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Research Article

Combining ability effects and heterotic grouping in newly developed early maturing yellow maize (*Zea mays* L.) inbreds under sub-tropical conditions

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Abstract
A field experiment was conducted at Experimental Farm, Shivalik Agricultural Research and Extension Centre, Kangra representing subtropical conditions of north western Himalayasecology during *Kharif* 2017 to estimate combining ability of newly developed early maturing yellow maize inbred lines. Twenty two crosses were generated by crossing 11 new developed yellow maize inbreds with 2 diverse testers using Line x Tester mating design. The experiment was conducted using randomized block design with two replications. The mean square due to genotypes, parents and parents v/s crosses were significant for all the traits, except for days to 50 per cent silking due to genotypes, kernel rows, days to 50 per cent tasseling and days to 50 per cent silking due to parents. This revealed presence of appreciable amount of genetic variability in the experimental material of the present investigation. The ratio of σ^2gca / σ^2sca for all the studied traits indicated the preponderance of non-additive gene effects in the inheritance of these traits. Among female inbred lines, L_9 had significant GCA effects for grain yield per plant (21.64) and yield component traits like shelling percentage (3.24) , ear length(2.37), ear diameter(1.07), number of kernels/row(3.84) and 1000- kerenel weight (8.68) , indicated that best general combiner for these traits, while in male parent T_2 was the best general combiner for yield contributing traits viz., ear length (0.47), ear diamter (0.19), number of kernel rows per ear (0.59), number of kernels/row (1.02) and 1000-kernel weight (10.05). On the basis of mean grain yield and SCA effects, three test crosses, viz., L_9xT_2, L_5xT_1, and L_1xT_1 were identified most promising and may be further tested at multi environments for use as single cross hybrids. L_9xT_2 manifested highest mean grain yield (102.17g/plant) and significant positive specific combining ability effect (15.93). Based on the SCA effect for grain yield, the newly developed inbreds were classified into two heterotic groups. The lines L_1, L_2, L_4, L_5 and L_6 belonged to tester group CM-212, while L3, L9, and L11 belonged to heterotic group of HKI-1105. Inbred lines assigned into two opposite heterotic groups could be used as parents to develop hybrids and inbred lines with same heterotic group with positive GCA may be used for synthetic variety development.

Key words
Combining Ability, Heterotic grouping, Maize, GCA, SCA

Introduction

Exploitation of hybrid vigour 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). 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). Information on the heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development (Beck *et al*. 1990).

Knowledge on the genetic heterogeneity and progeny performance are significant for deciding breeding schemes, assigning the parental lines, defining heterotic groups and predicting future hybrid performance. Thus, information on genetic diversity among genetic materials has an utmost importance for hybrid maize breeding programmes for development of lines, the assigning of lines into different heterotic groups and the preference of testers for hybrid combinations (Xia *et al.* 2004). Thus, assigning of maize lines into different heterotic group is very vital for hybrid breeding programmes in giving information about the germplasms (Hallauer*et al*. 2010). Heterotic response based grouping will enable development of new inbred lines with-in group and hybrid development between lines of opposite heterotic group. Hence, for systematic exploitation of heterosis characterization of populations, genetic pools and even lines for heterotic pattern and establishing heterotic groups is important. It enhances the efficiency of hybrid development. Heterotic grouping in maize is done across the world. SCA effect is useful in determining the heterotic grouping of population and inbred lines for enhancing efficiency of hybrid breeding Vasal*et al*. (1992a, b).

Indian maize lines form a complex genetic structure, coming from diverse sources, which makes heterotic grouping very difficult. A similar kind of situation is seen in tropical CIMMYT maize germplasm where complementary heterotic patterns failed because of the complex genetic structure between populations (Xia *et al.* 2004). Hence, there is need to group new inbred lines continuously developed every year based on heterotic response. Heterotic grouping based on multi-location and over years may sometimes distort the combining ability results. This is because most of the variation is attributed to Genotype Environment Interaction (GEI). Hence, in the present study heterotic grouping is done with single year one location data.

Combining ability is one of the powerful tool to identify the best combiner parents in a series of its crosses and it provides information on the nature and magnitude of gene actions (Uddin*et al.* 2008). The two types of combining ability are: general combining ability (GCA) and specific combining ability (SCA). GCA is average performance of parents in a series of crosses and SCA designates those cases in which certain combinations relatively better or worse than would be expected on the basis of average performance of parents. Heterotic grouping is a group of related or unrelated genotypes from the same or different populations that indicate similar combining ability and heterotic response when crossed with testers from other genetically diverse germplasm groups (Melchinger*et al.*1998).

