Study of heterosis, genetic depression and estimation of genetic parameters of some morphological traits in chickpea genotypes by generation mean analysis

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Highlights

• The success of breeding programs to produce hybrid seed depends on the ability of the reformer to identify high-yielding hybrid parental lines.
• To study the heritability of various agronomic and physiological traits in the progeny of six chickpea cultivars using generation mean analysis to determine the effects of genes.
• The estimation of the genetic parameters of the genes and finally the determination of the breeding methods was appropriate.

Graphical Abstract
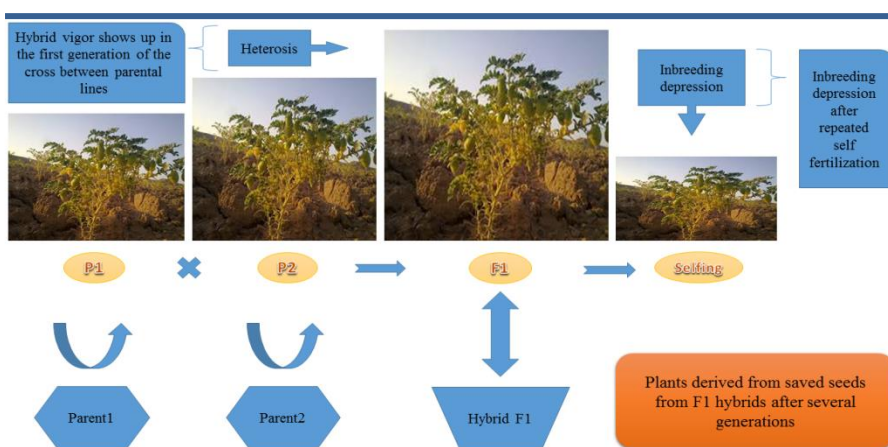
Abstract

In this study, six chickpea cultivars (Azad, Pirouz, Bivanich, Kaka, ICCV2, and Flip87-51C) and the progeny resulting from their crosses (F1, F2, Bc1, and Bc2) were examined to determine the inheritance, heterosis, and genetic depression of a number of different morphological traits. The cultivars and their progeny were planted in Sarab Niloofar Lake of Kermanshah in spring 2018 in a randomized block design with three replicates. The species of the crosses included Pirouz♀× ICCV2♂, ICCV2♀× Flip87-51C♂, Kaka♀× Flip87-51C♂, Azad♀× Flip87-51C♂, Bivanich♀× Flip87-51C♂, Azad♀× ICCV2♂, Kaka♀× Azad♂, and ICCV2♀× Bivanich♂. The results showed a significant difference between generations with respect to the studied traits, indicating a high genetic diversity in the studied materials. According to the results of generation mean analysis, additive and dominant as well as epistasis effects were involved in the inheritance of most of the measured traits. The mean degree of dominance in most of the traits showed the effect of gene dominance when these traits were controlled. The highest relative heterosis compared to the average parent (83.35) was related to the fourth cross in grain yield and the lowest (0.07) to the number of hollow pods per plant in the eighth cross. The lowest mean genetic regression in all crosses was related to 100-seed weight (3.92) and the highest (26.52) to the number of hollow pods per plant.

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1. Introduction

Chickpea (*Cicer arietinum L.*) is a self-pollinating and diploid annual plant (2n = 2x = 16) that has a relatively small genome (740Mb) which is ranked third in the world in terms of legume and the first place in Asia and North Africa (Rahbarian et al., 2013). Among legumes, chickpeas have the highest area under cultivation in the world after beans. According to statistics available in 2011, the global area under chickpea cultivation is reported to be 13.5 million hectares. 80% of it is cultivated in South and Southwest Asia, especially India (68%), Pakistan (9.8%) and Myanmar (3.2%), and the other major producers of chickpeas are Australia, Turkey, Ethiopia, Iran, Mexico, Canada and the United States (Thompson, 2008). In Iran, chickpeas, with 65% of the total area under cereals, ranks first in terms of area under cereals. One of the most useful parameters in estimating performance is the rate of heterosis and finding the parents with the most heterosis in their progeny (Park et al., 2021). Success in hybrid seed production breeding programs depends on the ability of the reformer to recognize the parent lines that have high hybrid production efficiency (Olfati et al., 2013). Heterosis means that hybrids are superior to their parents in terms of yield, stress resistance or fertility, and therefore heterosis is used to increase the production and quality of agricultural products (Gwanama et al., 2001; Huang et al., 2006; Ahmed et al., 2003) also stated that heterosis means a prominent role of dominance variance in controlling traits. In another study, Moll and Stuber (1974) identified the existence of heterosis as suggesting that the parents had dominant, super-dominant, or epistatic genes (Moll and Stuber, 1974). Therefore, with the presence of heterosis in hybrids, it is possible to detect the presence of different alleles in a genetic locus in hybrid parents. Heterosis or vigor of a hybrid indicates the development and superiority of F1 hybrids produced from cross-line inbred compared to the superior parent, average parent or a control variety.

Heterosis is caused by complete or partial dominance, which is achieved by the aggregation of desirable alleles, often from both parents, into a hybrid (Mather and Jinks, 1972). On the other hand, the predominant phenomenon is also a factor in causing heterosis and causes the value of the heterozygous genotype to be higher than the value of each of the homozygous genotypes (Comstock and Robinson, 1948). At the same time, some believe that heterosis is caused by an interaction between gene loci or epistasis. Some other hereditary factors of cytoplasm and their interaction with existing hereditary factors are included in heterosis (Gwanama et al., 2001). Sarkar and Sirohi (2011) expressed positive and significant heterosis compared to the superior parent of cucumber for total yield per plant unit (Sarkar and Sirohi, 2011). Singh et al., (1993) used the generation mean analysis method to analyze the effects of a gene on yield in chickpeas (Singh et al., 1993). The results showed that the additive and non-additive effects were effective for the number of days to flowering, number of primary and secondary branches, number of pods per plant and seed yield. Estimation of incremental components, dominance and epistasis determination is important to determine the corrective method. It is also important to recognize the need to produce a hybrid or pure line, as well as to predict the probability of obtaining lines that are better than the original lines. This study aimed to study the heritability of several agronomic and physiological traits in the progeny of six chickpea cultivars through generation mean analysis to determine the effects of genes. It was also appropriate to estimate the genetic parameters of the genes and finally to determine the breeding methods.

2. Materials and Methods

This study was conducted in Sarab Niloofar of Kermanshah in 2018 with the title of the study of heterosis, genetic depression and estimation of genetic parameters of some morphological traits in chickpea genotypes. The soil condition of the project according to the soil test is as follows (Table 1):

Table 1. Results of soil test.

Soil texture class	Sand %	Clay %	Silt %	FC	PH	EC dS/m	TNV %	P mg/kg	Fe mg/kg	Zn mg/kg	Cu mg/kg	Mn mg/kg
Clay silt	9	49	42	20.4	7.8	0.35	32.1	11	6.2	1.7	1.9	2.87

In this study, parent seeds (P1 and P2) were prepared with the following characteristics:

(A) ICCV2, (B) Flip87-51C, (C) Azad, (D) Kaka, (E) Pirouz, and (F) Bivanich

(A) ICCV2: Early, ripening drought resistant, good yield and almost large seed size.

(B) Flip87-51C: Early ripening, drought-resistant, high yield and large seed size

(C) Azad: Late ripening, high yield, drought-sensitive and large seed size.

(D) Kaka: Late ripening, medium yield, drought-sensitive, small seed size, black seed color, native to Kurdistan province.

(E) Pirouz: Late ripening, high yield, drought drought-sensitive, small seed size and yellow seed color.

(F) Bivanich: Large seed size, high yield, early ripening and native to Kermanshah.

