



Diallel Analysis for Yield Contributing Traits of Seven Inbred lines and Their F1 Crosses of Yellow Maize

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Abstract

The field experiment was performed during two successive 2022 and 2023 summer seasons at the experimental farm Faculty of Agricultural, Moshtohor, Banha University. Seven diverse maize inbred lines (line 635 (P₁), line 524 (P₂), line 423 (P₃), line 231 (P₄), line 418 (P₅), line 200 (P₆) and line 202 (P₇)). The lines were obtained from Faculty of Agricultural Moshtohor, Banha University, Egypt. To estimate of mean performance, combining ability, genetic parameters and heritability for ear weight, number of ear/plant, ear length, ear diameter, number of rows/ear, number of kernels/row, cub weight, 100-kernel weight, kernel weight/ear and kernel yield/plant. The results showed that mean of squares of GCA and SCA were highly significant for all traits. The ratio of (GCA/SCA) variance was less than unity for all traits, this emphasized that non-additive gene action was the prevailed type in controlling in this trait; consequently, hybrid breeding system would be the most efficient method for improving of these traits. The results reveal that positive and highly significant GCA effects were manifested in the parental lines P₂ and P₆ Indicating that these lines considered to be good combiner for kernel yield/plant and can be used breeding programs. The SCA effects of kernel weight/ear are given positive and highly significant SCA effects were registered by the crosses (P₁ x P₅), (P₁ x P₆), (P₂ x P₄), (P₂ x P₆), (P₂ x P₇), (P₃ x P₄) and (P₃ x P₇). Narrow sense heritability evaluate were recorded high for ear weight (76.158%), number of ears/plant (70.324%), ear length (88.019%), ear diameter (84.911%), cub weight (76.633%), rows/ear (84.210%), number of kernels/row, 100-kernel weight (84.468%), kernel weight/ear (71.667%) and kernel yield/plant (54.730%).

Keywords: Maize, combining ability, genetic parameters and heritability.

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1. Introduction

Maize, *Zea mays* L. (corn), is the most abundantly produced cereal in the world. It is grown in every continent except Antarctica. White, yellow, and red are the most common cultivated maize types. The white and yellow varieties are preferred by most people depending on the region. The global maize area (for dry grain) amounts to 197 M ha [1]. It is an established and important human food crop in a number of countries, especially in SSA, Latin America, and a few countries in Asia, where maize consumed as human food contributes over 20% of food calories [2].

In Egypt, it is used as human food, livestock and poultry feed as well as a raw material for industrial products such as oil and starch [3]. Maize production in 2023 in Egypt was estimated at a near-average level of 7.1 million tons [4]. [5] in Egypt the maize is one of the most important strategic crops, because it is a food crop for humans and animals, and it is also used in many food industries, one solution for this is the development of a hybrid variety with higher yields and broader environment adaptability [6]. The first step to achieve

these highly desirable characteristics of hybrid varieties is the development of promising inbred lines. The analysis of diallel design can be applied using Griffing's method, which explores GCA and SCA [7,8,9]. Furthermore, this analysis can be employed to study the additive and non-additive effects of studied traits [10,11]. SCA is related to dominance effects; however, GCA is ascribed to additive impacts [12]. Numerous studies investigated how yield traits in maize are genetically controlled. Non-additive and additive gene actions are crucial for yield contributing trait inheritance in recommended conditions [13,14]. However, non-additive effects predominantly influence these traits. Other studies presented contrasting evidence, indicating additive gene actions as the primary influence on grain yield inheritance [15,16].

Inbred lines serve as fundamental genetic resources for maize improvement efforts. Understanding the extent and distribution of genetic diversity among maize inbred lines is crucial for effective breeding strategies to develop promising

hybrid and introgression favorable alleles to enhance crop productivity and resilience [17].

[18] reported that the view of the importance of maize, researchers are utilizing available genetic resources to reconstruct the ideotype of the plant in order to meet the ever increasing requirements of the population through improvement in grain yield, other desirable agronomic and phenological characters as well as quality [19].

The success of any crop improvement program not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection [20,21]. Genetic variability for agronomic characters therefore is a key component of breeding programs for broadening the gene pool of crops [22].

Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to

determine the relative importance of genetic effects [23]. The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value.

Therefore, the main objectives of this study were as follows:

1. Studied the general and specific combining ability of some lines of maize lines.
2. Studied the genetic diversity and gene action of the yield and its components for maize lines.
3. Studied the heritability in maize lines.

