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Combining ability and heterosis for yield contributing and quality traits in medium maturing inbred lines of maize (Zea mays L.) using line x tester

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Abstract

Sixty crosses of maize were developed through Line x Tester design using two male testers and thirty medium maturing female inbred lines. These 60 crosses along with parents and two commercial checks, *viz.*, Bio 9544 and Palam Sankar Makka-2 were evaluated during *Kharif* 2016. The mean square due to parents, crosses and parents v/s crosses were significant for all the traits, except, days to 75% brown husk. The ratio of $\sigma^2 \text{GCA}/\sigma^2$ SCA was less than one for all the traits except plant height. This indicated that the preponderance of non-additive gene effects in the inheritance of these traits. Among female inbred lines, L₂₈ was observed to be a good general combiner for grain yield, cob length, biological yield and protein content. Tester T₁ was found to be a good general combiner for 1000 grain weight, biological yield and protein content whereas tester T₂ for grain yield, cob girth, harvest index, plant height and cob placement. High level of heterosis over best check was observed for yield contributing and quality traits. Three cross combinations L₂₈ × T₂, L₁₅ × T₂ and L₂₃ × T₁ were identified most promising on the basis of their *per se* performance, SCA effects and significant heterosis for different traits mainly for yield and earliness indicated potential for exploiting hybrid vigour in breeding programme and might be used for obtaining high yielding maize hybrids.

Keywords: Combining ability, gene action, heterosis, hybrids, line × tester, Zea mays

Introduction

In India, maize is the third most important food crop after rice and wheat. It is cultivated on 9.5 million ha area with production of 24.3 million tonnes and productivity of 24.5 q/ha (Anonymous, 2017)^[2]. It is primarily used for feed (59%) followed by human food (28%), industrial (starch) products (12%), beverages and seed (1%). It is the world's feeding crop and is widely cultivated as cereal grain that was domesticated in Central America. It is one of the most versatile emerging crops having wider adaptability. Globally, maize is known as queen of cereals because of its highest genetic yield potential. It is the only food cereals crop that can be grown in diverse seasons, ecologies and uses. Beside this maize have many types like normal yellow/white grain, sweet corn, baby corn, popcorn, waxy corn, high amylose corn, high oil corn, quality protein maize etc. Apart from this, maize is an important industrial raw material and provides large opportunity for value addition.

Combining ability analysis is one of the most powerful tool in identifying the best combiners that may be used in crosses either to exploit heterosis or to accumulate productive genes. It also helps to understand the genetic architecture of various characters that enable to breeder to design effective breeding plan for other improvement of the existing breeding material. Exploitation of hybrid vigor and selection of parents based on combining ability has been used as an important breeding approach in crop improvement. Selection of parents on the basis of *per se* performance with good GCA effect is the high approach to assess the nature of gene action involved in the inheritance of character (Vasal, 1998)^[27]. Combining ability analysis is one of the powerful tools in identifying the better combiners which may be hybridized to exploit heterosis and to select better crosses for direct use or further breeding work (Nigussie and Zelleke, 2001)^[19]. Information on the heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development (Beck *et al.*, 1990)^[3].

Heterosis and combining ability is prerequisite for developing good economically viable hybrids of maize. Information on the heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. In succesful hybridization programme, the ability of a parent to combine well and produce segregations in succeeding generations is an important criterion in selecting parents. The concept of general and specific combining ability was proposed by Sprague and Tatum (1942)^[26]. They defined general combining ability as "an average of a line in hybrid combination" and used specific combining ability to designate "deviation of certain crosses rom expectation on the basis of the average performance of the line involved". Their studies in a set of F₁ crosses of maize revealed that general combining ability is the function of additive gene effect whereas, specific combining ability results from intra-allelic interaction (dominance) and interallelic interaction (epistasis). Comstock et al. (1949) [5] designated breeding procedure to make maximum use of both general and specific combining ability. The present study was, therefore, undertaken with a view to estimate general and specific combining ability variances and effects to identify superior maize hybrids for good yield potential and quality traits.

Materials and Methods

The experimental material consisted of 30 medium maturing inbred lines (L₁- L₂) crossed with two diverse testers *viz.*, BAJIM-08-26 (T₁) and BAJIM-08-27 (T₂) using line x tester mating design during *Kharif*, 2015 in experimental field at CSK Himachal Pradesh Krishi Vishva Vidyalaya, Hill Agricultural Research & Extension Center, Bajaura, Kullu, H.P. (India). The list of the inbred lines and testers used in this experiment is given in Table 1.

The 60 F_1 hybrids along with 32 parents and 2 checks *viz.*, Bio-9544 and Palam Sankar Makka-2 were evaluated in randomized block design (RBD) with two replications during *Kharif*, 2016. The experimental material consisting of a total of 94 entries (60 F_1 hybrids, 32 parents and 2 checks) were sown in randomized block design with two replications with a two row plot of four meter length, maintaining crop geometry of 60 x 20 cm. Observations were recorded on 10 randomly selected plants per treatment per replication for the traits namely plant height (cm), cob placement (cm), cob length (cm), cob girth (cm), kernel rows per cob and kernels per row and were used for statistical analysis. However, days to 50 per cent pollen shed, days to 50 per cent silking, days to 75 per cent brown husk, grain yield (q/ha), 1000 grain weight (g) and biological yield (q/ha) were recorded on plot basis. Data recorded were subjected to analysis of variance according to Panse and Sukhatme (1985) ^[21] to determine significant differences among genotypes. Combining ability analysis for line x tester mating design was performed as per method suggested by Kempthorne (1957) ^[8]. Estimation of protein content and tryptophan were done as per Micro Kjeldahl's method given by Lindner (1944) ^[14] and Mertz *et al.* (1975) ^[17], respectively. The magnitude of heterosis was estimated in relation to the best standard check (SC). The statistical analysis was carried out using OPSTAT online Agriculture Data Analysis software (Sheoran *et al.* 1998) ^[25].

 Table 1: Description of the lines, testers and checks used in the study

Code	Genotypes	Code	Genotypes
	Lines		
L ₁	BAJIM-12-01	L19	CML-337
L ₂	BAJIM-13-01	L ₂₀	CML-439
L ₃	BAJIM-13-02	L ₂₁	CML-465-B-B
L ₄	BAJIM-15-08	L ₂₂	DMRQPM-58
L ₅	BAJIM-15-09	L ₂₃	HKI-1040-7
L ₆	BAJIM-15-10	L ₂₄	HKI-1105
L7	BAJIM-15-11	L25	LQPM-15-01
L ₈	BAJIM-15-12	L26	MRCQPM-16
L9	BML-6	L27	MRCQPM-18
L10	BML-7	L28	TNAU/CBE-83
L11	CML-44	L29	TNAU/CBE-115
L ₁₂	CML-141	L30	V-334
L ₁₃	CML-269	Testers	
L14	CML-269-1	T1	BAJIM 08-26
L15	CML-292	T ₂	BAJIM 08-27
L16	CML-294	Checks	
L17	CML-334	Check-1	Bio 9544
L ₁₈	CML-336	Check-2	Palam Sankar Makka-2

Results and Discussion

The mean square values for fifteen traits are presented in Table 2. The analysis of variance revealed significant differences among the genotypes for all the traits studied. The mean squares due to males were recorded to be significant for all characters except for grain yield, kernel rows per cob and cob length. The mean squares due to females were highly significant for all traits studied. The mean squares due to male vs. female were non-significant for all the characters except for 1000 grain weight and shelling per cent. The mean squares due to crosses and parents vs. crosses were found to be significant for all characters. This revealed presence of appreciable amount of genetic variability in the experimental material of the present investigation.

