



STUDY OF COMBINING ABILITY USING QPM DONORS AS TESTERS FOR YIELD AND YIELD TRAITS IN MAIZE (*Zea mays* L.)

L. RAM*, R. SINGH and S. K. SINGH

Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, India 221005

* Corresponding author's email: lekhamscientist@gmail.com

Email addresses of co-authors: rsingh6361@gmail.com, shravanranchi@yahoo.co.in

SUMMARY

Ten maize inbreds were crossed as female parent to 8 testers (QPM donors) as male parents to generate 80 F₁ crosses. The 99 genotypes including hybrids along with their parents and check were evaluated in randomized complete block design to estimate the GCA and SCA of parents as well as crosses. Combining ability analysis revealed that significant mean square was due to line GCA for all traits except shelling per cent while tester GCA was significant only for 100 grain weight. Mean square due to SCA was significant for all traits. Variance due to SCA was greater than GCA for most of the traits and variance due to GCA was greater than SCA for 100 grain weight indicating the predominance of non-additive and additive type of gene action, respectively. The crosses CM 141 × CML 161, V335 × CML 141, V351 × CML 141 were the best hybrids based on *per se* performance and SCA effects. The line V335 and the testers CML 141 was found to be the best general combiner for yield and yield contributing traits. Currently, based on combining ability estimates the lines V335 and V351 are being converted into QPM lines using QPM donor CML 141 to develop local QPM hybrid.

Key words: QPM donors, lines, testers, yield, *Zea mays* L., GCA and SCA

Key findings: The aim was to identify appropriate parental lines, hybrid combinations with useful gca, sca effects, heterotic combinations, high *per se* performance to breed local QPM hybrids and use these inbreds in DNA aided conversion of non-QPM lines into QPM one.

Manuscript received: July 11, 2014; Decision on manuscript: January 8, 2015; Manuscript accepted: February 7, 2015.

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Communicating Editor: Bertrand Collard

INTRODUCTION

Maize (*Zea mays* L.; 2n = 20) is an important cereal crop of India, which plays an important role in human and animal nutrition. It has assumed greater significance due to its demand for food, feed, fodder and industrial utilization. However, its protein quality is deficit in essential amino acids particularly, lysine and tryptophan. Quality protein maize (QPM) is a genotype in which *opaque-2* gene has been incorporated

along with associated modifiers. QPM contains twice the amount of lysine and tryptophan as compared to normal maize endosperm. QPM donors with sufficiently higher quantity of lysine and tryptophan have been developed at CIMMYT, Mexico (Vasal, 1999). In a QPM conversion program, a QPM line selected as a donor, by virtue of being elite, should possess good modifiers and the ability to pass them further when crossed and should have high combining ability (Vivek *et al.*, 2008).

Combining ability analysis is not only the quickest method of understanding the genetic nature of quantitatively inherited traits, but also gives useful information about the selection of parents to plant breeders for formulating an efficient breeding program (Jebaraj *et al.*, 2010). Inbred lines developed recently, are available in the maize breeding program at Institute of Agricultural Sciences, BHU, Varanasi, whose combining ability has not yet been studied for utilization in QPM conversion program. Most efficient use of such materials would be possible only when adequate information on the amount and type of genetic variation and combining ability effects in the materials is available. Introgression of the *opaque-2* (*o2*) trait in to normal maize lines is essential to improve the nutritional security of maize in India. In this context, $L \times T$ analysis (Kempthorne, 1957) has widely been used for evaluation of inbred lines by crossing them with testers (Kanagarasu *et al.*, 2010; Sundararajan and Kumar, 2011; Abrha *et al.*, 2013; Elmyhum, 2013, Kambe *et al.*, 2013). The present study was undertaken for estimation of combining ability of normal inbred lines with QPM donors as tester for initiating a successful quality protein maize conversion program.

MATERIALS AND METHODS

The experimental materials

Materials for this experiment consisted of 98 genotypes including 80 F_1 crosses and 18 parents. Ten lines and 8 testers were crossed in a line \times tester mating design in the Kharif (rainy) season, 2012. Ten maize inbreds i.e., HUZM185, HUZM97-1-2, HUZM509, HKI 287, HUZM478, V336, V341, V351, CM 141 and V335 obtained from BHU, Varanasi; VPKAS, Almora were used as lines (female). Many of these lines were early and medium duration. Eight tropical and subtropical Quality Protein Maize (QPM) donor inbreds i.e., CML 141, CML 193, DMRQPM 58, HKI 164-7-6, HKI 162, CML 169, CML 176 and CML 161 were obtained from Directorate of Maize Research (DMR), New Delhi, but originally introduced from CIMMYT, Mexico and Karnal,

India were used as testers (males). The characteristic features, origin and source of these parents (lines as well as testers) are given in Table 1.

Field plot technique and layout

The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications during Rabi (winter) season, 2012-13 at the Agriculture Research Farm, Institute of Agricultural Sciences, BHU, Varanasi, UP, India. Varanasi is situated at 25.2° N latitude and 83.0° E longitudes with an altitude of 128.9 m above mean sea level. Each genotype was planted in 2 row plot of 3 m length having a uniform inter and intra row spacing of 60 and 25 cm, respectively. Two seeds per hill were planted and later 1 plant was thinned from each hill to maintain the optimum plant population. Border rows were maintained at end of each replication to minimize border effect. The recommended agronomic package of practices was adopted to raise a good and healthy crop.

