Estimation of Combining Ability and Gene Action Effects on Yield and Yield Components in (Zea Mays L.) Using Factorial Mating Design

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Abstract

This study was carried out in the experimental field of the College of Agricultural Engineering Sciences, University of Duhok, in the autumn season of 2024. Thirteen locally sourced inbred lines were planted, and then crossed between them (four females × nine males) according to a factorial mating design to produce 36 F_1 crosses. In the spring season of 2025, the parents, their crosses, and a commercial check variety were designed in a complete block design with three replications. The results indicated highly significant differences among genotypes for all studied traits except the number of ears per plant. Cross 28 (ZP-593×DKCC6022) was superior in 500-grain weight (154.34 g), grain yield per plant (203.32 g), and total grain yield (13.55 tonnes). Both parents (4×12) (ZP-593×DKCC6022) gave positive general combining ability in 500 grain weight; also, the cross 4×12 (ZP-593×DKCC6022) had positive significant specific combining ability in 500 grain weight (7.0775), yield per plant (38.0729), and total grains per hectare (2.538196), respectively. Genetic parameter estimates revealed that dominance variance exceeded additive variance for all traits except 500-grain weight, which means most traits were under the dominance gene effect, indicating that the cross was the best for improving these traits. Broad-sense heritability was more than narrow-sense heritability, and the values ranged between 51% for yield per plant to 82% for rows per ear. Degrees of dominance were greater than 1 for all traits, confirming the presence of overdominance. Expected genetic advance as a percentage of the mean was low for all studied traits .

Keywords: combining ability, gene action, heritability, factorial mating design.

***This paper is part of the MSc research of the first author.**

Introduction

When starting a breeding program, the plant breeder evaluates inbred lines and their resulting hybrids to determine the type of gene action involved. Inbred lines are selected based on their genetic performance by estimating the general combining ability (GCA) of the lines and the specific combining ability (SCA) of their hybrids, as well as identifying the genes controlling the traits under study. Knowledge of combining ability and gene action is essential for improving maize productivity and addressing frequent deficits and severe food shortages [1 .[

Variance in general combining ability is associated with additive genetic effects, while the variance in specific combining ability includes non-additive genetic effects such as dominance and epistasis for certain traits. In an organized breeding program, it is important to identify superior parents for crossing in order to increase genetic variation, which supports the selection of improved genotypes

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[2]. One of the initial steps in hybrid development is evaluating pure lines based on their general combining ability effects. In plant breeding, various mating systems are employed, including the factorial mating design. The assessment of combining ability has been widely applied by maize breeders, as reported in several studies [3,4,5,6,7,8]. Understanding gene action is crucial for plant breeders, as alleles with dominant, additive, or harmful effects influence heritability differently based on whether they are homozygous or heterozygous [9]. Estimating the type of gene action, the extent of additive effects, and the degree of dominance is essential for selecting appropriate breeding strategies to improve specific traits. Several studies on maize have addressed this topic, including those by [10,11,12,13.[

The objective of this study is to estimate the general and specific combining abilities of thirteen maize inbred lines and their single crosses, as well as to investigate the gene action controlling grain yield and its components using a factorial mating design, to identify superior parental lines and cross combinations.

Materials and Methods

A field experiment was conducted at the College of Agricultural Engineering Sciences, University of Duhok, Kurdistan Region of Iraq. During the autumn season, thirteen inbred lines are involved in this study, as shown in Table 1. Before sowing, the land was plowed, smoothed, and leveled. Seeds of the thirteen inbred lines were sown on 15/7/2024; four lines were designated as female and nine as male. Each female line was planted in five rows, while each male line was planted in three rows. The length of the row was 4 meters, with a spacing of 0.75 meters between rows and 0.25 meters between plants. Fertilization was applied according to recommendations: NPK fertilizer (20:20:18) was applied at a rate of 200 kg/ha^{-1} before planting on 8/7/2024, and nitrogen fertilizer (urea 46%) at a rate of 200kg/ha-1 in two split doses, first on 9/8/2024 when plants reached 30 cm in height. The second was before flowering. A systemic insecticide (thiamethoxam) was sprayed on the plants twice between 7/8/2024 and 12/8/2024. Thinning was done on 14/8/2024 .

When the tasseling and silking began to appear, the tassels and silks were covered by (paper bags) to prevent self-pollination, and Crosses between male and female lines were made according to a factorial mating design Table 2.