In this plan, the types of parents along with generations F1, F2, Bc1, and Bc2 are related to the types of crosses, which were: First cross (Pirouz♀× ICCV2♂), second cross (ICCV2♀× Flip87-51C ♂), third cross (Kaka♀× Flip87-51C♂), fourth cross (Azad♀× Flip87-51C♂), fifth cross (Bivanich♀× Flip87-51C♂), sixth cross (Azad♀× ICCV2♂), seventh cross (Kaka♀× Azad♂), eighth cross (ICCV2♀× Bivanich♂). Which are shown in the tables as C7, C6, C5, C4, C3, C2, C1C8, respectively. The experiment was performed in a randomized complete block design with three replications. The planting was done in 2017 and the date of the first irrigation was considered for uniformity and coordination of germination of 2018 seeds. The studied traits included the number of pods per plant, number of seeds per plant, 100-seed weight, grain yield per plant, biological yield per plant, harvest index, the height of the lowest pod from the ground and the number of hollow pods per plant.

2.1. Statistical Analysis

Analysis of variance for different traits was performed using SAS statistical software. The results of weight analysis of variance showed that there was a significant difference between all generations, so the generation means analysis for all traits was performed using Minitab software. In this method, the overall average of each attribute is calculated as follows:

Equation 1: $$Y=m+[d]+\beta[h]+\alpha2[i]+ \alpha2 [j]+\beta2[l]$$

The components of the formula were: Y: average of one generation, m: average of all generations in a cross, [d]: sum of additive effects, [h]: sum of dominance effects, [i]: sum of interactions additive × additive, [j]: sum of interactions additive × dominance, [l]: Total interaction of dominance × dominance and α, β, $\alpha2$, $\alpha\beta2$ and $\beta2$.

Equation 2: Absolute heterosis compared to the mean parent (Matzinger et al., 1971) $\quad \overline{F}_1-mpv$

Equation 3: Relative heterosis compared to the average parent (Matzinger et al., 1971) $\quad \left(\frac{\overline{F}_1-mpv}{mpv}\right) \times 100$

Equation 4: Absolute heterosis over the superior parent (Matzinger et al., 1971) $\quad \overline{F}_1-hpv$

Equation 5: Relative heterosis to the superior parent (Matzinger et al., 1971) $\quad \left(\frac{\overline{F}_1-hpv}{hpv}\right) \times 100$

Equation 6: T-test for heterosis based on mean parents (Wynne et al., 1970) $\quad t = \frac{\overline{F}_1-MP}{\overline{F}\sqrt{\frac{3}{8}\alpha_P^2}}$

Equation 7: T-test for heterosis based on superior parent (Jinks and Pooni, 1976) $\quad t = \frac{\overline{F}_1-HP}{\sqrt{\frac{1}{2}\alpha_e^2}}$

2.2. Inbreeding depression

Inbreeding depression, which indicates a decrease in progeny produced by inbreeding, is due to increased homogeneity in segregating generations.

Equation 8: Inbreeding depression $\quad ID = \frac{\overline{F}_1-\overline{F}_2}{\overline{F}_1} \times 100$

Equation 9: T test for Inbreeding depression (Alam et al., 2004) $\quad t=\frac{ID}{\sqrt{\delta_{\overline{F}_1}^2+\delta_{\overline{F}_2}^2}}$

Where the ID indicates the Inbreeding depression and $\delta\frac{2}{F_1}$ the mean variance of F1 and $\delta_{\overline{F}_2}^2$ the mean variance of F2, respectively.

3. Results and Discussion

According to Table 2, which showed the results of weight analysis of variance of traits, there was a significant difference between all generations. Therefore, the mean generation analysis for the desired traits was performed as follows.

Table 2. Weight analysis of variance of the studied generations.

Traits	Crosses	Block effect	Generation effect	Error	Standard deviation
Number of seeds per plant	c1	9.05*	5.82*	1.78	3.49
	c2	5.05 ns	24.32**	2.12	3.93
	c3	2.20 ns	225.79**	2.94	3.71
	c4	2.27 ns	11.65**	1.72	4.10
	c5	0.27 ns	13.25**	0.65	2.22
	c6	0.32 ns	29.47**	0.23	1.40
	c7	4 ns	329.60**	2.13	3.03
	c8	11.72 ns	12.05**	2.12	4.15
Harvest index	c1	1.79**	6.99**	0.2	3.67
	c2	0.26 ns	9.18**	0.51	4.27
	c3	0.21 ns	29.76**	0.55	5.69
	c4	12.09 ns	23.08 ns	12.06	23.19
	c5	0.09 ns	9.68**	0.38	3.86
	c6	0.041 ns	6.29**	0.2	3.48
	c7	0.09 ns	4.55**	0.46	5.33
	c8	0.37 ns	5.46**	0.69	6.01
Number of pods per plant	c1	1.38 ns	9.42**	0.85	2.39
	c2	2.16 ns	29.2**	1.76	3.56
	c3	1.27 ns	232.14**	1.89	2.98
	c4	1.05 ns	8.72*	1.92	4.34
	c5	1.16*	15.43**	0.3	1.51
	c6	0.16 ns	26.9**	0.16	1.17
	c7	2.63 ns	324.75**	9.12	6.19
	c8	10.88*	10.18**	2.22	4.26
100-seed weight	c1	0.04 ns	6.42**	0.49	4.66
	c2	1.71*	22.08**	0.31	2.38
	c3	0.93 ns	90.62**	4.89	11.03
	c4	0.003 ns	10.02**	0.09	1.42
	c5	0.008 ns	1.87**	0.24	2.09
	c6	0.07 ns	5.78**	0.065	1.22
	c7	0.037 ns	64.66**	0.27	4.78
	c8	0.009 ns	8.11**	0.037	0.90
Seed yield per plant	c1	0.27 ns	0.69**	0.11	5.78
	c2	0.60 ns	4.30**	0.21	5.34
	c3	0.55 ns	10.12**	1.31	12.88
	c4	0.13 ns	1.55**	0.064	3.72
	c5	0.05 ns	0.36**	0.058	2.79
	c6	0.065 ns	1.55**	0.028	2.32
	c7	0.13 ns	17.48**	0.12	4.04

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	c8	0.51 ns	1.13*	0.14	5.04
Number of hollow pods per plant	c1	48.38**	21.68*	6.18	26.97
	c2	70.72**	39.65**	7.18	28.89
	c3	114.32**	34.11*	8.45	34.06
	c4	6.16 ns	50.63**	5.50	42.04
	c5	50.88 ns	52.08**	10.55	40.05
	c6	3.16 ns	36.23**	5.3	39.46
	c7	3.23 ns	40.02**	7.72	48.56
	c8	68.16**	36.63**	7.1	29.06
Biological yield per plant	c1	1.79**	6.92**	0.2	3.67
	c2	0.26 ns	9.18**	0.51	4.27
	c3	0.21 ns	29.76**	0.55	5.69
	c4	12.09 ns	23.08*	12.06	23.19
	c5	0.09 ns	9.68**	0.38	3.86
	c6	0.04 ns	6.29**	0.2	3.48
	c7	0.09 ns	4.55**	0.46	5.33
	c8	0.37 ns	5.46**	0.69	6.02
Lowest pod height from the ground	c1	0.8*	11.92**	0.18	2.36
	c2	0.12 ns	17.57**	0.65	3.16
	c3	0.55 ns	36.45**	1.36	5.32
	c4	0.55 ns	21.94**	0.53	3.23
	c5	0.25 ns	8.60**	0.48	2.82
	c6	0.002 ns	4.20**	0.18	2.11
	c7	3.60 ns	26.06**	3.25	8.57
	c8	0.08 ns	6.60****	0.4	2.98

* Significant level of 5%, ** Significant level of 1%, and ns: Not Significant.