Source of Variation	Replications	Parents	Males	Female	Male vs. Female	Crosses	Parents vs. Crosses	Error
Df	1	31	1	29	1	59	1	91
Grain yield	5.77	73.74*	11.66	77.97*	12.96	446.38*	168,230.72*	10.62
1000 grain weight	0.27	3,336.10*	19,600.0*	2,863.20*	786.62*	2,687.6*	246969.4*	25.05
Shelling percent	0.95	30.43*	14.59*	31.611**	12.27*	6.03*	307.74*	1.39
Rows / cob	0.32	4.00*	0.03	4.26**	0.33	1.99*	54.950*	0.39
Kernels / row	2.28	23.53*	18.79*	24.49*	0.44	30.83*	6,630.78*	2.63
Cob length	0.33	4.88*	1.78	5.16*	0.05	6.90*	1,261.02*	1.17
Cob girth	0.04	3.05*	2.00*	3.23*	0.02	3.61*	315.21*	0.17
Biological yield	1.33	1591.51*	3470.97*	1575.13*	186.95	3430.43*	535157.13*	69.28
Harvest index	0.01	0.01*	0.01*	0.01*	0.01	0.01*	0.72*	0.01
Days to 50% pollen shed	0.14	27.60*	6.25	28.32*	28.02*	12.75*	486.05*	1.79
Days to 50% silking	0.05	27.51*	6.25	27.67*	44.20*	14.23*	537.81*	1.65
Days to 75% brown husk	2.17	61.19*	0.25	61.35*	117.60*	15.99*	8.452	2.42

Table 2: Analysis of variance for parents and crosses for grain yield, yield related characters and quality traits

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Plant height	6.30	674.71*	18.78	707.36*	383.02*	541.06*	83,957.34*	47.94
Cob placement	0.21	271.33*	100	285.49*	32.05	336.18*	28,406.84*	38.49
Protein content	0.02	3.07*	0.16*	3.27*	0.19*	2.07*	107.34*	0.03
Tryptophan content	0.01	0.01*	0.01	0.01*	0.04**	0.02*	0.01*	0.01

*Significant at 5% level of significance; Df, degree of freedom

Estimates of combining ability variance

Combining ability variance of yield contributing and quality traits are presented in Table 3. The analysis of variance for combining ability revealed that variance due to lines was of higher magnitude than that of testers for grain yield, 1000-grain weight, shelling percentage, kernel rows/cob, kernels/row, cob length, biological yield, days to 50 per cent pollen shed, days to 75 per cent brown husk and tryptophan content. This indicated that the contribution of lines for these traits, towards σ^2 GCA was greater. Variance due to testers was of higher magnitude than that of lines for cob girth, harvest index, days to 50 per cent silking, plant height, cob placement and protein content. This indicated that the

contribution of testers for these traits, towards σ^2 GCA was greater. The estimates of SCA variance were of higher magnitude than GCA variance for all the traits except plant height. Besides this the ratio of σ^2 SCA/ σ^2 GCA was less than unity for all the traits except plant height for which the σ^2 GCA/ σ^2 SCA ratio was more than unity indicating that additive type of gene action was present. This indicated that the preponderance of non-additive gene effects in the inheritance of these traits. These results are in accordance with the findings of Kumar *et al.* (1998) ^[10], Joshi *et al.* (1998) ^[7], Amiruzzaman *et al.* (2013) ^[11], Verma *et al.* (2014) ^[28] and Sharma *et al.* (2015) ^[24].

Table 3: Analysis of variance for combining ability for grain yield, yield related characters and quality traits

Source of Variation	Replications	Tester	Lines	Line × Tester	Error	σ ² GCA	σ ² SCA	$\sigma^2 \text{ GCA} / \sigma^2 \text{ SCA}$
Df	1	1	29	29	59			
Grain yield	20.52	158.47*	499.75*	402.94*	12.47	-9.22	780.94	0.12
1000 grain wt.	0	1470.0*	3643.79*	1773.45*	25.89	97.93	3495.1	0.03
Shelling Percentage	2.78	1.47	7.81*	4.415*	1.21	0.07	6.39	0.01
Kernel rows/cob	0.92	0.98	2.68*	1.33*	0.45	0.062	1.77	0.04
Kernels/row	11.65	0.47	31.53*	31.18*	3.13	-1.89	56.10	0.03
Cob length	0.73	4.48	9.71*	4.17*	1.64	0.36	5.06	0.07
Cob girth	0.24	7.12*	3.99*	3.11*	0.0.19	0.31	5.84	0.05
Biological yield	70.64	2748.41*	4450.93*	2433.45*	76.40	44.56	1178.52	0.04
Harvest index	0.01	0.02*	0.01*	0.01*	0.01	0.001	0.02	0.01
Days to 50% pollen shed	0.67	14.01*	20.55*	4.90*	2.21	1.54	5.37	0.29
Days to 50% silking	0.20	23.40*	22.40*	5.75*	1.85	2.14	7.80	0.28
Days to 75% brown husk	1.63	9.63*	26.88*	5.32*	2.07	1.61	6.49	0.25
Plant height	62.73	3,698.08*	837.81*	135.45*	48.42	266.56	174.05	1.53
Cob placement	0.84	1,498.74*	494.03*	138.24*	45.11	107.26	186.28	0.058
Protein content	0.01	4.45*	3.16*	0.88*	0.03	0.36	1.71	0.21
Tryptophan content	0.01	0.01*	0.02*	0.01*	0.01	0.001	0.02	0.06

*Significant at 5% level of significance; Df, degree of freedom

Estimates of combining ability effects

The combining ability analysis revealed that among the lines L₂₈ and L₁₂ were good general combiners for grain yield and biological yield (Table 4). The lines identified on the basis of their GCA were good general combiners viz., L₁₄ for 1000 grain weight, L₂₂ for rows per cob, L₃ for kernels per row and for cob length, L₁₉ for cob girth, L₁₈ for harvest index, L₁₅ for shelling percentage, L₄ for days to 50 per cent pollen shed, L₁₇ for days to 50 per cent silking and 75 per cent brown husk, L₇ for plant height and cob placement, L_{12} for protein content and L_{11} for tryptophan content. Among the testers T_1 was a good general combiner for 1000 grain weight, biological yield, protein content and tryptophan content in endosperm protein whereas T₂ for grain yield, cob girth, harvest index, plant height, cob placement and days to 50 per cent silking. High general combining ability effects (GCA) observed were due to additive and additive x additive gene effects (Sprague and Tatum, 1942)^[26].