Data collection

Ten competitive plants in each plot were randomly selected prior to tasseling and tagged to record the observations for height, yield and yield related traits. Details of procedure for each trait are: *Plant height* was measured and recorded in centimetre by measuring the plant stalk from the ground level to the base of the last leaf sheath of the matured plant; *Ear height* was measured and recorded in centimeter as the length of plant from the ground level to the upper most ear bearing node; *Ear length* was measured and recorded in centimetre at the time of harvest as its total length (from the base to the tip of the ear); *Ear girth* was measured and recorded in centimeter as the thickness of the ear at the middle of the dehusked cob; The number of kernel rows per ear was counted and recorded; The number of kernels per row was recorded as number of kernels in each kernel row was counted and averaged; *Shelling percentage* were computed by the pith weight and grain weight of the randomly selected plants per plot using the given formula, *Shelling*

Table 1. Characteristic features, pedigree and sources of lines (10) and testers (8) used in present study.

Code	Inbred	Pedigree and Source	Characteristic Features
Non QPM Inbred (Lines)			
L 1	HUZM185	Seed tec-1250-1-2-2-1-# #, BHU, Varanasi	Yellow, Flint kernel, medium duration, tassel and leaf angle is small, tall height and good grain yield.
L 2	HUZM97-1-2	Devaki × VCZ, BHU, Varanasi	Yellow kernel, early duration, wide leaf angle with tassel anthocyanin coloration.
L 3	HUZM509	BHU, Varanasi	Yellow kernel, Late duration, leaf angle small with narrow tassel angle.
L 4	HKI 287	CML 287, Karnal	Yellow kernel, Late duration, leaf and tassel angle is wide, tall height with high grain yield.
L 5	HUZM478	BH-3427, BHU, Varanasi	Yellow, Flint Kernel, Late duration, wide leaf angle with narrow tassel angle, anthocyanin coloration is present.
L 6	V336	CML 145,P 63 CDHC 181-3-2-1-4 #2-BBBB # F-BBBBB #, VPKAS, Almora	Yellow, Flint Kernel, medium duration, leaf and tassel angle is small, straight leaf attitude.
L 7	V341	Mexico Acc No. 3136 @-3-2-3-8-1, VPKAS, Almora	Yellow, Flint Kernel, Early duration, tall with drooping leaf attitude, straight tassel.
L 8	V351	Shakti (So) HE 25, VPKAS, Almora	Orange yellow, Flint Kernel, Early duration, straight leaf attitude and better yield
L 9	CM 141	Pool 33 (Alm), VPKAS, Almora	Yellow kernel, Medium to late duration, curved tassel.
L 10	V335	TZI-25, VPKAS, Almora	Orange, flint kernel, short to medium duration, straight tassel.
QPM Inbred (Testers)			
T 1	CML 141	Pop 62, CIMMYT	White, flint kernel, medium to late duration, dwarf height.
T 2	CML 193	CY0162-B-1-1-B Africa), CIMMYT (S)	Yellow, Flint, Medium to late duration, medium height.
T 3	DMRQPM 58	Shakti 1, DMR	Orange yellow, Flint Kernel, Early duration, tall height.
T 4	HKI 164-7-6	CML164, Karnal	Yellow, Semi Dent, Medium in height, dark green plant, spares tassel, Late duration.
T 5	HKI 162	CML162, Karnal	Yellow, flint kernel, late duration, tall plant, small tassel, anther and silk purple, erect and narrow leaves.
T 6	CML 169	P26 QPM, CIMMYT	Yellow, Flint Kernel, Medium duration, curved tassel.
T 7	CML 176	(P63-12-2-1/P67-5-1-1)-1-2-B-B, CIMMYT	White kernel, Medium to Late duration.
T 8	CML 161	G25Qc18MH520-1-1# - 1-2#-5-3-B-1-B-B-B- B- #, CIMMYT	Orange yellow, Flint Kernel, Late duration, dwarf height with small leaf angle and straight leaf attitude.

percentage = [Grain weight / Total weight (Grain weight + pith weight) × 100]; *100-grain weight* was recorded as weight of 100 grains drawn from a random sun dried sample of 10 randomly selected ears in each plot was recorded in grams; *Grain yield per plant* expressed in gram was recorded by weighing the grains obtained after shelling of ears from 10 randomly selected plants and averaged.

Statistical analysis

The Analysis of Variance was carried out using mean values of observations on 10 randomly selected plants for each character. Initially the test of significance among the genotypes involving crosses and parents was estimated. When these differences were found significant, then Line × Tester analysis was performed. Treatment sum of square was partitioned into sum of squares due to parents, crosses and

parents vs. crosses with appropriate degree of freedom. Combining ability analysis using Line \times Tester procedures (Kempthorne, 1957 and Singh and Chaudhary, 1985) was performed using Windostat 9.1 software program (Indostat Services, Hyderabad).

