HETEROSIS AND GENETIC PARAMETERS FOR YIELD AND YIELD COMPONENTS IN MAIZE USING HALF DIALLEL CROSS

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ABSTRAC

The study was aimed to determine heterosis, GCA, SCA and some genetic parameters in maize (*Zea mays L.*). Seeds for half diallel crosses among eight inbred lines Planted in spring season 2021 during fall season 2021, the eight parents and 28 hybrids were sowing (10/7/2021) using Randomize Complete Block Design with three replications at the field of College of Agricultural Engineering Sciences, University of Duhok. The results revealed that the mean square for all genotypes was highly significant effects in all studied traits except number of ears per plant. The (Un44052) line was superior in number of rows per ear and grain yield per plant, while the cross (Zp-505 x Un44052) was superior in number ear per plant and number of rows per ear. Six crosses exhibited significant positive heterosis, the crosses Dkc-f-59 x Dk-17, Dkc-f-59 x Un44052, Dkc-f-59 x Zp-430, Zp-505 x Un44052, Zp-607 x Zp-505 and Zp-179 x Un44052. The heritability in broad sense was higher than the heritability narrow sense in studied traits, between 0.33 and 0.97 for number of ear per plant and grain yield per plant. The average degree of dominance was higher than one in studied traits.

Key words: heritability, combining ability, degree of dominance

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مجلة العلوم الزراعية العراقية- 2024:55(5):1859-1869 سعيد وحسين

قوة الهجين و بعض المعالم الوراثية للحاصل و مكونات الحاصل في الذرة الصفراء باستعمال التهجين التبادلي النصفي

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المستخلص

الهدف من الدراسة تحديد قوة الهجين وقابيلة القدرة العامة والخاصة للائتلاف وبعض المعالم الوراثية في الذرة الصفراء، باستعمال التضريب تبادلي نصفي بين ثمانية سلالات من الذرة الصفراء زرعت في العروة الربيعي 2021 لاستنباط 28 هجين فردي و في العروة الخريفية زرعت ثمانية السلالات مع هجنها 28 بتصميم القطاعات العشوائية الكاملة وبثاث مكررات في حقل كلية علوم الهندسة الزراعية، جامعة دهوك. اظهرت النتائج فروقات عالية المعنوية بين التراكيب الوراثية ولجميع الصفات ماعدا صفة عدد العرانيص بالنبات. تفوقت السلالة (Un44052) معنويا في الصفات حاصل الحبوب بالنبات وعدد الصفوف بالعرنوص،اما الهجين (Zp-505 x Un44052) اظهر تفوقا ملحوظا في الصفات عدد الصفوف بالعرنوص و عدد العرانيص بالنبات. اظهرت ستة هجن قوة هجين موجبة و معنوية لأغلب الصفات (Dkc-f-59 x Dk-17), (Dkc-f-59 x Un44052), (Dkc-f-59 x Zp-430), (Zp-505 x Un44052), (Zp-607 x Zp-505) and (Zp-179 x Un44052). كان التوريث بالمعنى الواسع اعلى من التوريث بالمعنى الضيق لكل الصفات وتراوحت قيمتها بين 0.33 و0.95 لعدد العرانيص بالنبات وحاصل الحبوب بالنبات وكان معدل درجة السيادة اكبر من الواحد لكل الصفات المدروسة.

الكمات المفتاحية: التوريث، قابلية الائتلاف، درجة السيادة

***جزء من اطروحة الدكتوراه للباحث الاول.**

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INTRODUCTION

Maize (*Zea mays L.*) is one of the most important cereal crops, which is cultivated throught the world to provid raw material for the food industrial and feed animals. Several breeding producers have been established to increase the grain yield of the maize populations, also hybrids are chosen to improve the traits of the resulting plants, such as better yield, greater uniformity, improve color, disease resistance (17). Diallel crossing programe have been applied to achieve this goal by providing asystematic approach for the detection suitable parents and crosses for the investigate traits, also dialle cross analysis give plant breeders the opportunity to choose the most efficient selection method by alowing to estimate several genetic parameters, (2). Hella *et. al.,* (8) indicated that significant differences were found among parental and their crosses for No. of rows ear^{-1}, No. of grains row^{-1}, grains weight and grain yield, Murtadha *et. al.,* (13) reported significant difference among parents and their crosses for No. of rows ear^{-1}, No. of grains row^{-1}, 300 grin weight. Plant breeding strategies that result in hybrid selection require a certain level of heterosis as well as a specified combining capacity within a breeding population, the relative impact of additive (GCA)and non-additive (SCA) gene activity is critical in determining which breeding strategy will most effectively improve the performance of the traits interest, (20), Several researchers found significant desirable heterosis for grain yield and yield components measured as departure of F1 of mid parents, best parents and check hybrid (5, 8, 10, 12, 14, 19). Fayyad and Hammadi (6) exhibited significant differences traits number of ears per plant, number of grains per row, 300 grain weight and grains yield per plant, indicating the variance pure lines involved in hybridization. Ali *et. al.,* (2) reported that values of heritability in a broad sense were high in days to silking, and tasseling, plant height and number of grains per row and medium for grain yield per plant. The heritability broad sense high for number of rows per ear, number of grain per row, grains weight per ear, weight of ear and shelling percent. (12, 20). While the heritability of narow sense was low for 300 grain weight, number of grain per row, number of row per ear and grain yield per plant, (6, 18, 22). Gene action refers to the behaviors or mode expression of gene in genetic population, knowledge of gene action helps in the selection parents for used hybridization programs. Several investigators reported that non-additive gene action was responsible for inheritance of grain yield and most of its characters in maize (20). Hella *et. al.,* (8) indicated that dominant gene action was more influential than additive genetic action in controlling the inheritance of these traits, there for the values of broad sense heritability were high for all traits. Hella *et. al.,* (8) reported that non-additive gene action was responsible for inheritance of all the traits (plant height, leaf area, number of rows per ear, number of grains per row). Rohman *et. al.,* (16) indicated that when using half diallel cross of ten pure lines of maize, the ratio of $\sigma 2gca \backslash \sigma 2sca$ was less than one for a 100-grain weight and reached 0.05. The average degree of dominance was exceeded one for number of ears per plant, number of rows per ear, number of grains per row, grain weight and grain yield per plant (8). Panda *et. al.,* (15) observed the genetic advance percentage ranged between low to medium for number of rows per ear, number of grains per row, 300 grain weight and grain yield per plant. This study aimed to estimate heterosis, general and specific combining ability and some genetic parameters in maize genotypes using half diallel cross.