Line x tester mating design is an efficient procedure as it allows the inclusion of more entries, estimate combining ability, gene effects, male and female relationship, heterotic grouping and aid to select desirable parents and crosses (Sharma, 2006). The knowledge of combining ability is important to develop desired hybrids (Mwimali*et al*. 2016). Thus, this study was carried out to estimate the combining ability of parents and hybrids, nature and magnitude of gene action for yield and yield components, to identify best hybrid combination of lines and testers and to determine heterotic groups of newly developed early maturing yellow maize inbreds.

Materials and Methods

The material for present investigation was developed during *Kharif,* 2016 at Research Farm of Shivalik Agricultural Research and Extension Centre, Kangra. The 11 newly developed early maturing yellow maize inbred lines, used as female parents, were crossed with two diverse testers in a line × tester mating design The list of the inbred lines and testers used in this experiment is given in Table 1. The 22 test crosses along with 13 parents and 2 checks *viz.*, Bisco-855 and PalamSankar Makka-2 were field tested in randomized block design (RBD) with two replications during *Kharif,* 2017 for yield performance and their agronomic traits at Experimental Farm of SAREC, Kangra, representing subtropical conditions of north western Himalayas. The experimental material consisting of a total of 37 entries (22 F_1s, 13 parents and 2 checks) were sown in randomized block design with two replications. Each experimental unit was represented by two rows of 2 m length with inter and intra-row spacing of 60 cm and 20 cm, respectively. Standard agronomic practices were followed and plant protection measures were taken when required to ensure normal growth and development of the plants. At maturity, 10 ears from the consecutive plants in middle of row of each experimental unit were harvested for recording data on grain yield/plant (g), shelling (%), ear length (cm), ear diameter (cm), days to 50 per cent tasseling, days to 50 per cent silking, plant height (cm), ear height (cm) rows/ear and kernels/row. After harvest, the kernels were air dried until a grain moisture content of 15% was achieved and then 1000-kernel weight (g) was recorded. However, days to 50 per cent tasseling and days to 50 per cent silking were recorded on plot basis. Data recorded were subjected to analysis of variance according to Panse and Sukhatme (1985) to determine significant differences among genotypes. Combining ability analysis for line x tester mating design was performed as per method suggested by Kempthorne (1957). Heterotic grouping of inbred lines were done based on SCA effect of crosses and mean grain yield performance as per procedure described by Menkir*et al.* (2004).

Results and Discussion

The mean square due to genotypes, parents and parents v/s crosses were significant for all the traits, except for days to 50 per cent silking due to genotypes, kernel rows, days to 50 per cent tasseling and days to 50 per cent silking due to parents. This revealed presence of appreciable amount of genetic variability in the experimental material of the present investigation. The results agree with the findings of Mohan *et al*. (2017).

Mean squares due to crosses were significant for grain yield/plant, shelling (%), ear length, ear diameter, and number of kernels per row, thousand-kernel weight, plant height and ear height. This indicated that, the crosses were sufficiently different from each other for these traits and hence, selection is possible to identify the most desirable crosses. Amiruzzaman*et al*. (2010) and Shushay*et al.* (2013) also found significantly different among crosses for yield and yield related traits. The mean square due to lines were significant for traits like grain yield/plant, shelling (%), ear length, ear diameter, number of kernels per row, thousand-kernel weight, plant height and ear height (Table 2). Significant differences among lines indicate greater diversity in the parental lines. Hailegebrial *et al*. (2015) also observed significance difference among GCA effects of lines in grain yield, plant height, ear height, ear length number of kernels per row. Mosa (2010) also reported similar results. Punewar *et al*. (2017) found significant difference for all the traits studied in their study of Genetic dissection of heterosis and combining ability in castor (*Ricinus communis* L.) with line × tester analysis. The mean square due to testers showed significant difference for grain yield/plant, ear length, ear diameter, no of kernel rows/ear ,number of kernels per row, thousand-kernel weight, plant height and ear height. These results are consistent with the earlier study of Girma *et al*. (2015).