3.1. Number of pods per plant

There was a significant difference between all crosses for the number of pods per plant according to Table 2, which showed the results of weight analysis of variance, so the mean generation analysis was performed for the desired trait. Table 3 shows the results of comparing the mean of traits and their standard error in different generations. The amount of standard error in different generations indicates the difference between different people within generations. Placement of progeny between two parents in this trait is an indication of additive effects in controlling this trait. For all crosses in this trait, the parameter m is significant at the level of 1% probability, which indicates the existence of common genes between the two parents. In most crosses to justify the inheritance of the number of pods per plant, in addition to the simple effects of three parameters including m, [d] and [h] epistatic effects are also included in the model, which indicates the complex inheritance of this trait. Table 4 presents the results of the study of relative heterosis and absolute heterosis based on the average of parents and higher parents as well as genetic depression. According to this table, the relative number of pods per plant in crosses 2, 3, 5, 7, and 8 was relatively higher than the mean of parent and parent higher. The highest rate of heterosis based on the parental mean and higher parent is related to the second crosses (14.15) and (-19.11). Mean genetic depression in this trait is in all crosses (11.13). The genetic parameters of different traits are presented in Table 5. According to Table 5, only crosses 2, 1, 4, 5, and 6 parameters [h] became significant and did not even appear in other crosses. The positivity and significance of the dominance parameter [h] at the intersections of 2, 1, 4, 5, and 6 are the indicators of hybrid production to improve this trait. It can also be stated that the alleles that increase this trait in the mentioned crosses should be dominant over the alleles that reduce

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it. In the first, second, third, fourth, and eighth crosses, the effects of [h] and [l] are opposite for the number of pods per plant, indicating dual-type epistasis in the inheritance of this trait. The degree of dominance in crosses 5, 8, 2, 1, and 4 indicates the existence of a dominant effect and in crosses 7, 6, and 3 indicate the effect of incomplete dominance for the number of pods per plant.

3.2. Number of seeds per plant

For the number of seeds per plant according to Table 2, which showed the results of weight analysis of variance, there was a significant difference between all crosses, so the mean generation analysis was performed for the desired trait. Table 3 shows the results of comparing the mean of traits and their standard error in different generations. The standard error values of different generations indicate differences between different individuals within generations. Table 4 presents the results of the study of relative heterosis and absolute heterosis based on the mean of parents and higher parents as well as genetic depression. According to this table, the relative number of seeds per plant in crosses 2, 3, 5, 7, 7, 6 and 8 was relatively higher than the average of parents and parents. The highest rate of heterosis based on the average parent and higher parent is related to the eighth (13.39) and third (-20.12) crosses. The mean genetic depression in this trait is in all crosses (5.99). Table 5 presents the genetic parameters of different traits. For the number of seeds per plant, the five-parameter model consisting of m, [d], [h], [i], [j] showed the best fit. In most crosses, the traits [h] and [l] have opposite signs for the number of seeds per plant, which indicates the existence of dual-type epistasis in the inheritance of this trait. The degree of dominance in crosses 5, 4, 2, 1, and 8 indicates the existence of a dominant effect and in crosses 3, 6, and 7 indicate the incomplete dominance effect for the number of seeds per plant.

3.3. 100-seed weight

For the 100-grain weight trait according to Table 2, which showed the results of weight analysis of variance of the traits, there was a significant difference between all crosses, so the mean generation analysis was performed for the trait. Table 3 shows the results of comparing the mean of traits and their standard error in different generations. The amount of standard error in different generations indicates the difference between different people within generations. The genetic parameters of different traits are presented in Table 5. For all crosses in this trait, the parameter m is significant at the level of 1% probability, which indicates the existence of common genes between the two parents. Table 4 presents the results of the study of relative heterosis and absolute heterosis based on the average of parents and higher parents as well as genetic depression. According to this table, for the trait of 100-grain weight in crosses 2, 3, 5, 7, 1, 4, 6, and 8, relative heterosis was significantly higher than the mean parent and higher parent. The highest rate of heterosis based on the average parent and higher parent is related to the seventh (34.47) and third (20) crosses. The mean genetic depression in this trait is in all crosses (3.92), which has the lowest value among all traits in all crosses tested. According to Table 5, in addition to the simple effects of three parameters including m, [d] and [h], the effects of epistasis have also been included in the model, which indicates the complex inheritance of this trait. Therefore, it can be concluded that the significant presence of all genetic parameters in the model indicates the role of both additive and non-additive effects in the genetic control of 100-grain weight. Of course, due to the multi-gene trait of 100-grain weight, these results will not be unexpected. The positive and significant dominance parameter [h] in crosses 2, 1, 5, 6, and 7 indicates the possibility of producing a hybrid to improve this trait. It can also be stated that the alleles that increase this trait in the mentioned crosses should be dominant over the alleles that reduce it. In the third cross, the effects [d] and [i] are opposite for the weight of 100 grains, which indicates the opposite nature of the interaction for this attribute. These results are consistent with the other research (Kandic et al., 2019). The degree of dominance in crosses 6, 7, 2, 1, and 8 indicates the existence of a dominant effect and in crosses 4 and 3.5 indicates the incomplete dominance effect for the 100-grain weight trait.

Table 3. Mean generation and standard error in different generations at crosses.

Traits	Crosses	Cross1	Cross2	Cross3	Cross4	Cross5	Cross6	Cross7	Cross8
Number of pods per plant	P1	37±3.52[dc]	32±3/18[d]	32±3/18[d]	32±3/18[ab]	32±3/18[d]	37±3/02[b]	29±2/06[c]	37±3/45[a]
	P2	40±2.96[ab]	37±3/02[bc]	59/33±2/71[a]	29±2/06[c]	37±3/45[bc]	29±2/06[c]	59/33±2/70[a]	37±3/02[a]
	F1	39±3.01[ab]	39/6±3/45[a]	47/99±3/12[b]	31/3±2/96[b]	38/67±2/88[a]	37±2/65[a]	52/44±2/65[b]	32/33±1/85[b]
	F2	36±5.44[d]	34/66±5/50[c]	46/33±5/48[b]	32/33±4/8[ab]	37/33±3/95[b]	35±3/25[c]	51/66±3/25[b]	34/67±3/02[ab]
	BC1.1	38.67±2.44[bc]	39±2/68[ab]	43/33±2/46[c]	34±3/21[a]	36±3/12[c]	35±3/25[c]	52/62±3/25[b]	35±1/50[ab]
	BC1.2	40.67±3.85[a]	39/66±2/56[a]	47/4±2/15[b]	33±3/54[ab]	36±3/25[c]	36±2/95[b]	47/3±2/95[b]	33/67±3/95[b]
Biological yield per plant	P1	15.16±1.85[a]	19.33±1.10[a]	19.33±1.10[a]	19.33±1.100[a]	19.33±1.1000[a]	15.16±1.85[a]	13.83±2.5[ab]	14.83±3.20[a]
	P2	12.33±2.80[b]	15.16±1.85[c]	11±2.0000[c]	13.83±2.5[ab]	14.83±3.200[dc]	13.83±2.6[b]	11±2.00000[d]	15.16±1.85[a]
	F1	12.5±1.780[b]	18.33±0.35[a]	12.91±1.10[b]	16.5±1.50[ab]	16.33±1.5800[b]	13.66±2[b]	14.16±1.320[a]	15.16±0.20[a]
	F2	10.5±1.750[c]	15±1.1000[a]	11.5±1.85[bc]	13.83±1.65[ab]	14.33±1.5600[d]	11±4[d]	11.66±1.29[dc]	12.5±0.500[b]
	BC1.1	11.83±1.78[b]	16±1.200[bc]	11.5±1.56[bc]	15.16±1.58[ab]	15.16±2.12[bcd]	12.33±3.69[c]	12.83±2.65[bc]	12.83±0.20[b]
	BC1.2	12.16±1.65[b]	16.83±1.20[b]	12±1.540[bc]	11.16±2.000[b]	15.16±2.250[bc]	12.5±4.01[c]	13.16±2.22[ab]	12.5±0.150[b]
Harvest index	P1	43±1.1000[a]	42±1.2100[b]	42±1.2100[b]	42±1.210[ab]	42±1.2100[c]	43±1.100[d]	43±1.520[e]	57±1.2900[a]
	P2	44±1.5800[a]	43±1.1000[b]	51±1.5000[b]	43±1.520[ab]	57±1.290[ab]	43±1.520[d]	51±1.500[d]	43±1.1000[b]
	F1	47±1.2500[a]	53±1.6200[a]	74±1.4000[a]	39±1.48000[b]	56±1.500[ab]	57±1.240[c]	71±1.350[c]	47±1.5000[b]
	F2	50±1.2400[a]	56±1.4400[a]	94±1.2000[a]	47±1.24000[a]	60±1.8700[a]	68±1.880[a]	92±1.800[a]	59±1.2300[a]
	BC1.1	47±1.6900[a]	60±1.2000[a]	79±1.8000[a]	45±1.9800[ab]	55±2.020[ab]	62±1.280[b]	86±1.400[b]	58±1.5800[a]
	BC1.2	45±1.5800[a]	55±1.5000[a]	82±2.0000[a]	42±2.2000[ab]	54±2.6000[b]	59±2.70[bc]	71±2.400[c]	58±2.2000[a]
Number of seeds per plant	P1	37.00±2.95[ab]	32.66±3.520[c]	32.660±3.520[d]	32.66±3.520[a]	32.66±3.520[d]	37.00±2.950[a]	28.66±1.970[e]	37.66±4.260[a]
	P2	39.33±3.120[a]	37.0±2.95[ab]	59.670±3.030[a]	28.66±1.970[b]	37.66±4.26[ab]	28.66±1.970[c]	59.67±3.030[a]	37.00±2.95[ab]
	F1	39.00±3.330[a]	39.33±3.120[a]	47.660±3.110[b]	31.33±3.800[a]	38.66±4.010[a]	37.00±2.230[a]	49.00±2.12[dc]	32.33±0.950[c]
	F2	36.00±4.870[b]	34.67±4.75[bc]	46.33±4.56[bc]	32.33±4.260[a]	37.33±3.50[ab]	35.66±2.490[b]	53.00±2.400[b]	34.67±0.56[bc]
	BC1.1	38.67±3.560[a]	39.33±3.500[a]	43.33±3.2100[c]	34.00±4.010[a]	35.66±1.500[c]	35.33±3.020[b]	51.58±3.00[bc]	35.0±0.99[abc]
	BC1.2	39.33±3.250[a]	39.33±3.570[a]	47.40±3.6000[b]	33.00±3.500[a]	36.33±1.21[bc]	35.66±3.420[b]	47.25±3.300[d]	33.66±0.670[c]