Positive as well as negative and significant estimates of SCA effects were observed among the crosses for grain yield

(Table 5). Out of the 60 crosses, thirteen crosses have shown significant positive SCA effects for grain yield. The cross L₁₅ \times T₂ (31.11) followed by L₇ \times T₁ (23.07), L₂ \times T₁ (22.47) and $L_{28} \times T_2$ (14.56) showed high positive significant effect for this trait. The cross $L_{15} \times T_2$ for 1000 grain weight, $L_1 \times T_2$ for shelling percentage, $L_2 \times T_2$ for number of rows per cob, $L_2 \times$ T_1 for cob girth, $L_2 \times T_1$ for biological yield and $L_{19} \times T_2$ for harvest index showed the highest positive significant sca effect. Whereas, highest significant negative SCA effect for maturity and physiological traits was shown by $L_7 \times T_1$ for days to 50 per cent pollen shed and days to 50 per cent silking, $L_2 \times T_1$ for days to 75 per cent maturity and $L_2 \times T_2$ for plant height and cob placement. The cross $L_{21} \times T_2$ showed the highest significant positive SCA for protein content and $L_9 \ \times \ T_2$ for tryptophan content. Similar finding for identification of superior inbred lines and hybrids based on gca and sca effects for grain yield and its components in maize were also reported by Miranda et al. (2008) [18] and Jampatong et al. (2010)^[6] and Rastgari et al. (2014)^[23].

Parents	GY	GW	SP	KRC	KPR	CL	CG	BY	HI	DP	DS	DBH	PH	СР	PC	ТС
								Lines								
L ₁	-14.23*	-20.50*	-0.43	0.82*	-1.36	-2.87*	-1.39*	-37.94*	0.01	-2.02*	-2.19*	-4.30*	-20.742*	-21.078*	-0.73*	0.03*
L ₂	-13.32*	-90.50*	0.18	-0.17	-1.36	-3.87*	-1.30*	-0.10	-0.06*	3.47*	3.80*	3.45*	-10.907*	-9.076*	1.10*	-0.03*
L ₃	2.20	-0.50	-1.78*	0.48	4.80*	2.35*	1.13*	32.52*	-0.05*	1.22	1.80*	2.95*	3.553	16.424*	-0.26*	-0.02*
L ₄	-3.94*	-30.50*	0.28	1.40*	-1.49	-0.14	1.11*	11.68*	-0.05*	-4.27*	-3.69*	-3.05*	-20.074*	-2.243	-0.69*	0.12*
L ₅	1.54	9.50*	1.14*	0.40	-2.69*	0.60	-0.51*	2.18	-0.00	0.22	0.05	-2.05*	-9.490*	-1.576	-0.75*	-0.01
L ₆	6.66*	-0.50	-0.50	1.32*	-1.78*	0.24	0.65*	-14.26*	0.05*	-1.27	-1.19	-0.80	3.596	3.004	-1.01*	0.01
L7	-10.31*	-10.50*	0.93	-0.26	-5.49*	-1.79*	0.04	-67.78*	0.11*	1.22	1.05	1.20	-36.825*	-27.576*	0.39*	-0.02*
L ₈	-12.19*	9.50*	-1.25*	-0.84*	-1.28	0.68	0.77*	-29.55*	-0.00	-0.27	-0.94	-2.05*	-11.407*	-9.283*	-0.77*	0.02*
L9	1.65	-0.50	0.76	-0.67*	-0.19	-2.08*	-1.12*	4.64	-0.01	1.72*	1.80*	1.70*	7.426*	5.172	-0.12	0.02*
L ₁₀	14.40*	9.50*	1.43*	-1.51*	2.17*	-0.01	-0.61*	58.88*	-0.04*	1.97*	1.80*	3.20*	14.011*	10.839*	1.25*	-0.09*
L ₁₁	10.24*	9.50*	0.38	0.90*	0.01	-1.18	-0.74*	48.66*	-0.04*	-0.77	-0.44	-1.05	-1.407	4.007	-0.65*	0.14*
L12	21.46*	59.50*	0.57	-0.92*	-2.94*	2.35*	0.75*	15.37*	0.06*	0.72	0.80	-0.55	27.593*	13.922*	2.56*	-0.08*
L13	0.62	29.50*	1.01	0.15	-2.53*	1.81*	1.29*	-30.92*	0.06*	2.47*	2.05*	0.70	8.928*	8.872*	-0.26*	-0.02*
L14	8.62*	69.50*	0.17	-0.84*	-0.70	1.24	0.21	25.76*	-0.01	0.72	0.55	0.45	13.596*	6.839*	0.88*	-0.08*
L15	4.28*	9.50*	3.10*	-1.26*	4.34*	1.04	0.65*	20.14*	-0.04*	2.97*	3.30*	3.45*	5.593	-1.661	-1.09*	0.07*
L16	14.13*	-20.50*	-1.24*	-0.01	2.92*	-0.02	0.94*	38.03*	-0.01	3.72*	3.55*	3.45*	15.258*	13.257*	0.35*	0.01
L17	-2.74	19.50*	1.02	0.48	2.42*	1.85*	1.19*	22.32*	-0.04*	-3.77*	-4.69*	-4.80*	-16.824*	-21.078*	0.23*	-0.01
L18	-10.96*	-0.50	1.07	-0.17	3.63*	1.10	-1.36*	-56.52*	0.08*	-0.77	-0.69	0.45	-10.992*	-10.243*	0.54*	-0.12*
L19	-0.49	29.50*	-1.59*	1.03*	3.71*	0.08	1.66*	-20.99*	0.05*	-2.02*	-1.94*	-2.80*	8.258*	0.672	0.62*	-0.03*
L20	-13.18*	-20.50*	-1.09*	0.48	4.17*	-0.63	0.10	-14.24*	-0.03*	-0.02	0.05	-0.05	3.093	0.504	-0.71*	0.09*
L ₂₁	1.15	-20.50*	-0.55	0.07	2.59*	0.39	0.11	-12.31*	0.03*	4.22*	4.05*	4.70*	12.676*	16.507*	1.10*	-0.10*
L22	-10.59*	9.50*	1.11*	1.73*	-4.32*	-1.48*	0.75*	-28.38*	-0.00	-1.02	-1.19	-2.05*	-25.157*	-8.743*	-0.99*	0.06*
L ₂₃	10.91*	19.50*	1.57*	0.57	-3.11*	-0.18	1.65*	-14.60*	0.08*	-3.02*	-3.19*	-2.55*	-5.239	7.587*	-0.77*	0.05*
L ₂₄	6.36*	-25.50*	-3.69*	-0.59	-2.61*	0.14	-1.18*	23.16*	-0.02*	1.22	1.05	1.70*	5.841	1.839	-0.15	0.07*
L ₂₅	-15.51*	-40.50*	1.03	-0.01	-1.11	1.51*	-0.24	-20.25*	-0.04*	0.47	-0.19	-0.55	10.261*	-3.331	-0.43*	-0.03*
L ₂₆	7.41*	-20.50*	0.46	-1.01*	1.96*	-2.23*	-1.58*	-22.40*	0.08*	-2.27*	-1.94*	-1.05	-7.575*	-6.411	-0.76*	0.08*
L ₂₇	-14.42*	9.50*	-2.27*	-0.67*	-2.03*	0.74	-0.66*	35.85*	-0.12*	-3.02*	-3.19*	-2.30*	6.260	-6.828*	1.18*	-0.06*
L ₂₈	25.13*	-20.50*	0.72	-0.42	1.96*	1.87*	-0.47*	72.24*	-0.02*	1.72*	3.30*	3.95*	18.178*	13.172*	0.72*	-0.11*
L29	-3.59*	29.50*	-1.60*	-0.09	1.59	-0.41	-0.99*	-13.93*	0.01	-1.52*	-1.44*	1.20	2.428	5.589	0.13	0.01
L30	-11.30*	-0.50	-0.91	-0.34	-1.28	-1.12	-0.84*	-27.24*	-0.00	-2.02*	-2.19*	-2.55*	10.093*	0.919	-0.84*	0.04*
			_		_			Testers	_	_		_				
T1	-1.14*	3.50*	-0.11	0.09	0.06	0.19	-0.24*	4.79*	-0.02*	0.34	0.44*	-0.28	5.551*	3.534*	0.19*	0.01*
T ₂	1.14*	-3.50*	0.11	-0.09	-0.06	-0.19	0.24*	-4.79*	0.02*	-0.34	-0.44*	0.28	-5.551*	-3.534*	-0.19*	-0.01*

