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Combining ability and gene action analysis for yield and yield attributing traits in maize (*Zea mays* L.)

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Abstract
In present study forty-five crosses produced from 9 lines and 5 testers using line × tester mating design were evaluated in Randomized Block Design. Estimation of general combining ability (GCA) gives important information for the selection of parents in terms of performance of hybrids and elucidate the nature and magnitude of gene action involved in the expression of quantitative characters. Present study was caried out to determine the type of gene action and identify inbred lines and crosses with good combining ability for yield and its contributing traits. Variance due to specific combining ability (SCA) was larger than general combining ability (GCA) for the all characters except plant height and ear height. It indicates the preponderance of non-additive gene action in expression of those character except plant height and ear height. Inbred lines WNC 40406 followed by BLD 2, BLD 125 and WNC 40080 showed good combining ability (*gca*) effect for yield and some of the important yield contributing characters. Among Forty-five hybrids, BLD 2 × BLD 103, WNC 40406 × BLD 125, BLD 114 × IMR 113, WNC 40456 × IMR 113 and BLD 114 × BLD 98 exhibited high specific combining ability (*sca*) effects for yield. These hybrids are recommended for further evaluation to determine their performance.

Keywords: Line × tester, combining ability, gene action, maize (*Zea mays* L.)

Introduction
Among the cereal crops, Maize (*Zea mays* L.) is one of the most important cereal crop and it occupies a prominent position in global agriculture after wheat and rice. Maize (2n = 2x = 20) belongs to the family *Poaceae.* It was domesticated over the past 10,000 years from the grass teosinte in Central America and has been subject to cultivation and selection (Doebley *et al*. 2006) [3]. In addition to staple food for human being and quality feed for animals, maize serves as a basic raw material to the industry for production of starch, oil, protein, alcoholic beverages, food sweeteners and more recently bio-fuel. Combining ability analysis is an important tool for selecting parents with good general combining ability and these parents can be used for hybridization program in order to produce superior hybrids. It also helps in understanding the nature of gene action of a particular character. General combining ability (GCA) is due to result of additive gene effects, while the specific combining ability (SCA) is due to result of non-allelic interactions (Jinks, 1954) [5]. The estimate of combining ability is useful to predict the relative performance of different lines in hybrid combinations. The information on the magnitude of gene action is important in understanding the genetic potential of a population and deciding the breeding procedure to be adopted in a given population.

Materials and Methods
Plant materials: The experimental material consisted 60 entries having 45 hybrids produced from line × tester mating design which involved 14 parental lines (9 lines and 5 testers) with a standard check GAYMH 1.

Field experiments: The above mentioned experimental material was evaluated in Randomized Block Design with three replications in *kharif* 2020 at Maize Research Station, Sardarkrushinagar Dantiwada Agricultural University, Bhiloda. Seeds were sown in two rows of four meters length. In this experiment, the spacing of 60 cm between the rows and 20 cm between the plants was maintained. All the plant protection and agronomic practices applicable for maize crop were adopted as per crop production guide.

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Different thirteen observations were recorded *viz.*, days to tasseling (days), days to silking (days), anthesis-silking interval (days), days to maturity, plant height (cm), ear height (cm), cob length (cm), cob girth (cm), kernels row per cob, kernels per row, 100 kernel weight (g), kernels yield per plant (g) and shelling percentage (%). All the observations were recorded from randomly selected five plants from each genotype in each replication.

Statistical analysis: The mean performance of each parent and hybrid was subjected to statistical analysis. Analysis of variance to test the significance for all traits was carried out as per methodology given by Panse and Sukhatme (1985) [8]. Combining ability analysis for parents and their crosses (line × tester method) was conducted as per methodology given by Kempthorne (1957) [6].

Result and Discussion
The results of analysis of variance are presented in Table 1. It revealed highly significant differences due to genotypes for all the characters under study. This indicating a high degree of variability in the material. The presence of significant differences among parents showed greater diversity in the fourteen parental lines. Similarly, in case of hybrids, significant differences were found for all the traits under study.