2. Material and Methods

2.1. Material and experimental design

The field experiment was performed during two successive summer seasons 2022 and 2023 at the experimental farm Faculty of Agricultural, Moshtohor, Banha University. Seven diverse maize inbred lines (line 635 (P₁), line 524 (P₂), line 423 (P₃), line 231 (P₄), line 418 (P₅), line 200 (P₆) and line 202 (P₇)). The lines were obtained from Faculty of Agricultural Moshtohor, Banha University, Egypt. The origin of the seven maize lines is presented in Table (1)

Table 1: The origin and name of the seven maize lines under this study

Number	Name	Origin
P ₁	Line 635	Egypt
P ₂	Line 524	Egypt
P ₃	Line 423	Egypt
P ₄	Line 231	Egypt
P ₅	Line 418	Egypt
P ₆	Line 200	Egypt
P ₇	Line 202	Egypt

The lines were sown in the first season 2022 at 30 may. All possible parental combinations, excluding reciprocates were made among the seven parental lines to produce twenty-one crosses. Necessary precautions were adopted during the crossing operations to avoid contaminations of the genetic material. The seed of the twenty-one hybrids along with seven lines parents were grown in second season 2023 and evaluated under all recommend practices for maize productions were applied from sowing till harvesting. Using randomized complete block design in three replications. The experimental plot consists six rows 6 m., long and 70 cm for width and inter between plant distances was kept 20 cm.

2.2. The following data were recorded individual plant basis

2.2.1. Grain yield and its Contributing

Number of ears/plants, ear weight (g), ear length (cm), ear diameter (cm), number of rows/ear, number of kernels/rows, cub weight (g), 100-kernels weight, kernel weight/ear and kernel yield/plant.

2.3. Diallel analysis

The collected data were subjected to the standard analysis of variance of the randomized complete blocks design according to [24].

Griffing,s approcha: Estimation of the both general (GCA) and specific (SCA) combining ability were computed according to [25], designated as method 2, model 1 for the studied traits. The parameters of GCA and SCA for studied traits were estimated as follows:

$$SS \text{ due to } GCA = \frac{1}{P+2} \{ \sum (X_i + X_{ii})^2 - \frac{4}{P} \chi^2 \}$$

$$SS \text{ due to } = \sum_j \sum_i j \chi^2 ij - \frac{1}{P+2} \sum I (\chi_i + \chi_{ii})^2 + \frac{1}{(P+1)(P+2)} \chi^2$$

The general (gi) and specific (Sij) combining ability effects are estimated as follows: $gi = \frac{1}{P+2} [\chi_i + \chi_{ii} - \frac{2}{P} \chi]$

$$Sij = \chi_{ii} - \frac{1}{P+2} [\chi_i + \chi_{ii} + \chi_j + \chi_{jj}] + \frac{1}{(P+1)(P+2)} \chi$$

Standard error for effects and differences between effects were calculated as follows: $SE(gi) = [\frac{P-1}{P(P+2)} \delta^2 e]^{\frac{1}{2}}$

$$SE(S_{ij}) = \left[\frac{P_2 + P + 2}{(P+1)(P+2)} \delta^2 e \right] \frac{1}{2}$$

Where: P: is the number of parents. Xi: is the sum of the means of parent (i). and its crosses. Xii: is the mean of the parent (i). X...: is the sum of the means of all genotypes. Xj: is the sum of means of parent (j) and its crosses. Xjj: is the mean of the parent. $\delta^2 e$: is the error mean of square for the randomized complete block design.

2.3.1. Genetic variance and derived parameters

According to [26,27,28], the components of D, H1, H2, h2, F and \hat{E} were calculated using the following equation:

$$D = V_{O}L_0 - \hat{E}. H_1 = V_{O}L_0 - 4W_{O}L_0 + 4V_{i}l_i - (3n-2) \hat{E}/n. H_2 = 4V_{i}l_i - 4V_{O}l_i - 2 \hat{E}. F = 2V_{O}L_0 - 4W_{O}L_0 - 2(n-2) \hat{E}/n. h^2 = 4(M_{Li} - M_{IO})^2 - 4(n-1) \hat{E}/n^2$$

$$\hat{E} = [\text{Error SS} + \text{Reps SS}/df \text{ error}] / \text{number of replicates}$$

Where: D: Variation due to additive effects. H1: Component of variation due to the dominance of the genes summed over loci. H2: the component of variation arising from the (h) increment of all segregating genes. F: Refers to the relative frequencies of dominant versus recessive genes in the parents. h²: Dominance effects as the algebraic sum overall loci in heterozygous phase in all crosses. n: Number of parents of arrays. E: The expected environmental component of variation.

2.3.2. Derived parameters in F1

- a- **(H1/D)** = The mean average degree of dominance. It could be classified as follows:
 - D>H1 and the intercept is positive refers to partial dominance.
 - D=H1 and regression line passes through the point of origin indicates complete dominance.
 - D<H1 and the intercept is negative refers to over dominance.
- b- **(H2/4H1)** = Refers to the proportion of genes with positive and negative effects in the genetic constitution of parental genotypes.