* Significant at 5% level of significance

Note: GY, grain yield; GW, 1000 grain weight; SP, shelling percentage; KRC, kernel rows per cob; KPR, kernels per row; CL, cob length; CG, cob girth; BY, biological yield; HI, harvest index; DP, days to 50% pollenshed; DS, days to 50% silking; DBH, days to 75% brown husk; PH, plant height; CP, cob placement; PC, protein content; TC, tryptophan content

Table 5: Estimates of specific combining ability (SCA) effects of crosses for grain yield, yield related characters and quality traits

Crosses	GY	GW	SP	KRC	KPR	CL	CG	BY	HI	DP	DS	DBH	PH	СР	PC	ТС
$L_1 \times T_1$	-0.86	16.50*	-2.24*	-1.09*	2.52*	0.70	0.16	9.76	-0.03*	-0.59	-0.69	0.53	-1.63	2.88	-0.09	0.05*
$L_1 \times T_2$	0.86	-16.50*	2.24*	1.09*	-2.52*	-0.70	-0.16	-9.76	0.03*	0.59	0.69	-0.53	1.63	-2.88	0.09	-0.05*
$L_2 \times T_1$	22.47*	26.50*	0.52	1.24*	3.68*	-0.26	2.57*	59.25*	0.00	-1.59	-1.69	-3.71*	16.53*	17.21*	0.23	0.01
$L_2 \times T_2$	-22.47*	-26.50*	-0.52	-1.24*	-3.68*	0.26	-2.57*	-59.25*	-0.00	1.59	1.69	3.71*	-16.53*	-17.21*	-0.23	-0.01
$L_3 \times T_1$	10.50*	-43.50*	-2.07*	0.57	-3.31*	-0.90	-0.52	-19.38*	0.08*	0.65	0.30	-0.71	9.32	11.06*	-0.61*	0.03*
L ₃ ×T ₂	-10.50*	43.50*	2.07*	-0.57	3.31*	0.90	0.52	19.38*	-0.08*	-0.65	-0.30	0.71	-9.32	-11.06*	0.61*	-0.03*
L ₄ ×T ₁	-2.12	6.50	0.57	-0.67	-3.44*	-0.90	0.24	-2.04	-0.00	-0.34	-0.19	-1.21	3.36	1.38	0.22	0.01
$L_4 \times T_2$	2.12	-6.50	-0.57	0.67	3.44*	0.90	-0.24	2.04	0.00	0.34	0.19	1.21	-3.36	-1.38	-0.22	-0.01
L ₅ ×T ₁	-8.60*	6.50	1.35	-1.01*	-7.64*	-1.23	0.53	-31.37*	0.02	-0.84	-0.94	-0.21	-4.71	-5.94	0.02	0.01
L5×T2	8.60*	-6.50	-1.35	1.01*	7.64*	1.23	-0.53	31.37*	-0.02	0.84	0.94	0.21	4.71	5.94	-0.02	-0.01
$L_6 \times T_1$	-2.79	-3.50	-0.41	0.41	-1.06	-0.75	-1.21*	-9.31	0.01	0.15	0.30	1.03	2.03	1.80	-0.13	-0.01
$L_6 \times T_2$	2.79	3.50	0.41	-0.41	1.06	0.75	1.21*	9.31	-0.01	-0.15	-0.30	-1.03	-2.03	-1.80	0.13	0.01
$L_7 \times T_1$	23.06*	26.50*	0.23	-0.50	2.89*	-0.75	-0.60	36.51*	0.02	-3.34*	-3.44*	-1.46	7.95	7.88	-0.47*	0.03*
L ₇ ×T ₂	-23.06*	-26.50*	-0.23	0.50	-2.89*	0.75	0.60	-36.50*	-0.02	3.34*	3.44*	1.46	-7.95	-7.88	0.47*	-0.03*
$L_8 \times T_1$	0.11	-13.50*	0.09	-0.42	-1.89	0.01	-0.58	-13.12*	0.03*	0.15	1.05	0.78	0.03	-5.74	0.19	-0.01
$L_8 \times T_2$	-0.11	13.50*	-0.09	0.42	1.89	-0.01	0.58	13.12*	-0.03*	-0.15	-1.05	-0.78	-0.03	5.74	-0.19	0.01
L ₉ ×T ₁	-4.42	-3.50	2.23*	0.41	0.76	0.74	0.51	3.85	-0.02	0.65	0.30	0.03	2.36	3.29	0.94*	-0.13*
L ₉ ×T ₂	4.42	3.50	-2.23*	-0.41	-0.76	-0.74	-0.51	-3.85	0.02	-0.65	-0.30	-0.03	-2.36	-3.29	-0.94*	0.13*
$L_{10} \times T_1$	5.20*	6.50	1.32	-0.09	-0.19	-1.17	-1.06*	8.36	0.01	0.90	0.80	1.03	8.61	3.96	0.01	-0.03*
$L_{10} \times T_2$	-5.20*	-6.50	-1.32	0.09	0.19	1.17	1.06*	-8.36	-0.01	-0.90	-0.80	-1.03	-8.61	-3.96	-0.01	0.03*
$L_{11} \times T_1$	-5.46*	6.50	0.43	-0.01	4.47*	1.05	0.18	15.10*	-0.04*	1.15	1.05	1.78	-2.63	-3.20	-0.65*	-0.03*
$L_{11} \times T_2$	5.46*	-6.50	-0.43	0.01	-4.47*	-1.05	-0.18	-15.10*	0.04*	-1.15	-1.05	-1.78	2.63	3.20	0.65*	0.03*
$L_{12} \times T_1$	0.67	-3.50	-0.41	0.16	1.02	0.18	-0.48	6.96	-0.01	2.15*	2.30*	0.28	1.69	-1.28	0.76*	0.01
$L_{12} \times T_2$	-0.67	3.50	0.41	-0.16	-1.02	-0.18	0.48	-6.96	0.01	-2.15*	-2.30*	-0.28	-1.69	1.28	-0.76*	-0.01
$L_{13} \times T_1$	-3.53	6.50	-0.36	-0.09	-2.06	-1.35	-0.56	-11.99	0.01	1.40	1.55	0.53	-8.96	-4.40	0.20	-0.05*