RESULTS

Analysis of variance (ANOVA) and combining ability analysis

The analysis of variance revealed that differences between treatments, parents and lines were highly significant ($P \leq 0.01$) for all the characters. Among the testers highly significant differences ($P \leq 0.01$) were found for grain yield and yield component traits i.e., ear length, ear girth, kernels per row, shelling percent and 100-grain weight, while among line vs testers for grain yield, ear length, shelling percent, 100-grain weight and ear height. The differences between parent vs crosses and crosses were also highly significant ($P \leq 0.01$) for all the characters (Table 2).

The combining ability analysis revealed that mean squares due to line effect were highly significant ($P \leq 0.01$) for all the characters except ear length, ear girth and shelling percent, while significant ($P \leq 0.05$) for ear length and ear girth only. The mean square due to tester effect was highly significant ($P \leq 0.01$) for 100-grain weight. The mean squares due to line \times tester interaction effect were also highly significant ($P \leq 0.01$) for grain yield, ear length, ear girth, kernels rows per ear, kernels per row, shelling percent and 100-grain weight, while significant ($P \leq 0.05$) for plant height and ear height (Table 3). Combining ability study is an important step of plant breeding to identify the suitable parents for the further hybrid development program. The analysis of variance indicated that sufficient genetic variability present among treatments, parents and lines for all the characters. Combining ability study indicated that grain yield per plant, ear length, ear girth, number of kernel rows per ear, number of kernels per ear, number of kernels per row, shelling percentage, plant height and ear height were controlled predominantly by non additive

type of gene action which was further supported by higher values of specific combining ability variance than general combining ability variance, while 100-grain weight was controlled preponderantly by additive gene action. These results were consistent with those of Kanagarasu *et al.* (2010), Premlatha *et al.* (2011) and Kambe *et al.* (2013). The importance of non additive gene action for grain yield and some other traits have been reported earlier by Subramaniyan and Subbraman (2006), Jayakumar and Sundram (2007), Vijayabharathi *et al.* (2009) and Kambe *et al.* (2013) whereas, contrarily, importance of additive gene effects was reported by Alamnie *et al.* (2006).

General combining ability (GCA) effects

The estimates of General Combining Ability (GCA) effects of the parents for different characters are presented in Table 4. A wide range of variability for GCA effects was observed among the parents for different characters. Among the lines, V335 exhibited high positive GCA effect of 17.49 g followed by CM 141(16.20 g) and V351 (4.39 g), while the tester CML 141 exhibited maximum positive GCA effect of 6.13 g followed by HKI 164-7-6 (3.34 g) and CML 161 (3.20 g) for grain yield per plant. The GCA effects are important indicators of the value of inbreds in hybrid combinations. It was observed from the GCA effects that, none of the parents individually expressed good general combiner for all the characters. The high and significant positive GCA effects suggested that line V335 was the best general combiner for grain yield along with the most of the yield contributing traits, whereas QPM tester CML 141 was the best general combiner for grain yield along with the ear girth and 100 grain weight. For the number of kernels per row, V335 exhibited significant and positive GCA effect followed by V341, whereas HKI 287 exhibited significant and negative GCA effect. The positive GCA effect is desirable for number of kernels per row as it is the most important yield component trait that directly contributes to enhance the grain yield. Hence, inbred lines with high GCA effects for this trait

Table 2. Analysis of variance for parents and crosses for yield and its contributing characters in maize.

Source of Variation	Df	GYP	EL	EG	KRE	KR	SP	GW	PH	EH
Replications	2	55.99	0.21	0.52	0.18	3.78	17.59	2.95	245.41	59.04
Treatments	97	945.46**	6.28**	2.21**	4.52**	49.75**	49.25**	16.61**	1129.78**	544.40**
Parents	17	487.60**	8.20**	3.13**	5.14**	70.93**	84.22**	23.48**	1010.07**	536.73**
Parents (Line)	9	622.42**	8.63**	4.25**	8.36**	86.23**	42.94**	13.85**	1604.16**	750.68**
Parents (Testers)	7	210.57**	6.61**	1.76**	1.71	60.96**	112.18**	4.14**	369.8	219.88
Parents (L vs T)	1	1213.49**	15.48**	2.71*	0.26	3.06	260.03**	245.58**	145.21	829.15**
Parents vs Crosses	1	21993.50**	84.68**	29.49**	43.85**	1432.18**	929.99**	115.08**	52935.30**	23743.33**
Crosses	79	777.55**	4.87**	1.67**	3.89**	27.69**	30.57**	13.89**	499.78**	252.39**
Error	194	56.23	2.15	0.64	1.2	8.68	12.87	1.03	201.14	132.67

Table 3. Combining ability analysis and genetic components for yield and its contributing characters in maize.

