

Genetic Analysis of Combining Ability and Gene Action of Yield and Its Components in Maize (*Zea Mays* L.) Using Full Diallel Cross

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ABSTRACT: A field study was conducted at a private farm in AL-Anbar Governorate city of Ramadi- the village of Albu Shaban, during the successive spring and autumn seasons (2020). Five pure lines of maize (*Zea mays* L.) (ART-B-17, Zm-1, SYn-33, Inb-27, Zm-5) were crossed in all possible combinations including reciprocal, during the spring season of 2020 to produce 20 diallel and reciprocal crosses. planted single cross and parents in autumn seasons by using Randomized Complete Block Design (R.C.B.D), with three replications to determine the best pure lines and their single crosses, depending on its performance, genetic analysis for General and Specific Combining Ability (GCA; SCA), Gene Action, and Heritability, using the approach of Griffing method 1 with the fixed model for traits: days to 50% silking, plant height, number of ears per plant (NEPP), number of grains per row, 300-grain weight, and grains yield per plant. The results of indicated that there were highly significant differences for all the studied traits. Where parent line (5) gave the highest mean for most of the studied traits, including Grains Yield per plant 156.73 gm. Regarding the crosses, the diallel cross (1×5) gave the highest mean Grains Yield per plant reach 231.15 gm, while in reciprocal crosses, the cross (4×1) gave the highest mean Grains Yield per plant reached 186.35 gm. The results show that the estimation of the reciprocal effect was significant in most of the reciprocal crosses. The results of the genetic analysis showed that there were high significant differences in MS_{gca}, MS_{sca}, and MS_{rca} for all studied traits except for the mean squares of days to 50% silking trait. The parent line (5) showed the best effect of the general combining ability in Grains Yield per plant traits reached 13,691, and the number of grains per row was 1,280 and 300 Grain Weight reached 2,326, while the cross (1×2) and reciprocal cross (5×4) showed the best effect of Specific Combining Ability of Grains Yield per plant traits was 15,285 and 15,718, respectively. The ratio of $\sigma^2_{sca}/\sigma^2_{gca}$ and $\sigma^2_{rca}/\sigma^2_{gca}$ was less than one for all the studied traits in the diallel and reciprocal hybrids. This was reflected in the value of the mean value of the degree of dominance that was greater than one in all the studied traits of the diallel and reciprocal crosses. The ratio of broad-sense heritability was high and in the narrow sense low in most traits studied in the diallel and reciprocal crosses.

Key words: maize, additive gene action, degree of dominance, combining ability, Heterosis, (*Zea mays* L.), heritability.

Introduction

Maize (*Zea mays* L.) is one of the major grain crops in the world and is widely cultivated as a grain crop, it's one of the cross-pollinated species. It is the only highly adaptable grain crop that can be grown in two seasons, in addition to successful in temperate, tropical, and subtropical regions of the world (Shree *et al.*, 2018). Its grains are used as human food and as a concentrated

diet for poultry and animals because it contains carbohydrates, starch, and some vitamins, in addition to using its vegetable parts as animal feed (Sweed and Al-Jumaily, 2017) In addition to the use of maize in biofuels. The hybridization program is one of the most important plant breeding and improvement programs to transmit genes existing in more than one parent and collect them in a specific genetic structure. This program provides an opportunity for plant breeders to estimate the components of genetic variation and determine the appropriate breeding method (Ahmed and Al-Hamdani, 2014). The Diallel cross between different parents is considered one of the important mating systems through which conclusions can be reached about the nature of the genes and general and Specific Combining Ability with an appreciation of some genetic parameters through which it is possible to determine the best method for plant breeding, well benefit of the phenomenon of heterosis that won the interest of the breeders of this crop. Many researchers and plant breeders have used pure lines of maize in the full diallel cross programs, such as Ibraheem and Hamadi (2010), Ramadan (2010), Ahmed and Al-Hamdani, (2014), Rovaris *et al.* (2017), and Obaidi (2018). Waheeb *et al.* (2016), Ramadan *et al.* (2020) studied five pure lines of maize, found that the ratio of additive variation to diallel and reciprocal dominance variation was more than one. As well as the degree of dominance mean for most of the studied traits of the diallel and reciprocal crosses, which indicates that the non-additive genetic action controlling the traits, as well as that the diallel and reciprocal effects were positive and negative for the studied traits, and that gca/sca and gca/rca were less than one. Abd *et al.* (2017), when studying full diallel cross on five pure lines of maize, reported that the dominant effect was the largest and the basis with an additive effect to a lesser degree where the effect of both general and specific (diallel and reciprocal) was high significant and the ratio between gca/sca And gca/rca is greater than one for all traits, and the variance components belonging to the dominant were higher than the components of the additive variation and the broad-sense heritability was high their lower values in the narrow sense of the diallel crosses and the higher the rate of dominance than the one and for all the traits of the reciprocal crosses. Ali *et al.* (2017) studied full diallel cross on four pure lines of maize, where broad-sense heritability of the traits of plant height, number ear per plant, number of grains per row, grain weight, and grain yield were (86.6%, 59.7%, 45.4%,12.2%, and 99.7%) for traits respectively. Sadalla *et al.* (2017), estimated the general and specific combining ability of four pure lines of maize, which were included in the full diallel cross, and reported that the ratio between variance of general and specific combining ability was less than one for studied traits, and this indicates that the non-additive effect of genes is more important than additive effect. Yuwono *et al.* (2017), performed the full diallel cross, obtained an estimate of general and specific combining ability of the diallel and reciprocal crosses with high significance for the traits of days to 50% silking and plant height, as well as effects of specific combining ability of diallel and reciprocal crosses was positive and negative values for the same traits. Al-Obaidi *et al.* (2018), when studying the full diallel cross of six pure lines of maize, found that squares mean of diallel and reciprocal general and specific combining ability were highly significant for all traits except for the number of ear per plant was significant for general and specific combining ability for diallel crosses and not significant for reciprocal crosses. The non-additive gene action is more important in the inheritance of the studied traits, as it obtained effects of the general and specific combining ability with positive and negative values in all the studied traits, and the variance ratio of general