L	13×T2	3.53	-6.50	0.36	0.09	2.06	1.35	0.56	11.99	-0.01	-1.40	-1.55	-0.53	8.96	4.40	-0.20	0.05*
L	$_{14} \times T_1$	6.12*	-13.50*	0.08	-0.59	-0.32	-1.38	-1.06*	-16.97*	0.06*	-0.34	-0.44	-0.71	0.86	-0.86	0.88*	-0.03*
L	$_{14} \times T_2$	-6.12*	13.50*	-0.08	0.59	0.32	1.38	1.06*	16.97*	-0.06*	0.34	0.44	0.71	-0.86	0.86	-0.88*	0.03*

Crosses	GY	GW	SP	KRC	KPR	CL	CG	BY	ні	DP	DS	DBH	РН	СР	РС	ТС
L15×T1	-31.10*	-53,50*	-0.05	0.49	-0.10	0.03	-0.38	-49.18*	-0.04*	0.40	0.30	0.28	0.19	-5.86	0.10	0.07*
$L_{15} \times T_2$	31.10*	53.50*	0.05	-0.49	0.10	-0.03	0.38	49.18*	0.04*	-0.40	-0.30	-0.28	-0.19	5.86	-0.10	-0.07*
$L_{16} \times T_1$	4.37	-3.50	0.36	-0.59	5.56*	1.63	0.24	-2.07	0.03*	0.15	0.05	0.28	2.53	3.54	-0.87*	0.05*
L ₁₆ ×T ₂	-4.37	3.50	-0.36	0.59	-5.56*	-1.63	-0.24	2.07	-0.03*	-0.15	-0.05	-0.28	-2.53	-3.54	0.87*	-0.05*
L ₁₇ ×T ₁	-2.38	-3.50	0.09	0.57	-2.27	0.18	0.41	34.76*	-0.06*	-0.84	-0.69	-0.96	-9.88*	-5.45	0.27*	-0.04*
L ₁₇ ×T ₂	2.38	3.50	-0.09	-0.57	2.27	-0.18	-0.41	-34.76*	0.06*	0.84	0.69	0.96	9.88*	5.45	-0.27*	0.04*
$L_{18} \times T_1$	5.11*	36.50*	-0.14	-0.59	2.35	1.84*	1.18*	29.50*	-0.06*	0.15	-0.19	-0.21	0.11	1.54	0.24	0.01
$L_{18} \times T_2$	-5.11*	-36.50*	0.14	0.59	-2.35	-1.84*	-1.18*	-29.50*	0.06*	-0.15	0.19	0.21	-0.11	-1.54	-0.24	-0.01
L ₁₉ ×T ₁	-12.87*	-13.50*	1.79*	0.78	-1.39	-0.25	-0.35	27.41*	-0.13*	-0.59	-0.94	-1.46	0.36	-2.20	-0.34*	0.02*
L19×T2	12.87*	13.50*	-1.79*	-0.78	1.39	0.25	0.35	-27.41*	0.13*	0.59	0.94	1.46	-0.36	2.20	0.34*	-0.02*
$L_{20} \times T_1$	1.15	16.50*	1.08	-0.59	0.22	-0.78	-0.62*	-46.38*	0.09*	-0.09	0.05	-0.21	0.19	1.46	0.24	-0.10*
$L_{20} \times T_2$	-1.15	-16.50*	-1.08	0.59	-0.22	0.78	0.62*	46.38*	-0.09*	0.09	-0.05	0.21	-0.19	-1.46	-0.24	0.10*
$L_{21} \times T_1$	-4.41	-23.50*	-0.03	-0.01	1.97	1.38	1.57*	19.02*	-0.06*	-0.34	-0.44	-0.46	-4.38	-4.20	-1.14*	0.02*
$L_{21} \times T_2$	4.41	23.50*	0.03	0.01	-1.97	-1.38	-1.57*	-19.02*	0.06*	0.34	0.44	0.46	4.38	4.20	1.14*	-0.02*
$L_{22} \times T_1$	3.63	-33.50*	-1.34	0.16	-0.94	-0.48	-1.15*	3.02	0.01	-0.59	-0.69	0.78	-9.55	-11.95*	-0.19	0.04*
$L_{22} \times T_2$	-3.63	33.50*	1.34	-0.16	0.94	0.48	1.15*	-3.02	-0.01	0.59	0.69	-0.78	9.55	11.95*	0.19	-0.04*
$L_{23} \times T_1$	7.42*	16.50*	0.24	0.99*	3.10*	1.05	0.53	-18.58*	0.08*	-0.59	-0.19	0.28	-2.80	-1.61	0.04	0.06*
$L_{23} \times T_2$	-7.42*	-16.50*	-0.24	-0.99*	-3.10*	-1.05	-0.53	18.58*	-0.08*	0.59	0.19	-0.28	2.80	1.61	-0.04	-0.06*
$L_{24} \times T_1$	2.17	21.50*	-2.01*	-0.01	-1.98	-0.02	0.28	12.84*	-0.01	1.15	1.05	1.53	0.78	4.80	0.16	0.04*
$L_{24} \times T_2$	-2.17	-21.50*	2.01*	0.01	1.98	0.02	-0.28	-12.84*	0.01	-1.15	-1.05	-1.53	-0.78	-4.80	-0.16	-0.04*
$L_{25} \times T_1$	6.14*	-3.50	0.72	-0.09	3.27*	2.26*	0.68*	8.01	0.02	-1.09	-1.19	-0.71	-8.46	-1.53	0.20	-0.02
$L_{25} \times T_2$	-6.14*	3.50	-0.72	0.09	-3.27*	-2.26*	-0.68*	-8.01	-0.02	1.09	1.19	0.71	8.46	1.53	-0.20	0.02
$L_{26} \times T_1$	3.07	-3.50	-0.33	0.07	-1.23	0.01	-0.26	6.36	-0.00	2.15*	2.55*	1.28	3.69	-0.28	0.29*	-0.02
$L_{26} \times T_2$	-3.07	3.50	0.33	-0.07	1.23	-0.01	0.26	-6.36	0.00	-2.15*	-2.55*	-1.28	-3.69	0.28	-0.29*	0.02
$L_{27} \times T_1$	-2.34	26.50*	-0.15	-0.09	-2.48*	-0.50	-0.52	-26.06*	0.03*	-1.09	-1.19	-0.46	-2.96	-2.36	-0.17	0.01
$L_{27} \times T_2$	2.34	-26.50*	0.15	0.09	2.48*	0.50	0.52	26.06*	-0.03*	1.09	1.19	0.46	2.96	2.36	0.17	-0.01
$L_{28} \times T_1$	-14.55*	-23.50*	0.26	-0.17	-1.98	0.61	0.91*	-31.25*	0.00	0.15	1.30	1.28	-0.55	2.63	0.26*	-0.02
$L_{28} \times T_2$	14.55*	23.50*	-0.26	0.17	1.98	-0.61	-0.91*	31.25*	-0.00	-0.15	-1.30	-1.28	0.55	-2.63	-0.26*	0.02
$L_{29} \times T_1$	-3.42	6.50	-1.13	0.82	1.06	0.57	0.59	9.40	-0.03*	0.40	0.05	1.53	1.19	2.71	-0.43*	-0.03*
L ₂₉ ×T ₂	3.42	-6.50	1.13	-0.82	-1.06	-0.57	-0.59	-9.40	0.03*	-0.40	-0.05	-1.53	-1.19	-2.71	0.43*	0.03*
L30×T1	-2.35	16.50*	-0.70	-0.09	-0.56	-1.54	-1.21*	-12.44*	0.02	0.40	-0.19	-0.71	-5.30	-9.28	-0.17	0.01
$L_{30} \times T_2$	2.35	-16.50*	0.70	0.09	0.56	1.54	1.21*	12.44*	-0.02	-0.40	0.19	0.71	5.30	9.28	0.17	-0.01

