher estimates for SCA variance (σ^2SCA) than variance due to GCA (σ^2GCA) for all the traits evaluated (Table 1b). Furthermore, the dominance genetic variance (σ^2_D) showed higher estimates than additive genetic

Table 1a: Analysis of variance for combining ability of various agro-morphological traits.

S.O.V.	df.	DT (50%)	DS (50%)	PH (cm)	CL (cm)	CD (cm)	GC	GW(g)	GYP (g)
Replication	2	13.01	17.92	73. 29	1.40	0.51	4550.48	25.36	162.63
Treatments	53	40.56**	45.55**	2014.13**	4.81**	3.34**	16050.91**	18.94**	2223.48**
Parents (P)	13	37.89**	36.79**	1586. 80**	2.08*	3.82**	14754.62**	11.96**	531.52**
P. vs C.	1	299.06**	420.36**	39865.18**	40.45**	21.71**	120473.06**	75.66**	56761.36**
Crosses (C)	39	34.82**	38.86**	1186.03**	4.80**	2.71**	13805.51**	19.82**	1389.06**
Lines (L)	9	25.00**	30.15**	1247. 28**	7.24**	3.31**	17975.79**	31.32**	2245.52**
Testers (T)	3	128.01**	156.76**	3661. 73**	6.31**	4.83**	19542.169**	11.38**	1730.04**
Line × testers	27	27.74**	28.66**	890.53**	3.82**	2.28**	11778.02**	16.92**	1065.68**
Error	106	3.51	3.04	118.03	0.57	0.55	3034.94	3.30	193.72

Table 1b: Estimation of the components of genetic variance.

σ^2GCA	2.32	3.09	74.48	0.14	0.09	332.43	0.21	43.91
σ^2SCA	8.18	8.65	266.46	1.09	0.61	2862.41	4.63	282.59
σ^2A	4.64	6.17	148.95	0.28	0.17	664.85	0.42	87.82
σ^2D	8.18	8.65	266.46	1.09	0.61	2862.41	4.63	282.59
σ^2GCA/σ^2SCA	0.28	0.36	0.28	0.13	0.15	0.12	0.05	0.16
2 σ^2GCA/ 2σ^2GCA + σ^2SCA	0.36	0.42	0.36	0.21	0.22	0.19	0.08	0.24
Average degree of dominance	1.33	1.18	1.34	1.97	1.89	2.08	3.32	1.79

S.O.V: Source of variance, DT 50%: Days to 50% tasseling, DS 50%: Days to 50% silking, PH: Plant height, CL: Cob length, CD: Cob diameter, GC: Number of grains/cob, GW: 100-Grain weight and GYP: Grain yield/plant.

*and **, significant at 0.05 and 0.01 levels of probability.

Table 2: Proportion of contributions of lines, testers and line × tester to the total variance for 8 traits.

Parameters	DT (50%)	DS (50%)	PH (cm)	CL (cm)	CD (cm)	GC	GW (g)	GYP (g)
Lines	16.57	17.91	24.27	34.79	28.13	30.05	36.47	37.31
Testers	28.28	31.03	23.75	10.10	13.69	10.89	4.42	9.58
Line × testers	55.15	51.07	51.98	55.11	58.18	59.06	59.11	53.11

Table 3: Estimates of general combining ability (GCA) effects of parents in respect of 8 traits.

