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Heterosis, Genetic Parameters of Maize (*Zea Mays* L.) Using the Half Diallel Cross Method

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ABSTRACT: A field experiment was conducted in the spring season to conduct single crosses with half diallel cross, and autumn from the year 2020 For comparing eight genotypes (Zm-1, Zm-2, Zm-3, Zm-4, Zm-5, S2, S5 and S6) in a comparison experiment using a randomized complete block design (RCBD). The results showed significant differences in the traits: days to 50% silking (DTS), plant height (PLH), number of ears per plant s per plant (NEPP), number of grains per row (NGPR), 300 grain weight (300 GW) and grains yield per plant (GY), indicating the variance pure lines involved in hybridization. pure line (2) was distinguished by its superiority in the trait of plant height, number of ears per plant s per plant and grains yield per plant. It was also found that the pure line (1) in the traits of days to 50% silking, the pure line (5) in 300 grain weight, and pure line (8) in the trait of number of grains per row. the cross (5×7) was the best hybrid in traits, with 300 grain weight and plant grain yield. The results of the study of Heterosis Relative to Mean Parents showed that (28) crosses in days to 50% silking, (27) crosses in plant height, (20) crosses for number of ears per plant s per plant, (28) in number of grains per row and grains yield per plant, (26) crosses 300 grain weight gave Heterosis Relative to Mean Parents in the desired significant direction in single crosses, As for the Heterosis Relative to Higher Parents, it was (28) crosses in traits of days to 50% silking, (26) crosses in plant height, (18) crosses for number of ears per plant s per plant, (24) in number of grains per row, (20) crosses At a 300 grain weight and (22) in grains yield per plant. The highest values of Heterosis Relative to Mean and best parents in traits of grains yield per plant, were 24.08% and 23.18 for the cross (5×7), respectively. It can be concluded that the heterosis depends on the diversity between the lines, which was evident in the lines (5) and (7). The ratio of σ^2sca\$\sigma^2$gca was less than one for all the studied traits in crosses. This was reflected in the value of degree of dominance, which was greater than one in all the studied traits of crosses. The ratio of broad sense heritability was high and in the narrow sense low in all traits studied in the crosses.

Key words: maize, Heterosis, genetic parameters, gene action, (*Zea mays* L.).

Introduction:

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 variance and determine the appropriate breeding method (Ahmed and Al- Hamadany, 2014). some genetic features must be estimated through dividing the components of genetic variance into additive variance and dominance and superiority variance, and knowing broad sense and narrow sense heritability, which means the amount of transfer of produced individuals in the trait to its offspring resulting from it in the first generation as well as concerned about this matter many researchers in the crop of maize, including EL-Shamarka *et al*. (2015), Ofori *et al.* (2015), AL- Tikrity and Al-Karkhi (2016), Nyombayire *et al.* (2016), Erdeaan (2017), Mussarbat and Aldulaymy (2017). AL-Obaidy *et al.* (2015) explained that the ratio of broad sense heritability was low in number of ears per plant s per plant, and number of grains per row, and high for the two traits of 500 grain weight grains yield per plant. AL-rawi *et al.* (2017) found that dominant gene action was more influential than additive genetic action in controlling the inheritance of these traits. The values of broad sense heritability were high for all traits. narrow sense heritability was an average of the traits of plant height, number of ears per plant s per plant and number of grains per row. 300 grain weight and grains yield per plant, it is high for days to 50% silking and low for the rest of traits, that the mean degree of dominance was greater than one correct for all traits, which indicates the existence of Superior dominant genes of these traits, except for days to 50% silking that was less than one which means so there is a partial dominant gene. Panda *et al.* (2017) indicated that when using half diallel cross of ten pure lines of maize, the ratio of σ^2sca\$\sigma^2$gca was less than one for a 100-grain weight trait and reached 0.05, which illustrates the importance of the dominant genetic action for this trait as the value of σ^2sca was greater than the value of σ^2gca. It was 2.22 and 0.10, respectively, for the 250- grain. indicate. Both Al-Jumaily and Al-Zubaidy (2018) indicated that the values of the components of the dominant gene action were the highest values of the components of the additive gene action, and that the heritability ratio in its narrow sense was of average values for all the studied traits.

The aim of this study is to introduce a group of pure lines (eight pure lines) into a half diallel cross program in order to estimate the heterosis relative to better parents and the general and special combining ability.

