

RESEARCH PAPER

Studies on combining ability and identification of good single cross hybrids for grain yield and its component traits of maize (*Zea mays* L.)

K. L. NAVEEN KUMAR AND G. SHANTHAKUMAR

Department of Genetics and Plant Breeding, College of Agriculture
University of Agricultural Sciences, Dharwad - 580 005, Karnataka, India
E-mail: nkumar8074@gmail.com

(Received: January, 2017 ; Accepted: December, 2017)

Abstract: Thirty inbred lines were crossed with each of three testers in a line $\times$ tester design to evaluate combining ability and heterosis to identify promising hybrids of maize for various characters *viz.*, days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent dry husk, ear length, ear girth, number of kernels row per ear, number of kernel per row, hundred seed weight, shelling percentage and grain yield per hectare. The resulting F_1 s along with three checks and the parents were evaluated during summer 2013. Analysis of variance revealed highly significant differences among the genotypes. Crosses excelled their perspective parents in performance for most of the traits studied. DMIL767, DMIL318 and DMIL326 among the parental lines and DMIL011 among the testers were identified as the best general combiner for grain yield. Whereas among the hybrids, DMIL765 $\times$ DMIL031, DMIL318 $\times$ DMIL011 and DMIL639 $\times$ DMIL011 were identified as a potential cross combination for grain yield while the cross DMIL765 $\times$ DMIL031 recorded highest magnitude of economic heterosis of 13.95 percentages over the best standard check. So the crosses DMIL765 $\times$ DMIL031, DMIL318 $\times$ DMIL011 and DMIL639 $\times$ DMIL011 can be utilized for developing high yielding hybrid varieties as well as for exploiting hybrid vigor.

Key words: Combining ability, Hybrids, Genotypes, Heterosis

Introduction

Maize (*Zea mays* L.; $2n=20$) is one of the most important staple food crops in the world after wheat and rice and belongs to the family *Poaceae*. It is grown from 58° N latitude to 40° S latitude and at altitudes higher than 3000 m as also in areas with rainfall of 250 mm to more than 5000 mm per year (Chandrashekara *et al.*, 2014). Maize occupies an important position among the crops both as food and feed as well as raw material in industrial production starch, oil, protein, alcoholic beverages, recently biofuel, food sweeteners, pharmaceuticals, cosmetics, films, textiles, gums, package and paper industries *etc.* It is the most versatile photo insensitive crop with high adaptability hence maize is referred to as "Miracle Crop". Being a C_4 plant, it is physiologically more efficient, has higher grain yield potential compared to other grass family members and is also regarded as "Queen of Cereals" (Sandeep, *et al.*, 2012).

The concept of combining ability is landmark in the hybridization programme. Combining ability analysis is one of the effective approaches available for estimating the combining ability effects that helps in selecting desirable parents and crosses for the exploitation of heterosis. Knowledge on the nicking ability of genotypes in hybrid combination is of paramount importance, since the combining ability of parents and hybrids does not always depends on the per se performance. In order to identify potential cross combinations, it is very important to screen out the parent materials for their genetic diversity and combining ability. Line $\times$ Tester method is considered one of the effective ways for estimating the general and specific combining ability, hybrid vigor and gene action to select the inbred lines for the late generation (Kumar, *et al.*, 2012 and Talukder *et al.*, 2016). The present investigation was

carried out to determine the nature and magnitude of gene action and heterosis for yield and other important traits in maize.

Material and methods

The basic material for the present study comprised 33 parents that is, thirty diverse, vigorous and productive maize inbred lines *viz.*, DMIL218, DMIL233, DMIL247, DMIL130, DMIL136, DMIL318, DMIL326, DMIL466, DMIL145, DMIL147, DMIL152, DMIL497, DMIL516, DMIL559, DMIL561, DMIL606, DMIL630, DMIL639, DMIL655, DMIL688, DMIL699, DMIL703, DMIL736, DMIL749, DMIL762, DMIL765, DMIL767, DMIL769 and DMIL771 and three well adapted testers of varying genetic base *viz.*, DMIL011, DMIL021 and DMIL031 (Table 1). Hybridization among the genotypes has been done by line $\times$ tester method developed by Kempthorne, 1957, during anthesis as the tassels of male parent and the silks of females appeared, they were isolated and covered with special papers bag takes and butter to avoid self-pollination among them, crossing was done for all the genotypic materials (33 parents) the seeds of each hybrid and parent were harvested and dried to be used in summer 2012 at Main Agriculture Research Station (MARS), University of Agriculture Sciences (UAS), Dharwad to generate 90 hybrids.