*Significant at 5% level of significance **Note:** GY, grain yield; GW, 1000 grain weight; SP, shelling percentage; KRC, kernel rows per cob; KPR, kernels per row; CL, cob length; CG, cob girth; BY, biological yield; HI, harvest index; DP, days to 50% pollenshed; DS, days to 50% silking; DBH, days to 75% brown husk; PH, plant height; CP, cob placement; PC, protein content; TC, tryptophan content.

Table 6: Estimation of heterosis over best standard check

Entry	GY	GW	SP	KRC	KPR	CL	CG	BY	HI	DP	DS	DBH	PH	СР	PC	ТС
Crosses																
$L_1 \times T_1$	-29.01*	-17.65*	-3.93*	-6.45	-11.52*	-23.72*	-19.21*	-31.53*	-13.14*	-3.28	-3.17	-4.06*	-1.97	-15.49*	-6.72*	26.74*
$L_1 \times T_2$	-25.49*	-29.41*	1.59	6.45	-24.28*	-32.16*	-18.27*	-41.12*	6.03	-2.46	-2.38	-4.57*	-6.60	-29.05*	-9.12*	-2.33
$L_2 \times T_1$	-7.81*	-35.29*	0.02	2.16	-8.64	-32.94*	-4.43	-2.73	-20.65*	4.10	4.76*	-0.51	14.58*	12.33	19.33*	2.33
$L_2 \times T_2$	-45.11*	-52.94*	-0.93	-15.06*	-27.16*	-32.35*	-32.01*	-44.96*	-16.44*	8.20 *	8.73*	7.61*	-11.53*	-31.51*	9.00*	-9.30
L ₃ ×T ₁	-4.69	-29.41*	-5.32*	2.16	-10.70*	-6.66	-8.37*	-17.90*	-2.72	4.10	4.76*	2.03	18.87*	32.77*	-7.44*	9.30
L ₃ ×T ₂	-21.06*	-5.88*	-0.19	-6.45	5.35	0.00	0.74	-8.28*	-27.88*	0.82	2.38	4.06*	1.28	1.92	2.76	-9.30
$L_4 \times T_1$	-21.11*	-23.53*	0.21	0.00	-26.54*	-18.42*	-3.93	-19.05*	-18.37*	-6.56*	-4.76*	-4.57*	1.38	2.82	-2.40	39.53*
$L_4 \times T_2$	-15.39*	-29.41*	-0.87	7.52	-9.88*	-11.76	-3.93	-20.87*	-10.42*	-6.56*	-5.56*	-1.52	-9.16*	-7.57	-12.42*	27.91*
L ₅ ×T ₁	-21.98*	-11.76*	2.13	-8.61	-39.91*	-16.47*	-11.82*	-31.86*	-4.07	0.00	0.00	-2.54	2.86	-4.22	-5.52*	9.30
L5×T2	-4.93	-17.65*	-0.78	3.23	-2.47	-6.66	-15.25*	-14.33*	-7.03	1.64	1.59	-1.52	1.87	0.88	-10.80*	-2.33
L ₆ ×T ₁	-12.42*	-17.65*	-1.87	6.45	-21.40*	-15.88*	-15.25*	-30.00*	4.76	-0.82	0.00	0.00	14.58*	8.80	-10.68*	4.65
L ₆ ×T ₂	-5.54	-17.65*	-0.65	0.00	-16.46*	-10.59	1.98	-27.02*	8.46*	-2.46	-2.38	-1.52	5.62	-2.47	-12.00*	6.98
L7×T1	-4.65	-11.76*	0.57	-9.68*	-20.78 *	-25.48*	-15.25*	-32.54*	18.47*	-2.46	-2.38	-0.51	-5.81	-17.08*	2.28	9.30
L7×T2	-43.00*	-29.41*	0.28	-4.29	-35.40*	-20.19*	-5.17*	-59.78*	18.70*	7.38*	7.14*	3.05*	-21.77*	-41.19*	9.00*	-9.30
L ₈ ×T ₁	-26.38*	-17.65*	-2.16	-12.90*	-22.22*	-10.19	-10.82*	-36.30*	-3.10	0.82	1.59	-1.52	4.53	-12.14	-3.84	11.63*
L ₈ ×T ₂	-24.57*	-11.76*	-2.11	-8.61	-13.17*	-12.16*	-0.98	-30.80*	-8.64*	-0.82	-3.17	-2.54	-2.07	-7.48	-13.09*	9.30
L ₉ ×T ₁	-18.23*	-17.65*	2.72*	-6.45	-12.96*	-19.81*	-15.52*	-19.43*	-14.96*	4.92*	4.76*	1.52	17.05*	12.68	13.09*	-18.60*
L ₉ ×T ₂	-8.49*	-17.65*	-2.27	-12.90*	-17.07*	-28.64*	-18.71*	-25.13*	2.40	1.64	2.38	2.03	7.68	-1.76	-14.17*	39.53*
$L_{10} \times T_1$	1.34	-11.76*	2.44	-15.06*	-9.47*	-19.01*	-21.90*	-0.06	-15.02*	5.74*	5.56*	4.06*	24.63*	19.37*	18.25*	-23.26*
$L_{10} \times T_2$	-5.76	-17.65*	-0.39	-15.06*	-8.85*	-9.81	-6.38*	-8.73*	-13.50*	1.64	1.59	2.54	7.88	3.52	13.57*	-9.30
$L_{11} \times T_1$	-11.63*	-11.76*	0.16	1.06	-3.30	-14.12*	-15.25*	-1.21	-25.02*	1.64	2.38	0.51	8.87*	4.58	-12.6*	32.56*
$L_{11} \times T_2$	-0.07	-17.65*	-0.59	0.00	-25.72*	-25.88*	-14.51*	-14.32*	-2.27	-3.28	-2.38	-2.54	5.42	3.88	-1.44	44.19*
$L_{12} \times T_1$	3.55	0.00	-0.61	-9.68*	-19.14*	-1.58	-10.35*	-14.87*	1.93	5.74*	6.35*	-0.51	28.57*	17.08*	43.10*	-11.63*