Materials and methods:

The experiment was carried out in Ramadi city/ Albu Shaban village in the spring and autumn seasons of 2020 using eight pure lines of maize: (Zm-1, Zm-2, Zm-3, Zm-4, Zm-5, S2, S5 and S6), obtained from the Department of Agricultural Research/Abu Ghraib Research Station, soil service operations were conducted, including plowing, smoothing, leveling, and fertilization with compound fertilizer N: P (18:18) at a rate of 100 kg / dunum, followed by lines opening operations. The seeds of the pure lines were planted in the spring season on 20/3/2020 with lines with distances 0.75m between the lines and 0.25m between the lines and a length of 7m by two lines for each pure line, and at a rate of 3 seeds per pit, then it was reduced to one plant in the pit. Urea fertilizer (46% N) was added at a rate of 100 kg/ dunam in two batches, the first after 30 days of emergence and the second at the start of male flowering. weeds control operation was carried out after the first irrigation and before germination, and for this purpose, Atrazine was used at a concentration of 80% at a rate of 3.2 kg/ ha. During the growing season, the crop service operations were carried out from irrigation, weeding and hoeing, and the maize leg borer insect (*Sesamia Criteca*) was controlled using the granulated diazinon pesticide 10% topically. Feeds for the plant were added twice, the first when the plant reached the 6-leaf stage and the second after 20 days of the first control, these operations were in both The two seasons. When the female inflorescences appeared and before the emergence of the calories, they were covered with paper bags to avoid open pollination and to ensure access to the required crosses, The male was covered with paper bags the day before the start of the pollination process and after the release of pollen grains, and hybridization process continued until all the required crosses between the eight pure lines were completed, at a rate of five ears for each cross to ensure that sufficient seeds were obtained for planting in the comparison experiment. Half diallel cross was carried out between pure lines to obtain individual crosses (diallel) and according to what Griffing said according to the second method (Method 2) and the first (fixed) model (model 1), so the number of the resulting genotypes is equal to p (p-1)/2. The seeds of the parental pure lines were propagated by self-pollination, and at the end of the season ears resulting from parents and crosses were taken and dried and core for the purpose of using them in a comparison experiment that includes parents and F1 crosses. Parents and individual crosses were sown on July 22, 2020 in the comparison experiment. The number of 28 crosses is in the form of lines with dimensions 0.75 between the lines and 0.25 between the lines and a length of 7 m and with 2 lines for each individual hybrid and with three replications according to Randomize Complete Block Design (R.C.B.D) taking into account all agricultural operations to serve the soil and crop. The data for each of the traits under study were taken of 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 crosses in the studied traits were tested using the least significant difference (L.S.D) with probability level 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 by using the approach of Griffing method 2 with fixed model.

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

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

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

$\sigma^2E = Mse^{-} = MSe / r$

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

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

The heritability ratio was estimated in its broad sense ($h^2b.s$) and narrow sense ($h^2n.s$) for diallel crosses according to (Singh and Chaudhary, 2007):

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

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

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

heterosis of diallel crosses was estimated in based on the basis of the average and best parents according to the following equation: (Singh and Chaudhary, 2007):

$$\text{Heterobeltiosis}\,\% = \overline{\text{F1}} - \overline{\text{BP}}/\overline{\text{BP}} \times 100$$

$$\text{Heterosis}\,\% = \overline{\text{F1}} - \overline{\text{MP}}/\overline{\text{MP}} \times 100$$

Results and discussion

Performance evaluation of genotypes

The results shown in Table (1), which include the values of the mean of the pure lines and individuals of the first generation, the studied traits resulting from the half diallel cross, show that there are differences between the values of those means. The differences were significant at a probability level of 1% and for all the studied traits. Studies confirmed by Shah *et al.* (2016), Yuwono *et al.* (2017) and Abed and Hammadi (2018) Begum *et al.* (2018), Murtadha *et al.* (2018), Tulu *et al.* (2018), Zhou *et al.* (2018), Ramadan *et al.* (2020), Keimeso *et al.* (2020), Yu *et al.* (2020) showed that there are significant differences between individual crosses and their parents for several studied traits.

The date of silking is effectd by many factors as the temperature, the length of the photoperiod, the growing season, and the nature of the genotype directly affect this trait. Pure line (2) had the longest flowering period of 73.73 days. As for the resulting crosses, crosses (1×5) surpassed in reaching the stage of 50% silking, as it took 65.03 days, while the longest flowering period was 69.43 days for cross (3×4). This great genetic variance between the pure lines at the time of flowering led to Significant differences in this trait for their diallel crosses. The reason for these differences in flowering of crosses is due to the genetic and environmental differences of the diallel crosses and their parents, and this calls for the continuation of the study of their combining ability, the highest average plant height reached 184.30 cm in the Pure line (2), while the Pure line gave (1) The lowest average plant height was 167.34 cm. The cross (2×5) showed the highest average plant height of 205.31 cm, while cross (1×8) showed the lowest average plant height of 170.07 cm.