Parents	DT (50%)	DS (50%)	PH (cm)	CL (cm)	CD (cm)	GC	GW(g)	GYP(g)
Lines/Females								
CML508	0.67	0.49	23.17**	1.14**	0.92**	44.13**	1.65**	29.19**
CML510	-1.47**	-1.52**	-14.72**	-0.57**	-0.01	-27. 93*	0.21	-0.85
CML511	-0.85	-0.57	0.04	-0.35	0.03	-20.75	1.19*	7.34
CML163-D	2.47**	2.83 **	-0.77	1.23**	0.75**	44.77**	2.70**	13.77**
CML167	1.83**	1.83 **	7.04**	0.63**	-0.02	-25.22*	-2.79**	-11.89**
CML170	-0.93*	-1.11*	1.40	-0.60*	-0.39	-1.04	0.18	-5.0
CML179	-1.12**	-2.11 **	-9.59**	-0.05	-0.53**	13.71	0.09	-1.41
DMRQPM03-104	-0.7	-0.50	-3.4	-0.54*	0.16	-34.45**	-0.38	-12.93**
H.K.I.163	-1.21**	-0.73	-4.84	0.16	-0.12	17.86	-1.52**	-2.47
H.K.I.193-1	1.36**	1.39**	1.71	-1.05**	-0.77**	-11. 07	-1.32**	-15.66**
SE (Female)	0.49	0.45	2.62	0.21	0.18	13.57	0.48	4.04
Testers/males								
CML154-2	-3.08**	-3.41**	-15.63**	-0.55**	-0.31*	1.28	0.28	-4.83*
CML165	1.16**	1.30**	0.01	-0.19	-0.19	-5.73	-0.78**	-5.35*
CML169	0.69*	0.77**	7.58**	0.46**	0.59**	22.79**	0.65*	10.97**
DMR QPM 103	1.23**	1.34**	8.03**	0.28*	-0.08	-18.33*	-0.15	-0.80
SE (Male)	0.28	0.26	1.51	0.12	0.11	7.83	0.28	2.33

Table 4: Top three best performing crosses in terms of specific combining ability (SCA) for the traits under study and the GCA of the parents involved.

Characters	Crosses	GCA of parents
Days to tasseling-50%	CML167 × CML154-2 (-6.56**),	Poor × Good,
	H.K.I.193-1 × CML165 (-4.29**),	Poor × Poor,
	CML511 × CML 154-2 (-3.76**)	Average × Good
Days to silking-50%	CML167 × CML154-2 (-6.01**),	Poor × Good,
	H.K.I.193-1 × CML165 (-3.85**),	Poor × Poor,
	CML511 × CML154-2 (-3.53**)	Average × Good
Plant height (cm)	CML511 × CML165 (-23.61**),	Average × Average,
	CML167 × DMRQPM103 (-21.26**),	Poor × Poor,
	CML163-D × CML165 (-20.89**)	Average × Average
Cob length (cm)	CML179 × CML165 (3.03**),	Average × Average,
	CML167 × CML169 (1.85**),	Good × Good,
	DMRQPM03-104 × DMRQPM103 (1.35**)	Poor × Good
Cob diameter (cm)	CML179 × CML165 (1.41**),	Poor × Average,
	CML167 × CML169 (1.21**),	Average × Good,
	H.K.I 163 × CML165 (1.09**)	Average × Average
No. of grains/cob	CML170 × CML169 (109.95**),	Average × Good,
	CML508 × CML154-2 (63.82**),	Good × Average,
	CML179 × CML169 (60.40*)	Average × Good,
100 grain weight (gm)	CML170 × CML169 (4.78**),	Average × Good,
	CML508 × CML154-2 (4.24**),	Good × Average,
	DMRQPM03-104 × DMRQPM103 (3.36**)	Average × Average,
Grain yield/plant (gm)	CML170 × CML169 (35.27**),	Average × Good,
	H.K.I.193-1 × CML165 (26.66**),	Poor × Poor,
	DMRQPM03-104 × DMRQPM103 (25.50**)	Poor × Average

Table 5: Top three heterotic combinations (mid parent, better parent/heterobeltiosis, standard heterosis) over 900M Gold and HQPM1.