MATERIALS AND METHODS

The study was carried out at the fields of College of Agricultural Engineering Sciences, University of Duhok. The materials under study consist from eight inbred lines (Table 1), which were selected based on different agronomic traits. During spring season 12th of march 2020. Grains of eight inbred lines were sown to perform half diallel crosses between them. the seed of inbred lines were sown in a row 3m long for each genotype, 0.75m between the rows and 0.25m within the row to produce twenty-eight hybrids. In the fall season prepared the field by agricultural practices were done and planting genetic materials (parents (8) and hybrids (28)) were seeding during 10/7/2021 in rows, the long of row 3m, 0.75m between rows and 0.25m within row using randomize complete block design (RCBD) with three replications. Urea (46%) 300 kg h^{-1} was added in two times, the first after two weeks from planting and the second at the beginning of tasseling, all the recommended agronomic package of management and protection of plant measure were followed to obtain good healthy crop. The data was collected on five plants taken randomly from each row, and the data recorded on **GYP^{-1}** (grain yield $plant^{-1}$), **300WG** (300 weight grain), **NGR^{-1}** (No. of grain Row^{-1}), **NRE^{-1}** (No. of Rows Ear^{-1}), **EL** (Ear Length), **ED** (Ear diameter).

The parameters were calculated by the following formulas:

Estimation of heterosis (H)

Heterosis was determined for different characters for each hybrid from the replicates mean related to the differences of F1 hybrids generation from the mid parent value, better parent and local variety and the equation to estimate each heterosis as follows: Heterosis at mid parents (H) %

$$\frac{\bar{F1} - M.P}{M.P} \times 100$$

Heterosis at best parents (H) %

$$= \frac{\bar{F1} - b.P}{b.P} \times 100$$

Heterosis at best parents (H) %

$$= \frac{\bar{F1} - C.C}{C.C} \times 100$$

where:

F1: mean of hybrid

P1: parent one

P2: parent two

BP: better parent

CC: check hybrid

The significance of heterosis was tested from calculation of **t** value for each hybrid according to the following equation:

$t = \frac{H}{\sqrt{V(H)}}$ =====Where the heterosis variance V (H) will be

$$V(H) = (3/2)(Mse/r)$$

Estimation of general and Specific combining effect

$$\hat{g}i = \frac{1}{r(n+2)}[zi.. - \frac{z...}{n}]\text{-----}$$

$$\hat{S}ij = \frac{yij.}{r} - \frac{[zi.. + zj..]}{r(n+2)} + \frac{2y...}{r(n+1)(n+2)}$$

ĝi= effect of general combining ability

Ŝij= effect of specific combining ability

yij= F1's overall mean as a result of crossing parent " i" with parent " j

y…= sum of the overall mean of all parent and F1's hybrid non- reciprocal

The estimation of standard error for each GCA and SCA

$$S.E\ (\hat{g}i - \hat{g}j) = \sqrt{\frac{2Mes}{n+2}}$$

$$S.E\ (\hat{S}ij - \hat{S}jk) = \sqrt{\frac{2(n+1)Mes}{n+2}}$$

Estimation of component of variance and genetic enterpretion: The Additive, Dominance and Environmental variances were estimated by using EMS from (9) analysis. and their significance from zero were tested in the manner explained by (14).