When $U \neq V$, it means unequal allelic frequencies and the ratio is less than its maximum value (0.25) and *vice versa*.
- c- **KD/KR** = $\frac{(4DH1)^{0.5} + F1}{(4DH1)^{0.5} - F1}$

This ratio refers to the proportion of dominance and recessive genes in the studied parents.
- d- **Hertability in narrow T(n) sense:** Was estimated according to [29].

3. Results and discussion

3.1. Mean Performance

The mean performance of seven lines and their F1 crosses for ear length presented in Table (2), it ranged from 10 to 14.7 cm for parents, as well as it changed from 13.3 to

19.0 cm for crosses. The parent P2 and the crosses (P4 x P6), (P5 X P7), (P3 x P7) and (P5 X P7) were given the highest values for ear length cm. but the parent P3 and cross (P6 X P7) were given lowest values for this trait. The mean performance it ranged from 2.7 to 4.2 cm for parents, as well as it changed from 2.2 to 4.3 cm for crosses. The parent P1 and the crosses (P1 x P3), (P2 x P4), (P3 x P4) and (P4 x P7) were given the highest values for ear diameter cm. but the parent P5 and cross (P4 X P5) were given lowest values for this trait. The mean performance it ranged from 14.3 to 27.7 cm for parents, as well as it changed from 11.4 to 39.7 cm for crosses. The parent P7 and the crosses (P1 x P3), (P2 x P4), (P2 x P5), (P4 x P5), (P4 x P6), (P4 x P7) and (P5 x P7) were given the highest values for cub weight. But the parent P5 and cross (P3 x P6) were given lowest values for this trait. The mean performance of seven lines and their F1 crosses for number of rows/ear it ranged from 8.00 to 12.00 for parents, as well as it changed from 10.7 to 18 rows for crosses. The parent P6 and the crosses (P1 x P5), (P1 x P6), (P2 x P3), (P2 x P4), (P3 x P4), (P3 x P7) and (P4 x P7), were given the highest values for number of rows/ear. But the parent P4 and cross (P2 x P6) were given lowest values for this trait. The mean performance of seven lines and their F1 crosses for ear weight (g) it ranged from 57.0 to 83.3 (g) for parents, as well as it changed from 106.3 to 197.0 (g) for crosses. The parent P2 and the crosses (P1 x P7), (P2 x P4), (P2 x P6), (P2 x P7), (P4 x P5) and (P5 x P7), were given the highest values for ear weight. But the parent P1 and cross (P1 x P3) were given lowest values for this trait. The results are in agreement with those obtained by [30,31].

The present in Table (3) show the mean performance of seven lines and their F1 crosses for number of ear/plant, the mean performance it ranged from 1.0 to 1.3 (ear) for parents, as well as it changed from 1.00 to 2.9 (ear) for crosses. The parent P7 and the crosses (P1 x P2), (P2 x P4), (P2 x P6), (P2 x P7) and (P4 x P6), were given the highest values for number of ear/plant. The mean performance of seven lines and their F1 crosses for number of kernels/row it ranged from 12.7 to 13.00 (kernel) for parents, as well as it changed from 22.0 to 40.0 (kernel) for crosses. The parents P6, P7 and the crosses (P1 x P2), (P1 x P4), (P2 x P3), (P2 x P6), (P2 x P7), (P3 x P5), (P4 x P6) and (P4 x P7), were given the highest values for number of kernels/row. But the parent P3 and cross (P3 x P4) were given lowest values for this trait. The mean performance for 100-kernel weight (g) it ranged from 21.00 to 30.00 (g) for parents, as well as it changed from 24.8 to 40.3 (g) for crosses. The parents P1, P6 and the crosses (P1 x P3), (P1 x P5), (P1 x P7), (P2 x P3), (P2 x P4), (P2 x P5), (P2 x P6), (P3 x P5), (P3 x P7), (P4 x P5) and (P4 x P7), were given the highest values for 100-kernel weight. The results are in agreement with those obtained by [30,31]. But the parent P5 and cross (P3 x P6) were given lowest values for this trait. The mean performance kernel weight/ear (g) it ranged from 31.7 to 67.0 (g) for parents, as well as it changed from 79.0 to 155.0 (g) for crosses. The parents P2, P4 and the crosses (P1 x P7), (P2 x P4), (P2 x P6) and (P5 x P7), were given the highest values for kernel weight/ear. But the parent P1 and cross (P1 x P3) were given lowest values for this trait. The mean performance of seven lines and their F1 crosses for kernel yield/plant (g) it ranged from 31.7 to 67.0 (g) for parents, as well as it changed

from 91.27 to 405.5 (g) for crosses. The parents P₂, P₄ and the crosses (P₁ x P₆), (P₂ x P₄), (P₂ x P₆), and (P₂ x P₇), were given the highest values for kernel yield/plant. But the parent P₁ and cross (P₆ x P₇) were given lowest values for this trait. [32] showed that the significant differences in the days to 50% silking, plant height, number of ears/plant number of kernels/row, 300 kernel weight distinguished by its

superiority in the trait of plant height, number of ears / plant and kernel yield plant. It was also found that the pure line in the traits of days to 50% silking, the pure line in 300 kernel weight, and pure line in the trait of number of grains / rows. the cross (5x7) was the best hybrid in traits, with 300 grain weight and plant grain yield. The results are in agreement with those obtained by [30,31].