The study of *per cent* contribution of line, tester and hybrid (Table 2) revealed that among the parents, female parent contributed more to total variance for all traits except plant height, ear height and kernels per row. While, comparative study of *per cent* contribution of parents and hybrids to total variance indicates, the hybrids contributed more to total variance for majority of characters except plant height, ear height and days to maturity. Whereas, for character *viz.*, plant height, ear height and days to maturity parental contribution is more than the hybrid to the total variance.

The ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ was less than unity for majority of the characters except plant height and ear height. If the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ was less than unity than it indicates non-additive component of genetic variance was predominantly involved in expression of character. In this study for plant height and ear height, the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ was found more than unity, suggesting a greater role of additive genetic variance in the inheritance of this trait.

Among all the parental genotypes under study WNC 40406, BLD 2, WNC 40080 and BLD 125 were reported good general combiner for kernel yield per plant (Table 3). Apart from the yield, the genotype WNC 40406 was good general combiner for days to silking, anthesis silking interval and kernels per row. While genotype BLD 2 was also found good general combiner for anthesis silking interval, cob length, kernels row per cob, 100 kernels weight and shelling percentage.

Specific combining ability effects for each cross are presented in Table 4. Out of 45 crosses under study, 14 crosses were showed significant and positive *sca* effect for kernel yield per plant. The crosses *viz.*, BLD 2 × BLD 103, WNC 40406 × BLD 125, BLD 114 × IMR 113, WNC 40456 × IMR 113 and BLD 114 × BLD 98 were considered as good specific combiner on their *sca* effects. Therefore, in such crosses desirable transgressive segregants would be expected in the subsequent generation. These results of GCA and SCA were in accordance with Amiruzzaman *et al.* (2013) [1], Habtamu zeleke (2015) [4], Ram *et al.* (2015) [10], Kumar *et al.* (2016) [7], Yerva *et al.* (2016) [11], Bharti *et al.* (2017) [2] and Rajesh *et al.* (2018) [9].

Out of 45 hybrids, for days to tasselling, anthesis-silking interval and ear height number of crosses found significant in desired direction were two. While, for days to silking (3), plant height (1), days to maturity (5), cob length (4), cob girth (1), kernels row per cob (6), kernels per row (8), 100 kernel weight (9), kernels yield per plant (14) and shelling percentage (6) hybrids exhibited significant SCA in desired direction. The crosses found good specific combiner for kernel yield per plant were also reported either good or average specific combiners for its yield contributing traits.

In present study, overall result concluded that among all the parental genotype WNC 40406, BLD 2, BLD 125 and WNC 40080 were reported good general combiner for kernel yield plant and its component traits. This may be useful in future breeding programme. The crosses BLD 2 × BLD 103, WNC 40406 × BLD 125, BLD 114 × IMR 113, WNC 40456 × IMR 113 and BLD 114 × BLD 98 were found most promising for kernel yield per plant and its component traits. Considering their *per se* performance and *sca* effects, there would be a chance of getting good transgressive segregant in future breeding programme.

Table 1: Analysis of variance (mean sum of square) for combining ability and estimates of components of variance for various characters