These 90 hybrids and thirty three parental lines with three standard checks are, Super 900M, Bio-9681 and Arjun were grown in a randomized block design in three replications. Each entry was sown in two rows having 60×20 cm crop geometry. Data were recorded on randomly selected five plants in each replication for fourteen characters *viz.*, days to 50

Table 1. List of the pedigree of lines used in experiment

Sl. No.	Lines (females)	Pedigree	Sl. No.	Lines (females)	Pedigree
1	DMIL103	CML430×CML338-x-x-x-4	18	DMIL630	PINNACLE×K138-x-x-x-3
2	DMIL218	CML430×CML338-x-x-x-8	19	DMIL639	NK6240×NE1412-x-x-x-12
3	DMIL233	NK6240×CML412-x-x-x-4	20	DMIL655	CML430×CML338-x-x-x-3
4	DMIL247	NK6240×NE1412-x-x-x-11	21	DMIL688	25K45-5-1-4-139
5	DMIL130	PINNACLE×K132-x-x-x-7	22	DMIL699	PINNACLE×K326-x-x-x-14
6	DMIL136	PINNACLE×K132-x-x-x-14	23	DMIL703	NK6240×CML426-x-x-x-10-14
7	DMIL318	NK6240×CML412-x-x-x-5-6-7	24	DMIL736	VA-2-3-65
8	DMIL326	NK6240×CML412-x-x-x-10-12	25	DMIL749	CML460×CML338-x-x-x-8-4
9	DMIL466	25K60-5-1-4-139	26	DMIL762	CML430×CML338-x-x-x-4-12
10	DMIL145	M-IG8011-6-2-4-147	27	DMIL765	NK6240×NE1412-x-x-x-1-4
11	DMIL147	DMH8255-3-4-8-41	28	DMIL767	CML430×CML436-x-x-x-8-4
12	DMIL152	DMH8255-6-8-4-42	29	DMIL769	CML430×CML436-x-x-x-8-12
13	DMIL497	NK6240-6-8-15-8	30	DMIL771	NK6240×NE1412-x-x-x-6-11
14	DMIL516	NK6240-6-8-12-13	Tester (males)		
15	DMIL559	PINNACLE×K132-x-x-x-7-5	1	DMIL011	900M Gold x NEI- 004
16	DMIL516	NK6240×CML412-x-x-x-1-9	2	DMIL021	NS x 052030
17	DMIL606	VA-2-3-65	3	DMIL031	NK 640 XCML412

per cent tasseling, days to 50 per cent silking, days to 75 per cent dry husk, ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, test weight (g), shelling percentage and grain yield (q/ha). Combining ability and heterosis analysis was carried out according to formulae given by Kempthorne (1957) and Talukder *et al.*, 2016, through computer generated program, WINDOSTAT (edition 9.1).

Results and discussion

Analysis of variance to test the significance of difference among the genotypes (Table 2 and 3) revealed highly significant differences for all ten traits reflecting thereby presence of adequate diversity in the genetic material chosen for the study. Line × tester interactions were found to be significant for all the characters except days to 75 percent dry husk. The estimation of specific combining ability (SCA) variance were much higher for all the characters except for number of rows per ear and number of kernels per row as compare to the

respective general combining ability (GCA) variance (Table 4) implied the greater importance of non-additive gene effects in inheritance of grain yield and its component traits. These results were also supported by the earlier findings of Yousif, *et al.* (2011), Sandeep, *et al.* (2012), Senhorinho *et al.* (2015) and Talukder *et al.* (2016).