Table 2: Mean performance for some ear traits in 7 in-beard lines and their F₁ crosses

Genotypes	Ear length/cm	Ear diameter/cm	Cub weight/g	Number of rows/ear	Ear weight (g)
P1	12.7	4.2	25.3	10.7	57.0
P2	14.7	3.7	16.3	8.0	83.3
P3	10.0	2.8	17.3	8.7	64.3
P4	13.7	4.1	15.2	8.0	76.3
P5	11.0	3.2	14.3	10.7	74.7
P6	12.7	2.7	16.8	12.0	68.7
P7	13.3	3.5	27.7	10.0	65.3
P1 x P2	17.7	2.7	18.5	12.0	107.0
P1 x P3	16.7	3.8	27.3	12.7	106.3
P1 x P4	14.77	3.13	16.90	12.67	119.0
P1 x P5	14.7	3.6	20.0	14.0	132.3
P1 x P6	16.7	3.3	17.6	14.7	138.0
P1 x P7	15.4	3.6	21.7	13.3	152.3
P2 x P3	14.0	2.2	18.2	14.7	130.3
P2 x P4	15.0	4.3	28.9	15.3	171.7
P2 x P5	16.3	2.6	29.0	14.0	115.0
P2 x P6	15.7	2.9	18.7	10.7	162.5
P2 x P7	16.3	3.6	22.8	12.7	151.3
P3 x P4	13.7	4.2	17.0	16.0	131.5
P3 x P5	15.7	2.9	24.5	13.3	113.0
P3 x P6	14.7	3.0	11.4	13.3	103.3
P3 x P7	17.3	3.3	26.3	14.7	143.0
P4 x P5	15.7	2.3	35.8	14.0	163.7
P4 x P6	19.0	3.7	30.3	13.3	123.3
P4 x P7	15.5	3.7	30.7	18.0	135.7
P5 X P6	15.7	4.0	19.3	12.7	141.2
P5 X P7	18.7	3.3	39.7	18.0	197.0
P6 x P7	13.03	3.83	25.05	14.00	116.3
Mean	15.0	3.4	22.6	12.9	119.4
l. S. D _{0.05}	1.204	0.563	1.759	2.062	3.008
L.S.D _{0.01}	1.597	0.746	2.333	2.735	3.991

Table 3: Mean performance for yield and its components traits in 7 in-beard lines and their F₁ crosses

Genotypes	Number of ear/plant	Number of kernels/row	100-kernel weight/g	Kernel weight/ear	Kernel yield/plant
P1	1.0	17.0	30.0	31.7	31.7
P2	1.0	17.7	24.3	67.0	67.0
P3	1.0	14.0	25.0	47.0	47.0
P4	1.0	15.3	23.7	61.2	61.2
P5	1.0	12.7	21.0	60.3	60.3
P6	1.2	23.0	26.3	51.8	60.8
P7	1.3	23.0	22.8	34.7	47.0
P1 x P2	2.3	32.0	27.9	88.5	206.7
P1 x P3	1.7	25.0	40.3	79.0	131.3
P1 x P4	1.03	32.00	24.97	102.10	102.10
P1 x P5	1.5	24.0	31.9	113.3	169.5
P1 x P6	1.8	23.07	26.4	120.4	220.6
P1 x P7	1.0	29.7	30.1	130.7	130.7
P2 x P3	1.8	34.0	31.1	112.2	205.3
P2 x P4	2.0	25.0	34.7	142.8	285.5
P2 x P5	1.3	29.0	37.0	86.0	112.7
P2 x P6	2.9	32.0	35.6	141.7	405.5
P2 x P7	2.3	32.0	25.8	128.5	299.3
P3 x P4	1.7	22.0	26.7	114.5	191.2
P3 x P5	1.7	34.0	39.0	88.5	152.9
P3 x P6	1.0	24.0	24.8	91.9	91.9
P3 x P7	1.7	24.0	37.3	116.7	194.2
P4 x P5	1.1	23.7	34.1	127.8	127.8
P4 x P6	2.0	37.7	26.8	93.0	186.0
P4 x P7	1.1	40.0	35.7	105.0	115.4
P5 X P6	1.3	34.3	31.1	121.9	162.9
P5 X P7	1.0	37.7	36.7	155.0	155.0
P6 x P7	1.0	26.67	30.33	91.27	91.27
Mean	1.5	26.6	30.0	96.6	146.9
1. S. D _{0.05}	0.557	3.465	1.861	3.730	54.513
L.S.D _{0.01}	0.740	4.597	2.469	4.948	72.319