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Table 3. Continue.

100-seed weight	P1	18.00±1.540ᵃ	25.00±1.504ᵃ	25.00±1.8100ᵃ	25.00±1.800ᵃ	25±1/8ᵃ	18±1/54ᶜ	21/3±1/9ᵃ	22/6±0/55ᵃ
	P2	14.00±1.290ᵇ	18.00±1.810ᶜ	9.500±2.0200ᶜ	21.30±1.900ᵇ	22/6±0/55ᶜ	21/3±1/9ᵇ	9/5±2/02ᶜ	18±1/54ᵈ
	F1	15.16±2.370ᵇ	25.00±2.900ᵃ	20.00±2.8500ᵇ	20.83±2.46ᵇᶜ	23/86±0/32ᵇ	21/20±1/01ᵇ	20/26±2/11ᵃᵇ	22/2/08ᵇ
	F2	14.66±4.440ᵇ	24.33±3.62ᵃᵇ	23.66±3.56ᵃᵇ	20.40±3.25ᵈᶜ	23/33±0/60ᵇᶜ	21/33±1/10ᵇ	20/51±1/42ᵃᵇ	21/5±1/51ᶜ
	BC1.1	14.55±3.150ᵇ	24.66±3.15ᵃᵇ	21.16±3.20ᵃᵇ	20.23±3.010ᵈ	23/83±0/21ᵇ	21/83±0/99ᵃ	21/50±1/01ᵃ	21/66±1/13ᵇᶜ
	BC1.2	14.33±3.700ᵇ	23.66±2.130ᵇ	21.00±2.15ᵃᵇ	20.36±2.19ᵈᶜ	23/50±0/12ᵇᶜ	21±0/86ᵇ	20±1/12ᵇ	21/83±1/26ᵇᶜ
Lowest pod height from the ground	P1	21.82±2.1ᵃ	27.5±2.14ᵃᵇ	27.49±2.14ᵃ	27.51±2.14ᵃ	27.49±2.14ᵃ	21.82±2.10ᵃ	19.86±2.5ᵈᶜ	23.34±2.60ᵃ
	P2	17.84±2.7ᵇᶜ	21.82±2.1ᵉ	16.66±2.21ᶜ	19.86±2.5ᶜ	23.34±2.60ᶜ	19.86±2.50ᵇ	16.66±2.21ᵈ	21.82±2.10ᵇ
	F1	18.41±1.98ᵇ	28.16±2ᵃ	22.48±2.25ᵇ	23.02±2.54ᵇ	25.56±2.54ᵇ	21.51±0.1ᵃ	24.62±1.5ᵃ	22.28±0.9ᵃᵇ
	F2	15.78±2.12ᵈ	23.44±2.02ᵈ	22.45±2ᵇ	20.42±2.68ᶜ	23.04±2.59ᶜ	18.61±0.12ᶜ	22.53±1.24ᵃᵇᶜ	19.95±0.45ᶜ
	BC1.1	17.46±2.5ᶜ	25.7±2.65ᶜ	20.67±2.36ᵇ	22.70±2.21ᵇ	23.66±2.25ᶜ	20.04±0.1ᵇ	23.92±1.65ᵃᵇ	20.42±0.5ᶜ
	BC1.2	17.79±2.16ᵇᶜ	26.14±2.2ᵇᶜ	21.95±2.54ᵇ	22.38±2.02ᵇ	24.2±2.30ᶜ	19.99±0.1ᵇ	20.61±1.78ᵇᶜ	19.84±0.5ᶜ
Number of hollow pods per plant	P1	11±3/23ᵃ	13/33±3/23ᵃ	13/33±3/23ᵃ	13/33±3/23ᵃ	13/33±3/23ᵃ	11±3/23ᵃ	2/66±6/25ᵈᶜ	12/66±4/85ᵃ
	P2	11/66±2/95ᵃ	11±3/01ᵃᵇ	9/22±3ᵃᵇ	2/66±6/25ᵇ	12/66±4/29ᵃ	2/66±6/25ᶜ	9/22±3ᵃᵇ	11±3/22ᵃᵇ
	F1	10/66±2/12ᵃ	11±3/15ᵃᵇ	9/66±3/4ᵃᵇ	5±5/61ᵇ	8/66±6/50ᵃᵇ	5±8/80ᵇᶜ	10/11±13/52ᵃ	11±3/62ᵃᵇ
	F2	7/33±2/02ᵃᵇ	7/33±5/95ᵇᶜ	7/33±5/5ᵇᶜ	6±5/50ᵇ	6±3/77ᵇ	2/33±5/50ᶜ	7±12/20ᵃᵇᶜ	7/3±2ᵇᶜ
	BC1.1	4/66±1/36ᵇ	3±4/73ᶜ	3±4/65ᶜ	4±4/70ᵇ	4/33±2/50ᵇ	5±9/75ᵇᶜ	4/33±8/50ᵇᶜᵈ	3±3/01ᶜ
	BC1.2	10±1/50ᵃ	10±9/20ᵃᵇ	8/66±8/89ᵃᵇ	2±4/12ᵇ	3/66±5/55ᵇ	9±12/6ᵃᵇ	1±2/55ᵈ	10±4/5ᵃᵇ
Seed yield per plant	P1	6.660±0.580ᵃ	8.160±0.560ᵇ	8.160±0.56ᵇ	8.160±0.560ᵃ	8.160±0.560ᶜ	6.660±0.580ᶜ	6.030±0.570ᵈ	8.510±0.540ᵃ
	P2	5.510±0.500ᵇ	6.660±0.580ᶜ	5.660±0.550ᶜ	6.030±0.570ᶜ	8.510±0.54ᵇᶜ	6.030±0.570ᵈ	5.660±0.550ᵈ	6.660±0.580ᶜ
	F1	5.910±1.100ᵇ	9.830±1.020ᵃ	9.560±1.00ᵃᵇ	6.520±1.100ᵇ	9.220±0.550ᵃ	7.840±0.520ᵃ	10.12±1.200ᵇ	7.110±0.55ᵇᶜ
	F2	5.280±1.100ᵇ	8.440±1.040ᵇ	10.95±1.120ᵃ	6.590±1.110ᵇ	8.700±0.350ᵇ	7.610±0.54ᵃᵇ	10.86±2.020ᵃ	7.450±0.850ᵇ
	BC1.1	5.630±0.480ᵇ	9.700±0.440ᵃ	9.170±0.95ᵃᵇ	6.870±0.940ᵇ	8.500±0.54ᵇᶜ	7.710±0.95ᵃᵇ	11.08±1.550ᵃ	7.580±0.670ᵇ
	BC1.2	5/620±0/550ᵇ	9.300±0.520ᵃ	9.530±0.91ᵃᵇ	6.710±0.880ᵇ	8.530±0.62ᵇᶜ	7.490±0.660ᵇ	9.440±1.230ᶜ	7.340±0.84ᵇᶜ

