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**Sawan Kumar**

Department of Crop  
Improvement, CSK Himachal  
Pradesh Agricultural University,  
Palampur, Himachal Pradesh,  
India

**Uttam Chandel**

CSKHPKV, SAREC, Kangra,  
Himachal Pradesh, India

**Satish Kumar Guleria**

CSKHPKV, HAREC, Bajaura,  
Himachal Pradesh, India

**R Devlash**

CSKHPKV, HAREC, Bajaura,  
Himachal Pradesh, India

**Correspondence****Sawan Kumar**

Department of Crop  
Improvement, CSK Himachal  
Pradesh Agricultural University,  
Palampur, Himachal Pradesh,  
India

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

**Sawan Kumar, Uttam Chandel, Satish Kumar Guleria and R Devlash**

**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  $\sigma^2$  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, L<sub>28</sub> was observed to be a good general combiner for grain yield, cob length, biological yield and protein content. Tester T<sub>1</sub> was found to be a good general combiner for 1000 grain weight, biological yield and protein content whereas tester T<sub>2</sub> 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 L<sub>28</sub> × T<sub>2</sub>, L<sub>15</sub> × T<sub>2</sub> and L<sub>23</sub> × T<sub>1</sub> 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 successful 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 from expectation on the basis of the average performance of the line involved”. Their studies in a set of F<sub>1</sub> 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 inter-allelic 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 (L<sub>1</sub>- L<sub>2</sub>) crossed with two diverse testers *viz.*, BAJIM-08-26 (T<sub>1</sub>) and BAJIM-08-27 (T<sub>2</sub>) 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<sub>1</sub> 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<sub>1</sub> 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
<b>Lines</b>			
L <sub>1</sub>	BAJIM-12-01	L <sub>19</sub>	CML-337
L <sub>2</sub>	BAJIM-13-01	L <sub>20</sub>	CML-439
L <sub>3</sub>	BAJIM-13-02	L <sub>21</sub>	CML-465-B-B
L <sub>4</sub>	BAJIM-15-08	L <sub>22</sub>	DMRQPM-58
L <sub>5</sub>	BAJIM-15-09	L <sub>23</sub>	HKI-1040-7
L <sub>6</sub>	BAJIM-15-10	L <sub>24</sub>	HKI-1105
L <sub>7</sub>	BAJIM-15-11	L <sub>25</sub>	LQPM-15-01
L <sub>8</sub>	BAJIM-15-12	L <sub>26</sub>	MRCQPM-16
L <sub>9</sub>	BML-6	L <sub>27</sub>	MRCQPM-18
L <sub>10</sub>	BML-7	L <sub>28</sub>	TNAU/CBE-83
L <sub>11</sub>	CML-44	L <sub>29</sub>	TNAU/CBE-115
L <sub>12</sub>	CML-141	L <sub>30</sub>	V-334
L <sub>13</sub>	CML-269	<b>Testers</b>	
L <sub>14</sub>	CML-269-1	T <sub>1</sub>	BAJIM 08-26
L <sub>15</sub>	CML-292	T <sub>2</sub>	BAJIM 08-27
L <sub>16</sub>	CML-294	<b>Checks</b>	
L <sub>17</sub>	CML-334	Check-1	Bio 9544
L <sub>18</sub>	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.

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

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

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  $\sigma^2$  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  $\sigma^2$  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  $\sigma^2$ SCA/ $\sigma^2$ GCA was less than unity for all the traits except plant height for which the  $\sigma^2$ GCA/ $\sigma^2$ 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 $\times$ Tester	Error	$\sigma^2$ GCA	$\sigma^2$ SCA	$\sigma^2$ GCA / $\sigma^2$ 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 L<sub>28</sub> and L<sub>12</sub> 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.*, L<sub>14</sub> for 1000 grain weight, L<sub>22</sub> for rows per cob, L<sub>3</sub> for kernels per row and for cob length, L<sub>19</sub> for cob girth, L<sub>18</sub> for harvest index, L<sub>15</sub> for shelling percentage, L<sub>4</sub> for days to 50 per cent pollen shed, L<sub>17</sub> for days to 50 per cent silking and 75 per cent brown husk, L<sub>7</sub> for plant height and cob placement, L<sub>12</sub> for protein content and L<sub>11</sub> for tryptophan content. Among the testers T<sub>1</sub> was a good general combiner for 1000 grain weight, biological yield, protein content and tryptophan content in endosperm protein whereas T<sub>2</sub> 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  $\times$  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 L<sub>15</sub>  $\times$  T<sub>2</sub> (31.11) followed by L<sub>7</sub>  $\times$  T<sub>1</sub> (23.07), L<sub>2</sub>  $\times$  T<sub>1</sub> (22.47) and L<sub>28</sub>  $\times$  T<sub>2</sub> (14.56) showed high positive significant effect for this trait. The cross L<sub>15</sub>  $\times$  T<sub>2</sub> for 1000 grain weight, L<sub>1</sub>  $\times$  T<sub>2</sub> for shelling percentage, L<sub>2</sub>  $\times$  T<sub>2</sub> for number of rows per cob, L<sub>2</sub>  $\times$  T<sub>1</sub> for cob girth, L<sub>2</sub>  $\times$  T<sub>1</sub> for biological yield and L<sub>19</sub>  $\times$  T<sub>2</sub> 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<sub>7</sub>  $\times$  T<sub>1</sub> for days to 50 per cent pollen shed and days to 50 per cent silking, L<sub>2</sub>  $\times$  T<sub>1</sub> for days to 75 per cent maturity and L<sub>2</sub>  $\times$  T<sub>2</sub> for plant height and cob placement. The cross L<sub>21</sub>  $\times$  T<sub>2</sub> showed the highest significant positive SCA for protein content and L<sub>9</sub>  $\times$  T<sub>2</sub> 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].