3.2. General and specific combining ability

Analyses of variance for general and specific combining abilities for ear weight, number of ear/plant, ear length, ear diameter, number of rows/ear, number of kernels/row, cub weight, 100-kernel weight, kernel weight/ear and kernel yield/plant are presented in Table (4 and 5). Showed that the mean of squares of GCA and SCA were highly significant, suggesting the importance of additive

and non- additive gene effects in the expression of ear weight. Similar results were recorded by [33,34,35,32,37,31] The ratio of (GCA/SCA) variance was less than unity, this emphasized that non-additive gene action was the prevailed type in controlling in this trait; consequently, hybrid breeding system would be the most efficient method for improving these traits. These results were agreement with reported by [33,34,37,38,32,37,31].

Table 4: Mean squares of general (GCA) and specific combining ability (SCA) of 7 in-beard lines and their f1 crosses

S. V	Df	Ear weight (g)	Number of ear/plant	Ear length/cm	Ear diameter/cm	Cub weight/g
GCA	6	41465.33**	6.65**	634.70**	32.67**	1593.90**
SCA	20	8257.69**	1.37**	70.77**	3.77**	263.68**
Error	55	3.37	0.12	0.53	0.12	1.15
GCA/(SCA+GCA)		0.834	0.829	0.9	0.897	0.858

*and ** = significant at 0.05 and 0.01 levels of probability, respectively.

Table 5: Mean squares of general (GCA) and specific combining ability (SCA) of 7 in-beard lines and their f1 crosses

S. V	Df	Number of rows/ear	Number of kernels/row	100-kernel weight/g	kernel weight/ear	kernel yield/plant
GCA	6	475.37**	2047.67**	2551.30**	27050.12**	76042.46**
SCA	20	64.51**	372.05**	331.80**	6468.63**	30767.93**
Error	55	1.58	4.46	1.29	5.17	1105.15
GCA/(SCA+GCA)		0.881	0.846	0.885	0.807	0.712

*and ** = significant at 0.05 and 0.01 levels of probability, respectively

The estimates of GCA and SCA effects in Tables (6 and 7). The results of GCA for ear weight reveal that positive and highly significant GCA effects were manifested in the all parental lines GCA effects. Indicating that these lines considered to be good combiner for ear weight and can be used breeding programs. The SCA effects of ear weight are given positive and highly significant SCA effects were registered by the crosses (P1 x P3), (P1 x P4), (P1 x P5), (P2 x P3), (P2 x P4), (P2 x P6), (P2 x P7), (P3 x P4), (P3 x P7), (P4 x P5), (P4 x P6), (P4 x P7), (P5 x P6) and (P5 x P7). Therefore, these crosses are considered to be the promising for ear weight improvement. Moreover, the estimates of GCA effects for number of ears/plant reveal that positive and highly significant GCA effects were manifested in the parental line P2 and two lines parental P1 and P6 were reveal positive and significant GCA effects under this study. Indicating that these lines considered to be good combiner for ear weight and can be used breeding programs. The SCA effects of number of ears/plant are given positive and highly significant SCA effects were registered by the crosses (P1 x P2), (P2 x P6), (P2 x P7) and (P4 x P6). Therefore, these crosses are considered to be the promising for number of ears/plant improvement.

Meanwhile the GCA effects for ear length are shown reveal that positive and highly significant GCA effects were manifested in the all parental lines GCA effects under this study. The results are in agreement with those obtained by [34] reported that the general combining ability GCA affects for six parental lines indicating that the parental inbred line P4 was good combiner for ear length. The SCA effects of ear length are given positive and highly significant SCA effects were registered by the crosses (P1 x P2), (P1 x P3), (P1 x P6), (P2 x P5), (P3 x P5), (P3 x P7), (P4 x P6) and (P5 x P7). The estimates of GCA effects for ear diameter reveal that positive and highly significant GCA effects were manifested in the parental lines P1, P4 and P7 GCA effects under this study. Indicating that these lines considered to be good combiner for ear diameter and can be used breeding programs. The results are in agreement with those obtained by [38]. The SCA

effects of ear diameter are given positive and highly significant SCA effects were registered by the crosses (P2 x P4), (P3 x P4) and (P5 x P6). Therefore, these crosses are considered to be the promising for ear diameter improvement.