$\sigma^2 A = 2\,\sigma^2 g$

$\sigma^2 D = \sigma^2 s$

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

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

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

$\sigma^2 P = \sigma^2 A + \sigma^2 D + \sigma^2 E$

where:

σ^2A: Additive genetic variance

σ^2D: Non-additive (dominance and epistasis) genetic variance,

σ^2g: Variance of general combining ability

σ^2s: Variance of specific combining ability

σ^2E: Variance of experimental error, i.e. environmental variance

σ^2G: Total genetic variance, and

σ^2P: Phenotypic variance (genetic and environmental variance)

Heritability: Heritability was calculated in broad sense (H^2) and narrow sense (h^2) concept and average degree of Dominance for each characteristic were calculated as follows:

Heritability broad sense, $h^2.b.s = \frac{\sigma^2 G}{\sigma^2 P}$

Heritability Narow sense, $h^2.n.s = \frac{\sigma^2 A}{\sigma^2 P}$

The average degree of dominance

$$(\bar{a}) = \sqrt{\frac{2\sigma^2 D}{\sigma^2 A}}$$

Where:

H.b.s: heritability in broad sense
H.n.s: heritability in narrow sense,
If: ā = zero denote no dominance,
ā < 1 denote partial dominance
ā =1 denote complete dominance
ā > 1 denote over dominance

Expected genetic advance

EGA = (i) (h_{ns}) (σ^2P)
EGA% = (EGA/ȳ) x 100
Where:
EGA: Expected genetic advanced
i: intensity of selection (which equals 1.76 when 10% of plants are selected
$h_{n.s}$: narrow sense heritability
σ^2P: phenotypic deviation

Table 1. Inbred lines used in the study

	Inbred lines	Source
1	Pol-f-53	Locally devised
2	Zp-607	Locally devised
3	Dkc-f-59	Locally devised
4	Zp-505	Locally devised
5	Zp-179	Locally devised
6	Dk-17	Locally devised
7	Un44052	Locally devised
8	Zp-430	Locally devised

RESULTS AND DISSCUSSION

Table 2. show the analysis of variance for genotypes (parents and hybrids), GCA and SCA for six studied traits, it was revealed that the genotypes were highly significant effects on studied traits except NEP^{-1}**,** also the data in the same Table exhibited significant differences among genotypes, indicating that there is a genetic diversity between parental lines using in this study, and had a greater divergence between the resulting hybrids, for general combining ability (GCA), also the result exhibited highly significant effect in EL, NRE^{-1}, 300 WG, GYP^{-1} and significant effect in NEP^{-1} and NGR-1, while the specific combining ability (SCA) showed highly significant effect in studied traits except NEP^{-1}, The average degree of dominance is less than one for ear length, number of ears per plant, number of rows per ear, number of grains per row, 300 weight grain and grain yield per plant indicating that the dominant gene action were controlling inheritance of these traits. The results are generally analogous to the fining of (2, 3, 15) when study half diallel cross in maize for these parents.

Table 2. Analysis of variance for genotypes (parents and hybrids) and Combining ability for studied traits in maize genotypes

Source of variation	Df	MS Traits EL (cm)	NEP $^{-1}$	NRE^{-1}	NGR^{-1}	300 WG (g)	GYP $^{-1}$ (g)
Replications	2	1.54	0.07	5.03	0.49	5.36	34.02
Genotypes	35	11.37**	0.05	4.23**	58.71**	311.04**	1073.26**
GCA	7	10.68**	0.09*	4.09**	15.04*	552.27**	358.95**
SCA	28	11.54**	0.05	4.27**	69.63**	250.73**	1251.84**
σ^2e	70	3.48	0.07	0.82	6.65	15.32	27.58
σ^2g/σ^2s		0.02	0.26	0.01	0.09	0.22	0.02

* **Significant at 0.05 Probability**
**** Significant at 0.01 Probability**

The data in Table 3a shows that the parent 1 gave the highest value 22.28 for EL, while the parent 6 exhibited a lowest value 16.00 in same trait. concerning the NEP^{-1} the parent 1 recorded the maximum value 1.50 and the minimum value 1.0 obtained by parent 8. For NRE^{-1}, the parent 6 record highest value 14.25, whilst the lowest value 12.16 recorded by parent 1. Regarding to the NGR^{-1} the parent 2 gave the maximum value 34.40, whereas the parent 1 had the minimum value 30.84. For 300 GW, the parent 8 exhibited the highest value 90.34g while the parent 5 had the lowest value 64.72g. For GYP^{-1} the maximum value 138.47g recorded by parent 7 whilst the minimum value 107.26g obtained by parent 4. Based on the data in Table 3acould be concluded that the parent 7 was best parental NEP^{-1}, NRE^{-1}and GYP^{-1}. These results are generally in accordance with the finding of (8,9,16).