and specific combining ability was less than one in all the studied traits. Sugiharto *et al.* (2018), used the full diallel cross between 7 pure lines of maize, found that the plant height was significant in mean squares of diallel general and specific combining ability, and reciprocal was not significant, whereas mean squares of diallel specific combining ability in the trait of grain yield was significant, and not significant of reciprocal general and specific combining ability mean squares, effects of general and specific combining ability were positive and negative values for all diallel and reciprocal crosses in grain yield traits. Afolabi *et al.* (2019), when studying six pure lines of maize using the full diallel cross, indicating that the ratio of GCA/SCA was less than one for days to 50% silking, plant height, and grain yield traits. Onejeme *et al.* (2020) found that when using a full diallel cross on four pure lines of maize, the effects of diallel and reciprocal crosses general and specific combining ability, were of positive and negative values for all studied traits. The aim of this study is to insert a group of pure lines (five pure lines) into a full diallel cross program in order to estimate general and specific combining ability and effects of diallel and reciprocal crosses in addition to estimate the variation of general and specific effects and genetic parameters for purpose of determining best pure lines and crosses and thus including it in subsequent breeding programs, and knowing the genetic action that controls these traits for determining the breeding method that is used to improve these traits.

MATERIALS AND METHODS:

A field study was conducted at a private farm in AL-Anbar Governorate city of Ramadi- the village of Abu Shaban, during the successive spring and autumn seasons (2020) using five pure lines of maize, namely ART-B-17, Zm-1, SYn-33, Inb-27, and Zm-5 provided by the Department of Agricultural Research/ Abu Ghraib Research Station. Soil service operations were conducted which included plowing, smoothing, leveling, and fertilization with compound fertilizer N: P (18:18) at a rate of 400 kg/h, followed by line opening operations. The seeds of pure lines were planted in the spring season on 20/3/2020 with lines at distances. The space between the adjacent furrows and pits is 0.75 and 0.25 cm respectively. The seeds were planted at the rate of 2 to 3 seeds per pit. Two lines were planted for each pure line with a length of 7 m. Urea fertilizer (46% N) at the rate of 400 kg.h-1 split into two batches, the first batch was added 30 days after emergence while the second was added at the flowering stage. Weeds were controlled after the first irrigation and before germination, using Atrazine at a concentration of 80% at a rate of 3.2 kg/ ha. During the growing season, crop service operations were carried out such as irrigation, weeding, and hoeing. The maize leg borer insect (*Sesamia Criteca*) was controlled using the granulated diazinon pesticide 10% applied using placement method twice, the first when the plant reached the 6-leaf stage and the second after 20 days of the first control, these processes were in both seasons. When the female inflorescences appeared and before the emergence of silking, covered with paper bags to avoid open pollination and to ensure access to the required crosses, and the male was covered with paper bags a day before the start of the pollination process and after the release of pollen grains, and the hybridization process continued until all the required crosses between the five pure lines were completed, at a rate of five ears for each cross to ensure that sufficient seeds are obtained for planting in the comparison experiment.

The full diallel cross was carried out between pure lines in two directions diallel and reciprocal crosses, using the approach of Griffing method 1 with the fixed model, so that the number of resulted genotypes is equal to p^2 . The seeds of the pure lines were propagated by self-pollination, and at the end of the season, the produced ears from the pure lines and crosses were dried and squandered separately for the purpose of using them in a comparison experiment that included the pure lines and first-generation F1 hybrids (diallel and reciprocal crosses). Pure lines and Single crosses seed were planted on 27/7/2020 in the comparison experiment, which consisted of 10 diallel single crosses and 10 reciprocal single crosses. Randomize Complete Block Design (R.C.B.D) with three replications was used taking into account all agricultural operations service of the soil and crop. The data for each trait under study were taken such as days to 50% silking, plant height (PLH), number of ears per plant (NEPP), number of grains per row (NGPR), 300- grain weight (300 GW), and grains yield per plant (GY) after weight adjustment to 15.5% moisture content (wolf *et al.* 2000). Statistical analysis of each trait was carried out according to a randomized complete block design (RCBD) with three replicates according to the fixed territory model mentioned by Steel and Torri (1980). The arithmetic means of the hybrids in the studied traits were tested using the least significant difference (L.S.D) with probability levels 0.05 and 0.01. In view of the presence of significant differences between the genetic crosses, the data for each trait of the study were analyzed genetically according to the approach of Griffing method 1 with the fixed model, and the division of the mean squares of the genetic hybrids into the mean of the squares of general combining ability (GCA) and diallel (SCA) and reciprocal (RCA) specific combining ability, components of genetic variation of the effect of σ^2_{gca} , σ^2_{sca} , and σ^2_{rca} was calculated from expected variance EMS according to the equations mentioned by it. (Singh and Chaudhary, 2007) as follows:

$$Mse^- = mse/ r$$

$$\sigma^2_{gca} = (MS_{gca} - Ms\bar{e})/ 2P$$

$$\sigma^2_{sca} = (MS_{sca} - Ms\bar{e})$$

$$\sigma^2_{rca} = (MS_{rca} - Ms\bar{e})/ 2$$

Either effect of general combining ability (\hat{g}_i), effect of specific combining ability to diallel crosses (\hat{S}_{ij}) and effect of specific combining ability to reciprocal crosses (\hat{r}_{ij}) were estimated according to the following equations:

$$\hat{g}_i = 1 / 2P (Y_{i.} + Y_{.j}) - (1 / P^2) Y_{..}$$

$$\hat{S}_{ij} = 1 / 2(Y_{ij} + Y_{ji}) - 1 / 2P (Y_{i.} + Y_{.i} + Y_{.j} + Y_{.j}) + (1 / P^2) Y_{..}$$

$$\hat{r}_{ij} = 1 / 2 (Y_{ij} - Y_{ji})$$

The standard error of effect of general combining ability S.E (\hat{g}_i) was estimated as follows:

$$S.E(\hat{g}_i) = \sqrt{\frac{Mse^-}{P}}$$

The standard error of effect of combining ability S.E (\hat{S}_{ij}) for diallel crosses was estimated as follows:

$$S.E(\hat{S}_{ij}) = \sqrt{\frac{Mse^-}{P}}$$

The standard error of effect of combining ability S.E (\hat{r}_{ij}) for reciprocal crosses was estimated as follows:

$$S.E(\hat{r}_{ij}) = \sqrt{(\sigma^2 e)/2}$$

The additive genetic variance ($\sigma^2 A$) and the dominant genetic variance ($\sigma^2 D$) as well as the environmental variance ($\sigma^2 E$) were estimated through the components of the expected EMS variance (Griffing, 1956b) and according to the following equations:

$$\sigma^2 A = 2\sigma^2 gca$$

$$\sigma^2 D = \sigma^2 sca$$

$$\sigma^2 E = Ms\bar{e} = MSe / r$$

The ($\sigma^2 G$) genetic variance and ($\sigma^2 P$) phenotypic variance can also be estimated according to the following:

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

Assuming no superiority (Epistasis)

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

The heritability ratio was estimated in its broad sense and narrow sense for diallel and reciprocal crosses according to (Singh And Chaudhary, 2007):

$$h^2_{b.s} = \sigma^2 G / \sigma^2 P, \quad h^2_{b.s-r} = \sigma^2 G / \sigma^2 P - r, \quad h^2_{n.s} = \sigma^2 G / \sigma^2 P, \quad h^2_{b.n-r} = \sigma^2 G / \sigma^2 P - r$$

Estimate the mean degree of dominance for diallel and reciprocal crosses according to the following (singh and Chaudhary, 2007):

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

$$\bar{a} - r = \sqrt{2\sigma^2 A - r / \sigma^2 A}$$

Reciprocal Eff

Results and Discussion

The analysis of variance informed significant genotype effect for all the characters under study, which include pure lines, diallel and reciprocal crosses at the level of 1% for all studied traits, and this indicates differences between the genotypes under study clearly as a result of having different genes for the studied traits, consequently, this difference allows us to conduct the genetic analysis of these traits to identify the pure lines, diallel and reciprocal crosses and introduce it into breeding and improvement programs. Many researchers found significant differences between genotypes such as: Abdel-Moneam *et al.* (2014), Al-Falahy (2015), Wuhiab *et al.* (2016), Aslam *et al.* (2017), Al-Salim *et al.* (2017), Aslam *et al.* (2017), Hussain and Hussen (2018), Afolabi *et al.* (2019), Al-Azawi *et al.* (2020), Ali *et al.* (2020), Onejeme *et al.* (2020). Table (1) showed that the general mean trait of pure lines, diallel and reciprocal crosses for days to 50% silking reached 67.24 days, whereas pure line (3) took the least period of 68.01 days, this great genetic variation between the pure lines at the time of days to silking appeared in their diallel and reciprocal crosses, cross (1×5) was earliest cross which took 64.09 days, while