The estimates of GCA effects for cub weight the results reveal that positive and highly significant GCA effects were manifested in the parental lines P1, P2, P4, P5 and P7 GCA effects under this study. Indicating that these lines considered to be good combiner for cub weight and can be used breeding programs. The results are in agreement with those obtained by [34]. The SCA effects of cub weight are given positive and highly significant SCA effects were registered by the crosses (P1 x P3), (P2 x P4), (P2 x P5), (P3 x P5), (P3 x P7), (P4 x P5), (P4 x P6), (P4 x P7) and (P5 x P7). The estimates of GCA effects for number of rows/ear the results reveal that positive and highly significant GCA effects were manifested in the parental lines P1, P3, P4, P5, P6 and P7 GCA effects under this study. Indicating that these lines considered to be good combiner for number of rows/ear and can be used breeding programs. The results are in agreement with those obtained by [34], reported that the general combining ability GCA effects for six parental lines indicating that the parental inbred line P4 was good combiner for number of rows/ear. The SCA effects of number of rows/ear are given positive and highly significant SCA effects were registered by the crosses (P1 x P6), (P2 x P3), (P2 x P4), (P3 x P4), (P4 x P7) and (P5 x P7).

Moreover, the estimates of GCA effects for number of kernels/rows the results reveal that positive and highly significant GCA effects were manifested in the parental lines P1, P2, P4, P5, P6 and P7 GCA effects. The results are in agreement with those obtained by [34], reported that the general combining ability GCA affects for six parental lines indicating that the parental inbred line P5 was good combiner for kernel number/row. The SCA effects of number of kernels/rows are given positive and highly significant SCA effects were registered by the crosses (P1 x P2), (P1 x P4), (P2 x P3), (P2 x P6), (P3 x P5), (P4 x P6), (P4 x P7), (P5 x

P6) and (P5 x P7). Therefore, these crosses are considered to be the promising for this trait improvement.

The estimates of GCA effects for 100-kernel reveal positive and highly significant GCA effects were manifested in the all parental lines GCA effects. The results are in agreement with those obtained by [30,31]. The SCA effects of 100-kernel are given positive and highly significant SCA effects were registered by the crosses (P1 x P3), (P2 x P4), (P2 x P5), (P3 x P5), (P3 x P7), (P4 x P5), (P4 x P7), (P5 x P7) and (P6 x P7).

The estimates of GCA effects for kernel weight/ear. The results reveal that positive and highly significant GCA effects were manifested in the all parental lines GCA effects. The results are in agreement with those obtained by [37]. The SCA effects of kernel weight/ear are given positive and highly significant SCA effects were registered by the crosses (P1 x P4), (P1 x P5), (P1 x P6), (P1 x P7), (P2 x P3), (P2 x P4), (P2

x P6), (P2 x P7), (P3 xP4), (P3 xP6), (P3 xP7), (P4 xP5), (P4 xP7), (P5 xP6) and (P5 xP7).

The estimates of GCA effects for kernel yield/plant reveal that positive and highly significant GCA effects were manifested in the parental lines P₂ and P₆ GCA. Indicating that these lines considered to be good combiner for kernel yield/plant and can be used breeding programs. The results are in agreement with those obtained by [34], reported that the general combining ability GCA effects for six parental lines indicating that the parental inbred line P₄ was good combiner the parental inbred lines P₁ was good combiner for kernel yield. [37], indicated that the parental inbred lines P₁, P₆ and P₇ had significant positive G.C.A. effects for grain yield. The SCA effects of kernel weight/ear are given positive and highly significant SCA effects were registered by the crosses (P₁ x P₅), (P₁ x P₆), (P₂ x P₄), (P₂ x P₆), (P₂ x P₇), (P₃ xP₄) and (P₃ xP₇). Therefore, these crosses are considered to be the promising for this trait improvement.

Table 6: Estimates of general (GCA) specific (SCA) combining ability maize genotypes for some ear traits