Source of Variation	Df	GYP	EL	EG	KRE	KR	SP	GW	PH	EH
Line Effect	9	2961.77**	9.39*	3.06*	10.17**	99.74**	45.28	55.38**	1797.38**	614.18**
Tester Effect	7	460.27	3.82	2.4	2.1	7.63	43.59	38.59**	519.74	252
Line x Tester Effect	63	500.78**	4.34**	1.39**	3.20**	19.62**	27.03**	5.21**	312.18*	200.75*
Error	158	63.13	2.27	0.63	1.12	9.78	12.17	1.07	221.4	135.53
σ^2_{gca}		61.29	0.16	0.08	0.18	1.67	1.17	1.7	35.46	11.13
σ^2_{sca}		148.18	0.73	0.25	0.66	3.65	4.72	1.39	37.02	22.69
σ^2_D		148.18	0.73	0.25	0.66	3.65	4.72	1.39	37.02	22.69
σ^2_A		122.58	0.33	0.15	0.37	3.33	2.34	3.4	70.92	22.25
Degree of dominance		1.1	1.49	1.27	1.35	1.05	1.42	0.64	0.72	1.01

* and **, significant at 5% and 1% level of significance, respectively.

Table 4. General combining ability (gca) effects of parents for yield and its contributing characters in maize.

S.No.	Characters	GYP	EL	EG	KRE	KR	SP	GW	PH	EH
LINES										
L1	HUZM 185	-4.59**	-0.10	0.28	-0.24	-0.84	-1.55*	1.04**	2.13	5.09*
L2	HUZM 97.1-2	-15.26**	-0.26	-0.42*	0.04	-2.18**	-1.79*	-2.83**	-2.34	-4.53
L3	HUZM 509	-10.55**	0.17	-0.27	-0.76**	-1.21	-0.12	-0.25	-11.12**	-5.87*
L4	HKI 287	-11.85**	-1.46**	-0.68**	-0.33	-2.65**	1.26	-1.04**	-10.19**	-4.44
L5	HUZM 478	0.20	0.06	0.03	0.17	-1.20	-0.42	-0.29	-10.89**	-6.26**
L6	V 336	-0.22	0.07	0.20	1.11**	0.38	-1.57*	-1.38**	8.29**	2.92
L7	V 341	4.20**	0.44	-0.07	-1.00**	2.37**	0.98	1.00**	-0.11	4.56
L8	V 351	4.39**	-0.19	0.21	-0.03	0.24	0.19	0.50*	3.79	-2.08
L9	CM 141	16.20**	0.31	0.32	0.15	1.25*	2.39**	2.63**	13.83**	5.78*
L10	V 335	17.49**	0.97**	0.41*	0.88**	3.83**	0.63	0.63**	6.62*	4.84*
SE± GCA (Line)		1.53	0.30	0.16	0.22	0.60	0.73	0.21	2.89	2.35
SE± Gi- Gj (Line)		2.16	0.42	0.23	0.32	0.85	1.04	0.29	4.09	3.33
TESTERS										
T1	CML 141	6.13**	-0.13	0.42**	0.15	-0.28	-1.66*	0.86**	-3.11	-0.41
T2	CML 193	-3.70**	-0.06	-0.1	0.07	-0.47	-0.47	-0.91**	1.02	-3.39
T3	DMR QPM 58	-1.55	-0.44	-0.47**	0.04	0.52	2.22**	-1.31**	-2.28	-0.91
T4	HKI 164-7-6	3.34*	0.55*	0.30*	-0.27	0.56	-0.02	1.92**	1.94	2.78
T5	HKI 162	-5.10**	-0.31	0.01	0.31	0.12	-0.31	-0.88**	5.81*	5.13*
T6	CML 169	-2.5	0.35	-0.22	0.31	-0.89	-0.85	-0.68**	0.59	1.35
T7	CML 176	0.2	-0.27	-0.05	-0.34	0.14	-0.12	0.09	3.48	-2.1
T8	CML 161	3.20*	0.3	0.1	-0.28	0.29	1.2	0.89**	-7.44**	-2.45
SE ± GCA(Tester)		1.37	0.27	0.15	0.20	0.54	0.65	0.19	2.59	2.10
SE ± Gi-Gj (Tester)		1.94	0.38	0.21	0.28	0.76	0.93	0.26	3.66	2.97

* and **, significant at 5 % and 1 % level of significance, respectively.

can be suitable parents for inclusion in future maize breeding programs. Such parents contribute favourable alleles in the process of synthesis of new varieties. This result is in conformity with the findings of Fan *et al.* (2008); Abrha *et al.* (2013); Elmyhum (2013) and Kambe *et al.* (2013). Inbred lines CM 141, HUZM 185 and V341 were good general combiners while HUZM97-1-2, V336 and HKI 287 were poor combiners for 100-grain weight. Good as well as poor combiners have been reported in maize (Abrha *et al.*, 2013). In maize short height is advantageous for lodging resistance while positive GCA effect indicates the tendency to increase the height. For ear height, 2 inbred lines showed negative and significant GCA effects, whereas 4 inbred lines showed positive and significant GCA effect. HUZM478 (-6.26 cm) and HUZM509 (-5.87 cm) were good general combiners while CM 141 showed the highest GCA effect (5.78 cm) which indicates the tendency to increase ear height. This is in agreement with the findings of Abrha *et al.* (2013). Parents including V335, CM 141, V351, V341, CML 141, HKI 164-7-6 and CML 161 were identified as overall good general combiners.