In the spring season, the land preparation process included plowing, smoothing, and leveling. The experiment was planned, and arrangements were made for planting thirteen inbred lines, thirty-six crosses, and a check variety on 5/3/2025. The length of the rows was 4 m, with 0.75 m between the rows and 0.20 m between plants to plant each genotype was sown in one row, using a Randomized Complete Block Design (RCBD) with three replications .

The service operation related to weeding was carried out according to recommendations by applying 200kg/ha of Russian fertilizer (20:20:18) before planting on 27/2/2025. also, the Nitrogen fertilizer (urea 46%) was applied at a rate of 200kg/ha in two split doses: the first on 3/4/ 2025, when the plants reached 30 cm in height, and the second before flowering. A systemic insecticide (thiamethoxam) was sprayed on the plants twice between 28/4/2025 and 2/5/2025. Thinning was done on 4/4/2025. Data were recorded on ten plants from each experimental unit, taken randomly. and the data recorded on Number of grains per row, Number of ears per plant, Number of rows per ear, Yield per plant, 500-grain weight (g), Total grain yield per hectare (ton.(

The parameters were calculated by the following formulas :

-1Combining ability.

The General combining ability (GCA) and Specific combining ability (SCA) were estimated using the following model:

$Y_{ijk}= \mu+M_i+F_j+MF_{ij}+R_k+e_{ijk}$

Y_{ijk}=observed value of the experimental unit

μ = is an overall population mean

M_i = is the GCA effect of male i

F_j = is the GCA effect of female j

MF_{ij}=male and female interaction (SCA for the cross i×j(

R_k= replication block effect

e_{ijk}=experimental error effect

Estimation of general combining ability effects for male

$m_i =\bar{y}_{i..} - \bar{y}_{...}$

Estimation of the general combining ability for female

$f_i=\bar{y}_{.j.} -\bar{y}_{...}$

Estimation of the specific combining ability for the hybrid

$mf_{ij}=\bar{y}_{ij.} - \bar{y}_{i..} -\bar{y}_{.j.}+\bar{y}_{...}$

.2Estimation of components of variance

Additive variance

$\sigma^2A(2Øm +2Øf)/2$

Domin

ance variance

$Ømf=\sigma^2D$

Genetic variance

$\sigma^2G =\sigma^2A+\sigma^2D$

Phenotypic Variance

$\sigma^2p=\sigma^2G +\sigma^2E$

Environmental variance

$MSe= \sigma^2e =\sigma^2E$

The effect of males

$MSm= \sigma2e+ rfØm$

$Øm= (MSm -MSe)/ rf$

The effect of females

$MSf =\sigma^2e +rmØf$

$Øf=(MSf-MSe)/rm$

The effect of the interaction between males and females

$MSmxf=\sigma^2e +rØmxf$

$Ømxf= (MSmxf -MSe)/r$

.3Standard error for combining ability effects

For male and female parents

$SE (gi)=\sqrt{((2 \sigma^2e)/r(}$

$SE (gj)=\sqrt{((2 \sigma^2e)/r(}$

For cross

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$SE(S_{ij}) = \sqrt{(4\sigma^2 e)/r}$

.4Heritability

Heritability was calculated in a broad sense (Hb.s) and a narrow sense (Hn.s) as follows :

Heritability percentage

$h_{(b.s)}^2 = \sigma^2 G/(\sigma^2 p) \times 100$

According to [14[

The value of heritability is considered low when it is less than 40%.

The value of heritability is considered medium when the value is between 40-60%.

The value of heritability is considered high when it is more than 60%.

$h_{(n.s)}^2 = \sigma^2 A/\sigma^2 p \times 100$

According to [33[

Heritability is considered low when the value is less than 20%.

Heritability is considered medium when the value is between 20-50%.

Heritability is considered high when the value is more than 50%.

Where :

$h_{(n.s)}^2$= heritability in a narrow sense.

$h_{(b.s)}^2$= heritability in a broad sense.

.5Estimation of average degree of dominance (ā(

The average degree of dominance (ā) for each trait was estimated as follows:

$\bar{\alpha} = \sqrt{2\sigma^2 D/\sigma^2 A}$

Interpretation of the results follows these criteria:

$\bar{\alpha} = 0$ no dominance.

$\bar{\alpha} < 1$ partial dominance.

$\bar{\alpha} = 1$ complete dominance.