Genotypes	Ear weight (g)	Number of ear/plant	Ear length/cm	Ear diameter/cm	Cub weight/g
GCA					
P1	3.312**	0.117*	1.618**	0.488**	1.446**
P2	16.862**	0.450**	1.934**	0.218*	1.056**
P3	2.028**	0.137	0.694**	0.158	0.130
P4	16.162**	0.067	1.594**	0.594**	3.176**
P5	17.565**	-0.023	1.368**	0.158	3.883**
P6	8.615**	0.217*	1.504**	0.268*	-0.212
P7	19.045**	0.057	1.788**	0.474**	6.338**
S.E.(gi-gj)	0.474	0.088	0.189	0.089	0.277
SCA					
P1 x P2	-6.049**	0.633**	2.449**	-0.656**	-1.577**
P1 x P3	8.117**	0.280	2.689**	0.504*	8.183**
P1 x P4	6.651**	-0.283	-0.111	-0.566*	-5.297**
P1 x P5	18.581**	0.273	0.016	0.304	-2.904**
P1 x P6	33.197**	0.367	1.879**	-0.039	-1.242
P1 x P7	37.101**	-0.307	0.329	-0.013	-3.692**
P2 x P3	18.567**	0.113	-0.294	-0.759**	-0.594
P2 x P4	45.767**	0.350	-0.194	0.904**	7.093**
P2 x P5	-12.303**	-0.227	1.366**	-0.359	6.486**
P2 x P6	44.147**	1.067**	0.563	-0.203	0.248
P2 x P7	22.551**	0.693**	0.946*	0.324	-2.135**
P3 x P4	20.434**	0.330	-0.287	0.797**	-3.880**
P3 x P5	0.531	0.487*	1.939**	0.001	2.946**
P3 x P6	-0.186	-0.487*	0.803	-0.009	-6.058**
P3 x P7	29.051**	0.340	3.119**	0.084	2.292**
P4 x P5	37.064**	-0.110	1.039*	-1.036**	11.166**
P4 x P6	5.681**	0.583**	4.236**	0.187	9.795**
P4 x P7	7.584**	-0.157	0.453	-0.019	3.578**
P5 X P6	22.144**	0.007	1.129*	0.957**	-1.912
P5 X P7	67.514**	-0.167	3.846**	0.084	11.872**
P6 x P7	-4.203**	-0.407	-1.924**	0.474*	1.347
S.E.(sij - sji)	1.16	0.215	0.462	0.217	0.678

*and ** = significant at 0.05 and 0.01 levels of probability, respectively

Table 7: Estimates of general (GCA) specific (SCA) combining ability maize genotypes for kernel yield and its components traits

Genotypes	Number of rows/ear	Number of kernels/ear	100-kernel weight/g	kernel weight/ear	kernel yield/plant
GCA					
P1	1.017**	1.363**	3.120**	2.131**	-0.401
P2	0.483	3.323**	3.037**	15.754**	62.089**
P3	1.150**	0.490	3.885**	2.061**	3.262
P4	1.483**	2.490**	1.986**	13.144**	10.216
P5	1.683**	2.190**	4.150**	13.708**	-2.674
P6	1.217**	3.763**	1.734**	8.771**	25.159**
P7	2.017**	4.990**	3.118**	12.038**	5.166
S.E.(gi-gj)	0.325	0.545	0.293	0.587	8.584
SCA					
P1 x P2	0.444	6.636**	-1.659**	-4.503**	30.737
P1 x P3	0.444	2.469	9.927**	-0.309	14.230
P1 x P4	0.111	7.469**	-3.507**	11.707**	-21.957
P1 x P5	1.244	-0.231	1.295	22.377**	58.333**
P1 x P6	2.378**	-2.738*	-1.836**	34.414**	81.567**
P1 x P7	0.244	2.636*	0.454	41.381**	11.660
P2 x P3	2.978**	9.509**	0.760	19.234**	25.740
P2 x P4	3.311**	-1.491	6.276**	38.751**	98.987**
P2 x P5	1.778*	2.809*	6.445**	-18.579**	-60.990**
P2 x P6	-1.089	4.236**	7.494**	42.024**	204.043**
P2 x P7	0.111	3.009*	-3.723**	25.591**	117.837**
P3 x P4	3.311**	-1.658	-2.572**	24.177**	63.447**
P3 x P5	0.444	10.642**	7.643**	-2.419	38.103
P3 x P6	0.911	-0.931	-4.187**	5.917**	-50.797*
P3 x P7	1.444	-2.158	6.929**	27.451**	71.497**
P4 x P5	0.778	-1.691	4.596**	25.831**	6.017
P4 x P6	0.578	10.736**	-0.321	-4.033*	36.383*
P4 x P7	4.444**	11.842**	7.195**	4.701**	-14.223
P5 X P6	-0.289	7.702**	1.814*	24.271**	26.140
P5 X P7	4.244**	9.809**	6.030**	54.137**	38.267*
P6 x P7	0.711	-2.764	2.113**	-4.659**	-53.300
S.E.(sij - sji)	0.795	1.335	0.718	1.439	21.025

*and ** = significant at 0.05 and 0.01 levels of probability, respectively

3.3. Genetic Components and Derived parameters

The present data in Tables (8 and 9) show highly significant values of additive and non-additive gene action for ear length, ear diameter, cub weight, number of rows/ear, number of kernels/row and 100-kernels weight, suggesting

the importance of non-additive gene action of the inheritance this trait. Moreover, highly significant values of dominance (H_1 and H_2) and non-significant of additive (D) for ear weight, number of ears/plant, kernel weight/ear (g) and kernel yield/plant, suggesting the importance of non-additive gene action of the inheritance these traits.