Combining ability variance of grain yield and its contributing triats are presented in Table 3.The analysis of variance for grain yield/plant, shelling (%), ear length, ear diameter, number of kernels per row, thousand-kernel weight, days to 50 per cent tasseling , days to 50 per cent silking and ear height. This indicated that the contribution of lines towards σ^2gca was greater for these traits. Variance due to testers was of higher magnitude than that of lines for kernel rows/ear and plant height. This indicated that the contribution of testers for these traits, towards σ^2gca was greater. The estimates of sca variance were of higher magnitude than gca variance for all the traits. Besides this the ratio of σ^2gca/ σ^2sca was less than one for all the traits 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 Amiruzzaman*et al*. (2013), Verma*et al.* (2014) , Sharma *et al*. (2015) and Mohan *et al.* (2017).

Estimates of GCA effects of the 11 lines and 2 testers are presented in Table 4. Line L_9 exhibited the maximum GCA effect (21.64) followed by L_1 (14.64), whereas L_{10} exhibited the lowest GCA effect of all (-24.01) followed by L_{11} (-13.04), the results revealed the existence of the best and poorest general combiners in the group of inbred lines studied, respectively. Inbred lines L_1, L_9, L_5 and L_6 were observed with good GCA effect forgrain yield and could be utilized in maize grain yield improvement programs. Both positive and negative GCA effects for grain yield in maize were alsoreported earlier by Chandeland Mankotia (2014), Girma*et al.* (2015) and Ram *et al.* (2015). Non –significant GCA effects were also observed for lines L_4, L_7 and L_8. Hafiz *et al.* (2015) also found non-significant GCA effects for grain yield in line x tester analysis of maize inbred lines. For days to silking line L_2 showed negative GCA effects. Negative GCA effects indicated that this line may be good sources of genes for earliness. The present results are in general agreement with the findings of previous researchers. Mosa (2010) and Punewar *et al.* (2017) also reported significant positive and negative GCA effects for days to silking. The GCA estimates ranged from -17.50 to 13.50 for plant height. Among all lines, two inbred lines L_2 and L_8 showed positive GCA effects and could significantly contribute to taller plant stature. On the other hand, line L_2 showed significant negative GCA effects, indicated that this line may contribute to reduced plant stature in their crosses. The testers showed significant GCA effects in plant height. In line with the present finding, Punewar *et al.* (2017) also observed significant positive and negative GCA effects for plant height.

With respect to ear height, four lines L_1, L_2, L_5 and L_6 showed negative and significant GCA effects, which indicated their potential to decrease ear height. L_8, L_9 and L_{11} showed positive and significant GCA effects for ear length. L_2 and L_9 recorded positive and significant GCA effects for ear diameter. L_3, L_6, L_9 and L_{11} showed positive GCA effects for number of kernel rows per ear. Positive GCA effect for number of rows per cob is very important yield parameter and directly contributes to increased grain yield in its hybrid combinations. L_8 and L_9 showed positive and significant GCA effects for number of kernels per rows. Lines with high GCA effects for this trait can be used as parents for hybrid formation as well as for inclusion in future breeding programs. Such parents contribute favorable alleles in the process of synthesis of new varieties. L_1, L_4 and L_9 showed positive and significant GCA effects for shelling (%). L_2, L_7 and L_9 were good general combiners for thousand-kernel weight. Lines with positive GCA effect have vital potential for genetic improvement of this trait in breeding programs. Habtamu and Hadji (2010), Rahman*et al.* (2010), Chandeland Mankotia (2014), Girma*et al.* (2015) and Punewar*et al.* (2017) also reported similar results for GCA effects of yield contributing traits in maize.

Tester 1 is best combiner forgrain yield (1.22), shelling (0.48), days to silking (-0.50), plant height (-10.93) and ear height (-4.84), while Tester 2 is best combiner for ear length (0.47), ear diameter (0.19),number of kernels rows per ear (0.59), number of kernels per row (1.02), 1000- kernels weight (10.05) and days to tasseling (-0.18). Kamara*et al*. (2010) and Shushay*et al*. (2013) also reported best combiner tester for grain yield, thousand kernels weight, number of rows per ear and ear length.