Traits	MID-Parent heterosis	Heterobeltiosis	SH over SC1	SH over SC2
Days to tasseling-50%	CML511 × CML 154-2 (-16.32**)	CML511 × CML154-2 (-12.36**)	CML167 × CML154-2 (-12.41**)	CML167 × CML154-2 (-10.59**)
	CML167 × CML154-2 (-15.76**)	H.K.I 163 × CML154-2 (-11.46**)	CML511 × CML154-2 (-12.25**)	CML511 × CML 154-2 (-10.43**)
	CML510 × CML154-2 (-15.53**)	CML167 × CML154-2 (-10.96**)	CML510 × CML154-2 (-12.25**)	CML510 × CML154-2 (-10.43**)
Days to silking-50%	CML511 × CML 154-2 (-16.33**)	CML511 × CML 154-2 (-12.48**)	CML510 × CML154-2 (-11.38**)	CML510 × CML154-2 (-10.86**)
	CML510 × CML154-2 (-15.96**)	H.K.I 163 × CML154-2 (-11.86**)	CML167 × CML154-2 (-10.90**)	CML167 × CML154-2 (-10.37**)
	CML167 × CML154-2 (-15.73**)	CML179 × CML154-2 (-11.82**)	CML511 × CML154-2 (-10.80**)	CML511 × CML 154-2 (-10.27**)
Plant height (cm)	CML163-D × CML 165 (-7.56*)	CML163-D × CML165 (-14.88**)	CML179 × CML154-2 (-26.34**)	CML179 × CML154-2 (-17.28**)
	CML511 × CML 165 (-0.32)	H.K.I 163 × CML154-2 (-9.90*)	H.K.I163 × CML154-2 (-23.13**)	H.K.I 163 × CML154-2 (-13.67**)
	CML163-D × CML169 (0.83)	CML163-D × CML169 (-7.14)	H.K.I193-1 × CML154-2 (-22.73**)	H.K.I193-1 × CML154-2 (-13.23**)
Cob length (cm)	CML167 × CML169 (31.59**)	CML167 × CML169 (26.94**)	CML167 × CML169 (20.00**)	CML167 × CML169 (22.68**)
	CML508 × CML169 (25.56**)	CML508 × CML169 (24.21**)	CML179 × CML165 (18.97**)	CML179 × CML165 (21.63**)
	CML508 × DMRQPM103 (24.06**)	CML508 × CML154-2 (19.63**)	CML508 × DMRQPM103 (15.88**)	CML508 × DMRQPM103 (18.47**)
Cob diameter (cm)	CML508 × CML154-2 (30.95**)	CML508 × CML154-2 (29.91**)	CML167 × CML169 (8.26*)	CML167 × CML169 (11.24**)
	H.K.I 163 × DMRQPM103 (22.14**)	CML508 × DMRQPM103 (18.87**)	CML508 × CML169 (4.50)	CML508 × CML169 (7.38)
	CML508 × DMRQPM103 (21.97**)	H.K.I 163 × DMRQPM103 (18.56**)	CML508 × CML154-2 (4.36)	CML508 × CML154-2 (7.24)
No. of grains/cob	CML508 × CML154-2 (74.58**)	CML508 × CML154-2 (59.07**)	CML179 × CML169 (29.00**)	CML179 × CML169 (34.95**)
	CML170 × CML169 (61.19**)	CML179 × CML169 (41.74**)	CML170 × CML169 (27.54**)	CML170 × CML169 (33.42**)
	CML179 × CML169 (55.84**)	CML9170 × CML169 (40.12**)	CML163-D × DMRQPM103 (25.32**)	CML163-D × DMRQPM103 (31.10**)
100 grain weight (gm)	CML508 × CML154-2 (45.00**)	CML508 × CML154-2 (41.61**)	CML163-D × DMRQPM103 (20.86**)	CML163-D × DMRQPM103 (18.74**)
	CML508 × CML 165 (40.58**)	CML508 × CML165 (36.74**)	CML170 × CML169 (19.33**)	CML170 × CML169 (17.24**)
	CML163-D × CML154-2 (36.98**)	CML170 × CML169 (33.86**)	CML163-D × CML154-2 (16.31**)	CML163-D × CML154-2 (14.27**)
Grain yield/plant (gm)	CML508 × CML154-2 (132.42**)	CML508 × CML154-2 (115.74**)	CML508 × CML154-2 (27.15**)	CML508 × CML154-2 (31.89**)
	CML170 × CML169 (117.50**)	CML508 × DMRQPM103 (102.18**)	CML170 × CML169 (27.09**)	CML170 × CML169 (31.82**)
	CML508 × CML165 (117.38**)	CML508 × CML165 (98.63**)	CML163-D × DMRQPM103 (24.32**)	CML163-D × DMRQPM103 (28.95**)