The means with common letters in each column based on Duncan's multiple range test, at the level of 5%, are not significantly different.

Table 4. The rate of relative and absolute heterosis based on the meanparent and higher parent and genetic depression for traits measured at crosses.

Traits	Parameters	Cross1	Cross2	Cross3	Cross4	Cross5	Cross6	Cross7	Cross8
Number of pods per plant	Mean parents	38.5	34.5	45.66	30.5	34.5	33	44.16	37
	Absolute heterosis compared to the mean parent	0.5	5.16	2.32	0.83	4.17	4	8.27	-4.67
	Relative heterosis compared to the mean parent	1.29, t=0.89	14.95**, t=6.37	5.08* ,t=2.76	2.72, t=1.36	12.08**, t=12.63	12.12, t=16.66	18.37, t=4.49	-12.62**, t=5.13
	Absolute heterosis over the higher parent	-1	2.66	-11.34	-0.67	1.67	0	-6.89	-4.67
	Relative heterosis to the higher parent	2.5*, t=-1.53	6.70*, t=2.88	-19.11**, t= -11.67	-2.09, t= -0.78	4.51**, t=4.39	0	-11.61, t= -3.23	-12.62**, t= -4.44
	genetic depression	7.69	12.60	3.45	-3.19	3.46	5.4	1.48	-7.23
Biological yield per plant	Mean parents	13.74	17.34	15.16	16.58	17.08	14.49	12.41	14.99
	Absolute heterosis compared to the mean parent	-1.24	1.08	-2.25	-0.08	-0.75	-0.83	1.75	0.17
	Relative heterosis compared to the mean parent	4.59**, t=9.06	6.29*, t=2.51	-11.63**, t=-5	-0.48, t=-0.03	-4.39*, t=-2.02	-5.76*, t=-3.07	14.10**, t=4.26	1.13*, t=0.34
	Absolute heterosis over the higher parent	-2.66	-0.97	-6.42	-2.83	-3	-1.5	0.33	0
	Relative heterosis to the higher parent	-17.54**, t=-0.85	-5.01*, t=-1.8	-32.21**, t=-12.34	-14.64*, t=-1.15	-15.51**, t=-6.97	-9.89**, t=-4.83	2.38*, t=0.70	0
	genetic depression	16	18.16	10.92	16.18	12.24	19.47	17.65	17.54

Table 4. Continue.

Harvest index	Mean parents	43.5	42.5	46.5	42.5	49.5	43	47	50
	Absolute heterosis compared to the mean parent	3.5	10.5	27.5	-3.5	6.5	14	24	-3
	Relative heterosis compared to the mean parent	-8.04**, t=12.96	24.7**, t=41/24	59.13**, t=61.11	-8.23, t=-1.65	-13.3**, t=-17.56	32.55**, t=51.85	51.06**, t=58.5	-6**, t=-6
	Absolute heterosis over the higher parent	3	10	23	-4	-1	14	20	-10
	Relative heterosis to the higher parent	6.81**, t=9.67	23.25**,t=32.25	59.13**, t=44.23	-9.3*, t=-1.63	-1.75*, t=-2.32	32.55**, t=45.16	39.21**, t=42.55	-17.54**, t=-17.24
	genetic depression	-6.38	-5.66	-27.02	-20.51	-7.14	-19.29	-29.57	-25.53
Seed yield per plant	Mean parents	6.08	7.41	6.91	3.09	8.33	6.34	5.54	7.51
	Absolute heterosis compared to the mean parent	-0.17	2.42	2.65	3.43	0.88	1.49	4.57	-0.48
	Relative heterosis compared to the mean parent	-2.87, t= -0.85	32.65, t= 1.18	83.35**, t= 3.78	111**, t= 22.86	10.62**, t= 22.86	23.58**, t=14.9	82.52**, t=21.76	-6.26, t=-2.18
	Absolute heterosis over the higher parent	-0.75	1.67	1.4	-1.64	0.71	1.18	4.09	-1.4
	Relative heterosis to the higher parent	-11.26*, t= -3.26	20.46**, t=5.21	17.15, t=1.75	-20.09**, t= -9.64	8.34**, t=4.17	17.71**, t=10.72	67.82**, t=20.41	-16.45**, t= -5.38
	genetic depression	10.65	14.14	-14.53	-1.07	5.63	2.93	-7.31	-4.78

Table 4. Continue.

Number of seeds per plant	Mean parents	38.16	34.83	46.16	30.66	35.16	32.83	44.16	37.33
	Absolute heterosis compared to the mean parent	0.83	4.5	1.49	0.67	3.5	4.17	4.38	-5
	Relative heterosis compared to the mean parent	2.18*, t=1.06	13.10**, t=5.05	3.23, t=1.41	2.18, t=0.78	9.95**, t=7.14	12.70**, t=14.37	10.92**, t=5.42	-13.39**, t=-5.61
	Absolute heterosis over the higher parent	-0.39	2.33	-12.01	-1.33	1	0	-10.67	-5.33
	Relative heterosis to the higher parent	0.99*, t=-0.43	6.29*, t=2.28	**-20.12, t=-9.92	-4.07,t=-1.35	2.65, t=1.57	0	**-17.88, t=-10.35	-14.15**, t=-5.07
	genetic depression	7.69	11.84	2.79	-3.19	3.44	3.62	-8.16	-7.23
100-seed weight	Mean parents	16	21.5	17.25	23.15	23.8	19.65	15.4	20.3
	Absolute heterosis compared to the mean parent	-0.84	3.5	2.75	-2.32	0.06	1.55	5.26	1.7
	Relative heterosis compared to the mean parent	-5.25*, t=-2.38	16.27**, t=10.2	15.94**, t=2.03	-10.02**, t=-12.88	0.25**, t=0.2	7.88**, t=10.33	34.74**, t=16.96	0.83**, t=15.45
	Absolute heterosis over the higher parent	-2.84	0	-5	-4.17	-1.14	-0.1	-0.36	-0.6
	Relative heterosis to the higher parent	-15.77**, t=-5.79	0	-20*, t=-3.20	-16.68**, t=-19.85	4.56*, t=-3.35	-0.46*, t=-0.55	-1.69, t=1	-2.65*, t=-4.61
	genetic depression	3.29	2.68	-18.3	2.06	2.22	-0.61	0.007	2.27

Table 4. Continue.