Source of variation	d.f.	DT	DS	ASI	PH	EH	DM	CL	CG	KR/C	K/R	SI	KY/P	Shelling (%)
Replications	2	21.65**	25.62**	1.09	1905.64**	390.99**	5.34	5.7**	5.44**	5.1**	27.48**	21.09**	589.86**	4.6
Hybrid (Crosses)	44	4.07**	5.45**	0.83**	247.01*	160.95**	9.22**	1.87**	0.52**	1.79**	6.77**	22.88**	474.63**	22.17**
Female in hybrid	8	7.22**	5.98**	1.03*	289.24	222.54**	23.59**	2.53**	0.62*	3.99**	7.75**	56.5**	601.03**	20.05**
Male in hybrid	4	2.67	6.34*	1.06*	1052.45**	547.07**	10.42**	3.75**	0.67*	1.3**	16.17**	7.72**	473.03**	12.77
Females × Males (L × T)	32	3.45**	5.2**	0.76*	135.77	97.29	5.47**	1.47**	0.48**	1.3**	5.35**	16.37**	443.24**	23.87**
Error	88	1.74	2.08	0.4	145.97	68.27	1.87	0.34	0.24	0.27	1.35	2.12	25.26	5.38
Components of variance														
σ^2 Females		0.25	0.05	0.02	10.23	8.35*	1.21**	0.07	0.01	0.18*	0.16	2.67**	10.52	-0.25
σ^2 Males		-0.03	0.04	0.01	33.95**	16.66**	0.18	0.08	0.01	-0.001	0.40*	-0.32	1.10	-0.41
σ^2_{gca}		0.07	0.05	0.01	25.48**	13.69**	0.55**	0.08*	0.01	0.06	0.31*	0.75	4.47	-0.36
σ^2_{sca}		0.57**	1.04**	0.12*	-3.4	9.67	1.20**	0.37**	0.08**	0.34**	1.33**	4.75**	139.33**	6.16**
σ^2_{gca} / σ^2_{sca}		0.12	0.04	0.12	-7.49	1.41	0.46	0.21	0.10	0.19	0.24	0.16	0.03	-0.06
* and ** indicate level of significance at 5% and 1%, respectively														

Table 2: Percent contribution of lines, testers and their interactions to total variance

Percent contribution	DT	DS	ASI	PH	EH	DM	CL	CG	KR/C	K/R	SI	KY/P	Shelling (%)
Female	32.29	19.97	22.55	21.29	25.14	46.54	24.64	21.63	40.48	20.81	44.90	23.02	16.44
Male	5.98	10.58	11.52	38.73	30.90	10.28	18.25	11.74	6.59	21.71	3.07	9.06	5.24
L × T (Hybrid)	61.74	69.45	65.94	39.98	43.96	43.18	57.11	66.63	52.93	57.48	52.03	67.92	78.32

(DT = Days to tasseling, DS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, DM = Days to maturity, CL = Cob length, CG = Cob girth, KR/C = Kernels row per cob, K/R = Kernels per row, SI = 100 kernels weight, KY/P = Kernel yield per plant, Shelling (%) = Shelling percentage.

Table 3: The estimates of general combining ability (*gca*) effects of the parents for various characters in maize