Table 3a. Mean of parents for studied traits in maize

Parents	EL (cm)	NEP $^{-1}$	NRE^{-1}	NGR^{-1}	300 WG (g)	GYP $^{-1}$ (g)
1	22.58 a-c	1.50 ab	12.16 h	30.81 l	78.72 g-l	107.53 i
2	21.08 a-f	1.25 ab	12.23 h	34.40 i-l	85.61 b-g	115.26 hi
3	18.08 d-g	1.25 ab	14.13 e-g	32.33 kl	89.40 a-c	118.05 h
4	18.75 d-g	1.33 ab	13.50 gh	30.98 l	72.30 m-l	107.26 I
5	19.41 b-g	1.41 ab	13.66 gh	31.00 l	64.72 o	120.44 h
6	16.00 g	1.33 ab	14.25 e-g	32.50 kl	65.87 o	134.83 g
7	20.00 dg	1.41 ab	14.41 dg	32.66 kl	66.25 no	138.47 g
8	17.41 gf	1.00 b	13.83 e-h	33.61 j-l	90.34 a-c	120.49 h
Y¯	20.84	1.20	14.93	39.32	79.56	152.01
C.V.	10.10	22.67	6.70	6.47	4.87	3.54

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

The mean performance of single hybrids for the studied traits are present in the Table 3b. The hybrid 3x7 shows highest value 24.73 and 4x6 the lowest value 17.50 for EL, for NEP^{-1} maximum value 1.58 recorded by hybrid 4x7 and the minimum value 1.00 obtained by hybrids 1x2, 1x6, 1x8, 2x6,2x8, 3x5 and 4x8. In NRE^{-1}, the hybrid 4x7 produce the highest value 17.83, whilst the hybrid 2x3 had the smallest value 13.83. The largest value 45.25 was detected in hybrid 2x8, whereas the hybrid 2x6 gives lowest value 35.83 in NGR^{-1}. Concerning the 300 WG, hybrid 6x8 showed highest value 93.55g while, the hybrid 4x6 gave the smallest value 41.66g. For GYP^{-1} the hybrid 2x7 recorded highest value 174.46g and check hybrid had the lowest value 140.49g. This hybrid was superior in the most yield components, so that this reason could be due to superior the one parent in the most that. These results are generally in accordance with (9, 19)

Table 3b. Mean of hybrids for studied traits in maize hybrids

Hybrids	EL (cm)	NEP $^{-1}$	NRE^{-1}	NGR^{-1}	300 WG (gm)	GYP $^{-1}$ (g)
1x2	19.66 b-g	1.00 b	15.16b-g	41.03 a-g	67.91 n-o	143.86 g
1x3	20.58 a-f	1.41 ab	14.83 c-g	43.33 a-c	75.32 i-l	155.70 f
1x4	20.50 b-f	1.16 ab	14.33 e-g	38.16f-j	87.88 a-e	158.51 ef
1x5	20.08 b-g	1.25 ab	14.83 c-g	39.33 c-h	79.27 f-l	156.69 f
1x6	21.08 a-f	1.00 b	14.33 e-g	42.00 a-f	80.78 e-j	159.06 ef
1x7	21.75 a-e	1.16 ab	15.00 b-g	44.25 a-c	84.73 c-g	168.03 a-e
1x8	20.91 a-f	1.00 b	15.33 b-g	39.08 d-i	92.60 ab	160.89 d-f
2x3	20.41 b-f	1.16 ab	13.83 f-h	41.00 a-g	76.21 h-l	159.52 d-f
2x4	21.41 a-f	1.16 ab	15.33 b-g	41.08 a-g	87.52 a-e	172.16 ab
2x5	21.25 a-f	1.08 ab	15.50 b-f	41.58 a-g	79.89 f-k	171.59 a-c
2x6	19.50 b-g	1.00 b	15.16 b-g	35.83 j-k	83.49 c-h	161.42 c-f
2x7	22.00 a-d	1.33 ab	15.66 b-e	39.80 b-h	88.97 a-d	174.46 a
2x8	22.66 a-c	1.00 b	14.50 d-g	45.25 a	90.31 a-c	158.14 ef
3x4	22.75 a-c	1.16 ab	14.50 d-g	42.33 a-f	78.21 g-l	154.38 f
3x5	22.50 a-c	1.00 b	15.16 b-g	44.05 a-c	74.12 j-m	157.14 f
3x6	23.00 a-c	1.16 ab	17.66 a	43.66 a-c	72.86 k-n	158.09 ef
3x7	24.75 a	1.25 ab	16.66 ab	44.75 ab	89.15 a-d	159.13 ef
3x8	23.58 ab	1.16 ab	16.33 a-c	44.16 a-c	85.64 b-g	161.51 c-f
4x5	19.58 b-g	1.16 ab	15.00 b-g	39.83 b-h	75.56 i-l	164.80 a-f
4x6	17.50 e-g	1.16 ab	14.16 e-g	39.33 c-h	41.66 p	169.95 a-d
4x7	23.08 ab	1.58 a	17.83 a	41.16 a-g	80.60 e-j	163.43 b-f
4x8	21.83 a-d	1.00 b	16.40 a-c	42.58 a-f	75.04 i-m	162.56 b-f
5x6	21.16 a-f	1.33 ab	16.33 a-c	44.16 a-c	81.77 d-I	158.55 ef
5x7	20.08 b-g	1.16 ab	16.16 a-d	37.00 g-k	73.77 j-m	160.66 d-f
5x8	20.08 b-g	1.16 ab	15.50 b-f	41.00 a-g	86.43 a-f	161.53 c-f
6x7	21.41 a-f	1.08 ab	15.16 b-g	43.41 a-c	78.50 g-l	161.59 c-f
6x8	21.75 a-e	1.08 ab	14.66 c-g	38.16 f-j	93.55a	159.73 d-f
7x8	24.41 a-f	1.16 ab	14.16 e-g	40.83 a-g	87.59 a-e	168.50 a-e
Check	21.66 a-f	1.58 a	15.00 b-g	38.33 e-i	81.19 e-j	140.49 g
Y¯	20.84	1.20	14.93	39.32	79.56	152.01
C.V.	10.10	22.67	6.70	6.47	4.87	3.54