$\bar{\alpha} > 1$ over dominance [15.[

.6Expected genetic advance (EGA(

Genetic advance under selection was estimated according to [34] using the following formula:

$EGA = (i)(h_{(n.s)}^2)(\sigma P)$

$EGA\% = EGA/\bar{Y} \times 100$

Where:

-i: selection intensity (which equals 1.76 when 10% of plants are selected(

-$h_{(n.s)}^2$: narrow-sense heritability

-σP: phenotypic standard deviation

-$\bar{Y}$: trait mean

Genetic advance is categorized as high (>30%), moderate (10–30%), or low (<10%) [16.[

All statistical and genetic analyses were performed according to the experimental design by [17]. Statistical analyses were conducted using the Statistical Analysis System (SAS) and Microsoft Office Excel 2003 programs.

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Table 1. The inbred lines and source used in the study

No.	Inbred line	Sources
1	ZP-607	Locally devised
2	DK-17	Locally devised
3	H-4	Locally devised
4	ZP-593	Locally devised
5	IK58	Locally devised
6	ZP-707	Locally devised
7	ZP-430	Locally devised
8	Ma-F-53	Locally devised
9	Maximo	Locally devised
10	Iran Variety	Locally devised
11	DKCC6418	Locally devised
12	DKCC6022	Locally devised
13	UNN052	Locally devised

Table 2. A cross between male and female according to factorial mating design.

Males / Females	1	2	3	4	5	6	7	8	9
10	10×1	10×2	10×3	10×4	10×5	10×6	10×7	10×8	10×9
11	11×1	11×2	11×3	11×4	11×5	11×6	11×7	11×8	11×9
12	12×1	12×2	12×3	12×4	12×5	12×6	12×7	12×8	12×9
13	13×1	13×2	13×3	13×4	13×5	13×6	13×7	13×8	13×9

The analysis of variance for all genotypes is presented in Table 3. The results indicate a highly significant difference for all traits except the number of ears per plant. This means there is a high variation between the parents used in this study, which gives different crosses for the studied traits. These results are in line with those reported by [18,19,20,21,22.[

Table 4 exhibited the yield and yield components for all genotypes. Among the parents, Parent 11 exhibited superior performance with a high number of ears per plant (1.16), number of grains per row (41.03), yield per plant (150.17 g), and total grain yield per hectare (10.011 tonnes). It was followed by Parent 10, which recorded a high number of grains per row (41.00) and the highest number of rows per ear (19.73). Parent 7 also performed well, with the highest number of grains per row (41.86) and the greatest 500-grain weight (129.12 g), and Parent 1 recorded the

highest yield per plant (155.18 g) and total grain yield (10.345 tonnes) among the parents.

From the same Table 4, the results indicate that cross 48 had the highest number of ears per plant (1.30), a high number of grains per row (46.46), and yield per plant (197.51), while cross 28 gave the highest 500-grain weight (154.34 g), yield per plant (203.32 g), and total yield per hectare (13.555 tonnes). Cross 31 recorded a high number of rows per ear (18.53), yield per plant (191.09 g), and total grain yield (12.739 tonnes). On the other hand, the check variety showed a high 500-grain weight (147.22 g), yield per plant (197.05 g), and total grain yield (13.136). These findings are consistent with those of

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[23,24,25,26,12], who also reported that certain crosses exhibited favorable traits for yield and its components
.

Table 3: Analysis of variance for yield and yield components of all maize genotypes.

Source of variance	d. f	Mean square for traits					
		No. of ears per plant	No. of grains per row	No. of rows per ear	500-grain weight(g)	Yield per plant(g)	Total grain yield ton/ha
Rep.	**2**	0.002	9.22	2.88	849.27	327.28	1.45
Genotypes	**49**	0.014	49.23**	2.45**	371.30**	1931.83**	8.58**
Error	**98**	0.013	7.17	0.78	69.06	389.58	1.73
Total	**149**						

*and ** indicate significance at the 5% and 1% levels.

Table 4: Mean performance of yield and yield components of all maize genotypes.