With respect to grain yield, both positive and negative significant estimates of SCA effects observed among crosses. Estimation of SCA effects in crosses ranged from -27.50 to 27.50 (Table5). Out of 22 crosses, six crosses have shown significant positive SCA effects for grain yield /plant. The cross$L_{11}xT_2$ (27.50) followed by $L_{2x}T_1$ (18.98),L_9xT_2 (15.93), $L_{5x}T_1$ (11.73), L_3xT_2 (9.28) and $L_{10}xT_1$ (8.58) showed high positive significant effect for this trait. Best combiner crosses may be used in maize improvement program. Current findings are in pact with the earlier reports of Amiruzzaman*et al.* (2010) and Shushay*et al*. (2013).

The crosses viz., $L_{11xT2,}L_2xT_1$ and L_5xT_1 for shelling percentage, L_9xT_2, L_6xT_1 and $L_{11}xT_2$ for ear length, L_9xT_2, $L_{11}xT_2$, L_8xT_1 and L_2xT_1 for ear diameter, L_1xT_1, L_6xT_1, L_9xT_2 and L_3xT_2 for kernels/row, L_9xT_2, L_3xT_1,L_6xT_1, L_5xT_2 and $L_2xT_2$for 1000- kernel weight showed significant positive SCA effects.Whereas, highest significant negative sca effect for plant height and ear height were observed for L_3xT_2, $L_{11}xT_1$ and L_4xT_{21}. A cross with high negative SCA effects for plant height and ear height is advantageous in case of development of lodging resistant maize varieties. Wali*et al*. (2010) and Asif*et al*. (2014) also reported significant negative SCA effects for plant height and ear height in maize. 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 earlier by Miranda *et al*. (2008), Jampatong*et al.* (2010) and Rastgari*et al.* (2014). In general, the GCA effects of the parents were not reflected in the SCA effects of the crosses in some of the studied traits. This result is supported by Debnath and Sarker (1987)and Deitos*et al*. (2006), they suggested that good general combining parent does not always show high SCA effects in their hybrid combinations.Heterosis in crosses of line with either of the testers depends largely on complementation and overdominance effect. This is function of chromosomal blocks or alleles fixed during inbred line development.

Melchinger and Gumber (1988) defined a heterotic group "as a group of related or unrelated genotypes from the same or different populations, which display similar combining ability and heterotic response when crossed with genotypes from other genetically distinct germplasm groups. By comparison, the term heterotic pattern refers to a specific pair of two heterotic groups, which express high heterosis and consequently high hybrid performance intheir cross. The performance of test crosses manifested in SCA effect was used to group lines into dieverseheterotic groups.

The results exhibited that, from eleven inbred lines, six inbred lines *viz*., L_1, L_2, L_4, L_5, L_6 and L_7 were showing positive SCA effects with CM-212 and exhibited negative SCA effects with HKI-1105 and grain yield greater than the mean grain yield when crossed to CML -212. On the other hand three inbred lines viz., L_3, L_9 and L_{11} showed positive SCA effects with HKI-1105 and exhibited negative SCA effects with CML 1-212 and grain yield greater than the mean yield of lines when crossed to HKI-1105 (Table 6). Irrespective of SCA effects two inbred lines viz., L_8 and L_{10} recorded yield less than the mean grain yield when crossed to both testers were classified as C group. In the present study, it may be concluded that all the newly developed inbred lines were not derived from single pool. Menkir*et al.* (2004), Rovaris*et al*. (2014) and Ejigu*et al.* (2017) also classified inbred lines into two heterotic groups based on SCA effects of mean grain yield.

The two testers included in the study separated the inbred lines effectively intoheterotic groups. This will be useful for developing hybrids and synthetic varieties in future breeding. Breeding programmes can take advantage of this information on combining ability to find best breeding strategy for developing high yielding lines and hybrids. Inbred lines assigned into two opposite heterotic groups should be used as parental lines hybrid developmen to maximize heterosis and inbred lines with same heterotic group with positive GCA should be used for synthetic variety development.The parents with good GCA for yield and negative GCA for plant and ear height and days to silking may be extensively used in the hybridization program as a donor to obtain early and short statured lodging resistant hybrids with higher yield.The test crosses viz., L_9xT_2, $L_5xT_{1,}$ and L_1xT_1exhibited 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 test crosses either can be directly used as single cross hybrids after evaluation in multilocation trials or may be advanced for isolation of superiorhomozygous inbred lines for use in breeding programmes. Alternatively the population constituted from these inbreds is supposed to get sufficient improvement through recurrent and reciprocal recurrent selection which utilizes both GCA and SCA variances.