The distinction of Pure line (2) is that it gives the highest average number of ears per plant , which reached 1.59 ear, and the lowest average of 1.18 ear in Pure line (1), and for crosses, the values of this trait ranged between 1.58 ear in cross (1×5) and below 1.37 ear in the two crosses (2×5) and (3×4). In number of grains per row per row, the Pure line (8) outperformed the highest average for the trait of 39.91 grain, while pure line (4) gave the lowest average for number of grains per row of 34.16 grain. For crosses, the values of this trait ranged between 45.69 cm in the cross (2×5) and below 38.34 cm in cross (1×2). Pure line (5) achieved the highest average

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

Tratis Genotype	DTS	PLH	NEPP	NGPR	300 GW	GY
1	68.20	167.34	1.18	36.18	74.17	117.18
2	73.73	184.30	1.59	39.36	80.04	140.24
3	70.66	168.13	1.33	34.91	75.03	115.06
4	71.16	172.60	1.34	34.16	78.70	137.15
5	69.82	172.44	1.36	39.19	80.40	140.14
6	68.83	169.50	1.23	36.34	72.23	122.01
7	69.03	170.48	1.26	37.08	76.16	138.12
8	68.01	169.72	1.44	39.91	79.77	119.24
1×2	66.11	198.16	1.38	38.34	78.36	138.55
1×3	66.24	186.44	1.42	40.08	80.74	140.34
1×4	66.70	183.53	1.39	38.63	83.54	144.06
1×5	65.03	193.11	1.58	41.56	81.84	142.84
1×6	65.81	191.76	1.38	40.00	78.47	140.44
1×7	67.03	191.64	1.41	39.72	81.10	140.79
1×8	67.00	170.07	1.38	38.45	79.84	143.42
2×3	69.01	199.76	1.44	41.79	82.17	143.03
2×4	67.39	195.47	1.38	40.27	81.91	141.36
2×5	66.05	205.31	1.37	45.69	79.34	141.63
2×6	65.74	197.51	1.40	40.74	80.24	140.52
2×7	66.26	198.11	1.42	39.17	81.22	143.75
2×8	66.54	187.67	1.47	41.64	81.49	143.55
3×4	69.34	189.45	1.37	39.76	82.27	139.75
3×5	69.03	191.65	1.45	40.10	82.73	141.44
3×6	67.08	193.74	1.46	38.93	81.94	142.53
3×7	67.13	195.94	1.41	41.54	81.21	143.07
3×8	66.00	190.83	1.48	42.34	80.47	141.66
4×5	67.80	188.73	1.39	39.83	80.52	140.42
4×6	66.26	187.67	1.42	40.04	81.18	140.72
4×7	66.64	189.42	1.45	40.01	81.20	143.13
4×8	67.25	188.38	1.39	39.63	80.01	143.05
5×6	68.33	185.95	1.51	41.07	82.03	144.46
5×7	67.09	190.86	1.54	41.65	86.54	172.63
5×8	66.82	190.05	1.50	40.57	80.12	143.30
6×7	67.17	191.21	1.49	41.36	81.36	140.03
6×8	66.17	183.00	1.48	42.12	78.34	142.27
7×8	66.44	169.67	1.54	40.48	83.82	144.56
G. Mean	67.58	186.10	1.42	39.80	80.29	139.90
L.S.D 5%	0.194	3.893	0.015	0.163	0.899	0.069
L.S.D 1%	0.258	5.169	0.020	0.217	1.193	0.092

For a 300 grain weight, it reached 80.40 g, and in contrast, Pure line (6) showed the lowest average 300 grain weight , amounting to 72.23 g. In crosses, cross (5×7) was distinguished by giving it the highest average 300 grain weight of 86.54 g and the lowest average of 78.34 g was found in cross (6×8). The differences between genotypes are due to the different genetic factors that the individual carries and the extent of its vulnerability to environmental conditions, and whether it are genetically similar or different, that this matter calls for continuing to study their genetic behavior to know the gene action that controls the inheritance of the trait under study. And for grains yield per plant trait, as Table (1) shows the values of the averages of the pure lines and individual crosses resulting from it, the Pure line (2) produced the highest average of grains yield per plant trait reached 140.24 g in When Pure line (3) produced the lowest average for grains yield per plant trait, which was 115.06 g/ plant, and the mean values showed that cross (5×7) produced the highest average for grains yield per plant trait, which reached 172.63 g/ plant, while cross (1×2) produced the lowest average. The plant yield was 138.55g. These differences between pure lines and their crosses reflect the extent of the genetic differences between it.