The analysis of combining ability effects revealed that none of the parents possessed desirable GCA effects for all the traits studied (Table 5). However, DMIL767 was found to have the highest positive and highly significant GCA effect for grain yield followed by DMIL218, DMIL318, DMIL326, DMIL152, DMIL639, DMIL699, DMIL749, DMIL765, DMIL767 and DMIL769. These parents also showed significant positive GCA effect and simultaneously possessed high mean value indicating that the per se performance of the parents could prove as a useful index for combining ability. Sundararajan, and Senthil Kumar (2011) and Talukder *et al.* (2016), also observed similar phenomenon. Regarding maturity related traits,

Table 2. Analysis of variance for yield and its components traits, of parents and hybrids of maize during summer

Source of variation	Replications	Parents	Females	Males	Females vs Males	Parent vs Crosses	Crosses	Error
Characters								
Df	1	32	29	2	1	1	89	122
Days to 50 per cent tasseling	13.67**	4.69**	4.80**	3.50	3.79	34.27**	2.29*	1.47
Days to 50 per cent silking	14.15**	4.43**	4.43**	4.50*	4.42	23.19**	2.02*	1.40
Plant height (cm)	9.6	1129.67**	1197.84**	604.41*	203.18	8290.83**	795.70**	128.24
Ear height (cm)	9.25	458.68**	495.82**	147.92	3.081	3332.22**	350.04**	80.69
Days to 75 per cent dry husk	0.04	1.46	1.26	0.50	9.20*	0.99	3.52**	1.41
Ear length (cm)	2.08	7.81	8.19	6.00	0.45	434.50**	8.85*	6.28
Ear girth (cm)	0.55	4.58 **	4.96 **	1.29	0.17	87.03 **	2.01	2.07
No. Kernels rows /Ear	2.34	2.42	2.34	2.00	5.45	44.94**	4.11*	2.90
No. Kernels /row	21.66	54.50*	47.46	164.67**	38.3	3058.04**	33.19	31.92
Test weight (g)	6.13	80.98**	78.37**	72.67**	173.30**	2707.31**	76.98**	9.93
Shelling percentage	2.72	279.40**	302.81**	38.55	82.45	14142.29**	59.68*	39.32
Grain yield (q/ha)	2.36	164.48**	175.41**	55.2	66.29	95798.89**	425.03**	18.94

* - Significant at 5% level

** - Significant at 1% level

Table 3. Estimates of variance components in respect of fourteen quantitative characters during summer 2013

Characters	σ^2_{GCA}	σ^2_{SCA}	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	σ^2_D	σ^2_A/σ^2_D
Days to 50 per cent tasseling	0.05	0.35	0.14	0.10	0.35	0.29
Days to 50 per cent silking	0.23 **	0.58**	0.40	0.47	0.58	0.81
Plant height (cm)	45.62 **	201.79**	0.22	90.33	201.78	0.45
Ear height (cm)	0.08**	0.62**	0.13	0.16	0.62	0.25
Days to 75 per cent dry husk	7.56**	83.64**	0.09	15.12	83.64	0.18
Ear length (cm)	0.16**	1.98**	0.08	0.31	1.98	0.16
Ear girth (cm)	-0.01	-0.18	0.06	-0.01	-0.18	0.06
No. of kernel rows per ear	0.02*	0.26**	0.08	0.03	0.26	0.11
No. of kernels per row	0.48**	-3.55	-0.14	0.97	-3.55	0.27
Test weight (g)	2.89**	22.49 **	0.19	5.79	22.49	0.26
Shelling percentage	0.56**	7.09**	0.19	5.79	22.49	0.15
Grain yield (q/ha)	11.93**	132.88 **	0.09	23.86	132.88	0.18

DMIL497 revealed the most desirable negative and significant value for tasseling and silking while DMIL639 revealed the most desirable negative and significant value for dry husk. The inbred DMIL103, DMIL497 and DMIL767 exhibited highest positive and significant *GCA* value for various yield related components *viz.*, ear length, number of rows per ear and number of kernels per row besides being a good general combiner for maturity traits. The lines with desirable *GCA* should be extensively used in the crossing programme to exploit maximum genetic variability.