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Table 1. Details of the lines, testers and checks used in the study

Sr. no	Inbred line	Code	Stage	Source (Origin)
1.	KI-3A	L_1	S_5	AICRP on maize, Kangra
2.	KI-7C	L_2	S_5	AICRP on maize, Kangra
3.	KI-21A	L_3	S_5	AICRP on maize, Kangra
4.	KI-28B	L_4	S_5	AICRP on maize, Kangra
5.	KI-36A	L_5	S_5	AICRP on maize, Kangra
6.	KI-36B	L_6	S_5	AICRP on maize, Kangra
7.	KI-13-3-1	L_7	S_6	AICRP on maize, Kangra
8.	KI-13-179	L_8	S_6	AICRP on maize, Kangra
9.	KI-13-182	L_9	S_6	AICRP on maize, Kangra
10.	KI-13-194	L_{10}	S_6	AICRP on maize, Kangra
11.	KI-13-315	L_{11}	S_6	AICRP on maize, Kangra
12.	KI -57 (CM-212)	L_{12}	Inbred CM-212	VPKAS, Almora
13.	KI -58 (HKI-1105)	L_{13}	Inbred HKI-1105	CCSHAU, Karnal
14	PalamSankar Makka-2		Hybrid	CSKHPKV, Palampur
15.	Bisco-855		Hybrid	Bisco Biosciences

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

		Mean of squares										
Source of variance	**df**	**Grain Yield/Plant**	**Shelling (%)**	**Ear length (cm)**	**Ear diameter (cm)**	**Kernel rows/ear**	**Kernels per row**	**1000-kernel weight (g)**	**Days to 50% tasseling**	**Days to 50% silking**	**Plant height (cm)**	**Ear height (cm)**
Replications	1	10.53	1.51	0.34	0.94*	0.06	28.93	288.06*	0.06	9.66	169.73**	151.56*
Genotypes	34	1570.53*	58.05*	17.47*	6.43*	9.53*	90.50*	13075.98*	4.47*	18.36	2107.59*	719.74*
Crosses	21	655.49*	36.71*	5.19*	1.37*	1.86	18.07*	658.98*	1.43	21.47	583.75*	16.22*
Lines(GCA)	10	660.89*	39.73*	8.10*	0.85*	1.00	13.91*	482.10*	1.95	24.99	245.10*	173.04*
Testers(GCA)	1	65.98*	9.94	9.74*	1.60*	15.36*	46.02*	4440.09*	1.45	11.00	5258.20*	1031.11*
L×T(SCA)	10	709.04*	36.36*	1.83*	1.86*	1.36	19.42*	457.74*	0.90	19.00	454.95*	66.61*
Parents	12	54.5132*	23.34*	1.38*	1.98*	1.54	13.13*	807.79*	7.40	8.54	359.38*	406.62*
Parents Vs Crosses	1	38978.61*	922.67**	468.35*	166.15*	266.54*	2540.02*	421051.12*	33.10*	70.97**	55086.80*	16164.04*
Error	34	5.8366	2.7215	0.2254	0.1041	1.7042	3.9286	29.8218	1.4101	15.0689	23.7874	8.3513

*, ** Significant at 5 % and 1 % level of significance, respectively

Table 3. Analysis of variance for combining ability for different characters in maize

Source of variation	**Grain Yield/Plant**	**Shelling (%)**	**Ear length (cm)**	**Ear diameter (cm)**	**Kernel rows/ear**	**Kernels per row**	**1000-kernel weight (g)**	**Days to 50% tasseling**	**Days to 50% silking**	**Plant height (cm)**	**Ear height (cm)**
σ^2_L	48.01	51.54	74.3	29.65	25.64	36.67	34.84	65.00	55.42	19.99	50.48
σ^2_T	0.48	1.29	8.93	5.58	39.39	12.13	32.08	4.85	2.44	42.89	30.08
σ^2GCA	-1.64	0.011	0.104	-0.015	0.0152	-0.0418	6.19	0.016	0.076	3.960	2.970
σ^2SCA	350.40	16.61	0.756	0.888	-0.1255	8.4792	208.34	-0.314	-2.280	212.180	28.930
σ^2GCA / σ^2SCA	-0.005	0.001	0.137	-0.017	-0.121	-0.005	0.030	-0.051	-0.033	0.019	0.103