Specific combining ability (SCA) effects

The estimates of SCA effects of the normal maize and QPM crosses are presented in Table 5. High and positive SCA effect is desirable for grain yield, ear length, ear girth, kernel rows per ear, kernels per row, shelling percent and 100-grain weight. Both negative and positive and significant estimates of SCA effects were observed among the crosses for grain yield per plant (Table 5). Crosses CM 141 × CML 161, V351 × CML 141, HUZM509 × CML 176, V335 × CML 141 and CM 141 × CML 176 were good specific combiners, whereas crosses V341 × CML 161 and CM 141 × DMRQPM 58 were poor specific combiners. Highly significant SCA effects of the crosses indicate that significant deviation from what would have been predicted based on their parental performances. These crosses with high positive and significant estimates of SCA effect could be selected for their specific combining ability to use in maize improvement. These results are in agreement

with the findings of Iqbal *et al.* (2007) and Shams *et al.* (2010), who reported high and significant level of SCA effects in most of the crosses they studied for grain yield in maize. In most of crosses one or both of the parents were good combiner for grain yield per plant. This supports the argument that GCA of the parental lines plays a key role for higher grain yield. Earlier reports of Xingming *et al.* (2002) suggested that good GCA parents play positive role in high yielding crosses. Ivy and Howlader (2000) obtained high SCA effect for grain yield in low × low general combining parents. The results showed that, generally GCA effects of the parents did not reflected in their SCA effect for all the traits which is reported by Ivy and Howlader (2000). However, Amiruzzaman *et al.* (2011) also pointed out that the SCA effect is a result of the interaction of GCA effects of the parents and that it can improve or deteriorate the hybrid expression compared to the expected effect based on GCA only. The SCA effects of the crosses did not show any specific trends in cross combinations between parents possessing high, medium and low GCA. In most of the cases, the crosses those showed high SCA effects involved at least one good general combiner. For ear length, crosses CM 141 × CML 161, V336 × CML 161, HUZM185 × CML 141, HUZM478 × CML 176 and V341 × DMRQPM 58 were found good specific combiners as these crosses were found to exhibit significant and positive SCA effects. Similar trend was observed for ear girth, number of kernel rows per ear and number of kernels per row. Crosses HUZM478 × CML 193, V351 × CML 141, HUZM 509 × HKI 164-7-6, V351 × CML 161 and HKI 287 × V341 were found good specific combiners for ear girth, whereas crosses V351 × CML 141, V335 × CML 141, HUZM509 × CML 193, V341 × CML 176 and HUZM478 × HKI 164-7-6 were good specific combiners for number of kernel rows per ear. With respect to number of kernels per row, crosses V336 × CML 161, HUZM185 × DMRQPM 58, CM 141 × CML 161, HUZM185 × CML 141 and HUZM509 × CML 176 exhibited significant positive SCA effects. With respect to 100-grain weight, 25 crosses exhibited significant and highly significant estimates of SCA effects.

Table 5. Specific combining ability effects of F₁ crosses for yield and yield contributing characters in maize.

S.No.	Crosses	GYP	EL	EG	KRE	KR	SP	GW	PH	EH
1	L 1 × T 1	8.99*	2.35**	0.11	-0.98	4.92**	-1.97	0.06	-7.31	-2.88
2	L 1 × T 2	14.83**	0.88	0.43	0.31	0.99	1.83	2.16**	-3.7	1.43
3	L 1 × T 3	13.34**	1.39	-0.1	-0.73	5.83**	2.03	1.23*	-18.67*	-6.45
4	L 1 × T 4	8.12	0.3	0.23	0.84	1.16	3.12	-0.34	9.97	3.92
5	L 1 × T 5	-14.44**	-1.6	-0.4	-1.14	-4.43*	1.07	-0.21	10.91	8.91
6	L 1 × T 6	-2.37	-1.93*	0.63	1	-3.72*	1.75	1.59**	9.93	4.82
7	L 1 × T 7	-11.74**	-0.25	-0.05	1.25	-0.95	-4.19*	-3.51**	9.24	5.41
8	L 1 × T 8	-16.74**	-1.14	-0.86	-0.54	-3.81*	-3.64	-0.98	-10.38	-15.17*
9	L 2 × T 1	-10.67*	-0.22	-0.68	-2.13**	2.17	1.74	-0.73	-0.64	-4.46
10	L 2 × T 2	4.83	-0.63	0.04	0.56	-0.11	3.15	-0.63	-7.5	-8.29
11	L 2 × T 3	-7.32	-0.38	0.04	0.85	-2.44	-2.91	-0.23	-1.8	2.1
12	L 2 × T 4	4.45	1.17	0.78	0.29	-1.98	-0.29	-0.8	12.24	10.61
13	L 2 × T 5	14.90**	0.03	0.47	-0.09	2.65	0.66	2.33**	6.04	2.39
14	L 2 × T 6	-0.37	0.57	-0.13	0.05	1.15	-2.65	0.13	-3.34	-2.76
15	L 2 × T 7	-3.74	0.05	-0.11	0.23	-0.85	-1.03	0.7	-2.03	-0.78
16	L 2 × T 8	-2.07	-0.58	-0.42	0.24	-0.58	1.34	-0.77	-2.98	1.18
17	L 3 × T 1	-12.72**	-0.42	-0.87	0.07	-3.48*	-0.51	-0.98	5.8	-6.12
18	L 3 × T 2	6.78	0.34	1.28**	1.49*	0.98	-6.92**	-1.22*	25.94**	21.25**
19	L 3 × T 3	1.29	-1.21	-0.01	0.18	-1.01	0.55	0.52	-4.62	0.91
20	L 3 × T 4	-7.86	1.1	1.15*	-0.44	0.85	-1.48	1.62**	11.42	11.35
21	L 3 × T 5	-6.49	0.73	-0.68	-1.22	0.48	-0.23	0.08	-18.45*	-15.00*
22	L 3 × T 6	-4.42	-0.47	-0.86	0.72	-2.06	1.7	-1.78**	-23.96**	-14.42*
23	L 3 × T 7	22.88**	0.28	0.6	-0.1	3.74*	2.9	2.45**	-0.99	2.97
24	L 3 × T 8	0.54	-0.35	-0.61	-0.69	0.51	4.01	-0.68	4.86	-0.95
25	L 4 × T 1	-2.42	-0.75	-0.06	0.71	-0.66	3.27	-1.19*	-8.66	-8.02
26	L 4 × T 2	-3.26	0.44	-0.27	-0.13	1.6	-1.17	-0.43	2.55	5.15