cross (1×3) was late in flowering and took 69.28 days, whereas in reciprocal crosses, the cross (4×2) the earliest reciprocal crosses took 65.12 days. cross (3×2) was late in flowering and took 70.46 days. This illustrates the role of cytoplasmic inheritance and interaction between them and nuclear genetics in controlling the inheritance of this trait. pure line (2) in plant height trait had the highest mean reach 198.96 cm, while pure line (1) had the lowest mean reached 168.56 cm. genetic divergence between the pure lines was reflected in diallel and reciprocal crosses where the cross (1×5) gave the highest mean of the trait was 191.52 cm, while the cross (1×4) gave lowest values reached 174.05 cm, similarly, the reciprocal cross (4×3) had the highest mean reached 189.18 cm, and reciprocal cross (4×2) was with the lowest values reach 177.84 cm. The five to seven nodes under the main ear site also bear ears (antique), which usually do not succeed to produce ears with the exception of the first stem under the main ear in the event that the plant density allows this with the availability of other growth factors, but in the case of multiple varieties of ears, this happens more clearly, as we notice many plants with two ear and sometimes three with seeds in good condition. elshookie (1990). As pure line (5) had the highest mean for the trait, which was 1.44 ear/ plant, while the pure line (4) had the lowest mean for the trait, with a value of 1.00 ear/ plant. The genetic divergence between the pure lines was clearly reflected in the diallel and reciprocal crosses resulting from it, where the cross (1×5) had the highest number of ears in the plant reached 1.44 ear/ plant, while the two reciprocal crosses (4×1) and (5×4) were with highest number of ears, which reach 1.31, while the lowest number of ears was shown by two crosses (2×3) and (4×5), which reach 1.12 ear/ plant, and reciprocal cross (4×3) reached 1.08 ear/ plant. Plant. In number of grains per row trait pure line (5) had the highest mean reached 38.54 grains / row, while the pure line (1) had lowest mean for the trait reach 30.53 grain / row, while

Table (1) value means of pure lines and crosses (diallel and reciprocal) of the studied traits in maize by full diallel cross method 2020

Trait Genotype	DTS	PLH	NEPP	NGPR	300 GW	GY
1	69.33	168.56	1.12	30.53	75.24	121.33
2	68.09	198.96	1.01	36.54	72.45	134.93
3	68.01	182.06	1.01	32.43	82.35	126.73
4	68.57	172.56	1.00	34.63	84.65	130.84
5	75.01	168.60	1.14	38.54	89.16	156.73
1x2	67.14	176.87	1.23	38.65	81.16	157.24
1x3	69.28	182.93	1.28	44.76	83.75	161.35
1x4	66.11	174.05	1.33	46.72	85.09	174.10
1x5	64.09	191.52	1.44	49.05	90.17	231.15
2x3	65.13	182.54	1.12	44.74	83.46	163.76
2x4	65.00	184.74	1.23	46.12	86.17	157.84
2x5	67.03	180.99	1.18	45.17	84.14	187.11
3x4	65.09	185.92	1.18	42.65	83.43	182.44
3x5	67.01	184.79	1.16	46.53	85.04	188.16
4x5	66.03	181.56	1.12	42.86	83.13	180.24

2x1	66.09	186.26	1.25	46.24	81.17	159.35
3x1	67.11	186.84	1.26	44.35	81.08	180.54
3x2	70.46	188.96	1.20	44.07	82.17	177.23
4x1	66.22	181.74	1.31	45.08	81.55	186.35
4x2	65.12	177.84	1.24	44.26	84.03	171.65
4x3	67.09	189.18	1.08	43.85	85.09	170.26
5x1	70.18	178.86	1.17	45.75	82.14	182.36
5x2	66.00	181.96	1.27	44.26	86.25	181.09
5x3	66.05	186.75	1.28	42.55	82.04	180.43
5x4	65.82	188.54	1.31	46.13	83.33	183.66
G. Mean	67.24	182.54	1.20	42.66	83.13	169.07
L.S.D 5%	1.710	0.167	0.011	0.040	0.052	0.046
L.S.D 1%	2.282	0.223	0.015	0.054	0.069	0.061

The cross (1×5) gave the highest mean of the trait reach 49.05 grain/row. Regarding the reciprocal crosses, the two crosses (2×1) gave the highest mean for the trait, reach 46.24 grain/row, while the lowest means in diallel crosses were shown by the cross (1×2) with a value reached 32.65 grain/row, and in reciprocal crosses, the cross (5×3) was lowest mean in this trait reached 42.55 grain/row. Pure line (5) had the highest median 300 Grain Weight reached 89.16, while pure line (2) had lowest mean for a trait reach 72.45. diallel cross (1×5) gave highest mean reach 90.17 g, while reciprocal cross (5×2) gave highest mean reach 86.25 g, lowest mean for crosses showed the cross (1×2) was 81.16 g and reciprocal cross (3×1) It was 81.08 g. The pure line (5) had the highest mean for the trait of grains yield per plant reach 156.73 g/ plant, while the lowest mean was obtained from the pure line (1) reached 121.33 g/ plant, and the highest mean for the trait was 231.15 g / plant observed from the diallel cross (1×5), meanwhile, the lowest mean for the trait in diallel cross was 157.24 g/ plant for the cross (1×2), while in reciprocal crosses the highest mean for the trait was 186.35 g/ plant for the cross (4×1), while the lowest mean was 159.35 g/ plant for the cross (2×1), plant height (PLH), number of ears per plant (NEPP), number of grains per row (NGPR), 300-grain weight (300 GW) and grains yield per plant (GY).