Lowest pod height from the ground	Mean parents	19.83	24.66	22.07	23.68	25.41	20.84	18.26	22.58
	Absolute heterosis compared to the mean parent	1.42	3.5	0.41	-0.66	0.15	0.67	6.36	-0.3
	Relative heterosis compared to the mean parent	7.16**, t=5.68	14.19**,t=7.14	1.85,t= 0.57	-2.8**, t= -1.5	0.59, t=0.35	3.21*, t= 2.68	34.83**, t=5.67	-1.32, t=57.81
	Absolute heterosis over the higher parent	-4.41	0.66	-5.01	-4.49	-1.93	-0.31	4.76	-1.06
	Relative heterosis to the higher parent	-20.21**, t= -14.7	2.4, t= 1.15	t= -6.10	t = -8.80	-7.02**, t= -4.02	-1.42, t= -1.03	23.96**, t=3.68	-4.54**, t= -45.34
	genetic depression	14.28	16.76	0.13	11.29	9.85	13.48	8.48	10.45
Number of hollow pods per plant	Mean parents	11.33	12.16	11.27	7.99	12.99	6.83	5.94	11.83
	Absolute heterosis compared to the mean parent	-0.67	-1.16	-1.61	-2.99	-4.33	-1.83	4.17	-0.83
	Relative heterosis compared to the mean parent	5.91 , t= -0.44	-9.58 , t= -0.7	-14.33 , t= -0.9	-37.48, t= - 2.09	-33.37, t=-2.18	-26.79, t= - 1.30	70.20*, t=2.45	-0.07, t= -0.50
	Absolute heterosis over the higher parent	-1	-2.33	-3.67	-8.33	-4.67	-6	0.89	-1.66
	Relative heterosis to the higher parent	-8.57, t= -0.57	-17.47, t= -1.23	-27.53, t= -1.79	-62.49**, t= -5.04		-45.54**, t= -3.70	9.65, t=0.45	-13.11, t= -0.88
	genetic depression	31.32	33.36	24.12	-20		35.4	3.76	33.63

* Significant level of 5%, ** Significant level of 1%, and ns: Not Significant.

Table 5. Estimation of genetic parameters in the studied model by means of generation means analysis.

Traits	Crosses	Mean effect	Addtive effect	Dominance effect	Addtive× Addtive	Addtive× Dominance	Dominance× Dominance	Kai 2	Degree of dominance
Number of pods per plant	c1	24.13 ± 3.00**	− 1.70 ± 0.41**	32.60 ± 6.71**	14.36 ± 2.95**	---	− 17.73 ± 3.95**	0.34	−19.17
	c2	15.9 ± 3.01**	− 1.55 ± 0.39**	51.12 ± 6.64**	18.59 ± 2.94**	---	− 27.41 ± 3.93**	5.41	−32.98
	c3	45.66 ± 0.53**	− 13.66 ± 0.53**	− 3.08 ± 1.95ns	---	19.24 ± 1.45**	5.4 ± 1.88 **	1.78	0.22
	c4	30.44 ± 0.47**	1.35 ± 0.4**	10.06 ± 1.98**	---	---	− 9.17 ± 1.95**	3.10	7.45
	c5	34.38 ± 0.48**	− 2.49 ± 0.60**	4.18 ± 0.83**	---	4.90 ± 1.80**	---	5.11	− 1.68
	c6	33.17 ± 0.39**	4.06 ± 0.46**	4.04 ± 0.70**	---	− 10/24 ± 1/59**	---	1.4	0.99
	c7	50.86 ± 0.93**	− 15.16 ± 0.43**	1.56 ± 1.33ns	− 6.7 ± 1.05**	40/97 ± 1/57**	---	0.002	− 0.1
	c8	37.36 ± 1.94**	0.62 ± 0.43ns	− 5.70 ± 4.79**	− 0.28 ± 1.83**	---	0/71 ± 2/98**	2.36	− 9.9
Biological yield per plant	c1	8.55±0.55**	1.36±0.43**	4.03±0.84**	5.32±0.71**	-3.41±1.12**	----	0.51	5.39
	c2	11.68±0.26**	2.07±0.27**	6.64±0.29**	5.57±0.4**	-5.8±0.74**	----	0.1	3.2
	c3	15.16±0.29**	4.16±0.29**	-11.72±1.05**	-----	9.33±0.88**	9.46±0.91**	0.74	-2.81
	c4	16.58±0.35**	2.75±0.35**	-12.41±1.23**	-----	2.22±1.03*	12.33±1.08**	5.51	-4.51
	c5	12.26±0.5**	2.41±0.41**	3.95±0.74**	4.6±0.66**	- 4.88±1.23**	----	1.57	1.63
	c6	14.49±0.41**	0.66±0.41ns	-9.64±1.82**	---	-1.49±1.82ns	8.81±1.72**	4.63	-14.60
	c7	9.22±0.42**	1.47±0.41**	5.04±0.62**	3.44±0.58**	-3.87±1.30**	----	3.07	3.42
	c8	12.23±0.41**	0.31±0.03**	-10.26±1.24**	-----	-----	10.18±0.83**	7.07	-33.09
Harvest index	c1	59.5±0.97**	-0.5±0.24*	-25.5±2.55**	-16±0.19**	5±0.85**	13±1.67**	0.00	51
	c2	36.5±0.96**	-0.5±0.21*	61.5±2.38**	6±0.93**	11±0.71**	-45±1.56**	0.00	123
	c3	100.5±1.04**	-4.5±0.24**	0.5±2.82ns	-54±1.01**	3±0.94**	-27±1.87**	0.00	-0.11
	c4	54.97±0.43**	-0.47±0.25ns	-16.1±0.66**	-12.56±0.50**	6.84±1.0**	-----	2.18	34.25
	c5	71.5±1.39**	-7.5±0.22**	-30.5±3.6**	-22±1.37**	17±1.08**	15±2.31**	0/00	4.60
	c6	73±1.33**	0.00±0.24ns	-4±3.39**	-30±1.31**	6±1.33**	-12±2.14**	0.00	ns
	c7	101±1.27**	-4±0.27**	-6±3.22ns	-54±1.24**	38±0.99**	-24±2.05**	0.00	1.5
	c8	54±1.05**	7±0.21**	27±2.82**	-4±1.02**	-14±0.91**	-34±1.88**	0.00	3.85
Number of seeds per plant	c1	26.21 ± 2.86**	− 0.97 ± 0.40*	26.36 ± 6.71**	11.94 ± 2.80**	---	− 13.57 ± 4.13**	0.30	− 27.17
	c2	16.28 ± 2.85**	− 1.32 ± 0.46*	50.49 ± 6.70**	18.69 ± 2.78**	---	− 27.45 ± 4.17**	5.19	− 38.25
	c3	45.34 ± 0.49**	− 13.62 ± 0.59**	1.43 ± 0.86ns	---	18.79 ± 1.87**	---	7.85	− 0.06
	c4	30.29 ± 0.49**	1.77 ± 0.43**	10.26 ± 2.07**	---	---	− 9.22 ± 2.19**	4.96	5.79
	c5	40.31 ± 1.96**	− 0.92 ± 0.26**	− 10.27 ± 4.49*	− 5.44 ± 1.81**	---	8.62 ± 2.98**	5.66	11.16
	c6	32.28 ± 0.37**	4.34 ± 0.44**	4.14 ± 0.63**	--	− 9.28 ± 1.62**	---	3.03	0.95
	c7	56.87 ± 0.73**	− 15.45 ± 0.46**	− 7.98 ± 1.05**	− 12.84 ± 0.88**	39.46 ± 1.61**	---	0.88	0.51
	c8	39.07 ± 0.76**	1.27 ± 0.17**	− 10.86 ± 2.21**	− 1.40 ± 0.45**	---	4.12 ± 1.49**	2.12	− 8.55

Table 5. Continue.