A critical evaluation of the results with respect to specific combining ability effects showed that none of the cross combinations exhibited desirable significant *SCA* effects for all the characters. The estimates of specific combining ability analysis demonstrated various cross combinations having significant positive *SCA* effects (Table 6). The highest magnitude of desirable *SCA* effects for grain yield in q/ha was detected in DMIL318 x DMIL011 followed by DMIL136 x DMIL021, DMIL233 x DMIL011, DMIL247 x DMIL011 and DMIL703 x DMIL021 were regarded as good combiner these single cross hybrid were obtained from parents with low x high, high x low, high x low, low x low, low x high (Table 6). Mohamad, *et al.* (2007) and Talukder *et al.* (2016), also reported high positive specific combining ability effects along with high *per se* performance for grain yield. However for maturity related

traits, DMIL136 x DMIL031 showed the most desirable value for tasseling and silking while DMIL103 x DMIL031 and DMIL703 x DMIL021 were the most desirable value for test weight. The cross combination DMIL318 x DMIL011 was a good specific combiner for ear length. The superiority of crosses as parents could be explained on the basis of interaction between positive alleles from good combiners and negative alleles for the poor combiners as parents. The high yield of such crosses would be non-fixable and thus could be exploited for heterosis breeding.

All the crosses exhibited highly significant positive heterosis over mid parent and better parent for grain yield (Table 6). The cross combination DMIL765 x DMIL031 followed by DMIL318 x DMIL011 and DMIL699 x DMIL031 revealed magnitude of economic heterosis on far over the best check for grain yield in q/ha. Appreciable percentage of heterosis for grain yield in maize was also reported by Wali, *et al.* (2010), Kumar *et al.* (2010), Yusuf *et al.* (2009), and Singh *et al.* (2012). In another study, Amiruzzaman *et al.* (2013), and Talukder *et al.* (2016), observed 13.95 to 245.10% and -16.42 to 71.82% heterobeltiosis, respectively. The cross combination DMIL103 x DMIL011, DMIL233 x DMIL011 and DMIL145 x DMIL021 showed the most desirable value for heterosis for days to 50 per cent tasseling and silking. However the cross DMIL103 x DMIL031 and DMIL655 x DMIL021 revealed maximum

Table 4. Analysis of variance for combining ability of inbreds and hybrids of maize evaluated during summer 2013

Source of variation characters	Replications	Crosses	Females (Lines)	Males (Testers)	Females vs male	Error
df	1	89	29	2	58	89
Days to 50 per cent tasseling	10.27	19.09	19.26	14.74	19.15	19.06
Days to 50 per cent silking	0.356	3.943 **	5.825 **	12.689 *	2.700 **	1.502
Plant height (cm)	5.83	795.71 **	1240.64 **	1997.04 *	531.82 **	166.32
Ear height (cm)	5.77	350.04 **	572.22**	88.19	247.98 **	104.19
Days to 75 per cent dry husk	2.94	3.52 **	5.32 *	2.69	2.65 **	1.31
Ear length (cm)	0.01	6.51 **	7.84	6.27	5.84 **	2.14
Ear girth (cm)	0.69	2.01 **	2.69	1.06	1.70	1.73
No. Kernels rows /ear	0.8	3.65 **	4.87	1.16	3.13 **	1.65
No. Kernels /row	57.81 *	45.53 **	43.81	60.15	45.89 **	12.92
Test weight (g)	0.01	19.44 **	18.75	5.54	20.26 **	5.84
Shelling percentage	0.52	61.34 **	82.58 *	126.73	48.46 **	8.48
Grain yield (q/ha)	13.05	682.62 **	673.78	797.23	683.09 **	7.67

* - Significant at 5% level

** - Significant at 1% level

Table 5. Estimates of general combining ability effects of parents for fourteen traits of maize evaluated during summer 2013