Table (2) shows the mean squares for analyzing the variance of general combining ability and specific combining ability of studied traits in maize by the method of the full diallel cross according to the first method and suggested by Griffing (1956) the fixed model where mean squares of general combining ability and specific combining ability of diallel and reciprocal crosses differed significantly on the level of significance 1% for all traits except days to 50% silking trait of diallel crosses, in general, combining ability was significant at the level of 5%, and this explains the importance of the additive and non-additive genetic action in inheriting these traits. Whereas, the additive genetic action is determined based on general combining ability and non-additional genetic action on specific combining ability (Hassan, 2005). the results also indicated that the ratio of the variation component of general combining ability and specific combining ability in diallel and reciprocal crosses was less than one for all the studied traits, which explains the importance of the dominant genetic action in controlling the traits in which

the ratio was less than one, and thus these can be improved this trait by hybridization, and this is consistent with Moneam *et al.* (2014), Wuhiab *et al.* (2016b), Wuhiab *et al.* (2016a), Abed *et al.* (2017), Afolabi *et al.* (2019).

Table (2) mean squares for analysis of variance of general combining ability and specific combining ability of studied traits in maize by full diallel cross method (2020)

S.O.V	d.f	Mean Square					
		DTS	PLH	NEPP	NGPR	300 GW	GY
Block(Rep)	2	1.019	0.006	3.730	0.002	0.0006	0.001
Genotype	24	16.214**	147.117**	0.035**	67.215**	39.413**	1667.272**
GCA	4	1.114*	31.589**	0.012**	22.787**	39.192**	1264.493**
SCA	10	6.316**	51.909**	0.012**	25.682**	7.101**	488.689**
RCA	10	6.299**	53.150**	0.011**	18.975**	8.752**	339.331**
Error	48	1.086	0.010	4.430	0.0006	0.001	0.0008
		0.008	0.049	0.076	0.071	0.442	0.207
		0.108	0.095	0.172	0.192	0.716	0.596

effect of general combining ability was estimated for each pure line and its results are listed in Table (3), in which it is noticed that the effect general combining ability is desirable and significant for days to 50% silking trait for pure lines (2 and 4), the effects of plant height were positive and significant for pure lines (2 and 3) reached 3.265 and 2,660, respectively. the effect of general ability on the combination in the number of ears per plant trait was positive for pure lines (1 and 5) reached 0.054 and 0.0240 respectively. The effect of general ability on the combination of the number of grains per row was positive, with a significant difference for the pure lines (2, 4, and 5), which reached 0.001, 0.035, and 1.280, respectively. The pure lines (4 and 5) showed a positive effect of general ability on the combination in 300-grain weight traits were 0.982 and 2.326 respectively. Regarding the grains yield per plant trait, the pure line (5) had a positive and significant effect in the desired direction, which reached 13.691, from the previous results, we noted that the pure lines (2, 4 and 5) were the best pure lines in terms of its general ability on combination in a meaningful and desired direction, therefore, it can be concluded that the pure lines which had the general ability in desired direction has the ability to transfer its good qualities to crosses and thus obtain superior commercial hybrids as well as the knowledge of the plant breeder in determining the appropriate method for the genetic improvement of those traits, where we find a relationship between the general ability to combination of grains yield per plant trait and general ability to combination of components of grains yield per plant, where the pure line that has a general ability to combination is positive and significance often possesses a general ability to combination the main components of yield, and at the same time superiority in performance. These results are in agreement with Al-Falahy (2015), Wuhiab *et al.* (2016b), Wuhiab *et al.* (2016a), Al-Salim *et al.* (2017), Aslam *et al.* (2017), Al-Obaidi *et al.* (2018), Hussen (2018) and Sugiharto *et al.* (2018) and Onejeme *et al.* (2020).

Table (3) effects of general combining ability of studied traits in maize by full diallel cross method 2020

Trait Geno.	DTS	PLH	NEPP	NGPR	300 GW	GY
1	0.246	-2.924	0.054	-0.492	-1.471	-1.565
2	-0.427	3.265	-0.023	0.001	-1.785	-6.562
3	0.082	2.660	-0.039	-0.822	-0.054	-3.312
4	-0.880	-1.674	-0.017	0.035	0.982	-2.253
5	0.981	-1.326	0.024	1.280	2.326	13.691
SE($\hat{g}_i - \hat{g}_j$)	0072	0.001	2.950	4.020	6.690	5.180