Parents	Days to tasseling	Days to silking	ASI	Plant height (cm)	Ear height (cm)	Days to maturity	Cob length (cm)	Cob girth (cm)	Kernels row per cob	Kernels per row	100 kernels weight (g)	Kernel yield per plant	Shelling (%)
Female parents (Lines)													
BLD 2	1.07**	0.62	-0.40*	-4.42	-1.36	0.87*	0.69**	0.12	0.55**	0.40	1.84**	7.71**	1.26*
BLD 109	-0.39	-0.11	0.27	3.65	8.70**	-1.86**	-0.38*	0.14	0.25	-1.11**	3.24**	0.88	-2.48**
BLD 114	0.54	0.82*	0.27	7.23*	1.70	0.87*	-0.21	-0.28*	-0.23	-0.55	1.11**	2.39	0.93
WNC 40080	0.61	0.69	0.07	-2.75	-2.90	-0.79*	-0.23	-0.03	0.89**	-0.32	-2.49**	5.31**	1.14
WNC 40324	-0.66	-0.64	0.00	-3.62	-2.43	-1.53**	0.18	0.24	0.28*	-0.88**	-0.89*	-7.54**	-0.64
WNC 40406	-0.46	-0.78*	-0.33*	-4.49	-3.03	0.34	-0.44**	0.19	-0.68**	0.64*	-1.09**	7.84**	0.15
WNC 40456	0.01	-0.18	-0.13	1.31	-2.23	1.54**	0.41**	0.11	-0.41**	0.65*	-2.22**	-3.54**	-0.14
WNC 52313	0.34	0.29	-0.07	-1.75	-1.30	-0.73*	-0.35*	-0.23	-0.31 *	0.46	-0.69	-8.80**	0.25
WNC 52646	-1.06**	-0.71	0.33*	4.85	2.84	1.27**	0.33*	-0.25*	-0.33 *	0.72*	1.18	-4.25**	-0.48
S.Em. ±	0.34	0.37	0.16	3.12	2.13	0.35	0.15	0.12	0.13	0.30	0.37	1.31	0.60
Male parents (Testers)													
VL 109178	0.03	-0.10	-0.15	-5.79**	-4.87**	-0.80**	0.14	0.08	0.04	0.46*	-0.56*	-2.83**	0.97*
BLD 98	-0.30	-0.33	-0.04	-7.31**	-4.94**	0.01	-0.61**	-0.13	-0.23*	-1.25**	0.70*	-3.51**	-0.75
BLD 103	0.14	0.34	0.19	1.91	3.73*	-0.02	-0.07	-0.21*	-0.18	0.12	0.22	-0.55	0.16
BLD 125	0.44	0.64*	0.22	6.76**	2.50	0.94**	0.20	0.10	0.05	-0.09	-0.52	7.03**	-0.58
IMR 113	-0.30	-0.55	-0.22	4.43	3.58*	-0.13	0.34**	0.15	0.32**	0.77**	0.15	-0.14	0.20
S.Em. ±	0.25	0.28	0.12	2.32	1.59	0.26	0.11	0.09	0.10	0.22	0.28	0.98	0.45

Note: * and ** indicate level of significance at 5% and 1%, respectively

Table 4: The estimates of specific combining ability (*sca*) effects of the crosses for various characters

Sr. No.	Crosses	Days to tasseling	Days to silking	ASI	Plant height	Ear height	Days to maturity	Cob length
1.	BLD 2 × VL 109178	0.70	0.64	-0.12	10.46	5.40	-0.13	-0.13
2.	BLD 2 × BLD 98	-0.96	-0.81	0.10	-6.69	-2.86	-2.28**	-0.65
3.	BLD 2 × BLD 103	1.93*	2.53**	0.55	-2.91	-2.53	0.76	0.58
4.	BLD 2 × BLD 125	-1.04	-1.77*	-0.49	-3.42	-3.64	0.13	0.25
5.	BLD 2 × IMR 113	-0.63	-0.59	-0.04	2.57	3.62	1.53	-0.05
6.	BLD 109 × VL 109178	0.84	0.04	-0.79*	-13.94*	-0.00	-1.07	-0.01
7.	BLD 109 × BLD 98	1.50	1.93*	0.44	-10.42	-12.59**	1.12	0.18
8.	BLD 109 × BLD 103	-0.94	-1.07	-0.12	6.69	2.07	-0.84	0.04
9.	BLD 109 × BLD 125	-0.24	0.30	0.51	9.18	8.96	0.19	-0.45
10.	BLD 109 × IMR 113	-1.16	-1.19	-0.04	8.50	1.56	0.60	0.23
11.	BLD 114 × VL 109178	0.57	0.10	-0.45	2.14	-6.00	-0.80	-0.33
12.	BLD 114 × BLD 98	-0.10	-0.01	0.10	-5.01	0.41	0.39	1.10**
13.	BLD 114 × BLD 103	-0.21	-0.34	-0.12	7.43	7.07	0.09	0.17
14.	BLD 114 × BLD 125	-1.17	-0.97	0.18	-0.81	5.96	0.79	-1.09**
15.	BLD 114 × IMR 113	0.90	1.21	0.29	-3.75	-7.44	-0.47	0.16
16.	WNC 40080 × VL 109178	-0.83	-0.43	0.41	2.12	0.27	0.20	-1.13**
17.	WNC 40080 × BLD 98	-0.16	-0.21	-0.03	6.64	9.34	-0.95	1.35**
18.	WNC 40080 × BLD 103	-0.27	0.13	0.41	-0.25	-3.33	0.42	-0.04
19.	WNC 40080 × BLD 125	1.76*	1.83*	0.04	-3.09	-2.77	1.46	-0.11
20.	WNC 40080 × IMR 113	-0.50	-1.32	-0.84*	-5.43	-3.51	-1.13	-0.08
21.	WNC 40324 × VL 109178	0.77	1.57	0.81*	2.66	3.47	1.60*	1.47**
22.	WNC 40324 × BLD 98	-1.90*	-2.54**	-0.63	-0.82	-2.46	-1.21	-0.03
23.	WNC 40324 × BLD 103	0.33	0.13	-0.19	9.29	3.54	-0.18	-0.33
24.	WNC 40324 × BLD 125	1.03	1.16	0.11	-10.89	-10.24*	0.19	-1.00**
25.	WNC 40324 × IMR 113	-0.23	-0.32	-0.11	-0.23	5.69	-0.40	-0.11
26.	WNC 40406 × VL 109178	0.24	0.04	-0.19	3.52	1.73	0.07	-0.25
27.	WNC 40406 × BLD 98	0.24	-0.07	-0.30	5.04	0.14	-1.41	-0.35
28.	WNC 40406 × BLD 103	-1.54*	-1.74*	-0.19	-3.85	1.14	-1.71*	-0.46
29	WNC 40406 × BLD 125	-0.17	-0.37	-0.22	-3.36	-5.30	0.66	0.60
30	WNC 40406 × IMR 113	1.24	2.15*	0.89*	-1.36	2.29	2.40**	0.45