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

Characters/ Lines	**Grain Yield/Plant**	**Shelling (%)**	**Ear length (cm)**	**Ear diameter (cm)**	**Kernel rows/ear**	**Kernels per row**	**1000-kernel weight (g)**	**Days to 50% tasseling**	**Days to 50% silking**	**Plant height (cm)**	**Ear height (cm)**
L_1	14.64**	4.65**	-0.98**	-0.42**	0.00ns	0.84ns	5.68ns	0.50ns	1.30ns	-4.50ns	-10.55**
L_2	-6.89**	-0.42ns	-0.43ns	0.45**	0.00ns	-1.16ns	21.68**	0.00ns	-7.20**	-17.50**	-10.80**
L_3	-3.40*	-0.56ns	-0.43ns	-0.05ns	0.50ns	-1.41ns	-5.75ns	0.25ns	0.80ns	7.50*	3.70*
L_4	-2.18ns	2.16*	-2.21**	0.08ns	0.00ns	-1.16ns	-8.82*	-0.75ns	0.30ns	-2.25ns	1.45ns
L_5	11.28**	1.80ns	0.09ns	-0.10ns	-0.50ns	1.09ns	-13.82**	-0.50ns	-0.20ns	4.00ns	-3.30*
L_6	5.14**	-0.06ns	0.44ns	0.05ns	0.50ns	-0.16ns	-13.32**	0.75ns	1.30ns	-4.00ns	-4.05*
L_7	-1.06ns	0.40ns	-1.41**	-0.32*	0.00ns	-2.66**	11.18**	-0.75ns	0.50ns	2.75ns	0.95ns
L_8	-2.13ns	-0.89ns	2.07**	-0.53**	-1.00ns	2.09*	1.18ns	-0.25ns	0.30ns	13.50**	9.20**
L_9	21.64**	3.24**	2.37**	1.07**	0.50ns	3.84**	8.68*	1.50*	2.30ns	-1.25ns	7.70**
L_{10}	-24.01**	-6.67**	-0.71*	-0.40*	-0.50ns	-1.41ns	-3.07ns	-0.25ns	1.05ns	1.00ns	2.20ns
L_{11}	-13.04**	-3.65**	1.22**	0.18ns	0.50ns	0.09ns	-3.82ns	-0.50ns	0.05ns	0.75ns	3.45*
SE± (g)	2.02	1.25	0.39	0.28	0.89	1.11	4.53	0.87	3.43	3.91	2.09
Testers											
T_1	1.22ns	0.48ns	-0.47**	-0.19**	-0.59*	-1.02**	-10.05**	0.18ns	-0.50ns	-10.93**	-4.84**
T_2	-1.22ns	-0.48ns	0.47**	0.19**	0.59*	1.02**	10.05**	-0.18ns	0.50ns	10.93**	4.84**
SE± (g)	0.86	0.53	0.16	0.08	0.38	0.47	1.93	0.37	1.46	1.66	0.89

*, ** Significant at 5 % and 1 % level of significance, respectively

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Table 5. Specific combining ability effects for grain yield and its contributing characters in maize