Table (4) showed the effects of the diallel and reciprocal specific combining ability of studied traits in maize by the full diallel cross method. it is noticed that the trait of days to 50% silking had significant effects in the desired direction for crosses (2×1), (3×2) and (5×3) and (4×1), (4×2) and (5×1) and (54×) in reciprocal crosses. diallel crosses (1×2), (1×3), (1×4), (2×4), (2×5), (3×4), (3×5) and reciprocal crosses (2×1), (3×1), (4×2), (5×1), (5×2), and (5×4) a significant desired effect of the specific combining ability of diallel and reciprocal crosses of plant height Trait. In terms of the number of ears per plant Trait, the cross (1×2) and (3×5) and reciprocal crosses (3×2), (4×1), (4×2), (5×1) and (5×4) were shown a significant desired effect of specific combining ability of diallel and reciprocal crosses of the number of ears per plant trait. The Crosses (1×2), (1×3), (1×4), (2×3), (2×4) and (3×5) were distinguished in diallel crosses, and (2×1) and (3×2), (4×1), (5×1) and (5×4) in reciprocal crosses, by giving diallel and reciprocal positive and significant effects on the number of grains per row trait. The trait of 300-grain weight showed positive and significant effects of the diallel and reciprocal specific combining ability in diallel crosses (1×2), (1×4), (1×5), (2×3) and (4×5), as well as (3×2), (4×3), (5×1), and (5×4) in reciprocal crosses. So as to the grains yield per plant, the crosses (1×2), (1×3), (1×4), (2×3), (2×4) and (3×5), and reciprocal crosses (3×2), (5×1), (5×4) positive and significant effects of the diallel and reciprocal specific combining ability, while the rest of hybrids were positive, but did not reach the limits of significant and another significant negative but in the unwanted direction and for all the studied Traits. This is in agreement with Al-Falahy (2015), Wuhiab *et al.* (2016b), Wuhiab *et al.* (2016a), Al-Salim *et al.* (2017), Aslam *et al.* (2017), Yuwono *et al.* (2017), Al-Obaidi *et al.* (2018), Hussain and Hussen (2018). Sugiharto *et al.* (2018) and Onejeme *et al.* (2020).

Table (4) effects of diallel and reciprocal specific combining ability for studied traits in maize by full diallel cross method 2020

Trait Geno.	DTS	PLH	NEPP	NGPR	300 GW	GY
1x2	-0.938	3.359	0.109	4.557	1.190	15.285
1x3	-0.129	5.002	-0.017	0.599	-1.774	3.612
1x4	-1.425	6.536	-0.038	3.483	2.447	14.602

1x5	-0.085	-3.810	-0.075	-1.324	1.579	-20.376
2x3	-0.548	-3.121	-0.063	0.952	2.129	10.885
2x4	0.768	2.528	0.001	0.983	-1.710	5.934
2x5	1.016	2.003	-0.026	-0.790	-1.108	-8.670
3x4	-0.489	1.327	-0.036	-5.280	-0.969	-14.050
3x5	-1.394	1.015	0.017	0.735	-1.785	3.107
4x5	3.357	-5.446	-0.077	-2.125	0.119	-10.225
2x1	-0.062	2.262	-0.030	0.578	-0.190	-13.502
3x1	1.485	10.560	-0.118	-3.860	-5.790	-18.358
3x2	0.500	-0.287	0.028	1.155	0.508	3.435
4x1	-0.977	-3.318	0.020	0.442	-0.817	-3.248
4x2	-1.537	3.990	0.042	-0.697	-0.532	-0.908
4x3	0.983	-2.342	-0.137	-5.063	0.157	-26.847
5x1	-1.783	6.090	0.112	5.743	0.758	13.500
5x2	2.228	3.502	-0.033	-0.093	-2.037	-1.930
5x3	-0.365	-1.310	-0.055	-1.742	0.047	-0.610
5x4	-4.003	8.097	0.010	3.995	-2.060	15.718
SE($\hat{\sigma}_{ij}-\hat{\sigma}_{ik}$)	0.538	0.053	0.003	0.013	0.016	0.014
SE($r^{\wedge}_{ij}-r^{\wedge}_{ik}$)	0.602	0.059	0.003	0.014	0.018	0.016

Table (5) showed the estimation of effects variation of general and specific combining ability of each parent for the traits under study, where through these differences it is possible to know the most important pure lines in improving the studied traits to determine the effect of each parent to make a decision about the pure lines which can be included in the hybridization programs of subsequent generations for the purpose of obtaining superior hybrids, As well as the advantage of the phenomenon of segregation and obtaining also superior hybrids, and among the phenomena that can occur, the phenomenon of super- segregation through which it is possible to obtain genotypes that superior the line in quantitative traits such as the yield trait, and this phenomenon produces from the additive gene action when the dominant and recessive alleles are established in different individuals of the product from heterozygous individuals. The pure lines (2) and (4) outperformed and gave the highest effect of pure lines for days to 50% silking trait reaching -0.427 and -0.880, respectively, effect variation of specific combining ability for the pure line (2) was less and reached 7.689, indicating that pure line (2) had transferred its effect to most of its crosses, while the pure line (4) had an effect variation value of specific combining ability was greater, reached 17,817. This indicates that it transferred its effect to some of its crosses and that the effect of general ability to combination for plant height traits was significant and desirable in pure lines (2) and (3), and they achieved the highest value of 3.265 and 2.660 respectively. While effect Variation of specific combining ability was 3.265 and 2.660, indicating that the first pure line transferred its influence to some of its crosses, while the low special effect variation of the second pure line indicates that it inherited its traits to most of their crosses. In the number of ears per plant trait, the pure lines (1) and (5) showed the highest effect of general combining ability reach 0.054 and 0.024 respectively. The evidence showed that effect