31	WNC 40456 × VL 109178	-1.23	-0.56	0.61	-4.94	0.27	1.20	0.10
32	WNC 40456 × BLD 98	1.44	1.33	-0.16	3.58	1.01	1.72*	-0.93**
33	WNC 40456 × BLD 103	-0.01	-0.34	-0.39	-3.31	-5.99	0.76	-0.54
34	WNC 40456 × BLD 125	-0.64	-1.30	-0.76*	2.18	3.56	-1.87*	1.68**
35	WNC 40456 × IMR 113	0.44	0.88	0.69	2.50	1.16	-1.80*	-0.30
36	WNC 52313 × VL 109178	-0.23	-0.36	-0.12	-1.21	-8.00	0.13	0.09
37	WNC 52313 × BLD 98	-0.23	-0.47	-0.23	-0.36	1.74	1.32	-0.30
38	WNC 52313 × BLD 103	1.33	1.53	0.21	-2.91	0.07	-0.98	0.31
39	WNC 52313 × BLD 125	0.03	0.56	0.51	6.24	2.96	0.39	-0.04
40	WNC 52313 × IMR 113	-0.90	-1.25	-0.38	-1.76	3.22	-0.87	-0.07
41	WNC 52646 × VL 109178	-0.83	-1.03	-0.19	-0.81	2.87	-1.20	0.18
42	WNC 52646 × BLD 98	0.17	0.86	0.70	8.04	5.27	1.32	-0.37
43	WNC 52646 × BLD 103	-0.61	-0.81	-0.19	-10.18	-2.06	1.69*	0.27
44	WNC 52646 × BLD 125	0.43	0.56	0.11	3.98	0.50	-1.94*	0.15
45	WNC 52646 × IMR 113	0.84	0.41	-0.44	-1.03	-6.58	0.13	-0.23
	S.Em. ±	0.76	0.83	0.36	6.97	4.77	0.78	0.34
Range	Minimum	-1.9	-2.54	-0.84	-13.94	-12.59	-2.28	-1.13
	Maximum	1.93	2.53	0.89	10.46	9.34	2.4	1.68
	Total significant	4	7	5	1	2	9	8
	Number of +ve significant	2	4	3	0	0	4	4
	Number of –ve significant	2	3	2	1	2	5	4