100-seed weight	c1	12 ± 1.06**	1/76 ± 0/24**	2/83 ± 1/36*	3/27 ± 1/11*	---	---	9/18	1/60
	c2	21.77 ± 0.28**	− 3/54 ± 0/30**	4/20 ± 0/58**	---	8/66 ± 1/25**	---	5/66	− 1/18
	c3	27.27 ± 1.01**	7/75 ± 0/35**	− 7/30 ± 1/43**	− 10/03 ± 1/08**	− 15/13 ± 1/31**	--	0/024	− 0/94
	c4	19.31 ± 0.90**	1/85 ± 0/33**	1/12 ± 1/26^{ns}	3/62 ± 0/98**	− 3/37 ± 1/27**	---	5/79	0/60
	c5	22.86 ± 0.15**	1/38 ± 0/18**	1/007 ± 0/19**	1/15 ± 0/25**	− 2/11 ± 0/36**	---	1/27	0/72
	c6	19.65 ± 0.31**	− 1/65 ± 0/31**	5/39 ± 1/01**	---	4/94 ± 0/74**	− 3/84 ± 0/81**	0/25	− 3/26
	c7	15.4 ± 0.35**	5/9 ± 0/35**	15/85 ± 1/21**	---	− 8/77 ± 0/84**	− 10/59 ± 1/16**	1/46	2/69
	c8	20.49 ± 0.19**	2/16 ± 0/20**	2/18 ± 0/39**	---	− 4/73 ± 0/63**	---	4/69	1/00
Seed yield per plant	c1	4.64 ± 0.34**	0/57 ± 0/09**	1/25 ± 0/51*	1/43 ± 0/36**	− 1/13 ± 0/29**	---	0/016	2/19
	c2	3.23 ± 0.56**	0/57 ± 0/07**	14/23 ± 1/25**	4/18 ± 0/55**	---	− 7/63 ± 0/79**	5/79	24/96
	c3	12.21 ± 0.3**	1/24 ± 0/10**	− 2/78 ± 0/48**	− 5/33 ± 0/35**	− 3/19 ± 0/44**	---.	3/34	− 2/24
	c4	7.07 ± 0.09**	1/06 ± 0/10**	− 0/6 ± 0/2**	---	− 1/82 ± 0/43**	---	1/71	− 0/56
	c5	8.23 ± 0.07**	− 0/17 ± 0/10^{ns}	0/86 ± 0/14**	---	0/21 ± 0/31^{ns}	---	8/92	− 5/05
	c6	7.43 ± 0.16**	0/25 ± 0/08**	0/48 ± 0/24^{ns}	− 1/00 ± 0/19**	---	---	7/58	1/92
	c7	5.84 ± 0.10**	0/18 ± 0/10^{ns}	14 ± 0/64**	---	3/05 ± 0/62**	− 9/72 ± 0/72**	4/25	77/77
	c8	7.64 ± 0.008**	0/92 ± 0/10**	− 0/46 ± 0/14**	---	− 1/3 ± 0/37**	---	1/22	−0/50
Number of hollow pods per plant	c1	11.33±0.56**	− 0/33±0/56^{ns}	− 15/33 ± 1/82**	…	− 10/02±1/28**	14/66±1/50**	0/00	46/45
	c2	12.16±0.56**	1/16±0/57*	− 19/82±2/83**	…	− 17/29±3/03**	18/66±2/76**	0/58	−17/08
	c3	11.27±0.56**	2/05±0/56**	− 17/00±2/75**	…	− 17/22±2/95**	15/39±2/67**	2/11	− 8/29
	c4	20.48±3.51**	3/71±0/65**	− 42/46±8/4**	− 11/55±3/39**	…	26/97±5/49**	6/56	− 11/44
	c5	20.7±2.53**	0/45±0/55^{ns}	− 46/76±6/36**	− 7/73±2/48**	…	34/72±4/58**	0/86	103/91
	c6	− 0.77±2.25^{ns}	3/97±0/97**	7/02±3/71**	7/93±2/41**	− 13/66±4/93**	…	4/64	1/76
	c7	5.94±0.89**	− 3/28±0/89**	− 14/67±5/52**	…	15/39±3/07**	18/84±6/19	6/43	4/47
	c8	11.83±0.75**	0/83±0/75^{ns}	− 18/21±2/52**	…	− 16/52±2/14**	17/38±2/26**	2/78	−21/93
lowest pod height from the ground	c1	13.21±0.66**	1.96±0.43**	5.26±0.96**	6.70±0.8**	-4.65±1.32**	----	0/3	2/68
	c2	14.21±1.51**	2.84±0.38**	22.94±3.91**	10.44±1.46**	-7.08±1.28**	2.55±-9**	0/00	8/07
	c3	26.63±1.51**	5.41±0.39**	-12.58±3.93**	-4.56±1.46**	-13.39±1.30**	2.60±8.43**	0/00	-2.32
	c4	18.15±0.84**	3.78±0.42**	5.25±1.22**	5.80±0.95**	-7.03±1.23**	---	3/98	1/38
	c5	20.38±0.82**	2.10±0.43**	4.98±1.21**	4.89±0.94**	-5.29±1.29**	---	0/98	2/37
	c6	0.03±15.71**	0.41±0.89*	0.05±5.79**	0.07±5.60**	0.83±-1.69*	---	1/32	6/5
	c7	18.26±0.42**	0.46±1.6**	1.55±10.01**	----	1.41±3.40**	1.42±-3.74**	0/48	6/31
	c8	0.52±21.82**	0.1±0.59**	1.5±-7.92**	0.31±0.72**	----	1.03±8.41**	0/16	-13/42

* Significant level of 5%, ** Significant level of 1%, and ns: Not Significant.

3.4. *Seed yield per plant*

For grain yield traits per plant according to Table 2 which showed the results of weight analysis of variance of traits. There was a significant difference between all crosses, so the generation means analysis was performed for the desired trait. Table 3 shows the results of comparing the mean of traits and their standard error in different generations. The amount of standard error in different generations indicates the difference between different people within the generations. The superiority of the results over the average of parents can confirm the existence of dominance in most traits. Table 4 presents the results of the study of relative heterosis and absolute heterosis based on the average of parents and higher parents as well as genetic depression. According to this table, relative heterosis was significantly higher than the average parent and parent for higher grain yield per plant at crosses 2, 3, 5, 7, 7, 4, 6, and 8. The highest rate of heterosis based on the average parent and higher parent is related to the fourth (111) and seventh (67.12) crosses. The average rate of genetic depression in this trait is in all crosses (7.63). Due to the low heritability of the yield trait, morphological characteristics that have high heritability and high correlation with yield are usually used for its selection (Alam et al., 2004). The genetic parameters of different traits are presented in Table 5. For all crosses in this trait, the parameter m is significant at the level of 1% probability, which indicates the existence of common genes between the two parents. For grain yield per plant, the five-parameter model consisting of m, [d], [h], [i], and [j] showed the best fit. The significant presence of all genetic parameters in the model indicates the role of both additive and non-additive effects in the genetic control of grain yield. Of course, due to the multi-genetic nature of these traits, these results will not be unexpected. The significance of the dominance component [h] in all crosses except the sixth cross indicates the possibility of producing a hybrid to improve this trait. In the third and sixth crosses, the effects [d] and [i] are opposite for the grain yield trait in the plant, indicating the opposite importance of the interaction for this trait. In the second and seventh crosses for this trait, the effects [h] and [l] have the opposite sign, which indicates the existence of dual-type epistasis in the inheritance of the trait of grain yield per plant. The degree of dominance in crosses 5, 3, 2, 1, 6, and 7 indicates the presence of a dominant effect and in crosses 4 and 8 indicates the incomplete dominance effect for the grain yield trait per plant.