The non-additive gene effects (H_1 and H_2) for all studies traits were more than additive gene action (D). The dominance components (H_1) were more than (H_2) for this trait, revealing that dominance and recessive genes were unequally distributed in the parents for all study traits. These results are confirmed by the values of ($H_2/4H_1$) which was less than its maximum value (0.25).

F which indicates the relative frequency of dominant and recessive alleles in parents was found to be negative and non-significant values were observed for ear weight, number of ears/plant, ear length, ear diameter, cub weight, number of rows/ear, number of kernels/row, 100-kernel weight, kernel weight/ear and kernel yield/plant, revealing the importance of recessive alleles in these traits, it was supported by the sum of KD/KR which was greater than unity for these traits. The sum of dominant alleles in heterozygous phase over all loci, as indicated by (h^2), was positive and highly significant for

this studied trait, showing that dominant genes controlling this trait were mainly due to heterozygosity of loci.

The environmental components of variation (E) was non-significant for all studies traits, suggesting unimportant of environmental factor in determining. The degree of dominance (H_1/D)^{0.5} was more than unity for ear weight, number of ears/plant, ear length, ear diameter, cub weight, number of rows/ear, number of kernels/row, 100-kernel weight, kernel weight/ear and kernel yield/plant, confirming the importance of over-dominance gene action in controlling the inheritance of this trait.

The proportions of genes with positive and negative effects in the parents as indicated by ($H_2/4H_1$) were less than the theoretical value (0.25) for all studies traits. The proportions of dominant and recessive genes in the parents (KD/KR) were more than unity, suggesting that the recessive genes were more important.

Table 8: Genetic parameters D and derived parameters in 7 maize genotypes for some ear traits

Genetic component	Ear weight (g)	Number of ears/plant	Ear length/cm	Ear diameter/cm	Cub weight/g
Genetic parameters					
E	1.026	0.030	0.151	0.032	0.411
D	676.972	0.128	21.786**	1.744**	68.468**
F	-2667.561*	-0.417	-42.180**	-1.751**	-65.376
H_1	6987.513**	1.176**	50.536**	2.341**	234.112**
H_2	3975.659**	0.723**	24.028**	1.435**	138.368**
h^2	5076.411**	0.181	2.178	0.809**	4.384
Derived parameters					
{ H_1/D } ^{0.5}	3.213	3.026	1.523	1.158	1.849
$H_2/4H_1$	0.142	0.154	0.119	0.153	0.148
h^2/H_2	0.240	0.302	0.223	0.395	0.590
KD/KR	1.277	0.250	0.091	0.564	0.032
h(n.s)	76.158	70.324	88.019	84.911	76.633

*and ** = significant at 0.05 and 0.01 levels of probability, respectively

Narrow sense heritability evaluate were recorded high for ear weight (76.158%), number of ears/plant (70.324%), ear length (88.019%), ear diameter (84.911%), cub weight (76.633%), rows/ear (84.210%), number of kernels/row (76.74), 100-kernel weight (84.468%), kernel weight/ear (71.667%) and kernel yield/plant (54.730%). [39], showed that High heritability accompanied with high genetic advance had shown by the cob length. [40], recorded that the

heritability percentage in broad sense to moderate high for ear length trait. [41], found that high heritability for number of kernels/row. [42], observed that the uppermost heritability was in 1000 grain weight (96.91). [43], found that the heritability 86.79 for thousand kernel weight. [44], observed that the traits under study showed a wide range of heritability estimates (24%–90%). among the characters, highest heritability was recorded for kernel yield.

Table 9: Genetic parameters D and derived parameters in 7 maize genotypes for kernel yield and its components

Genetic component	Number of rows/ear	Number of kernels/ear	100-kernel weight/g	kernel weight/ear	kernel yield/plant
Genetic parameters					
E	0.420	1.137	0.353	1.699	282.391
D	13.390**	51.688*	83.175**	474.830	205.297
F	-29.868**	-123.925*	-160.040**	-1470.361	-3873.977
H1	50.909**	310.077**	259.585**	5559.854**	27629.112**
H2	24.462**	180.587**	134.160**	3310.093**	19336.896*
h2	12.066*	144.103**	14.858	4835.879**	22851.435**
Derived parameters					
{H1/D} ^{0.5}	1.950	2.449	1.767	3.422	11.601
H2/4H1	0.120	0.146	0.129	0.149	0.175
h2/H2	0.272	0.343	0.295	0.377	0.103
KD/KR	0.493	0.798	0.111	1.461	1.182
h(n.s)	84.210	76.722	84.468	71.667	54.730

*and ** = significant at 0.05 and 0.01 levels of probability, respectively

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