Note: * and ** indicate level of significance at 5% and 1%, respectively

S.N.	Crosses	Cob girth	Kernels row per cob	Kernels per row	100 kernels weight	Kernel yield per plant	Shelling (%)
1.	BLD 2 × VL 109178	-0.03	-0.01	1.21	1.49	9.20**	-2.18
2.	BLD 2 × BLD 98	-0.03	0.12	-1.21	-0.10	6.02*	-0.92
3.	BLD 2 × BLD 103	0.54	0.34	1.74*	-2.96**	25.53**	3.57**
4.	BLD 2 × BLD 125	0.39	0.37	-1.04	2.45**	-16.46**	1.38
5.	BLD 2 × IMR 113	-0.86**	-0.83**	-0.70	-0.88	-24.29**	-1.84
6.	BLD 109 × VL 109178	0.08	-1.32**	-0.08	-2.58**	5.76*	2.21
7.	BLD 109 × BLD 98	0.16	0.01	-0.04	1.83*	-7.42*	2.93*
8.	BLD 109 × BLD 103	0.13	0.64*	-1.55*	1.64	-9.25**	-0.51
9.	BLD 109 × BLD 125	-0.76**	0.13	-0.40	0.39	6.90*	-3.45*
10.	BLD 109 × IMR 113	0.39	0.53	2.07**	-1.28	4.01	-1.17
11.	BLD 114 × VL 109178	-0.30	-0.71*	0.16	-0.78	-4.88	-3.68**
12.	BLD 114 × BLD 98	0.39	0.09	1.47*	3.96**	12.94**	1.53
13.	BLD 114 × BLD 103	0.00	-0.08	0.09	0.44	-11.22**	-0.63
14.	BLD 114 × BLD 125	-0.09	-0.45	-0.36	0.19	-14.27**	-2.37
15.	BLD 114 × IMR 113	0.00	1.15**	-1.35*	-3.81**	17.43**	5.15**
16.	WNC 40080 × VL 109178	0.15	-0.09	-1.00	-0.51	-10.47**	0.34
17.	WNC 40080 × BLD 98	0.55	0.84**	-0.09	-3.44**	-0.12	-2.74*
18.	WNC 40080 × BLD 103	-0.10	-0.80**	1.53*	2.38**	0.39	0.52
19.	WNC 40080 × BLD 125	-0.08	0.96**	-0.65	-2.55**	6.54*	2.35
20.	WNC 40080 × IMR 113	-0.51	-0.91**	0.22	4.12**	3.65	-0.47
21.	WNC 40324 × VL 109178	0.02	0.79*	1.82**	-1.11	3.25	2.69*
22.	WNC 40324 × BLD 98	-0.69*	-0.68*	-0.33	2.63	0.67	-2.86*
23.	WNC 40324 × BLD 103	-0.10	-0.32	-0.31	-0.56	5.91*	3.15*
24.	WNC 40324 × BLD 125	0.46	-0.03	-1.36*	-1.48	-4.27	-0.98
25.	WNC 40324 × IMR 113	0.30	0.24	0.18	0.52	-5.57	-2.00
26.	WNC 40406 × VL 109178	-0.01	-0.39	-1.76*	0.42	-14.80**	-0.68
27.	WNC 40406 × BLD 98	-0.36	0.15	0.55	-1.50	-6.85*	-1.33
28.	WNC 40406 × BLD 103	0.31	0.24	-1.90**	1.98*	5.19	-0.32
29.	WNC 40406 × BLD 125	-0.14	-0.40	3.25**	0.39	20.08**	2.12
30.	WNC 40406 × IMR 113	0.19	0.40	-0.14	-1.28	-3.62	0.22
31.	WNC 40456 × VL 109178	0.23	1.08**	0.16	2.56**	0.79	-0.11
32.	WNC 40456 × BLD 98	-0.25	-0.65*	-1.27	-4.37**	-4.80	1.38
33.	WNC 40456 × BLD 103	-0.11	-0.03	-0.51	-1.22	-13.75**	-1.99
34.	WNC 40456 × BLD 125	0.39	-0.53	1.51*	1.19	0.80	1.16
35.	WNC 40456 × IMR 113	-0.26	0.13	0.11	1.85*	16.97**	-0.44
36.	WNC 52313 × VL 109178	-0.03	0.17	-0.19	-1.64	10.24**	2.41
37.	WNC 52313 × BLD 98	-0.11	-0.09	-0.81	0.10	-0.34	0.55
38.	WNC 52313 × BLD 103	-0.44	0.26	0.94	-0.09	5.83*	2.17
39.	WNC 52313 × BLD 125	-0.09	-0.51	-0.77	1.65	-12.08**	-4.97**
40.	WNC 52313 × IMR 113	0.68*	0.16	0.83	-0.01	-3.65	-0.16
41.	WNC 52646 × VL 109178	-0.10	0.47	-0.31	2.16*	0.89	-0.99
42.	WNC 52646 × BLD 98	0.34	0.20	1.73*	0.90	-0.09	1.47
43.	WNC 52646 × BLD 103	-0.23	-0.24	-0.04	-1.62	-8.65**	-5.96**