variation of specific combining ability of pure line (1) reached 0.027, which means that pure line (1) transferred its influence to some of its crosses, and for the pure line (5) reached 0.009, and this indicates that pure line (5) transferred its influence to most of the crosses. pure lines (4) and (5) outperformed the positive effect of general combining ability to the others pure lines for the number of grains per row, where their value reached 0.035 and 1.280 respectively, while effect Variation of specific combining ability was 21.198 and 6.265, and this indicates that the pure line (4) gave the largest value, meaning that inherited this trait to some crosses, while the pure line (5) gave a lower value, meaning that it inherited the effect of the genes for this trait equally to their crosses in 300-grain weight trait, pure lines (4) and (5) showed the highest effect of 0.982 and 2.326, and effect variation value of specific combining ability of pure line (4) was high at 5.910, indicating that this pure line had transferred its influence to some of its crosses. On the other hand, this value was low, reached 5.256 for the pure line (5), which means that this pure line transferred its influence to most of its crosses in that trait. Regarding the pure line (5), the highest effect of the general combining ability of grains yield per plant was 13.691, respectively, and the effect variance values of specific combining ability were 327.628, which indicated that the pure line (5) transferred its effect to some crosses for that trait. These results are consistent with Hussain, Sulaiman (2011), Chakraborty *et al.* (2012), and Al-Zehairy (2014).

Table (5) effects Variation of general and specific combining ability to studied traits in maize by full diallel cross method 2020

Trait Geno.	Var.	DTS	PLH	NEPP	NGPR	300 GW	GY
1	$\delta^2\hat{g}$	0.936	31.144	0.006	11.660	4.343	291.398
	$\delta^2\hat{s}$	6.160	161.315	0.027	48.192	34.778	590.534
2	$\delta^2\hat{g}$	0.601	8.410	0.002	0.943	2.904	136.915
	$\delta^2\hat{s}$	7.689	32.019	0.008	8.744	5.160	94.148
3	$\delta^2\hat{g}$	1.422	38.090	0.005	14.870	12.622	185.112
	$\delta^2\hat{s}$	1.225	25.269	0.027	29.697	5.609	843.936
4	$\delta^2\hat{g}$	5.055	20.668	0.009	10.268	0.329	278.611
	$\delta^2\hat{s}$	17.817	91.507	1.725	21.198	5.910	318.064
5	$\delta^2\hat{g}$	7.971	38.834	0.006	17.312	2.987	144.326
	$\delta^2\hat{s}$	14.065	39.528	0.009	6.265	5.256	327.628

Table (6) indicates the reciprocal effect of studied traits, where all crosses showed significant negative reciprocal effects ranging between -29.82% for the cross (3×2) to -100.00% for crosses (4×1), (5×1), (5×3), and (5×4) in days to 50% silking trait. Regarding the plant height trait the (6) reciprocal cross effects that outperformed its diallel crosses, where the reciprocal effect of these hybrids was positive and significant, the reciprocal effect (2×1) was more than the reciprocal crosses, reached 86.84%, while the reciprocal effect was a significantly negative in (4) reciprocal cross, where the crosses (4×1), (5×1), (5×3) and (5×4) showed the lowest negative and significant effect reach -100.00%. The results showed that all crosses had significant negative reciprocal effects that ranged between -98.69% for (3×1) to -100.00% for crosses (4×1), (5×1),

(5×3) and (5×4) in the number of ears per plant trait. Likewise, the number of grains per row and 300-grain weight traits, all crosses had a reciprocal negative effect ranged between -54.25% for the hybrid (3×2) to -13.75% for the cross (4×3) and between -100.00% for crosses (4×1), (5×1), (5×3) and (5×4) for the two traits respectively. Whereas, reciprocal effect in grains yield per plant was positive and negative values, where (6) had reciprocal effects that outperformed its diallel crosses, where the reciprocal effect of these crosses was positive and significant, where the reciprocal effect of the cross (3×1) was most reciprocal cross outperforming a diallel cross, reached 86.35%, while the reciprocal effect was negative and significant in (4) reciprocal cross, as the crosses (4×1), (5×1), (5×3) and (5×4) showed the lowest negative and significant effect that reached -100.00%. This Variation between diallel and reciprocal crosses demonstrates the role of cytoplasmic genetics in traits improving compared to the role of nuclear genetics in some cases, and this explains the importance of adopting reciprocal crosses in evaluating the management of genotypes.