$L_{12} \times T_2$	4.38	0.00	0.63	-12.90*	-24.48*	-5.11	-1.71	-22.62*	13.11*	-2.46	-2.38	-0.51	20.00*	12.32	20.17*	-16.28*
L ₁₃ ×T ₁	-18.35*	-5.88*	-0.03	-4.29	-25.72*	-11.36	-7.63*	-36.38*	7.56*	7.38*	7.14*	1.02	11.23*	8.45	2.52	-11.63*
$L_{13} \times T_2$	-10.16*	-11.76*	1.08	-4.29	-15.84*	-0.40	1.98	-31.63*	10.19*	1.64	0.79	0.51	15.27*	10.28	-7.08*	11.63*
$L_{14} \times T_1$	-2.91	0.00	-0.50	-13.97*	-16.88*	-14.12*	-17.00*	-19.33*	0.99	1.64	1.59	-0.51	19.81*	10.04	24.37*	-20.93*
Entry	GY	GW	SP	KRC	KPR	CL	CG	BY	HI	DP	DS	DBH	PH	СР	PC	ТС
$L_{14} \times T_2$	-11.62*	5.88*	-0.43	-7.52	-15.64*	-2.94	-1.48	-11.30*	-16.49*	1.64	1.59	1.52	12.22*	4.41	-1.44	-6.98
$L_{15} \times T_1$	-39.26*	-29.41*	2.79*	-9.68*	-3.91	-8.42	-10.35*	-31.81*	-25.33*	6.56*	7.14*	3.55*	14.68*	-4.23	-8.64*	41.86*
$L_{15} \times T_2$	17.15*	0.00	3.18*	-17.19*	-3.70	-10.59	-2.96	-2.53	0.78	4.10	4.76*	3.55*	7.88	0.71	-15.85*	2.33
$L_{16} \times T_1$	0.38	-23.53*	-1.83	-8.61	6.58	-5.88	-4.91	-10.37*	-6.16	7.38*	7.14*	3.55*	21.77*	21.48*	-3.12	20.93*
$L_{16} \times T_2$	-5.26	-23.53*	-2.42	-2.16	-21.20*	-23.13*	-4.91	-12.16*	-9.54*	5.74*	5.56*	3.55*	12.22*	6.52	13.33*	-9.30
$L_{17} \times T_1$	-20.29*	-11.76*	0.52	2.16	-13.99*	-3.93	-2.45	-3.41	-30.85*	-6.56*	-7.14*	-6.09*	-4.53	-24.30*	9.36*	-4.65
$L_{17} \times T_2$	-14.11*	-11.76*	0.56	-6.45	-3.09	-7.46	-4.43	-29.49*	2.11	-4.92*	-6.35*	-3.55*	0.59	-20.25*	-1.92	13.95*
$L_{18} \times T_1$	-20.92*	-5.88*	0.31	-9.68*	0.41	0.40	-13.04*	-31.14*	-3.68	0.00	0.00	0.00	4.83	-5.46	12.61*	-20.93*
$L_{18} \times T_2$	-27.86*	-29.41*	0.89	-3.23	-11.52*	-18.82*	-24.12*	-53.75*	30.69*	-1.64	-0.79	1.02	-1.87	-16.19*	2.16	-25.58*
$L_{19} \times T_1$	-27.50*	-11.76*	-0.56	7.00	-8.64	-14.31*	-4.17	-20.11*	-23.75*	-3.28	-3.17	-4.57*	16.35*	2.11	6.60*	4.65
$L_{19} \times T_2$	-2.98	-5.88*	-4.50*	-4.29	-2.06	-13.72*	2.87	-41.35*	38.60*	-2.46	-1.59	-1.02	9.36*	-0.70	10.14*	-11.63*
$L_{20} \times T_1$	-26.32*	-17.65*	-0.81	-5.39	-3.49	-20.19*	-15.02*	-42.22*	6.91	0.82	1.59	-0.51	13.20*	5.81	-2.40	4.65
$L_{20} \times T_2$	-26.34*	-29.41*	-3.08*	1.06	-4.94	-14.59*	-4.76	-14.79*	-27.58*	0.00	0.00	0.51	6.40	-4.75	-12.97*	51.16*
$L_{21} \times T_1$	-18.66*	-29.41*	-1.48	-4.29	-3.09	-5.11	-1.95	-20.02*	-14.83*	7.38*	7.14*	4.06*	16.16*	16.73*	2.64	-11.63*
$L_{21} \times T_2$	-8.93*	-17.65*	-1.15	-5.39	-13.17*	-20.00*	-17.74*	-35.72*	18.75*	7.38*	7.14*	5.58*	14.78*	18.14*	25.57*	-27.91*
$L_{22} \times T_1$	-21.89*	-23.53*	-1.06	7.52	-27.37*	-22.75*	-14.28*	-30.60*	-5.70	-1.64	-1.59	-1.52	-9.26*	-18.13*	-11.16*	32.56*
$L_{22} \times T_2$	-26.24*	-5.88*	2.34	4.29	-23.05*	-20.00*	2.22	-35.74*	-3.83	-0.82	-0.79	-2.54	-4.53	-0.35	-11.04*	6.98
$L_{23} \times T_1$	7.22*	-5.88*	1.34	5.39	-14.41*	-9.41	1.01	-33.17*	26.08*	-4.92*	-3.97	-2.54	6.50	10.04	-5.64*	34.88*
$L_{23} \times T_2$	-10.75*	-17.65*	1.03	-8.61	-30.04*	-21.18*	-2.45	-24.07*	-1.46	-4.10	-4.76*	-2.54	3.25	5.98	-11.22*	2.33
$L_{24} \times T_1$	-8.33*	-17.65*	-7.51*	-8.61	-25.72*	-12.94*	-17.23*	-10.36*	-14.30*	4.92*	4.76*	3.05*	15.17*	10.74	3.36	34.88*
$L_{24} \times T_2$	-10.14*	-32.35*	-2.51	-9.68*	-16.26*	-14.52*	-17.74*	-21.99*	-3.54	0.00	0.00	0.51	7.68	-6.87	-5.28*	9.30
$L_{25} \times T_1$	-24.00*	-29.41*	1.26	-5.39	-9.05*	4.31	-9.34*	-26.27*	-13.63*	0.00	-0.79	-1.52	12.32*	-1.41	0.36	-6.98
$L_{25} \times T_2$	-32.75*	-29.41*	-0.17	-5.39	-25.52*	-18.82*	-14.51*	-34.71*	-13.44*	2.46	1.59	0.51	15.77*	-5.64	-9.12*	2.33
$L_{26} \times T_1$	-6.63*	-23.53*	-0.64	-10.74*	-12.56*	-23.93*	-22.91*	-27.52*	7.91*	0.82	2.38	0.00	8.96*	-3.34	-2.40	20.93*
$L_{26} \times T_2$	-10.00*	-23.53*	0.40	-12.90*	-6.79	-25.88*	-16.85*	-34.87*	16.16*	-7.38*	-7.14*	-2.03	-1.97	-10.21	-14.17*	30.23*
$L_{27} \times T_1$	-30.47*	-5.88*	-3.64*	-9.68*	-25.52*	-12.35*	-18.95*	-19.00*	-28.05*	-5.74*	-5.56*	-3.05*	13.20*	-5.98	15.37*	-6.98
$L_{27} \times T_2$	-24.37*	-23.53*	-3.04*	-9.68*	-13.58*	-9.41	-9.84*	-4.97	-33.33*	-3.28	-3.17	-1.52	10.15*	-8.45	14.89*	-13.95*
$L_{28} \times T_1$	-6.55*	-29.41*	0.36	-8.61	-14.41*	-1.76	-9.34*	-8.72*	-14.20*	4.10	8.73*	5.08*	21.68*	20.42*	15.01*	-25.58*
$L_{28} \times T_2$	20.91*	-17.65*	0.01	-7.52	-4.94	-9.41	-17.23*	8.74*	-6.78	2.46	3.17	3.05*	15.77*	7.39	4.08	-18.60*
$L_{29} \times T_1$	-21.94*	-5.88*	-4.00*	0.00	-7.81	-12.75*	-14.28*	-23.73*	-14.25*	-0.82	-0.79	2.54	13.40*	12.50	-0.36	0.00
L ₂₉ ×T ₂	-13.95*	-11.76*	-1.09	-11.84*	-13.37*	-20.00*	-18.47*	-33.08*	7.79*	-3.28	-2.38	0.00	5.42	-0.70	5.40*	11.63*
$L_{30} \times T_1$	-27.76*	-11.76*	-2.69*	-7.52	-18.93*	-26.07*	-24.12*	-35.31*	-6.25	-1.64	-2.38	-3.55*	14.09*	-5.11	-9.12*	18.60*
$L_{30} \times T_2$	-21.63*	-23.53*	-0.79	-7.52	-16.46*	-13.34*	-6.89*	-30.27*	-5.42	-4.10	-3.17	-1.52	13.79*	7.04	-9.48*	11.63*