Heterosis:

In days to 50% silking, all crosses had significant negative values for Heterosis relatively to the mean and higher parents, The highest percentage of Heterosis relatively to the mean parents, was shown in Table (2) in the cross (2×5), it was -7.97%, and the lowest value appeared in the cross (5×6) was -1.43%. The highest Heterosis relatively to higher parents, was shown in Table (4) in cross (2×6), reached to -10.84%, and the lowest value appeared in the cross (1×8) reached to -1.76%. The phenomenon of Heterosis increased SCC in hybrid plant as a result of a gene action that affected the flowering trait that led to hybrid plant reaching flowering faster than its faster parent. This is in agreement with Aminu *et al.* (2014), Ghallab (2014), Tulu *et al.* (2018), Ramadan *et al.* (2020), Keimeso *et al.* (2020), Yu *et al.* (2020) in terms of heterosis values in combinations of maize. It ranged between positive and negative values for Heterosis relatively to the mean and higher parents for this trait.

As for the plant height, all the values were positive in relatively to the mean and the best parents except for cross (7×8). It had negative values for heterosis relative to mean and best parents, as the significant positive values calculated on the basis of the deviation of the average members of the first generation from the average parents ranged between 15.73% and 0.91% for the two crosses (3×7) and (1×8) respectively. As for heterosis relative to best parents, Table (3), the positive significant values ranged between 14.93% and 1.83% for the two crosses (3×7) and (2×8) respectively. Crosses that gave positive values for heterosis indicate the occurrence of the trait under the control of the super-dominance of genes, which gave negative values that were under the control of the partial dominance of the genes, this is consistent with what the Ghallab (2014), Erdeaan (2017), Sweed (2017), Darshan and Marker (2019), and Ramadan *et al.* (2020), in obtaining negative and positive values of heterosis relative to mean and best parents.

In the trait of number of ears per plant, (20) crosses with positive values and (8) crosses with negative values of heterosis relative to mean parents, (19) crosses with positive values and (9) crosses with values negative for heterosis relative to best parents, as the highest ratio of heterosis relative to mean parents appeared in Table (3) positive and high in significance reached 24.35% in cross (1×5) As for the low positive value for the heterosis, it was 2.59% for cross (4×5).

As for heterosis relative to best parents, Table (3), where cross (6×7) was significantly superior to the 1% probability level for number of ears per plant by 17.99%, followed by cross (1×5) with a value of 16.14%. The lowest positive value for the heterosis was 1.71% for cross (4×5). This is due to the genetic divergence between the pure lines, which was reflected in crosses in giving it a heterosis for that trait. These results are in agreement with the findings of Dhayif *et al.* (2013), Aminu *et al.* (2014), Ghallab (2014), Erdeaan (2017) and Ramadan *et al.* (2020), in obtaining of negative and positive values for heterosis relative to mean and best parents. In the trait of number of grains per row in Table (2), all crosses had significant positive values for heterosis relative to mean parents, as the values ranged between 16.33% for cross (2×5) and 1.06% for cross (1×8). As for heterosis relative to best parents, Table (3), most of crosses achieved a high positive and significant heterosis, and the highest percentage of 16.07% appeared in the cross (2×5), followed by the two crosses (2×5) and (3×4) with values of 16.07% and 13.88%, respectively, these results are in agreement with what was obtained by Ghallab (2014), Kanoosh (2014), AL- Tikrity and Al-Karkhi (2016), Erdeaan (2017), Mutlag *et al.* (2018) and Ramadan *et al.* (2020). In obtaining negative and positive values for heterosis relative to mean and best parents.

As for 300 grain weight trait, which is one of the most important main yield components, which represents the degree of fullness of the grain, its apparent density and quality. heterosis relative to mean parents founded in, Table (2) was positive and significant in most of crosses. Its values ranged between 11.28% in cross (3×6) and 0.05% in cross (5×8). As for heterosis relative to best parents, Table (3) for the 300 grain weight , the values for the positive heterosis ranged between 9.20% for cross (3×6) and 0.08% for cross (1×8). This result is consistent with what was mentioned by Ghallab (2014), Erdeaan (2017), Sweed (2017), Abdul-Hamed *et al.* (2017), Mutlag *et al.* (2018), Abdullah and Karim (2019) in their obtaining negative and positive values heterosis relative to mean and best parents.