*and **, significant at 0.05 and 0.01 levels of probability.

variance (σ^2_A), further corroborating the predominance of non-additive gene actions. Similar observations were earlier recorded in the investigations of several studies (Subramanian and Subbaraman, 2006; Vijayabharathi *et al.* 2009). The Baker's predictability ratio (1978) (2 σ^2 g/2 σ^2 g + σ^2 s) revealed that the values for all the traits were below unity; indicating that the performances of the F_1 hybrids cannot be determined with certainty only based on the GCA recorded for the consecutive parents involved. The proportional contributions of lines, testers and the interaction component were calculated (Table 2). The contribution of line × tester interaction was higher than the individual contribution of either of the parents; thus, indicating that the parents utilized in the present study can provide highly heterotic cross combinations. Similar observations were also reported by earlier workers in maize (Ali *et al.* 2013; Begum *et al.* 2016).

In the present study the GCA estimates for the lines and testers were evaluated (Table 3). High GCA estimates observed for a trait indicates a significant role of additive and additive × additive genetic variance in the expression of a given morphological trait (Griffing, 1956). The present investigations revealed that the lines CML 508 and CML 163-D were the best general combiners in terms of yield and yield attributing traits like number of grains per cob and 100-grain weight. Thus, the two QPM inbreds can be recommended as female parents for hybrid maize development in future breeding programs. Similarly, the QPM inbred CML 169 showed superior GCA for yield and yield attributing traits. Therefore, the inbred can be utilized as a male parent in future breeding programs. In the case of SCA for the hybrids, it was observed that the top three crosses with the highest SCA estimates had either or both the parents exhibiting poor or average GCA (Table 4). Thus, such observation can indicate the predominance of non-additive gene action determining the performance of the hybrids; which in the case of cross-pollinated species like maize is quite anticipated (Uddin *et al.* 2008; Dar *et al.* 2017). In the present study the top three crosses showing superior SCA in the desired positive direction include CML170 × CML169 (35.27), H.K.I.193-1 × CML 165 (26.66) and DMRQPM03-104 × DMRQPM103 (25.50). The heterosis over the better parent, mid parent and standard commercial checks were also estimated for the single cross hybrids (Table 5). Ultimately, from the commercial perspective heterosis over standard checks are essential for determining the success of a given cross combination. The top three cross combinations which showed significant yield heterosis over the two standard checks were CML508 × CML154-2, CML170 × CML169 and CML163-D × DMRQPM103. These hybrids exhibited a significant yield advantage over both the QPM check as well as the non-QPM hybrid check (*i.e.*, HQPM1 and 900M Gold, respectively). Thus, the hybrids mentioned above can be recommended for further evaluation and commercial cultivation.

CONCLUSION

The present investigation revealed valuable inbred lines of QPM which showed superior general combining ability and can be recommended for extensive use in future breeding programs aimed at developing single cross QPM hybrids. Furthermore, the analysis revealed a predominance of non-additive gene action governing the expression of all the traits, which in turn resulted in the detection of superior hybrids which showed considerable yield advantage over the existing commercial checks. These heterotic cross combinations namely, CML508 × CML154-2, CML170 × CML169 and CML163-D × DMRQPM103 can be recommended for multi-locational evaluation followed by large scale cultivation across maize growing regions of rural West Bengal and India.

ACKNOWLEDGEMENT

The first author is grateful towards the National Fellowship for Higher Education of ST students (NFST) by Ministry of Tribal Affairs, Govt. of India for providing the necessary fund for the research.

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