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

For estimation heterosis of mid parent, best parent and check hybrid were present in Table 4. Among the crosses, the calculated value for mid parents, best parents and check variety. Twelve hybrids had significant positive heterosis were found in EL over mid parents. The highest value was 5.95 for cross 3x6, while over best parents eight hybrids had significant positive heterosis and largest value 5.50 was recorded by cross 3x8. Over check hybrid observed the highest significant positive heterosis value 3.08 record by cross 3x7, while, lowest significant negative heterosis value -4.16 produce by 4x6. Regarding NEP $^{-1}$ over mid parents 24 hybrids showed negative heterosis except hybrids 1x6 and 3x5 significant gave negative heterosis, while over better parents most hybrids had negative heterosis except hybrids 1x2, 1x6 and 3x5 showed negative significant heterosis -0.50, -0.50 and -0.41 respectively, whereas, over check hybrid 22 crosses produced significant negative heterosis. For NGR^{-1} all hybrids had significant positive heterosis except hybrids 2x6 and 4x8 were non-significant over mid parents, while, over best parents also all hybrids recorded significant positive heterosis except cross 2x6. Over check hybrid negative heterosis are found in four hybrids and ten hybrids were significant positive heterosis. Heterosis values for NRE^{-1} over mid parents detected 22 crosses had significant positive heterosis and the maximum value 3.87 for cross 4x7 whereas, minimum value was 0.04 for cross 7x8. Over better parents 14 crosses showed significant positive heterosis and greater value 3.41 was recorded by cross 3x6 and 4x7, while, smallest value -0.30 recorded by cross 2x3, while over check hybrid six hybrids showed significant positive heterosis, the cross 4x7 gave highest value 2.83 and cross 2x3 lowest value -1.16. Regarding to 300 GW 18 crosses exhibited significant positive heterosis with maximum value 15.44 for cross 6x8 over mid parents. Over best parents 11 hybrids recorded significant negative heterosis, over check hybrid 7 hybrids produced significant positive heterosis and the hybrid 6x8 gave greater value 12.36, while, the hybrid 4x6 recorded smallest value -39.52. For estimating heterosis for GYP^{-1} over mid parents all hybrids showed significant positive heterosis and the maximum value 60.89 found in the hybrid 2x4, while, minimum value 24.93 found in the hybrid 6x7. Over best parents all hybrid showed significant positive heterosis and highest value was 64.90 which gave hybrid 2x4, whereas, lowest value 20.66 was detected in the 3x7. Over check hybrid all hybrids recorded significant positive heterosis except hybrid1x2 was non-significant and the greater value 33.97 was recorded in cross 2x7, and hybrid 1x2 showed smallest value 3.36. For the same traits, six hybrids exhibited significant positive heterosis over mid parent, best parent and check hybrid, the hybrids were 3x6, 3x7, 3x8, 4x7, 2x4 and 5x7. That heterosis is a quantitative phenomenon resulting from the action of a large group of genes that may work by partial dominant, dominant and over dominant that there are major genes directly related to yield or to metabolic activities that work complementary to show the trait and that the latter may be the one with the most effective role in showing heterosis. The results appeared that the hybrids gave positive value were under over dominant effect, while the hybrids that gave negative values were under partial dominant effect. Present results are in agreement with the finding of (5,8,11,12,13, 20).

Table 4. Heterosis based on deviation of F1 from mid parents, best parents and check variety for studied traits in maize