Genotypes	Mean square for traits					
	No. of ears per plant	No. of grains per row	No. of rows per ear	500- grain weight(g)	Yield per plant(g)	Total grain yield ton/ha
1.	1.00b	36.80h-k	16.93a-f	123.26e-k	155.18e-h	10.345c-h
2.	1.13ab	37.60f-k	16.53b-h	122.06e-l	149.95d-h	9.997e-h
3.	1.20ab	28.33n	15.06g-k	109.38k-n	90.27k	6.018k
4.	1.06ab	31.00mn	14.40jk	114.94h-m	96.32jk	6.421jk
5.	1.10ab	37.53i-k	16.00c-j	102.01m-n	118.88h-k	7.925h-k
6.	1.06ab	35.66ijk	15.46d-k	114.07i-m	118.98h-k	7.932h-k
7.	1.10ab	41.86a-h	14.13k	129.12d-i	146.24e-i	9.749d-i
8.	1.06ab	37.33i-k	16.66b-g	112.12j-m	131.44g-j	8.762g-j
9.	1.20ab	34.73kl	15.46d-k	106.17l-n	110.64ijk	7.375ijk
10.	1.03b	41.00b-h	19.73c-k	117.73g-m	143.12e-i	9.541e-i
11.	1.16ab	41.030b-h	15.46d-k	125.24d-k	150.17d-h	10.011d-h
12.	1.10ab	33.20l	16.66b-g	126.44d-j	134.31ghi	8.954f-i
13.	1.06ab	35.40kj	14.80h-k	95.73n	95.61jk	6.374jk
14.	1.06ab	44.33a-e	15.73c-k	124.00d-k	162.04b-g	10.803b-g
15.	1.03b	42.93a-f	17.20a-d	125.56d-k	172.13a-f	11.475a-f
16.	1.00b	42.53a-g	15.73c-k	131.71b-h	169.76a-g	11.317a-g
17.	1.03b	42.46a-g	16.00c-j	131.61b-h	170.3a-g	11.353a-g
18.	1.10ab	46.00abc	14.80h-k	130.02d-i	169.03a-g	11.269a-g
19.	1.06ab	42.46a-g	15.73c-k	123.51d-k	163.25b-g	10.883b-g

20.	1.03b	41.40a-h	17.20a-d	128.50d-j	172.45a-f	11.497a-f
21.	1.06ab	39.40e-k	16.13b-j	129.34d-i	155.69d-h	10.379c-h
22.	1.03b	43.86a-e	15.33e-k	137.28e-d	172.09a-f	11.473a-f
23.	1.13ab	40.53c-i	15.73c-k	132.46b-g	159.51b-g	10.634b-g
24.	1.16ab	41.93a-h	17.06a-e	132.77b-g	182.55a-e	12.169a-e
25.	1.00b	45.46a-d	16.93a-f	124.28d-k	183.12a-e	12.208a-e
26.	1.03b	46.53a	16.26b-i	132.31b-g	186.43a-d	12.429a-d
27.	1.06ab	43.66a-e	15.73c-k	137.21b-g	177.17a-e	11.811a-e
28.	1.03b	43.06a-d	16.26b-i	154.34a	203.32a	13.555a
29.	1.16ab	43.86a-e	14.66ijk	138.54b-e	172.34a-f	11.49a-f
30.	1.06ab	45.20a-d	14.80h-k	126.15d-j	158.88c-g	10.592c-g
31.	1.03b	43.06a-e	18.53a	128.66d-j	191.09abc	12.739abc
32.	1.10ab	43.86a-e	15.46d-k	127.10d-j	162.77b-g	10.851b-g
33.	1.23ab	45.93abc	17.86ab	117.18g-m	182.01a-e	12.134a-e
34.	1.20ab	45.53a-d	15.86c-k	130.55d-i	178.54a-e	11.903a-e
35.	1.00b	40.06e-j	14.80h-k	136.12b-f	149.77d-h	9.984d-h
36.	1.13ab	42.00a-h	16.26b-i	140.29a-d	177.47a-e	11.831a-e
37.	1.10ab	42.93a-f	14.80h-k	135.33b-f	163.05b-g	10.87b-g
38.	1.20ab	43.40a-e	15.06g-k	132.52b-g	162.92b-g	10.861b-g
39.	1.03b	43.66a-e	15.33e-k	123.50d-k	155.76c-h	10.384c-h
40.	1.06ab	40.20e-j	15.73c-k	137.85e-d	160.19c-g	10.679b-g
41.	1.03b	43.26a-e	15.20f-k	127.44d-j	156.07c-h	10.405d-h
42.	1.20ab	46.40ab	15.73c-k	125.77d-k	172.34a-f	11.49a-f
43.	1.03b	40.66e-i	17.46abc	132.82b-g	175.92a-e	11.728a-e
44.	1.13ab	41.20a-h	15.73c-k	142.17abc	171.26a-g	11.417a-g
45.	1.06ab	44.60a-e	16.26b-i	109.36k-n	155.62c-h	10.375c-h
46.	1.00b	41.66a-h	14.93g-k	124.06d-k	151.41d-h	10.094d-h
47.	1.13ab	44.33a-e	15.86c-k	120.27f-l	165.65b-g	11.044b-g
48.	1.30a	46.46ab	16.13b-j	138.05e-d	197.51ab	13.168ab
49.	1.10ab	44.73a-e	15.33e-k	122.61e.k	162.86b-g	10.858b-g
50.	1.00b	45.06a-d	15.46d-k	147.22ab	197.05ab	13.136ab