Table (6) estimating the reciprocal effect of studied traits in maize by full diallel cross method 2020

Trait Geno.	DTS	PLH	NEPP	NGPR	300 GW	GY
2x1	-32.89	86.84	-98.74	-55.65	-18.92	80.54
3x1	-33.78	81.74	-98.69	-54.92	-18.45	86.35
3x2	-29.82	78.86	-98.83	-54.25	-17.86	82.36
4x1	-100.00	-100.00	-100.00	-100.00	-100.00	-100.00
4x2	-34.88	77.84	-98.76	-55.74	-15.97	71.65
4x3	-34.00	81.96	-98.73	-55.74	-13.75	81.09
5x1	-100.00	-100.00	-100.00	-100.00	-100.00	-100.00
5x2	-33.95	86.75	-98.72	-57.45	-17.96	80.43
5x3	-100.00	-100.00	-100.00	-100.00	-100.00	-100.00
5x4	-100.00	-100.00	-100.00	-100.00	-100.00	-100.00
SE	10.91	29.79	0.21	7.25	13.54	29.48

The variance values of genetic parameters of studied straits listed in Table (7) showed that the variance values of (σ^2D) and (σ^2D-r) differed from zero and its value was greater than the variance values of (σ^2A) in all the studied traits in diallel and reciprocal crosses, Except for the 300-grain weight trait and grains yield per plant in reciprocal crosses. Also, the variance component (σ^2gca) was greater than the variance component (σ^2sca) in all studied traits in diallel crosses, with exception of the number of ears per plant trait, This result in agreement with Aslam *et al.* (2017), In reverse hybrids, the contrast component (σ^2gca) was less than the variance component (σ^2rca) in all traits understudy in reciprocal crosses, so the best way to improve the traits is selection in diallel crosses that showed additive gene action and hybridization in reciprocal crosses in hybrids that showed a dominant gene action for the traits, and this is in agreement with both Wuhiab *et al.* (2016a) and Wuhiab *et al.* (2016b) in reciprocal crosses. As evident from the table (7) same ratio ($h^2b.s\%$) and ($h^2n.s\%$) and rate (\bar{a}), where the ratio ($h^2b.s\%$)

and ($h^2b.sr\%$) had high values in all the studied traits in diallel and reciprocal crosses, where the values ranged between 94.363% for days to 50% silking to 99.999% for the number of grains per row and grains yield per plant respectively, due to the fact that the variance value (σ^2G) was high and the variance value (σ^2E) was low in the studied traits, and these results do not contradict these results. With the results found by Falahy Al- (2015), Wuhiab *et al.* (2016a), Wuhiab *et al.* (2016b), Al-Salim *et al.* (2017), Abed *et al.* (2017) in terms of their obtaining of ($h^2b.s\%$) and ($h^2n.s\%$) High in some traits, Regarding the ratio ($h^2n.s\%$), the values were low for all the studied traits, except for 300-grain weight trait grains yield per plant that was medium values for diallel crosses, where the values of ($h^2n.s\%$) ranged between 1.647% to 894.46% in the two traits of days to 50% silking and 300-grain weight respectively, these results are in agreement with Al-Falahy (2015), Wuhiab *et al.* (2016a), Wuhiab *et al.* (2016b) and Abed *et al.* (2017) in terms of having a low ratio ($h^2n.s\%$) in some traits. As to ($h^2n.sr\%$) in reciprocal crosses, the values were for two traits of days to 50% silking and plant height, medium for two traits of the number of ears per plant and number of grains per row, and high for two traits of 300-grain weight and grains yield per plant. The ratio ($h^2n.sr\%$) was low in some traits. Also, the rate of (\bar{a}) and ($\bar{a}-r$) in the same table was greater than one in all the studied traits in diallel and reciprocal crosses, and this showed the importance of the dominance of the superior gene in controlling these traits in diallel and reciprocal crosses. These results are in agreement with Wuhiab *et al.* (2016b), Wuhiab *et al.* (2016a), Al-Salim *et al.* (2017), Abed *et al.* (2017), Aslam, *et al.* (2017).

Table (7) the variance values of genetic parameters of the studied traits by full diallel cross 2020

Trait para.	DTS	PLH	NEPP	NGPR	300 GW	GY
	0.053	2.527	0.0009	1.823	3.135	101.159
	0.008	0.046	0.076	0.071	0.442	0.207
	2.924	26.573	0.005	9.487	4.376	169.666
	0.362	0.003	1.480	0.0002	0.0003	0.0003
	0.106	5.054	0.002	3.646	6.271	202.319
	5.954	51.905	0.012	25.682	7.101	488.689
	10.609	4.532	3.628	3.753	1.505	2.198
$h^2b.s\%$	94.363	99.994	99.896	99.999	99.998	99.999
$h^2n.s\%$	1.647	8.872	13.179	12.431	46.894	29.279
	2.924	26.573	0.005	9.487	4.376	169.666
	7.434	3.243	2.414	2.281	1.181	1.295
$h^2b.s-r\%$	89.326	99.959	99.798	99.998	99.996	99.999

h^2	3.12	15.977	25.507	27.76	58.895	54.359
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Conclusion:

We conclude from this study that there are significant differences between the pure lines and their diallel and reciprocal crosses, in addition to the dominant gene action was controlling Studied traits, and therefore the way to improve these traits was through hybridization.

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