Sr. No.	Crosses	Grain Yield/ Plant	Shelling (%)	Ear length (cm)	Ear diameter (cm)	Kernel rows	Kernel per row	1000-kernel weight (g)	Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Ear height (cm)
1	L_1xT_1	3.01ns	0.52ns	0.07ns	0.12ns	0.09ns	3.02*	-5.45ns	0.82ns	1.25ns	-5.32ns	-3.41ns
2	L_1xT2	-3.01ns	-0.52ns	-0.07ns	-0.12ns	-0.09ns	-3.02*	5.45ns	-0.82ns	-1.25ns	5.32ns	3.41ns
3	L_2xT_1	18.98**	3.78**	-0.38ns	0.49*	0.09ns	0.02ns	-9.45*	0.32ns	-6.25ns	3.68ns	0.34ns
4	L_2xT_2	-18.98**	-3.78**	0.38ns	-0.49*	-0.09ns	-0.02ns	9.45*	-0.32ns	6.25ns	-3.68ns	-0.34ns
5	L_3xT_1	-9.28**	-2.27ns	0.57ns	0.34ns	0.59ns	-2.73*	13.30**	0.07ns	0.75ns	21.18**	7.34**
6	L_3xT_2	9.28**	2.27ns	-0.57ns	-0.34ns	-0.59ns	2.73*	-13.30**	-0.07ns	-0.75ns	-21.18**	-7.34**
7	L_4xT_1	3.11ns	0.04ns	0.35ns	-0.13ns	0.09ns	1.52ns	5.05ns	-0.93ns	-0.75ns	10.93*	6.09**
8	L4xT_2	-3.11ns	-0.04ns	-0.35ns	0.13ns	-0.09ns	-1.52ns	-5.05ns	0.93ns	0.75ns	-10.93*	-6.09**
9	L_5xT_1	11.73**	2.84*	0.25ns	-0.41ns	-0.41ns	-1.73ns	-9.95*	-0.18ns	0.25ns	7.18ns	-1.16ns
10	L_5xT_2	-11.73**	-2.84*	-0.25ns	0.41ns	0.41ns	1.73ns	9.95*	0.18ns	-0.25ns	-7.18ns	1.16ns
11	L_{6x}T1	0.29ns	1.27ns	1.15**	-0.41ns	0.59ns	3.02*	10.55*	0.57ns	1.25ns	-7.32ns	1.09ns
12	L_6xT_2	-0.29ns	-1.27ns	-1.15**	0.41ns	-0.59ns	-3.02*	-10.55*	-0.57ns	-1.25ns	7.32ns	-1.09ns
13	L_7xT_1	9.04**	1.61ns	0.05ns	-0.13ns	0.09ns	0.02ns	5.05ns	-0.43ns	-0.00ns	-7.57ns	-0.91ns
14	L_7xT_2	-9.04**	-1.61ns	-0.05ns	0.13ns	-0.09ns	-0.02ns	-5.05ns	0.43ns	0.00ns	7.57ns	0.91ns
15	L_8xT_1	-2.03ns	1.36ns	-0.53ns	0.57*	0.09ns	-1.73ns	5.05ns	0.07ns	1.25ns	-9.32*	-2.16ns
16	L_8xT_2	2.03ns	-1.36ns	0.53ns	-0.57*	-0.09ns	1.73ns	-5.05ns	-0.07ns	-1.25ns	9.32*	2.16ns
17	L_9xT_1	-15.93**	-1.57ns	-1.18**	-1.63**	-1.41ns	-2.98*	-22.45**	-0.18ns	1.25ns	-1.57ns	-2.16ns
18	L_9xT_2	15.93**	1.57ns	1.18**	1.63**	1.41ns	2.98*	22.45**	0.18ns	-1.25ns	1.57ns	2.16ns
19	$L_{10}xT_1$	8.58**	-0.19ns	0.50ns	0.29ns	-0.41ns	2.27ns	0.80ns	0.07ns	1.00ns	4.18ns	1.84ns
20	$L_{10}xT_2$	-8.58**	0.19ns	-0.50ns	-0.29ns	0.41ns	-2.27ns	-0.80ns	-0.07ns	-1.00ns	-4.18ns	-1.84ns
21	$L_{11}xT_1$	-27.50**	-7.39**	-0.83*	0.92**	0.59ns	-0.73ns	7.55ns	-0.18ns	-0.00ns	-16.07**	-6.91**
22	$L_{11}xT_2$	27.50**	7.39**	0.83*	-0.92**	-0.59ns	0.73ns	-7.55ns	0.18ns	0.00ns	16.07**	6.91**
23	S.E ±(Sij)	2.80	1.77	0.56	0.29	1.27	1.56	6.40	1.23	4.85	5.53	2.95

*, ** Significant at 5 % and 1 % level of significance, respectively

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Table 6.Heterotic grouping of newly developed inbred lines correspondingto testers

Lines	**CM-212 (Group "B")**	**SCA**	**HKI-1105 (Group "A")**	**SCA**	**Heterotic group**
L_1	84.69	3.01ns	76.22	-3.01ns	B
L_2	79.14	18.98**	38.72	-18.98**	B
L_3	54.36	-9.28**	70.47	9.28**	A
L_4	67.97	3.11ns	59.31	-3.11ns	B
L_5	90.06	11.73**	64.14	-11.73**	B
L_6	72.47	0.29ns	69.44	-0.29ns	B
L_7	75.03	9.04**	54.5	-9.04**	B
L_8	62.89	-2.03ns	64.5	2.03ns	C
L_9	72.75	-15.93**	102.17	15.93**	A
L_{10}	51.61	8.58**	32	-8.58**	C
L_{11}	26.5	-27.50**	79.06	27.50**	A
Mean	67.04	3.01ns	76.22		

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