Parents	Days to 50 per cent tasseling	Days to 50 per cent silking	Plant height (cm)	Ear height (cm)	Days to 75 per cent dry husk	Ear length (cm)	Ear girth (cm)	No. of Kernels rows/ear	No. of Kernels / row	Test weight (g)	Shelling percentage	Grain yield (q/ha)
DMIL103	-0.40	-0.16	5.34	6.64	1.46 **	4.07 **	0.30	-1.72 *	0.63	11.53 **	-0.28	-0.62
DMIL218	0.13	0.34	28.79	9.09	-0.87	1.49	0.91	-0.72	1.30	1.77	0.11	5.09 **
DMIL233	-0.23	-0.66	9.29	2.88	-2.21 **	-0.36	-0.02	-0.39	0.97	0.24	0.19	-7.16 **
DMIL247	-0.07	0.05	-28.27 **	-16.91 **	-0.37	-0.84	-1.08	-0.72	-0.87	2.54	3.97	-13.51 **
DMIL130	-0.07	0.34	9.81	4.84	0.29	-1.59	-0.37	-0.72	-2.87	1.30	-4.99	-0.76
DMIL136	0.43	0.34	8.76	23.29 **	0.29	-0.51	0.87	-0.39	-1.87	-0.23	-5.90 *	-8.93 **
DMIL318	-0.07	0.18	-5.82 **	-3.47	0.13	0.99	0.67	1.28	2.97	5.94 **	1.73	11.94 **
DMIL326	0.60	0.34	0.49	-2.46	0.46	0.32	-1.02	-1.06	4.13	-0.90	0.95	8.03 **
DMIL466	-0.57	-0.82	7.09	-6.39	0.79	1.37	-0.12	0.94	2.97	-1.05	1.87	-6.97 **
DMIL145	-1.07 *	-0.99 *	-11.42 **	-1.92	-1.21 *	-0.97	-1.43 *	-0.06	-1.37	-1.80	-2.61	-9.15 **
DMIL147	-0.57	-0.49	-11.09 **	-6.957	0.46	-1.55	0.75	1.61 *	-3.03	-5.86 **	-11.94 **	-11.72 **
DMIL152	0.27	0.34	-7.89 **	-2.057	1.29 **	-1.35	0.83	0.28	-3.70	-4.10 **	-1.04	6.18 **
DMIL497	-1.08 *	-1.16 *	-10.37 **	-11.29 *	-0.37	-2.09 *	-0.18	2.28 **	-5.37 *	-8.40 **	-2.20	-11.37 **
DMIL516	-0.73	-0.32	-19.22 **	-10.39 *	0.29	-0.95	-0.23	-0.06	-0.87	-8.16 **	-4.44	-8.61 **
DMIL559	-0.95	-0.82	-43.47 **	-11.87 *	-0.37	-0.09	0.27 *	1.28	2.13	5.54 **	-1.11	2.59
DMIL561	0.43	0.34	-22.29 **	-20.24 **	-0.71	-1.01	-0.97	-1.72 *	-1.20	3.80 **	1.70	-16.63 **
DMIL606	1.10 *	1.01 *	-19.35 **	-15.09 **	-1.04 *	-0.18	-0.65	0.28	2.97	-4.46 **	4.88	-10.24 **