It is the final outcome sought by the producer and the plant breeder, and it is a result of the contribution of the main yield components, so improving any of the traits associated with the yield components results in an increase in grains yield per plant or per unit area. In the traits of grains yield per plant in Table (2), heterosis was positive and significant in all crosses, relative to mean parents, while in Table (3) heterosis relative to best parents that (27) cross with positive values and one hybrid with negative values. Most of crosses achieved a positive and significant heterosis towards the increase in plant yield, relative to mean parents, Table (2), the highest of which was 24.08% in the cross (5×7), followed by the cross (1×8) with a value of 21.33% As for heterosis relative to best parents, the highest percentage for heterosis in the significant positive direction was found in Table (3), reaching 23.18% in cross (5×7). That heterosis is a quantitative phenomenon resulting from the action of a large group of genes that may work by dominant or partial 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, especially if We learned that plant traits are governed by approximately ten million pairs of genes (Gleisman, 1998). These results are in agreement with the findings of AL- Tikrity and Al-Karkhi (2016), and Erdeaan (2017) in terms of their obtaining heterosis relative to mean and best parentsare positive in most crosses. Resulting in this trait.

Table (2) Heterosis MP% Relatively to the Mean parents for the studied traits in maize by half diallel cross method 2020

Traits Genotype	DTS	PLH	NEPP	NGPR	300 GW	GY
1×2	-6.84	12.71	-0.36	1.50	1.62	7.64
1×3	-4.59	11.15	12.88	12.74	8.22	20.86
1×4	-4.28	7.98	10.17	9.85	9.30	13.29
1×5	-5.76	13.67	24.35	10.30	5.90	11.02
1×6	-3.95	13.86	14.21	10.31	7.20	17.44
1×7	-2.31	13.45	15.69	8.44	7.89	10.29
1×8	-1.63	0.91	5.33	1.06	3.72	21.33
2×3	-4.40	13.36	-1.37	12.53	5.97	12.05
2×4	-6.98	9.54	-5.91	9.55	3.20	1.92
2×5	-7.97	15.10	-7.10	16.33	-1.09	1.03
2×6	-7.78	11.65	-0.94	7.64	5.39	7.17
2×7	-7.17	11.68	-0.23	2.49	3.99	3.28
2×8	-6.11	6.02	-3.18	5.06	1.98	10.64
3×4	-2.21	11.20	2.75	15.12	7.03	10.82
3×5	-1.71	12.55	7.56	8.24	6.44	10.85
3×6	-3.82	14.77	14.06	9.27	11.28	20.24
3×7	-3.89	15.73	8.76	15.41	7.42	13.02
3×8	-4.81	12.97	6.62	13.19	3.97	20.92
4×5	-3.81	9.40	2.59	8.62	1.22	1.28
4×6	-5.34	9.71	10.62	13.58	7.58	8.60
4×7	-4.94	10.42	11.79	12.32	4.88	3.99
4×8	-3.35	10.06	-0.36	7.01	0.97	11.59
5×6	-1.43	8.76	16.30	8.77	7.48	10.21
5×7	-3.37	11.31	17.41	9.23	10.55	24.08
5×8	-3.04	11.09	7.13	2.58	0.05	10.50
6×7	-2.56	12.48	19.25	12.67	9.66	7.66
6×8	-3.30	7.89	10.34	10.48	3.08	17.95
7×8	-3.05	-0.26	13.69	5.15	7.52	12.34
SE	0.35	0.70	1.52	0.79	0.61	1.20

Table (3) Heterosis HP% Relatively to the higher parents for the studied traits in maize by half diallel cross method 2020

Traits Genotype	DTS	PLH	NEPP	NGPR	300 GW	GY
1×2	-10.34	7.52	-13.18	-2.60	-2.10	-1.21
1×3	-6.25	10.89	6.78	10.77	7.60	19.77