Hybrids	EL			NEP $^{-1}$			NRE^{-1}			NGR^{-1}		
	M. P	B. P	Ch. V.	M. P	B. P	Ch. V.	M. P	B. P	Ch. V.	M. P	B. P	Ch. V.
1x2	-2.16	-2.91	-2.00	-0.37	-0.50*	-0.58**	2.96**	2.93**	0.16	8.42**	6.63**	2.70
1x3	0.25	-2.00	-1.08	0.04	-0.08	-0.16	1.68**	0.70	-0.16	11.75**	11.00**	5.00*
1x4	-0.16	-2.08	-1.16	-0.25	-0.33	-0.41*	1.50*	0.83	-0.66	7.26**	7.18**	-0.16
1x5	-0.91	-2.50	-1.58	-0.208	-0.25	-0.33	1.91**	1.16	-0.16	8.42**	8.33**	1.00
1x6	1.79	-1.50	-0.58	-0.41*	-0.50*	-0.58**	1.12*	0.08	-0.66	10.34**	9.50**	3.66*
1x7	0.45	-0.83	0.08	-0.29	-0.33	-0.41*	1.70**	0.58	0.00	12.50**	11.58**	5.91**
1x8	0.91	-1.67	-0.75	-0.25	-0.50	-0.58**	2.33**	1.50**	0.33	6.86**	5.46**	0.75
2x3	0.83	-0.67	-1.25	-0.08	-0.08	-0.41*	0.65	-0.30	-1.16	7.63**	6.60**	2.66
2x4	1.50	0.33	-0.25	-0.12	-0.16	-0.41*	2.46**	1.83**	0.33	8.39**	6.68**	2.75
2x5	1.00	0.17	-0.41	-0.25	-0.33	-0.50*	2.55**	1.83**	0.50	8.88**	7.18**	3.25
2x6	0.95	-1.58	-2.16	-0.29	-0.33	-0.58**	1.92**	0.91	0.16	2.38	1.43	-2.50
2x7	1.45	0.91	0.33	0.00	-0.08	-0.25	2.34**	3.08**	0.66	6.27**	5.40**	1.47
2x8	3.41**	1.58	1.00	-0.12	-0.25	-0.58**	1.46*	0.66	-0.50	11.24**	10.85**	6.91**
3x4	4.33**	4.00**	1.08	-0.12	-0.16	-0.41*	0.68	0.36	-0.50	10.67**	10.00**	4.00
3x5	3.75**	3.08*	0.83	-0.33*	-0.41*	-0.58**	1.26**	1.03	0.16	12.38**	11.72**	5.72**
3x6	5.95**	4.91**	1.33	-0.12	-0.16	-0.41*	3.47**	3.41**	2.66**	11.25**	11.16**	5.33
3x7	5.70**	4.75**	3.08*	-0.08	-0.16	-0.33	2.39**	2.25**	1.66*	12.25**	12.08**	6.41**
3x8	5.83**	5.5**	1.91	0.04	-0.08	-0.41*	2.35**	2.20**	1.33*	11.19**	10.55**	5.83**
4x5	0.50	0.16	-2.08	-0.20	-0.25	-0.41*	1.41*	1.33*	0.00	8.84**	8.83**	1.50
4x6	0.12	-1.25	-4.16**	-0.16	-0.16	-0.41*	0.29	-0.08	-0.83	7.59**	6.83**	1.00
4x7	3.70**	3.08*	1.41	0.20	0.16	0.00	3.87**	3.41**	2.83**	9.34**	8.50**	2.83
4x8	3.75**	3.75**	0.16	-0.16	-0.33	-0.58**	2.73**	2.56**	1.40*	10.28	8.96**	4.25*
5x6	3.45**	1.75	-0.50	-0.04	-0.08	-0.25	2.37**	2.08**	1.33*	12.41**	11.66**	5.83**
5x7	0.37	0.08	-1.58	-0.25	-0.25	-0.41*	2.12**	1.75*	1.16	5.16**	4.50*	-1.33
5x8	1.66	0.66	-1.58	-0.04	-0.25	-0.41*	1.75**	1.66*	0.50	8.69**	7.38**	2.66
6x7	3.41**	1.41	-0.25	-0.29	-0.33	-0.50*	0.83	0.75	0.16	10.83**	10.75**	5.08**
6x8	5.04**	4.33	0.08	-0.08	-0.25	-0.50*	0.62	0.83	-0.33	5.10**	4.55*	-0.16
7x8	2.70*	1.41	-0.25	-0.04	-0.25	-0.41*	0.04	0.33	-0.83	7.69**	7.21**	2.50

Hybrids	300 WG			GYP $^{-1}$		
	M. P	B. P	Ch. V.	M. P	B. P	Ch. V.
1x2	-14.25**	-17.70**	-13.28**	32.46**	28.59**	3.36
1x3	-8.74**	-14.08**	-5.87*	42.91**	37.65**	15.21**
1x4	12.37**	9.16**	6.69*	51.12**	50.98**	18.02**
1x5	7.545**	0.54	-1.92	42.70**	36.25**	16.20**
1x6	8.48**	2.05	-0.41	37.88**	24.23**	18.57**
1x7	12.24**	6.00*	3.54	45.025**	29.55**	27.53**
1x8	8.068**	2.26	11.41**	46.87**	40.39**	20.39**
2x3	-11.29**	-13.19**	-4.98	42.86**	41.47**	19.03**
2x4	8.57**	1.91	6.33	60.89**	64.90**	31.66**
2x5	4.72*	-5.71*	-1.29	53.73**	51.15**	31.09**
2x6	7.75**	-2.11	2.30	36.37**	26.59**	20.93**
2x7	13.04**	3.36	7.78**	47.59**	35.98**	33.97**
2x8	2.33	-0.03	9.12**	40.26**	37.65**	17.65**
3x4	-2.63	-11.19**	-2.97	41.73**	36.33**	13.89**
3x5	-2.94	-15.28**	-7.06**	37.89**	36.70**	16.64**
3x6	-4.77*	-16.54**	-8.32**	31.65**	23.26**	17.60**
3x7	11.32**	-0.25	7.96**	30.87**	20.66**	18.64**
3x8	-4.22	-4.69	4.45	42.24**	41.01**	21.02**
4x5	7.04**	3.26	-5.63*	50.95**	44.36**	24.31**
4x6	-27.42**	-30.63**	-39.52*	48.90**	35.12**	29.46**
4x7	11.32**	8.30**	-0.59	40.56**	24.95**	22.93**
4x8	-6.27*	-15.29**	-6.14*	48.68**	42.06**	22.06**
5x6	16.46**	15.89**	0.58	30.91**	23.72**	18.05**
5x7	8.288**	7.52*	-7.41*	31.20**	22.19**	20.17**
5x8	8.90**	-3.90	5.24	41.06**	41.03**	21.04**
6x7	12.43**	12.25**	-2.69	24.93**	23.11**	21.09**
6x8	15.44**	3.21	12.36**	32.07**	24.90**	19.24**
7x8	9.29**	-2.75	6.40*	39.01**	30.02**	28.00**