3.5. *Biological yield per plant*

For biological yield trait according to Table 2 which showed the results of weight analysis of variance of traits. There was a significant difference between all crosses, so the mean generation analysis was performed for the desired trait. Table 3 shows the results of comparing the mean of traits and their standard error in different generations. The amount of standard error in different generations indicates the difference between different people within the generations. Placement of progeny between two parents in this trait is an indication of additive effects in controlling this trait. Table 4 presents the results of the study of relative heterosis and absolute heterosis based on mean parents and higher parents as well as genetic depression. According to this table, relative heterosis was significantly higher than mean parents and higher parents for biological traits per plant at crosses 2, 3, 5, 7, 1, 4, 6 and 8. The highest rate of heterosis based on the average of parents and higher parents is related to the seventh (14.10) and third (33.21) crosses. The average rate of genetic depression in this trait is in all crosses (16.02). The genetic parameters of different traits are presented in Table 5. For all crosses in this trait, the parameter m is significant at the level of a probability of 1, which indicates the existence of common genes between the two parents. In all crosses to explain the inheritance of biological function, in addition to the simple three-parameter model consisting of m, [d] and [h], the additive and incremental effects of dominance are also significant at the level of one percent, which indicates the complex inheritance of this trait. The degree of dominance in all crosses indicates the existence of a dominance effect for the biological function trait.

3.6. *Harvest index*

For the harvest index trait according to Table 2, which showed the results of weight analysis of variance of the traits. There was a significant difference between all crosses, so the mean generation analysis was performed

for the desired trait. Table 3 shows the results of comparing the mean of traits and their standard error in different generations. The amount of standard error in different generations indicates the difference between different people within the generations. Placing the results between two parents in this trait is an indication of additive effects in controlling this trait. Table 4 presents the results of the study of relative heterosis and absolute heterosis based on mean parents and higher parents as well as genetic depression. According to this table, for the harvest index trait in crosses 2, 3, 5, 7, 4, 1, 6 and 8, relative heterosis was significant compared to mean parents and higher parents. The highest rate of heterosis based on the average parent and higher parent is related to the third (59) and third (59.11) crosses. The mean genetic depression in this trait is in all crosses (17.63). The genetic parameters of different traits are presented in Table 5. For all crosses in this trait, the parameter m is significant at the level of 1% probability, which indicates the existence of common genes between the two parents. The positive and significant dominance parameter [h] in crosses 2 and 8 indicates the possibility of producing a hybrid to improve this trait. It can also be argued that alleles that increase this trait at these crosses should be dominant over alleles that decrease it. In the second, sixth and eighth crosses, the effects [d] and [i] are also opposite for the harvest index, indicating the opposite nature of the interaction for this trait. In all crosses except the fourth, sixth and seventh crosses for this trait, the effects [h] and [l] have opposite signs, which indicates the existence of dual-type epistasis in the inheritance of the harvest index trait. The degree of dominance in crosses 1, 7, 8, 2, 5, and 4 indicates the existence of a dominant effect and in crosses 3 indicates the incomplete dominance effect for the harvest index trait.

3.7. Lowest pod height from the ground

For the trait, the height of the lowest pod from the ground in the plant according to Table 2, which showed the results of weight analysis of variance. There was a significant difference between all crosses, so the mean generation analysis was performed for the desired trait. Table 3 shows the results of comparing the mean of traits and their standard error in different generations. The amount of standard error in different generations indicates the difference between different people within the generations. The genetic parameters of different traits are presented in Table 4. For all crosses in this trait, the parameter m is significant at the level of 1% probability, which indicates the existence of common genes between the two parents. Table 4 presents the results of the study of relative heterosis and absolute heterosis based on mean parents and higher parents as well as genetic depression. According to this table, for the trait of the lowest pod height from the ground in crosses 2, 4, 6, 5, 1, 7, and 8, relative heterosis was significant compared to mean parents and higher parents. The highest rate of heterosis based on mean parents and higher parents is related to the seventh (34.83) and seventh (23.96) crosses. The average rate of genetic depression in this trait is in all crosses (10.59). According to Table 5 in all crosses, the five-parameter model consisting of m, [d], [h], [j], and[l] showed the best fit, which indicates the complex inheritance of this trait. Therefore, it can be concluded that the significant presence of all genetic parameters in the model indicates the role of both additive and non-additive effects in genetic control of the height of the lowest pod from the ground. However, due to the multi-gene trait of the lowest pod height above the ground, the results will not be unexpected. In the third cross, the effects [d] and [i] for the trait of the lowest pod height above the ground are also opposite, indicating the opposite nature of the interaction for this trait. In the second, third, seventh, and eighth crosses, the effects [h] and [l] have opposite signs for this adjective. Which indicates the existence of dual-type epistasis in the inheritance of the trait height of the lowest pod from the ground. The degree of dominance at all crosses indicates the existence of a dominant effect for the trait height of the lowest pod from the ground.

3.8. Number of hollow pods per plant

There was a significant difference between all crosses for the trait of hollow pods per plant according to Table 2, which showed the results of weight analysis of variance. Therefore, a mean generation analysis was

performed for the desired trait. Table 3 shows the results of comparing mean traits and their standard error in different generations. The amount of standard error in different generations indicates the difference between different people within the generations. Placing the results between two parents in this trait is an indication of additive effects in controlling this trait. Table 4 presents the results of the study of relative heterosis and absolute heterosis based on mean parents and higher parents as well as genetic depression. According to this table, the number of hollow pods per plant in crosses 4, 6, 7 and relative heterosis was significant compared to mean parents and higher parents. The highest rate of heterosis based on mean parents and higher parents is related to the seventh (70.20) and sixth (45.54) crosses. The genetic parameters of different traits are presented in Table 5. For all crosses in this trait, the parameter m is significant at the level of 1% probability, which indicates the existence of common genes between the two parents. According to Table 5, in addition to the simple effects of three parameters including m, [d] and [h], the effects of epistasis have also been included in the model, which indicates the complex inheritance of this trait. Therefore, it can be concluded that the significant presence of all genetic parameters in the model indicates the role of both additive and non-additive effects in genetic control of the number of empty pods per plant. However, due to the multi-genetic nature of the trait, the number of empty pods per plant will not be unexpected. The mean genetic depression in this trait in all crosses is higher than all traits (26.52), which is a reason to confirm the mentioned cases in the inheritance of this trait. The positive and significant parameter [h] in cross 6 indicates the production of hybrid to improve this trait. It can also be stated that the alleles that increase this trait in the mentioned cross must be dominant over the alleles that reduce it. In the fourth and fifth crosses, the effects of [d] and [i] for the trait are the opposite of the number of hollow pods per plant, indicating the opposite nature of the interaction for this trait. The degree of dominance in all crosses indicates the existence of a dominant effect for the number of hollow pods per plant.

4. Conclusions

Due to the presence of suitable heterosis in some of the studied compounds, including the fourth cross in the grain yield trait using hybridization between parents, it is possible to obtain hybrids with good yield and appearance traits. According to the results obtained by generation mean analysis, additive and non-additive effects and epistasis were involved in controlling most traits in crosses. However, the role of dominance effects in controlling traits was more important. Which indicates the complexity of inheritance of traits. Given that the additive parameter or additive × additive interaction is a function of the degree of dispersion of trait enhancing genes among parents. While the effects of dominance are the net product of dominance in each gene locus. Therefore, estimates of the additive effect may be small because of the high degree of dispersion. In general, it seems that in traits where the share of gene enhancement effect is higher, the selection is effective in early generations. However, in the case of traits where the effect of gene dominance is greater, selection should be delayed until later generations, ie, access to a high level of gene stabilization. The values obtained from the estimates of the average degree of dominance for most of the traits in most crosses indicated the existence of super-dominance and complete dominance effects in controlling the studied traits. In the case of traits with higher heterosis, the importance of the dominance component was more than the additive component in the genetic analysis of generations. Therefore, it can be concluded that hybrid parents had different alleles in each gene locus, among which there were alleles with a dominant to super-dominant effect.

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