Means values followed by the same letter for each trait are not significantly different from each other .

Table 5 indicates the analysis of variance of males and females and the interaction between them. For the male parents, the data gave a highly significant result for the number of rows per ear and 500-grain weight. While the female parents gave highly significant results for the number of grains per row, number of rows per ear and the 500-grain weight, and the interaction between male and female also gave a highly significant result for number of rows per ear and significant results for the number of grains per row and the 500-grain weight, However, the male and female parents, as well as their interaction, showed no significant effect on yield per plant and total grain yield per hectare. Based on the results in Table 5, the female parents and the interaction between male and female were more effective to produce the crosses. These results are consistent with those of [27,28.[

Table 6 exhibited general combining ability effects on yield and yield components for male parents. Male parent 4 showed significant negative GCA effects for yield per plant (-12.2291) and total grain yield per hectare (-0.81527), while it exhibited a positive effect for 500-grain weight (10.28796). Male parent 5 recorded significant negative GCA effects for 500-grain weight (-5.53954), yield per plant (-23.3618), and total grain yield per hectare (-1.55745), but showed significant positive effects for number of rows per ear (0.72963) and number of grains per row (1.19259). Male parent 6 exhibited significant negative GCA effects for number of rows per ear (-0.5037), yield per plant (-29.8403), and total grain yield (-1.98935), while showing a positive effect for 500-grain weight (5.258796). The rest of the male parents gave significant negative GCA for all studied traits. This is in accordance with the findings of [18,29,30,31,27.[

Table 7 exhibited general combining ability effects on yield and yield components for female parents. Female parent 1 recorded significant negative GCA effects for number of rows per ear (–0.544), yield per plant (–28.858), and total grain yield per hectare (–1.923), while exhibiting a positive effect for number of grains per row (1.44629). Female parent 3 showed significant negative GCA effects for yield per plant (–19.572) and total grain yield per hectare (–1.304), but gave positive GCA for 500-grain weight (6.6632). The remaining female parents showed significant negative GCA effects for all the studied traits. These findings are consistent with those of [18,29,30,31,27.[

Table 5: Analysis of variance for male and female parents and their interaction on yield and yield components in maize.

Source of variance	**d. f**	**Mean square for traits**					
		No. of ears per plant	No. of grains per row	No. of rows per ear	500- grain weight(g)	Yield per plant(g)	Total grain yield ton/ha
Rep.	**2**	0.0077	10.56	3.174	624.723	37.884	0.168
Crosses	**35**	0.016	11.24*	2.531**	193.060**	473.306	2.103
Male	**8**	0.010	8.222	2.434**	301.260**	621.530	2.762
Female	**3**	0.012	33.565**	4.173**	582.101**	668.485	2.970
M×F	**24**	0.018	9.460*	2.357**	108.363*	399.500	1.775
Error	**70**	0.012	6.274	0.683	67.717	409.827	1.821
Total	**107**						

*and ** indicate significance at the 5% and 1% probability levels.

Table 6: General combining ability effects on yield and yield components for male parents.

Males	No. of ears per plant	No. of grains per row	No. of rows per ear	500- grain weight	Yield per plant(g)	Total grain yield ton/ha
1	-0.0555*	-0.25741	0.22963	-2.09204	-28.489*	-1.89926*
2	-0.0222	-1.00741	0.02963	-2.47037	-31.9403*	-2.12935*
3	-0.0055	-0.37407	0.32963	1.386296	-22.7288*	-1.51525*
4	-0.0138	0.95925	-0.2037	10.28796*	-12.2291*	-0.81527*
5	0.01944	1.19259*	0.72963*	-5.53954*	-23.3618*	-1.55745*
6	0.01944	-0.69074	-0.5037*	5.258796*	-29.8403*	-1.98935*
7	-0.0055	-0.69074	-0.6037*	0.01463	-38.3122*	-2.55414*
8	0.01944	-0.10741	0.36296	-2.7812	-28.2609*	-1.88406*
9	0.04444	0.97592	-0.37037	-4.06454*	-27.6861*	-1.84574*
SE	0.05177	1.18085	0.38969	3.87923	9.543207	0.636232

*Indicate significance at the 5% probability level .