*Significant at 0.05 Probability

** Significant at 0.01 Probability

Estimation of general combining ability (GCA) effect was present in Table 5 for all studied traits. From the same Table the parent 7 gave highest positive significant values 6.17, 0.52 and 0.07 for GYP $^{-1}$, NRE^{-1} and NEP $^{-1}$ respectively, while parent 1 recorded lowest negative significant values -0.60 and -5.32 in NRE^{-1}and GYP $^{-1}$ respectively while parent 2 gave lowest value 0.03 in NEP $^{-1}$. Two maximum positive significant value 0.72 and 1.44 were present parent 3 for EL and NGR^{-1} respectively, whereas parents 8 and 1 recorded minimum negative value 0.02 and 0.53 in EL and NGR^{-1} respectively. For 300 GW shows the greater positive significant value 7.61 for parent 8, on the other hand, the lowest negative significant value 5.12 found in the parent 6. The parents which gave significant desirable GCA effect indicate that contribution of this parent increases the improvement of characters in their hybrids. The present results are corroboration with the finding of (9,11,13, 19)

Table 5. GCA effect of parents for studied traits in maize

Parents	Traits					
	EL (cm)	NEP $^{-1}$	NRE^{-1}	NGR^{-1}	300 WG (g)	GYP $^{-1}$ (g)
P1	0.31*	0.03*	-0.60**	-0.53*	1.02*	-5.32**
P 2	-0.07	-0.03*	-0.47**	0.02	2.98**	0.07
P 3	0.72**	0.02	0.22*	1.44**	1.46**	-2.93**
P 4	-0.24*	-0.02*	0.03	-0.77**	-4.45**	-1.06*
P 5	-0.03	0.03*	0.16*	-0.52*	-3.53**	0.08
P 6	-1.22**	-0.01	0.09*	-0.25*	-5.12**	2.70**
P 7	0.55**	0.07*	0.52**	0.23	0.01	6.17**
P 8	-0.02	-0.10*	0.03	0.38*	7.61**	0.27
S.E.	0.31	0.04	0.15	0.44	0.66	0.89

*** Significant at 0.05 Probability**
**** Significant at 0.01 Probability**

The data in Table 6 shows the Specific Combining Ability (SCA) effects of Hybrids for the different traits. The hybrid 3x7 gave highest value 2.89 and hybrid 3x8 gave lowest value -1.97 for EL. Concerning for NEP $^{-1}$ the hybrid 5x8 recorded maximum value 0.21, while the hybrid 3x5 recorded minimum value -0.24. The hybrid 4x7 gave 2.35 for NRE^{-1}, whereas, hybrid 7x8 recorded the smallest value -2.86. The largest and smallest values 5.59 and -7.64 were observed in hybrids 5x6 and 6x8 respectively. The hybrid 1x4 recorded the largest value 11.79 in 300 GW, on the other hand, the hybrid 4x6 obtained smallest value -28.26 in the trait 300 GW. The hybrid 7x8 gave highest value 16.50, while, the hybrid 4x8 gave lowest value -31.92 in GYP $^{-1}$. The hybrid 3x7 was more successful in studied traits, so that it could be concluded that parents could be used in breeding programs to get better hybrid combination for maize inbred lines. Positive relationship between SCA effect of kernel yield and yield contributory the significant estimates of GCA and SCA variances suggested the importance of both additive and non-additive gene actions for the expression of all the characters. Therefore, for yield improvement in maize both additive and non-additive genes should be exploited through a suitable breeding method., these results were in agreement with (1, 3, 11, 19).

Table 6. Specific combining ability effects of hybrids for studied traits in maize.