*Significant at 5% level of significance

Note: GY, grain yield; GW, 1000 grain weight; SP, shelling percentage; KRC, kernel rows per cob; KPR, kernels per row; CL, cob length; CG, cob girth; BY, biological yield; HI, harvest index; DP, days to 50% pollenshed; DS, days to 50% silking; DBH, days to 75% brown husk; PH, plant height; CP, cob placement; PC, protein content; TC, tryptophan content.

Estimation of magnitude of heterosis

The estimates of heterosis for 16 traits in maize are presented in Table 6. A wide range of heterosis was observed for grain yield and other traits in sixty crosses over the best standard check. The highest significant heterosis in positive direction over the best check was observed in cross $L_{28} \times T_2$ for grain yield (20.19%) and biological yield (8.74%), $L_{14} \times T_2$ for 1000 grain weight (5.88%), $L_{15} \times T_2$ for harvest index (36.60%), $L_{12} \times T_1$ for protein content (43.10%) and $L_{20} \times T_2$ for tryptophan content (51.16%). Cross combination $L_7 \times T_2$ for plant height (-21.77%) and cob height (-41.19%), $L_{26} \times T_2$ for days to 50 per cent pollenshed (-7.38%), $L_{17} \times T_1$ for days to 50 per cent silking (-7.14%) and 75 per cent brown husk (-6.09%) showed significantly negative heterosis as desirable for these traits. Two cross combinations $L_{28} \times T_2$ and $L_{15} \times T_2$ were identified as the best hybrid combinations as they showed highly significant heterosis and their per se performance was considerably more than that of the best check Bio-9544 (114.35 q/ha) and were also found to be early maturing.

Variable magnitude of heterosis as exhibited by different cross combinations for all the characters indicated sufficient divergence in parental material for these traits. Genetic variability among experimental material was also reported by Marker and Krupaker (2009) ^[16], Oliboni *et al.* (2012) ^[20], Kumar *et al.* (2013) ^[12] and Kumari *et al.* (2016) ^[14].

Reduction in plant height is desirable trait in maize and four crosses estimates significantly lesser plant height in comparison to check among 60 crosses developed. The cross $L_7 \times T_2$ (-21.77%) displayed the most negative heterosis for plant height hence can be used to produce short stature hybrids which can be useful where lodging is a problem. Bhatnagar et al. (2004)^[4], Kllaria and Sharma (2006)^[9] and Oliboni *et al.* (2012)^[20] earlier reported significant heterosis for dwarfness. Six crosses exhibited significant standard heterosis for earliness in respect of days to 50% tassel emergence and days to 50% silk emergence. Out of six crosses, three crosses, $L_{17} \times T_1$, $L_{17} \times T_2$ and $L_{27} \times T_1$ also exhibited significant standard heterosis for earliness in terms of days to brown. Manpreet et al. (2007) [15], Kumar (2008) ^[11] and Premlatha and Kalamani (2009) ^[22] observed significant heterosis for earliness in terms of days to 50% pollen shed and days to 50% silking in the case of hybrids included in their studies. Heterosis for earliness in terms of days to 50% maturity was also reported earlier by Nigussie and Zelleke (2001)^[19] and Bhatnagar et al. (2004)^[4].

The significant economic heterosis in the desirable direction over the best check is recorded in several cross combinations for all the characters except number of rows per cob, number of kernels per cob, cob length and cob girth. On the basis of high SCA effects, highly significant heterosis and *per se* performance for grain yield and other traits, three best hybrids *viz*; $L_{28} \times T_2$, $L_{15} \times T_2$ and $L_{23} \times T_1$ were identified.

Conclusion

Judicious choice of parents for hybridization and the selection procedure used in the breeding materials are among the factors on which the success of breeding primarily depends. Genetic information about the nature of combining ability, heterosis and the type of gene action controlling the inheritance of important traits, is a pre requisite in fixing the suitable parents and designing the appropriate breeding programme.

Based on per se performance and GCA effects for different traits, five lines viz., L15 (CML-292), L14 (CML-269-1), L23 (HKI-1040-7), L₁₂ (CML-141) and L₂₈ (TNAU/CBE-83) were identified as the best general combiners which could be involved in breeding programme for the development of composites or there is possibility of yield improvement which can be achieved by crossing these parents with some other inbred lines. Three hybrids TNAU/CBE-83 × BAJIM-08-27, CML-292 \times BAJIM-08-27 and HKI-1040-07 \times BAJIM-08-26 were identified as the best among sixty crosses on the basis of per se performance, earliness and highly significant heterosis. The cross combinations exhibited significantly positive SCA effects and the parents involved in these cross combinations showed positive and significant GCA effects which indicated the presence of both additive and non-additive gene action in the manifestation of heterosis. These crosses may be advanced for isolation of homozygous inbred lines for use in breeding programmes or may be used as single cross hybrids after evaluation in multilocation trials. Alternatively the population constituted from these inbreds is supposed to get sufficient improvement through recurrent and reciprocal recurrent selections which utilize both GCA and SCA variances.

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