Continuation of Table 5

S.No.	Crosses	GYP	EL	EG	KRE	KR	SP	GW	PH	EH
27	L 4 × T 3	-8.07	0.02	-0.53	-0.64	-2.86	-2.17	-2.03**	8.52	-0.99
28	L 4 × T 4	-15.63**	-0.93	-1.14*	-1.13	1.31	-2.88	-0.59	-9.84	-6.75
29	L 4 × T 5	3.48	0.4	0.19	-0.25	1.33	2.63	-0.79	-8.11	-4.43
30	L 4 × T 6	13.55**	1.44	0.82	-0.11	0.23	-1	3.01**	1.25	-0.98
31	L 4 × T 7	10.18*	0.39	0.92*	0.81	1.44	2.3	-0.76	6.35	1
32	L 4 × T 8	2.18	-1.01	0.07	0.75	-2.39	-0.98	2.78**	7.94	15.02*
33	L 5 × T 1	-18.46**	-2.07*	-0.4	-1.65**	-4.09*	2.72	1.06	-12.69	-7
34	L 5 × T 2	12.70**	1.06	0.56	0.03	1.36	0.38	0.16	-1.75	-5.56
35	L 5 × T 3	-0.78	0.84	-0.47	-0.21	0.23	5.33*	-1.11	-2.98	-7.1
36	L 5 × T 4	4.33	-0.55	0.39	1.30*	-0.75	-4	0.66	-2.81	-0.19
37	L 5 × T 5	7.44	0.25	0.52	0.85	0.32	-1.39	0.13	15.06	7.93
38	L 5 × T 6	0.84	0.18	0.25	0.73	1.34	1.17	-2.08**	4.08	2.77
39	L 5 × T 7	7.47	1.87*	-0.06	-0.63	1.55	-3.64	1.49*	4.19	6.16
40	L 5 × T 8	-13.53**	-1.56	-0.8	-0.42	0.03	-0.58	-0.31	-3.09	2.98
41	L 6 × T 1	-3.38	-0.95	0	-0.6	-1.9	-2.4	0.81	1.13	1.82
42	L 6 × T 2	-2.88	0.51	-0.65	-0.51	1.52	-1.49	-0.76	-5.39	-6.14
43	L 6 × T 3	0.97	-0.84	0.12	0.05	-1.32	3.97	0.98	-8.56	-8.75
44	L 6 × T 4	13.41**	0.51	0.09	0.35	1.19	-0.05	0.08	12.08	3.42
45	L 6 × T 5	-2.15	-1.43	0.19	1.11	-3.03	-0.5	-0.46	-0.72	-4.12
46	L 6 × T 6	6.59	0.57	0.58	0.71	-0.2	-0.84	0.34	0.64	3.86
47	L 6 × T 7	-10.11*	-1.01	-0.69	-0.77	-2.1	2.24	-0.76	-12.56	-4.16
48	L 6 × T 8	-2.45	2.63**	0.36	-0.34	5.85**	-0.93	-0.22	13.37	14.06*
49	L 7 × T 1	8.87*	0.41	-0.23	-0.22	1.34	4.81*	0.77	17.59*	14.78*
50	L 7 × T 2	-4.63	-0.19	0.12	0.27	-1.82	1.91	-0.47	3.53	-0.85
51	L 7 × T 3	5.88	1.79*	0.13	-0.11	2.46	-6.11**	1.27*	14.57	9.41
52	L 7 × T 4	-12.34**	-1.5	-0.83	-0.87	-2.86	0.19	0.03	-20.26*	-16.25*
53	L 7 × T 5	16.77**	0.86	0.06	0.95	3.40*	3.94	-0.17	-1.33	3.96
54	L 7 × T 6	5.5	0.33	0.35	-0.64	2.24	3.3	-0.03	10.9	8.41