Hybrids	Traits					
	EL (cm)	NEP $^{-1}$	NRE $^{-1}$	NGR $^{-1}$	300 WG (g)	GYP $^{-1}$ (g)
1x2	-1.31*	-0.18*	1.33**	2.19*	-15.62**	-3.21*
1x3	-1.19*	0.17*	0.30*	3.06**	-6.69**	11.63**
1x4	-0.30	-0.02	-0.009	0.11	11.79**	12.57**
1x5	-0.92*	-0.07	0.36*	1.03*	2.26*	9.60**
1x6	1.25*	-0.20	-0.06	3.44**	5.36**	9.35**
1x7	0.14	-0.12*	0.16	5.19**	4.16**	14.84**
1x8	1.11*	0.12*	-0.54*	-7.58**	1.58*	-20.65**
2x3	-0.97*	0.009	-0.82**	0.18	-7.76**	10.06**
2x4	0.99*	0.05	0.85**	2.48**	9.47**	20.82**
2x5	0.62*	-0.09*	0.8**	2.73**	0.92	19.09**
2x6	0.05	-0.13*	0.63*	-3.28**	6.11**	6.31**
2x7	-1.71**	0.11*	0.69*	0.19	6.45**	15.88**
2x8	1.84*	0.10*	-1.77**	0.50	0.30	-31.74**
3x4	1.53*	-0.007	-0.66*	2.30**	1.68*	6.05**
3x5	1.07*	-0.24**	-0.12	3.77**	-3.32*	7.65**
3x6	2.75**	-0.06	1.60**	3.12**	-2.99*	5.99**
3x7	2.89**	-0.02	1.00**	3.71**	8.15**	3.56*
3x8	-1.97**	0.09	-0.05	-6.59**	3.98**	-16.56**
4x5	-0.86*	-0.02	-0.10	1.77*	4.03**	13.44**
4x6	-1.76**	0.02	-0.87**	1.01*	-28.26**	15.97**
4x7	2.03**	0.10*	2.35**	2.34**	5.52**	5.98**
4x8	-0.13	-0.08	-0.06	-3.32**	-5.94**	-31.92**
5x6	1.68**	0.12*	1.16**	5.59**	1.91**	3.42*
5x7	-1.16*	-0.12*	0.56*	-2.06	-2.22*	2.06*
5x8	-0.50	0.21*	-1.17**	-5.52**	-4.88**	-23.23**
6x7	1.34*	-0.15*	-0.36*	4.08**	4.09**	0.37
6x8	-1.53*	0.19*	-1.22**	-7.64**	8.15**	-18.50**
7x8	-1.69*	0.11*	-2.86**	-6.29**	-12.86**	16.50**
S.E.	0.97	0.14	0.47	1.35	2.04	2.74

*** Significant at 0.05 Probability**

**** Significant at 0.01 Probability**

The genetic parameters for six studied traits are show in the Table 7., it is clear that additive, dominance and environmental variances were significant from zero for studied traits, indicating their important genetic controlling inheritance of these traits. The results showed that the values of dominance variance were greater than additive variance in these traits, indicating the dominance genetic effect were more important in the inheritance for all traits, also it is showed that phenotypic variance was greater than genotypic variance in studied traits, this caused to increase the values of heritability in broad sense compared with heritability in narrow sense in studied traits. The heritability in broad sense were maximum in all traits ranged between 0.77 and 0.97 except NEP $^{-1}$ plant $^{-1}$ was 0.33, while, heritability in narrow sense gave the smallest values for all traits ranged between ranged 0.03 to 0.29, which reflecting the lowest role of additive gene effect of these traits. Traits that revealed high heritability in broad sense reflect the high dominance genetic variation method, signifying the important of hybridization method to improve these traits. The ratio Vg/Vs was less than one for all studied traits. The average degree of dominance is more than one for all trait indicating the presence of over dominance gene action for all traits. For the expected genetic improvement as a percent was low for all traits and the value ranged between 0.75 to 7.26. The decrease in genetic advance values due to decrease in heritability narrow sense values. These results are a line with the results of (4,14, 16, 3,2, 20).

Table 7. variance components and genetic parameters for studied traits in maize.

Genetic parameters	Traits					
	EL (cm)	NEP $^{-1}$	NRE^{-1}	NGR^{-1}	300 WG (g)	GYP $^{-1}$ (g)
σ^2A	0.63 ± 0.33	0.004 ± 0.002	0.25 ± 0.12	0.85 ± 0.47	36.47 ± 17.35	23.31 ± 11.28
σ^2D	3.45 ±0.99	0.004 ± 0.002	1.33 ±0.36	22.47 ±5.99	81.87 ± 21.58	414.21 ± 107.74
σ^2E	1.16 ± 0.19	0.02 ± 0.004	0.27 ± 0.04	2.21 ± 0.36	5.10 ± 0.85	9.19 ± 1.53
σ^2G	4.09	0.01	1.58	23.32	118.35	437.53
σ^2P	5.25	0.03	1.86	25.54	123.46	446.72
H.b.s.	0.77	0.33	0.85	0.91	0.95	0.97
H.n.s.	0.12	0.11	0.13	0.03	0.29	0.05
Vg/Vs	0.09	0.26	0.09	0.01	0.22	0.02
$\bar{a}$	3.30	1.41	3.26	7.27	2.11	5.96
GA	0.48	0.04	0.32	0.29	5.77	1.94
GA%	2.35	3.41	2.19	0.75	7.26	1.27

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