L <sub>12</sub> ×T <sub>2</sub>	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 <sub>13</sub> ×T <sub>1</sub>	-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 <sub>13</sub> ×T <sub>2</sub>	-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 <sub>14</sub> ×T <sub>1</sub>	-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*
<b>Entry</b>	<b>GY</b>	<b>GW</b>	<b>SP</b>	<b>KRC</b>	<b>KPR</b>	<b>CL</b>	<b>CG</b>	<b>BY</b>	<b>HI</b>	<b>DP</b>	<b>DS</b>	<b>DBH</b>	<b>PH</b>	<b>CP</b>	<b>PC</b>	<b>TC</b>
L <sub>14</sub> ×T <sub>2</sub>	-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 <sub>15</sub> ×T <sub>1</sub>	-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 <sub>15</sub> ×T <sub>2</sub>	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 <sub>16</sub> ×T <sub>1</sub>	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 <sub>16</sub> ×T <sub>2</sub>	-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 <sub>17</sub> ×T <sub>1</sub>	-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 <sub>17</sub> ×T <sub>2</sub>	-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 <sub>18</sub> ×T <sub>1</sub>	-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 <sub>18</sub> ×T <sub>2</sub>	-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 <sub>19</sub> ×T <sub>1</sub>	-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 <sub>19</sub> ×T <sub>2</sub>	-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 <sub>20</sub> ×T <sub>1</sub>	-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 <sub>20</sub> ×T <sub>2</sub>	-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 <sub>21</sub> ×T <sub>1</sub>	-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 <sub>21</sub> ×T <sub>2</sub>	-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 <sub>22</sub> ×T <sub>1</sub>	-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 <sub>22</sub> ×T <sub>2</sub>	-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 <sub>23</sub> ×T <sub>1</sub>	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 <sub>23</sub> ×T <sub>2</sub>	-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 <sub>24</sub> ×T <sub>1</sub>	-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 <sub>24</sub> ×T <sub>2</sub>	-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 <sub>25</sub> ×T <sub>1</sub>	-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 <sub>25</sub> ×T <sub>2</sub>	-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 <sub>26</sub> ×T <sub>1</sub>	-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 <sub>26</sub> ×T <sub>2</sub>	-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 <sub>27</sub> ×T <sub>1</sub>	-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 <sub>27</sub> ×T <sub>2</sub>	-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 <sub>28</sub> ×T <sub>1</sub>	-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 <sub>28</sub> ×T <sub>2</sub>	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 <sub>29</sub> ×T <sub>1</sub>	-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 <sub>29</sub> ×T <sub>2</sub>	-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 <sub>30</sub> ×T <sub>1</sub>	-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 <sub>30</sub> ×T <sub>2</sub>	-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<sub>28</sub> × T<sub>2</sub> for grain yield (20.19%) and biological yield (8.74%), L<sub>14</sub> × T<sub>2</sub> for 1000 grain weight (5.88%), L<sub>15</sub> × T<sub>2</sub> for harvest index (36.60%), L<sub>12</sub> × T<sub>1</sub> for protein content (43.10%) and L<sub>20</sub> × T<sub>2</sub> for tryptophan content (51.16%). Cross combination L<sub>7</sub> × T<sub>2</sub> for plant height (-21.77%) and cob height (-41.19%), L<sub>26</sub> × T<sub>2</sub> for days to 50 per cent pollenshed (-7.38%), L<sub>17</sub> × T<sub>1</sub> 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<sub>28</sub> × T<sub>2</sub> and L<sub>15</sub> × T<sub>2</sub> 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<sub>7</sub> × T<sub>2</sub> (-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<sub>17</sub> × T<sub>1</sub>, L<sub>17</sub> × T<sub>2</sub> and L<sub>27</sub> × T<sub>1</sub> 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 Nigusie 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<sub>28</sub> × T<sub>2</sub>, L<sub>15</sub> × T<sub>2</sub> and L<sub>23</sub> × T<sub>1</sub> 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.*, L<sub>15</sub> (CML-292), L<sub>14</sub> (CML-269-1), L<sub>23</sub> (HKI-1040-7), L<sub>12</sub> (CML-141) and L<sub>28</sub> (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 × BAJIM-08-27 and HKI-1040-07 × 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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