Continuation of Table 5

S.No.	Crosses	GYP	EL	EG	KRE	KR	SP	GW	PH	EH
55	L 7 × T 7	0.14	-0.58	0.48	1.47*	-2.13	-0.66	0.2	-13.66	-10.54
56	L 7 × T 8	-20.20**	-1.11	-0.07	-0.85	-2.62	-7.37**	-1.60**	-11.34	-8.92
57	L 8 × T 1	24.68**	1.18	1.22**	2.68**	2.15	-1.64	1.27*	12.03	15.55*
58	L 8 × T 2	-19.49**	-0.76	-0.93*	-1.37*	-3.62*	0.66	0.7	-1.56	-5.14
59	L 8 × T 3	14.22**	0.42	0.91	0.79	1.97	0.04	-0.57	6.94	6.38
60	L 8 × T 4	-10.53*	-0.7	-0.43	-0.1	-0.73	1.28	-1.13	-9.75	-5.11
61	L 8 × T 5	5.24	0.9	-0.16	0.25	1.6	-2.34	-0.33	0.04	1.07
62	L 8 × T 6	-11.02*	-1.83*	-1.17*	-2.41**	1.59	-0.47	0.13	-5.17	-8.18
63	L 8 × T 7	-16.72**	-0.35	-0.44	-0.03	-2.66	0.79	-1.30*	-0.29	-2.56
64	L 8 × T 8	13.61**	1.15	1.01*	0.18	-0.31	1.67	1.23*	-2.24	-2.01
65	L 9 × T 1	-11.80**	0.21	0.11	0.23	-1.18	-4.92*	0.14	-5.81	-3.37
66	L 9 × T 2	-1.96	-0.53	-0.23	0.32	-0.5	2.93	-1.09	-3.4	-0.13
67	L 9 × T 3	-20.12**	-2.62**	-0.56	-0.46	-3.74*	0.83	0.31	3.77	6.66
68	L 9 × T 4	7	-0.2	0.1	0.25	0.99	-0.04	0.74	-0.73	0.03
69	L 9 × T 5	-20.23**	-0.51	-0.92*	-1.53*	-1.64	-1.7	-0.79	-9.99	-6.78
70	L 9 × T 6	-5.83	-0.07	-0.17	0.34	-1.07	-0.98	-1.99**	4.23	6.87
71	L 9 × T 7	16.80**	0.95	0.85	0.19	1.69	2.48	1.24*	6.47	-1.35
72	L 9 × T 8	36.14**	2.78**	0.81	0.67	5.44**	1.41	1.44*	5.46	-1.93
73	L 10 × T 1	16.91**	0.28	0.79	1.90**	0.73	-1.11	-1.19*	-1.47	-0.3
74	L 10 × T 2	-6.92	-1.12	-0.36	-0.95	-0.4	-1.28	1.58**	-8.73	-1.73
75	L 10 × T 3	0.59	0.59	0.48	0.28	0.88	-1.55	-0.36	2.84	-2.2
76	L 10 × T 4	9.04*	0.81	-0.36	-0.48	0.82	4.15*	-0.26	-2.32	-1.03
77	L 10 × T 5	-4.52	0.38	0.73	1.07	-0.69	-2.13	0.21	6.57	6.06
78	L 10 × T 6	-2.45	1.21	-0.3	-0.39	0.5	-1.97	0.68	1.44	-0.4
79	L 10 × T 7	-15.15**	-1.34	-1.50**	-2.41**	0.28	-1.18	0.24	3.28	3.85
80	L 10 × T 8	2.51	-0.81	0.52	1.00	-2.11	5.08*	-0.89	-1.6	-4.26
SE± (Sij)		4.33	0.85	0.46	0.63	1.70	2.07	0.59	8.19	6.65
SE± (Sij – Skl)		6.12	1.20	0.65	0.90	2.41	2.93	0.83	11.58	9.40

* and **, significant at 5% and 1% level of significance, respectively.

Best specific combination was observed for HKI 287 × CML 169, while poorest was HUZM185 × CML 176. For plant height, the estimates of SCA effect were found to be significant in 6 of the 80 crosses in the present study. Crosses HUZM509 × CML 169 and HUZM509 × CML 193 were found good and poor specific combiners, respectively. Similar trends were found for the ear height, where crosses V341 × HKI 164-7-6 and HUZM509 × CML 193 were good and poor specific combiners, respectively.

Best 3 crosses for grain yield per plant, ear length, ear girth, number of kernel rows per ear, number of kernels per ear, number of kernels per row, shelling percentage, 100-grain weight, plant height and ear height with higher *per se* performance along with desirable SCA effects and GCA effects of parents involved in the crosses are listed in Table 6. Three crosses i.e., CM 141 × CML 161, V 335 × CML 141 and V 351 × CML 141 had shown higher *per se* performance for grain yield per plant along with highly significant positive SCA effects and positive GCA effects of respective parents. Among them CM 141 × CML 161 (123.67 g) expressed highest *per se* performance along with maximum SCA effect for grain yield per plant. A critical evaluation of the results with respect to specific combining ability effects expressed that none of the cross combinations exhibited desirable significant SCA effects for all the characters. The highest yielding cross CM 141 × CML 161 revealed significant positive SCA effects and was the outcome of high × low combining parents. Surya and Ganguli (2004) also reported high and positive specific combining ability effects along with high *per se* performance for grain yield. The superiority of crosses involving high × low combiners as parents could be explained on the basis of interaction between positive alleles from good combiners and negative alleles for the poor combiners as parents. The high yield of such crosses would be non-fixable and thus could be exploited for heterosis breeding. The superior cross combinations involving low × low general combiners could result from over dominance and epistasis. The results obtained in the present study are mostly in conformity with the earlier findings of Mahto and Ganguli (2003), Malik *et al.* (2004) and Kanagarasu *et al.* (2010) for grain yield and

other component characters. It is evident that the best 3 crosses exhibiting desirable SCA effects for grain yield indicated the involvement of parents with high × average, average × high, low × low, high × high and high × low GCA effects.