1×4	-6.27	6.33	3.73	6.78	6.15	5.04
1×5	-6.85	11.98	16.14	6.06	1.79	1.93
1×6	-4.38	13.13	11.89	10.07	5.79	15.11
1×7	-2.90	12.41	12.17	7.13	6.49	1.93
1×8	-1.76	0.20	-4.16	-3.66	0.08	20.28
2×3	-6.40	8.39	-9.62	6.17	2.66	1.99
2×4	-8.60	6.06	-13.39	2.31	2.33	0.80
2×5	-10.41	11.40	-13.81	16.07	-1.32	0.99
2×6	-10.84	7.17	-12.13	3.51	0.25	0.20
2×7	-10.13	7.50	-10.67	-0.47	1.47	2.51
2×8	-9.75	1.83	-7.74	4.34	1.81	2.36
3×4	-2.56	9.76	2.24	13.88	4.54	1.90
3×5	-2.30	11.14	6.11	2.34	2.89	0.93
3×6	-5.06	14.30	10.05	7.13	9.20	16.82
3×7	-4.99	14.93	6.03	12.04	6.63	3.58
3×8	-6.59	12.44	2.31	6.11	0.88	18.81
4×5	-4.72	9.35	1.71	1.65	0.15	0.20
4×6	-6.89	8.73	6.22	10.17	3.16	2.60
4×7	-6.36	9.75	8.46	7.89	3.18	3.63
4×8	-5.49	9.15	-3.93	-0.69	0.30	4.30
5×6	-2.13	7.83	10.76	4.81	2.02	3.08
5×7	-3.91	10.68	12.96	6.29	7.63	23.18
5×8	-4.29	10.21	4.16	1.65	-0.35	2.26
6×7	-2.70	12.16	17.99	11.54	6.83	1.38
6×8	-3.87	7.82	2.31	5.55	-1.79	16.61
7×8	-3.76	-0.48	6.47	1.43	5.08	4.66
SE	0.52	0.72	1.80	0.92	0.59	1.42

Table (4) shows the variance values of the genetic parameters of the studied traits, as it shows that the variance values of (σ^2D) differed from zero and that its value was greater than the variance values of (σ^2A) in all the studied traits, and that the variance component of (σ^2gca) was less than variance component (σ^2sca) in all the studied traits, and this is in agreement with Aslam *et al.* (2017), Ambikabathy *et al.* (2019), Singh *et al.* (2019) and Ramadan *et al.* (2020) in terms of the importance of the dominant genetic action to control the inheritance of the studied traits, so the best way is to improve traits are crosses that show dominant genetic action for the traits. As can be seen from the table the same percentage (h^2b.s%) and (h^2n.s%) and rate (ā), as the percentage (h^2b.s%) had high values in all the studied traits, as the values ranged between 99.999% for grains yield per plant trait and 98 .275% for plant height trait, and this is due to the fact that the variance value (σ^2G) was high and the variance value (σ^2E) was low in the studied traits. These results do not contradict the results that were found by Sweed (2017), Ige *et al.* (2019) and Ramadan *et al.* (2020). As for the percentage (h^2n.s%), the values were low for all the studied traits, where the values of (h^2n.s%) ranged between 9.971% and 643.0% in two traits. number of grains per row and 300 grain weight respectively, these results are consistent with

Ramadan *et al.* (2020) in terms of having a low (h^2n.s%) in all traits. Also, the rate of (ā) in the same table was greater than one in all the studied traits. This indicates the importance of the superior dominance of genes in controlling these traits. These results were in agreement with the Erdeaan (2017) and Sweed (2017), in terms of their obtaining an average of a degree of dominance greater than one.

Table (4) the variance values of genetic parameters of the studied traits by half diallel cross 2020

Traits **para.**	**DTS**	**PLH**	**NEPP**	**NGPR**	**300 GW**	**GY**
	0.034	3.955	0.000	0.235	0.023	3.161
	3.093	100.623	0.007	4.246	7.145	83.700
	0.005	1.906	0.000	0.003	0.102	0.001
	0.068	7.910	0.000	0.471	0.047	6.321
	3.093	100.623	0.007	4.246	7.145	83.700
	0.011	0.039	0.023	0.055	0.003	0.038
σ^2 G	3.160	108.534	0.008	4.717	7.192	90.021
σ^2 P	3.165	110.439	0.008	4.720	7.293	90.022
h^2b.s%	99.851	98.275	99.615	99.929	98.608	99.999
h^2n.s%	2.137	7.163	4.431	9.971	0.643	7.022
$\bar{a}$	9.562	5.044	6.555	4.248	17.460	5.146

conclusion:

It can be concluded that the Heterosis depends on the diversity between pure lines, which was evident in pure lines (5) and (7). Also, the dominant gene action was controlling Studied traits, and therefore the way to improve these traits was through hybridization.

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