DMIL630	0.27	0.01	-18.17 **	-8.26	-0.37	0.41	-0.37	-0.06	0.30	0.37	4.29	-4.24 *
DMIL639	-0.57	-0.66	-10.79 **	-13.97 **	-2.37 **	-1.34	0.05	-0.06	-5.37 *	2.60 *	2.08	9.68 **
DMIL655	0.767	0.68	0.16	-2.89	-0.21	-2.18 *	-0.25	0.94	-1.20	-4.67 **	1.63	-0.33
DMIL688	1.27 *	0.84	2.16	-3.47	1.29 **	-1.18	-0.37	-0.72	-2.03	0.60	-0.18	-11.26 **
DMIL699	0.27	0.34	35.21	24.64 **	0.46	0.74	0.30	0.28	3.13	-0.03	-2.09	5.06 **
DMIL703	0.10	0.68	21.01	11.26 *	0.79	-1.56	-0.97	-0.72	-2.03	-2.06	1.08	-8.86 **
DMIL736	-1.08 *	-0.99 *	10.91	13.41 **	0.63	-0.39	0.25	-1.06	0.13	2.74 *	-0.80	3.37
DMIL749	0.10	0.18	5.86	9.08	-0.37	1.82	0.067	0.94	1.80	-1.30	1.64	18.29 **
DMIL762	0.77	1.01 *	39.03	24.29 **	1.13 *	0.49	0.35	-1.06	0.13	8.00 **	0.82	-3.64 *
DMIL765	-0.57	-0.66	3.41	11.31 *	0.79	1.47	0.25	0.61	1.30	3.50 **	2.78	23.11 **
DMIL767	0.77	0.34	11.81	3.64	-0.71	1.94	0.67	-0.06	6.63 **	-2.93 *	2.89	23.94 **
DMIL769	0.27	0.18	12.03	-4.12	0.13	1.00	0.72	0.94	-3.03	-3.36 *	0.99	0.47
DMIL771	0.43	0.18	-2.98	-2.62	0.46	2.07 *	0.52	-0.39	3.30	-1.10	3.97	16.26 **
S.Em±	0.49	0.48	6.60	5.03	0.49	1.02	0.59	0.69	2.31	1.29	2.56	1.78
C.D. at 5% female	0.98	0.96	82.44	10.00	0.96	2.03	1.17	1.38	4.58	2.56	5.09	3.53
C.D. at 1% female	1.30	1.27	17.37	13.25	1.28	2.69	1.55	1.83	6.07	3.39	6.74	4.68
DMIL011	-0.28	-0.31 *	1.02	0.58	0.12	-0.30	-0.13	-0.02	0.00	-0.62	-0.70	0.71
DMIL021	0.10	0.16	-2.71 **	-1.33	0.24	-0.19	0.14	0.14	-0.88	-0.80	0.93	-1.47 *
DMIL031	0.18	0.14	1.69	0.75	0.12	0.50	-0.01	-0.12	0.88	1.42 **	-0.24	0.76
S.Em±	0.15	0.15	2.09	1.59	0.15	0.32	0.19	0.22	0.73	0.41	0.81	0.56
C.D. at 5% male	0.31	0.30	26.07	3.16	0.30	0.64	1.17	0.44	1.45	0.81	1.61	1.12
C.D. at 1% male	0.41	0.40	5.49	4.19	0.40	0.85	1.55	0.59	1.92	1.07	2.13	1.48