Table 7: General combining ability effects on yield and yield components for female parents.

Females	No. of ears per plant	No. of grains per row	No. of rows per ear	500- grain weight	Yield per plant(g)	Total grain yield ton/ha
1	0.01111	1.44629*	-0.5444*	-1.12639	-28.8585*	-1.9239*
2	-0.0296	-0.9463	0.32963	-1.41157	-29.2407*	-1.94938*
3	0.01851	-0.80556	0.24074	6.663241*	-19.5726*	-1.30484*
4	0	0.30555	-0.0259	-4.12528*	-30.2609*	-2.01739*
SE	0.05177	1.18085	0.38969	3.87923	9.543207	0.636232

*Indicate significance at the 5% probability level

The data in the Table 8 indicate that for number of ears per plant 10 crosses gave significant specific combining ability, 7 from 10 had positive SCA and the rest recorded negative SCA and the values ranged from(0.079) for the cross (3×11) to (0.148) for the cross (9×12), for number of grains per row 8 crosses recorded significant positive and negative SCA, 5 of them gave positive combining ability the maximum value (2.972) recorded in cross (9×12), while the number of rows per ear 20 crosses gave significant SCA, and the maximum positive combing ability recorded by cross (5×11) with a value (1.53) and the lowest value (0.55) was in cross (3×12), regarding for 500 grain weight 10 crosses gave significant (positive and negative) SCA and the highest value (7.978) was found in cross (8×12), for yield per plant and total grain yield, 33 crosses showed positive and significant specific combining ability (SCA) effects. The highest yield per plant value (47.72) was recorded for the cross (9×12), followed by the cross (5×11) with a value of (46.64). For total grain yield, the highest value (3.1817) was also recorded by the cross (9×12), followed by the cross (5×11) with a value (3.1093). Based on the results in Table 8, crosses 9×12,3×13,5×13,6×10,8×10, and 8×11 recorded positive SCA effects in four traits. These findings are in agreement with those of [29,30,31,32.[

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From the data in Table 9, the dominance variance was more than the additive variance for yield and yield components except for 500-grain weight, indicating that these traits are under the control of dominance gene action. For heritability, the heritability in the broad sense was more than the heritability in the narrow sense for all traits, and the highest value was found in the number of rows per ear (82%), while the lowest value (51%) was in yield per plant and total grain yield per hectare, these results suggest that the cross is the best to improve these traits. For the degree of dominance, the value was greater than 1 for yield and yield components, indicating that dominance and overdominance control these traits. The genetic advance as a percentage of the mean was low for all studied traits, ranging from 7% for 500-grain weight to the lowest value of 1% for the number of ears per plant. These findings are consistent with those of [23,27,20.[

Table 8: Specific combining ability effects on yield and yield components crosses