The proportional contribution of lines, testers and their interactions

The proportional contribution of lines, testers and their interaction to the total variance showed that lines played an important role towards the total variance for all traits, indicating predominant lines influence. Contribution of lines for grain yield per plant and 100 grain weight was 43.39% and 45.44%, respectively. The greater contribution of line × tester interactions than testers for all the characters indicates higher estimates of specific combining ability variance. Contribution of line × tester interactions for ear length and shelling per cent was 71.10% and 70.50%, respectively. The contribution of lines than testers and line × tester interactions for 100 grain weight exhibited that lines played greater role in crosses for this trait (Table 7).

The line × tester studies revealed that lines V335, CM 141 and V351 are good combiner against testers CML 141, CML 161 and CML 141, respectively for grain yield and yield contributing traits. The lines V335 and V351 are promising and will be converted into QPM versions having agronomic background of V335 and V351. Based on the overall performance of the hybrids and parental lines, some of the lines could be used as parents of hybrids of maize with high quality and moderate yield potential. Hence, the information from this study may possibly be useful for researchers who would like to develop high yielding and high quality protein inbred lines and hybrids of maize.

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Table 6. Top ranking (First 3) cross combinations based on *per se* performance, SCA and GCA effects.

Characters	Significant Crosses	<i>Per se</i> performance			sca effects	gca effects	
		F ₁	Lines	Testers		Lines	Testers
GYP	L 9 × T 8	123.67	30.00	32.67	36.14**	16.20**	3.20*
	L 10 × T 1	108.67	59.00	30.67	16.91**	17.49**	6.13**
	L 8 × T 1	103.33	46.67	30.67	24.68**	4.39**	6.13**
	L 9 × T 8	17.07	10.00	9.73	2.78**	0.31	0.3
EL	L 6 × T 8	16.67	14.33	9.73	2.63*	0.07	0.3
	L 10 × T 6	16.20	12.64	14.07	1.21	0.97*	0.35
	L 8 × T 1	14.53	12.81	10.77	1.22**	0.21	0.42**
EG	L 10 × T 1	14.30	12.70	10.77	0.79	0.41*	0.42**
	L 8 × T 8	14.00	12.81	12.50	1.01*	0.21	0.10
	L 10 × T 1	17.07	13.96	11.87	1.90**	0.88**	0.15
KRE	L 8 × T 1	16.93	14.23	11.87	2.68**	-0.03	0.15
	L 6 × T 5	16.67	13.73	13.33	1.11	1.11**	0.31
	L 9 × T 8	32.63	8.48	15.22	5.44**	1.25*	0.29
KR	L 6 × T 8	32.18	26.08	15.22	5.85**	0.38	0.29
	L 7 × T 5	31.54	15.92	18.27	3.40*	2.37**	0.12
	L 5 × T 3	83.85	74.72	80.02	5.33*	-0.42	2.22**
SP	L 10 × T 8	83.63	77.45	59.49	5.08*	0.63	1.20
	L 9 × T 3	82.17	68.14	80.02	0.83	2.39**	2.22**
	L 9 × T 4	26.33	22.00	17.00	0.74	2.63**	1.92**
GW	L 9 × T 8	26.00	22.00	19.33	1.44*	2.63**	0.89**
	L 9 × T 7	25.00	22.00	15.67	1.24*	2.63**	0.09
	L 9 × T 7	189.87	119.27	130.93	6.47	13.83**	3.48
PH	L 6 × T 4	188.40	159.20	122.67	12.08	8.29**	1.94
	L 10 × T 5	185.09	126.04	118.07	6.57	6.62*	5.81*
	L 1 × T 5	110.53	79.47	74.93	8.91	5.09*	5.13*
EH	L 7 × T 1	110.33	46.13	64.37	14.78*	4.56	-0.41
	L 10 × T 5	107.44	63.40	74.93	6.06	4.84*	5.13*

* and **, significant at 5% and 1% level of significance, respectively.

GYP: Grain yield per plant (g.); EL: Ear length (cm); EG: Ear girth (cm); KRE: Number of kernel rows per ear; KR: Number of kernels per row; SP: Shelling percentage (%); GW: 100 Grain Wt. (g.); PH: Plant height (cm); EH: Ear height (cm).

Table 7. Percent (%) contribution of Lines, Testers and Line × Tester Interactions.

Characters	Lines	Testers	Line × Tester Interactions
GYP	43.39	5.25	51.36
EL	21.95	6.95	71.10
EG	20.89	12.72	66.39
KRE	29.75	4.77	65.47
KR	41.04	2.44	56.52
SP	16.87	12.63	70.50
GW	45.44	24.63	29.94
PH	40.97	9.21	49.81
EH	27.72	8.85	63.43

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