* - Significant at 5% level

** - Significant at 1% level

** - Significant at 0

Table 6. Top three desirable hybrids with per se performance, heterosis and their sca effects, gca status of parents for fourteen characters of maize evaluated during summer 2013

Characters	Desirable crosses				Per se		Heterosis			sca effects	Gca status
	Female	Male	F ₁	MP	BP	SH					
Days to 50 percent tasseling	DMIL 103 x DMIL 011	59.00	56.50	-3.00	-4.24*	-5.04*	Low x High	-1.22	Low x High		
	DMIL 233 x DMIL 011	59.00	56.50	-2.16	-4.24*	-5.04	Low x High	-1.38	Low x High		
	DMIL 145 x DMIL 021	59.50	56.50	-3.83*	-5.04*	-5.04*	Low x Low	-0.93	Low x Low		
Days to 50 percent silking	DMIL 103 x DMIL 011	60.00	58.00	-2.11	-3.33	-4.92*	Low x High	-1.53	Low x High		
	DMIL 233 x DMIL 011	60.00	58.00	-1.69	-3.33	-4.92*	Low x High	-1.03	Low x High		
	DMIL 145 x DMIL 021	61.50	58.00	-3.73*	-5.69*	-4.92*	Low x Low	-1.16	Low x Low		
Plant height (cm)	DMIL 771 x DMIL 031	178.25	238.50	46.93	33.80	33.14	High x High	0.62	High x High		
	DMIL 762 x DMIL 011	132.25	229.20	61.84**	51.79**	31.72**	Low x High	0.96	Low x High		
	DMIL 699 x DMIL 011	132.25	222.70	61.32**	54.81**	27.99**	Low x High	1.12	Low x High		
Ear height (cm)	DMIL 247 x DMIL 021	88.40	38.25	-49.72*	-56.73**	-59.49**	Low x Low	-27.33**	Low x Low		
	DMIL 561 x DMIL 031	102.75	49.40	-48.94*	-51.92**	-47.95**	Low x High	-0.25	Low x High		
	DMIL 145 x DMIL 021	88.40	61.90	-19.48	-29.98*	-34.83**	Low x Low	-18.66*	Low x Low		
Days to 75 per cent dry husk	DMIL 639 x DMIL 031	88.00	83.95	-5.08**	-5.62**	-6.15**	Low x Low	-2.54**	Low x Low		
	DMIL 561 x DMIL 011	88.50	86.50	-3.35**	-4.42**	3.35*	Low x High	-1.71*	Low x High		
	DMIL 233 x DMIL 021	87.50	86.50	-1.70	-2.26	-3.35*	Low x Low	-0.58	Low x Low		
Ear length (cm)	DMIL 103 x DMIL 031	12.50	23.50	70.91	56.67	14.63	Low x High	1.17	Low x High		
	DMIL 318 x DMIL 011	15.50	22.50	44.00	42.86	9.76	Low x High	4.05*	Low x High		
	DMIL 767 x DMIL 011	15.50	22.10	55.09	42.58	7.80	High x High	2.70	High x High		
Ear girth (cm)	DMIL 559 x DMIL 021	13.10	17.75	36.80**	35.50**	14.52	High x Low	1.41	High x Low		
	DMIL 147 x DMIL 021	13.10	17.65	31.72**	28.83**	13.87**	Low x Low	1.83	Low x Low		
	DMIL 136 x DMIL 021	13.10	16.75	23.30*	18.73	8.39	Low x Low	0.86	Low x Low		
Number of rows per ear	DMIL 655 x DMIL 021	15.00	18.00	28.57**	20.00	12.50	Low x Low	1.86	Low x Low		
	DMIL 497 x DMIL 021	15.00	18.00	21.43*	21.43*	13.33	Low x Low	0.52	Low x Low		
	DMIL 749 x DMIL 011	14.00	18.00	28.57**	28.57*	12.50	High x High	2.02	High x High		
Number of kernels per row	DMIL 767 x DMIL 011	16.00	46.50	106.67**	60.34**	25.68	High x High	3.83	High x High		
	DMIL 318 x DMIL 011	16.00	44.50	111.63**	68.52**	22.97	Low x High	6.50	Low x High		
	DMIL 326 x DMIL 031	27.00	45.00	91.49**	66.67**	21.62	Low x High	3.95	Low x High		
Test weight (g)	DMIL 103 x DMIL 031	39.60	58.50	56.36**	47.68**	93.00**	Low x High	9.90**	Low x High		
	DMIL 762 x DMIL 031	39.60	46.90	36.54**	18.43*	54.79**	Low x High	1.85	Low x High		
	DMIL 559 x DMIL 031	39.60	44.50	27.45**	14.90	15.17**	High x High	2.91	High x High		
Shelling percentage	DMIL 703 x DMIL 011	65.39	86.04	27.40**	23.49*	14.21	Low x High	6.64	Low x High		
	DMIL 247 x DMIL 011	65.39	85.84	43.26**	31.27**	13.95	Low x High	3.55	Low x High		
	DMIL 233 x DMIL 021	61.06	85.68	32.45**	25.41**	13.74	Low x Low	5.55	Low x Low		
Grain yield per ha (q/ha)	DMIL 765 x DMIL 031	24.71	108.91	483.89**	340.84**	13.95**	High x High	12.91**	High x High		
	DMIL 318 x DMIL 011	34.07	108.08	270.14**	217.28**	13.08**	Low x High	23.31**	Low x High		
	DMIL 699 x DMIL 031	24.71	107.20	442.64**	293.44**	1.69	Low x High	19.24**	Low x High		

positive and highly significant heterosis for ear length and number of kernel rows per ear. the cross combinations DMIL559 x DMIL021, DMIL767 x DMIL011 and DMIL703 x DMIL011 were recorded the highly significant heterosis for ear girth, number of kernels per row and shelling percentage, respectively. For hundred seed weight, the cross combination DMIL103 x DMIL031 followed by DMIL762 x DMIL031 showed highest magnitude of economic heterosis. Most crosses showing significant positive SCA effect and highest magnitude of economic heterosis for grain yield involved DMIL011 and DMIL031 as testers.