44	WNC 52646 × BLD 125	-0.08	0.45	-0.16	-2.21**	12.77**	4.76**
45	WNC 52646 × IMR 113	0.07	-0.88**	-1.22	0.79	-4.93	0.72
	S.Em. ±	0.28	0.30	0.67	0.84	2.93	1.34
Range	Minimum	-0.86	-1.32	-1.9	-4.37	-24.29	-5.96
	Maximum	0.68	1.15	3.25	4.12	25.53	5.15
	Total significant	4	14	13	16	26	12
	Number of +ve significant	1	6	8	9	14	6
	Number of –ve significant	3	8	5	7	12	6

Note: * and ** indicate level of significance at 5% and 1%, respectively.

References
1. Amiruzzaman M, Islam MA, Hasan L, Kadir M, Rohman MM. Heterosis and combining ability in a diallel among elite inbred lines of maize (*Zea mays* L.). Emirates Journal of Food and Agriculture. 2013;25(2):132-137.
2. Bharti B, Dubey RB, Kumar A, Bind HN, Jat BS. Combining ability analysis for grain yield and its contributing traits in maize (*Zea mays* L.) over environments. Electronic Journal of Plant Breeding. 2017;8(4):1069-1076.
3. Doebley JF, Gaut BS, Smith BD. Cell. 2006;127:1309.
4. Habtamu Zeleke Heterosis and Combining Ability for Grain Yield and Yield Component of Maize in Eastern Ethiopia. Science, Technology and Arts Research Journal. 2015;4(3):32-37.
5. Jinks J. The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. Genetics. 1954;39(6):767.
6. Kempthorne O. An Introduction to Genetic Statistics, New York, John Wiley and Sons, 1st Edn. 1957, 456-471.
7. Kumar V, Singh SK, Singh NP, Mahajan V. Combining ability studies for grain yield other agronomic traits in maize (*Zea mays* L.). Electronic Journal of Plant Breeding. 2016;7(3):544-554.
8. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 4th ed. ICAR, New Delhi, 1985, 97-156.
9. Rajesh V, Kumar SS, Reddy VN, Sankar AS. Combining ability and genetic action studies for yield and its related traits in maize (*Zea mays* L.). International Journal of Current Microbiology and Applied Sciences. 2018;7(6):2645-2652.
10. Ram L, Singh R, Singh SK, Srivastava RP. Heterosis and combining ability studies for quality protein maize. Ekin Journal of Crop Breeding and Genetics. 2015;1-2:8-25.
11. Yerva SR, Sekhar TC, Allam CR, Krishnan V. Combining ability studies in maize (*Zea mays* L.) for yield and its attributing traits using Griffing's diallel approach. Electronic Journal of Plant Breeding. 2016;7(4):1046-1055.