Crosses	No. of ears per plant	No. of grains per row	No. of rows per ear	500- grain weight	Yield per plant(g)	Total grain yield ton/ha
(1×10)	0.022222	-0.17963	0.111111	-3.09611	22.34119*	1.489411*
(1×11)	0.02963	0.812963	0.703704*	-1.24759	32.813*	2.187531*
(1×12)	-0.05185	0.272222	-0.67407*	-3.16907	20.77356*	1.384902*
(1×13)	0	-0.90556	-0.14074	7.512778*	32.00489*	2.133657*
(2×10)	0.022222	2.237037*	-0.62222*	3.302222	32.78052*	2.185366*
(2×11)	0.02963	1.096296	-0.56296*	-2.91926	27.38667*	1.825776*
(2×12)	-0.05185	-0.11111	0.992593*	-6.00741*	26.91656*	1.794435*
(2×13)	0	-3.22222*	0.192593	5.624444*	20.84889*	1.389925*
(3×10)	-0.06111	-0.52963	-0.38889	6.712222*	26.6326*	1.775505*
(3×11)	0.07963*	-1.47037	-0.86296*	2.174074	14.43575*	0.962382*
(3×12)	0.064815	-0.21111	0.559259*	-5.59074*	27.80064*	1.853374*
(3×13)	-0.08333*	2.211111*	0.692593*	-3.29556	39.06364*	2.60424*
(4×10)	-0.05278	0.803704	1.077778*	-7.16611*	30.4736*	2.031571*
(4×11)	0.021296	0.32963	-0.32963	-1.98093	21.59708*	1.439804*
(4×12)	-0.06019	-0.41111	0.292593	7.077593*	38.07297*	2.538196*
(4×13)	0.091667*	-0.72222	-1.04074*	2.069444	17.78897*	1.18593*
(5×10)	-0.05278	-0.76296	-1.32222*	2.508056	14.05127*	0.93675*
(5×11)	-0.04537	-0.5037	1.537037*	5.299907	46.64008*	3.109336*
(5×12)	-0.02685	0.155556	-1.44074*	-4.33824	8.653639	0.576909
(5×13)	0.125*	1.111111	1.225926*	-3.46972	38.58764*	2.572507*
(6×10)	0.080556*	1.453704	0.977778*	-3.89361	40.19719*	2.67981*
(6×11)	-0.0787*	-1.62037	-0.96296*	1.958241	11.801	0.786733
(6 ×12)	0.006481	0.172222	0.592593*	-1.94657	29.83222*	1.988813*
(6 ×13)	-0.00833	-0.00556	-0.60741*	3.881944	26.10222*	1.740146*
(7×10)	0.105556*	-0.67963	0.277778	3.323889	33.04802*	2.203199*
(7×11)	-0.02037	1.97963*	-0.32963	-5.41759	26.26283*	1.750854*
(7×12)	-0.03519	-1.62778	0.159259	0.857593	21.02672*	1.40178*
(7×13)	-0.05	0.327778	-0.10741	1.236111	27.59506*	1.839669*
(8×10)	0.080556*	1.737037*	-0.02222	-0.63028	32.41644*	2.161094*
(8 ×11)	-0.04537	-1.6037*	0.837037*	6.701574*	36.37592*	2.425059*
(8 ×12)	0.006481	-1.21111	-0.80741*	7.973426*	22.04581*	1.469719*

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(8 ×13)	-0.04167	1.077778	-0.00741	-14.0447*	17.09447*	1.13963*
(9 ×10)	-0.14444*	-4.07963*	-0.08889	-1.06028	10.9076	0.727173
(9 ×11)	0.02963	0.97963	-0.02963	-4.56843	25.53608*	1.702404*
(9×12)	0.148148*	2.972222*	0.325926	5.143426	47.72631*	3.181751*
(9×13)	-0.03333	0.127778	-0.20741	0.485278	23.76264*	1.584174*
SE	0.073221	1.669985	0.551114	5.48606	13.49613	0.899767

*Indicate significance at the 5% probability level .

Table 9: Estimation of variance components and genetic parameters for yield and yield components of maize.

	No. of ears per plant	No. of grains per row	No. of rows per ear	500-grain weight	Yield per plant(g)	Total grain yield ton/ha
Additive variance	0.00083	1.67662	0.33004	43.9473	60.1092	0.26711
SE (A)	0.00057	1.34782	0.18408	25.2245	32.2529	0.14332
Dominance variance	0.00486	2.45620	0.70999	28.5968	87.6305	0.38950
SE (D)	0.00173	0.88228	0.21834	10.0963	37.7055	0.16759
Total genetic variance	0.00570	4.13282	1.04004	72.5441	147.739	0.65662
Environmental variance	0.00402	2.09163	0.22779	22.5726	136.609	0.60718
SE (E)	0.00067	0.34860	0.03796	3.76210	22.7682	0.10119
Phenotypic variance	0.00972	6.22446	1.26783	95.1167	284.349	1.26380
Narrow-sense heritability	0.08559	0.26936	0.26032	0.46203	0.21139	0.21135
Broad-sense heritability	0.58637	0.66396	0.82032	0.76268	0.51957	0.51955
Expected genetic advance	0.01738	1.38436	0.60382	9.28263	7.34314	0.48946
Genetic advance %	1.59662	3.19537	3.78884	7.12325	4.31788	4.31722
Degree of dominance	3.42070	1.711707	2.074211	1.140795	1.707545	1.707755

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