Conclusion

The good combiners, DMIL767, DMIL318 and DMIL326 among the parental lines and DMIL011 among the testers were identified as the best general combiner for grain yield, hence

these lines can be used for the future hybrid breeding development programme and these promising crosses were identified as overall high general combiners and these could be utilized for development of either the synthetic varieties or an elite breeding population by allowing thorough mixing among them to achieve new genetic recombination and then subjecting the resultant population to recurrent selection. Whereas among the hybrids, DMIL765 x DMIL031, DMIL318 x DMIL011 and DMIL639 x DMIL011 were identified as a potential cross combination for grain yield while the cross DMIL765 x DMIL031 have highest magnitude of economic heterosis percentages over the best standard check. So the crosses DMIL765 x DMIL031, DMIL318 x DMIL011 and DMIL639 x DMIL011 can be utilized for developing high yielding hybrid varieties as well as for exploiting hybrid vigor.

References

- Amiruzzaman, M., Islam, M. A., Hassan, L., Kadir, M. and Rohman, M. M., 2013, Heterosis and combining ability in a diallel among elite inbred lines of maize (*Zea mays* L.). *Emir. J. Food Agri.*, 25 (2) : 132-137.
- Chandrashekara, C., Jha, S. K., Arunkumar, R. and Agrawal, P. K., 2014, Identification of new sources of resistance to *turicum* leaf blight and maydis leaf blight in maize (*Zea mays* L.). *Sabao J. Breed. and Genetics*, 46 (1): 44-55.
- Kemphorne, O., 1957, An introduction to genetic statistics. John Willy and Sons, New York.
- Kumar, T. S., Mohan Reddy, D., SaidaNaik, V., IshaParveen, S., and Subbaiah, 2012, Gene action for yield and morpho-physiological traits in maize (*Zeamays* L.) inbred lines. *J. Agric. Sci.*, 4: 13-16.
- Mohamad, A. A., Mohamad Amin, A. N. and Towfiq, S. I., 2007, Estimation of hetrosis, general and specific combining ability using diallel cross in maize (*Zea mays* L.). *Mesopotamia J. Agric.*, 35(3) : 307-316.
- Sandeep, K. T., Mohan, R. D., Saida, N. V., Isha, P. S. and Subbaiah, P. V., 2012, Gene action for yield and morpho-physiological traits in Maize (*Zea mays* L.) Inbred Lines. *J. Agric. Sci.*, 4(5) : 13-16.
- Senhorinho, H.J.C., Pinto, R.J.C., Scapim, C. A., Milani, K.F. and Nihei, N.H., 2015, Combining abilities and inbreeding depression in commercial maize hybrids. *Seminar: Ciencias Agrárias, Londrina*, 36(6): 4133-4150.
- Singh, P. K., Singh, A. K., Shahi, J. P. and Ranjan, R., 2012, Combining ability and heterosis in quality protein maize. *The Bioscan.*, 7(2) : 337-340.
- Sundararajan, R. and Senthil Kumar P., 2011, Studies on heterosis in maize (*Zea mays* L.). *Plant Archives.*, 11(1) : 55-57.
- Talukder, M.Z.A., Karim, A.N.M.S., Ahmed, S. and Amiruzzaman, M., 2016, Combining ability and heterosis on yield and its component traits in maize (*Zea mays* L.). *Bangladesh J. Agril. Res.*, 41(3): 565-577.
- Wali, M. C., Kachapur, R. M., Chandrashekar, C. P., Kulkarni, V. R. and Devaranavadagi, S. B., 2010, Gene action and combining ability studies in single cross hybrids of maize (*Zea mays* L.). *Karnataka J. Agric. Sci.*, 23(4) : 557-562.
- Yousif, M. A. and Sedeeq, F. A. Q., 2011, Estimation of combining ability for plant and ear height in Maize. *Tikrish J. Pure Sci.*, 16 (4) : 11- 13.
- Yusuf, M., Ado, S. G. and Ishiyaku, M. F., 2009, Heterosis in single crosses of quality protein maize inbred lines. *Afr. Crop Sci. Conf. Proc.*, 9 : 439 – 445.