



ESTIMATING THE PERFORMANCE AND GENE ACTION OF A NUMBER OF INDIVIDUAL GENOTYPES AND HYBRIDS ON THE CROP OF FABA BEAN (*VICIA FABA* L.)

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Abstract

10 faba bean crop genotypes were used, brought from the International Center for Agricultural Research in the Dry Areas (ICARDA), Parents and reverse hybrids were planted in the fields of one of the farmers at the Kirkuk irrigation project, by using randomized complete block design (RCBD) with three replicates, a traits of study were, nook length (cm), nook number. plant⁻¹, the number of seeds. nook⁻¹, weight 100 seeds (g), seed yield kg. ha⁻¹, the biological yield kg. ha⁻¹, harvest index (%). Analysis of variance showed that the mean squares of the genotype parents, parent vs. hybrids and hybrids were significant ($P \leq 0.05$) in all traits studied. The results indicated the superiority of parents 2, 5 and 9, the hybrids 2×7, 4×8, 5×8, 8×10, 4×5 and 1×5 by giving it higher mean in all traits studied. As genetic action, the values of the additional genetic variance were greater than the dominant genetic variance in all traits. The values of environmental variance were lower than the values of additional and dominant variance in all studied characteristics. The value of genetic variance increased compared to the environmental variance values for all traits. The values of phenotype variation have increased for all traits compared to genetic and environmental variations. The degree of dominance in all traits was less than one, except for the adjective number of seeds. nook⁻¹. The heritability was high in all studied traits. While the expected genetic improvement was low in length of nook (cm), nook number. plant⁻¹, the number of seeds. nook⁻¹ and harvest index (%), high in weight 100 seeds (g), seed yield kg. ha⁻¹ and the biological yield kg. ha⁻¹. In order for superior genotypes to contain the desired genes in most of the studied traits, it is well combine because they have general combination potential effects in the desired direction, it is possible to take advantage of these genotypes, after conducting many studies in other locations and seasons, for use in crossbreeding programs with other varieties. In order to transfer the desired genes into the species, and inserting those parents who have the highest percentage of genes prevalent in breeding programs, to benefit from the transfer of their other genetic traits, in addition to continuing to conduct subsequent studies, superior hybrids can be used to obtain the second generation and isolation generations, the selection procedure with the aim of developing new genotypes.

Key words : performance, genetics, individual genotypes, hybrids, faba bean (*Vicia faba* L.).

Introduction

Vicia faba L. (Fabaceae) was grown in all countries of the world, and its habitat is North Africa and Southwest Asia (Al-Shakarchi, 2010). China is one of the most producing and consuming countries for faba bean, then Ethiopia. In Iraq, the cultivated area reached 288.5 acres, total production reached (15) tons of seeds (Central Statistics and Information Technology Authority, 2018). It is a source of food in low-income countries, especially

in the Middle East, contains a number of amino acids, carbohydrates, vitamins and fatty substances, protein the main material in it and reaches 42%, therefore, it is one of the sources of protein, sometimes the percentage was affected by environmental conditions and genetic (Al-Jebouri, 2016). It is used in the treatment of many conditions, including eye diseases, liver impairment, kidney failure and stones, the importance of this plant in improving the properties of the soil through the process of stabilization of atmospheric nitrogen in the soil, contributing to the

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organization of the agricultural cycle (Jerri *et al.*, 2014). The basic goal of any breeding program is to develop genotypes with high productivity, necessary to estimate performance and genetic activity in order to understand how the yield and components were inherited, helps to efficiently and efficiently select the superior genotypes of the yield and components, the evaluation of any new genetic to compare with the prevailing local varieties in order to estimate phenotypic variations and components, the genetic variation is important in electing a superior genotype, the following research includes a different study in this field, in order to obtain varieties that were superior in terms of growth and productivity (Al-Jebouri, 2016). Variation is an important and fundamental factor in breeding and improvement programs, plant breeders were interested in estimating phenotypic variations, genetic and environmental components. Crop breeding for high yield and good quality needs to know the variance and the genetic origins, the availability of genetic variants was a continuous source of variation, which is the basis for selecting plants that are superior to their productive characteristics, the external appearance of any individual in the clan consists of the effect of interaction between the genotype and the environment, the environmental variation was the difference in the traits of plants with a genotype. Genetic variation was the difference in the phenotype of the traits of plants, due to the difference in genotype despite the equal effect of the environment (Elias and Abdel-Qader, 1985). Inheritance of an adjective is expressed as a ratio of hereditary to phenotypic variance (Allard 1960). A measure to determine the connection between parents and *offspring*, the value was useful in predicting the reliability of the phenotypic value as evidence of educational value (Lush, 1943). Two concepts were determined to calculate the inheritance percentage, the first of which is the hereditary rate, which includes additional and dominant genetic variation, the second was the hereditary ratio, which includes only the additional genetic variation, the second concept is more accurate

than the first in determining the electoral program, inheritance was important for plant breeders, to determining which one depends on the breeding material on which plant breeders work, the estimate of expected genetic improvement was the largest application of the theory of quantitative genetics in breeding and improvement programs, which is the product of the election intensity, inheritance, and standard deviation of phenotypic variance (Johanson *et al.*, 1955). Through of that, it is the evaluation of genotypes, study phenotypic variations and their genetic and environmental components, estimate some genetic features such as inheritance and expected genetic improvement, determine any of these important traits, considering a criterion for increasing the cereal yield in this crop, the idea for this study came for the purpose of arriving at a calendar of new genotypes first introduced into Iraq genetically and hybrids, estimate additional, dominant, environmental, genetic, and phenotypic variations, the inheritance percentage of the trait, the degree of dominance and the expected genetic improvement.

Materials and Methods

10 faba bean crop genotypes were obtained mentioned in table 1, brought from Dr. Maan Muhammad Salih Al-Badrani, College of Agriculture, University of Telafer, sourced from the International Center for *Agricultural Research in the Dry Areas (ICARDA)*, Genetic structures included (parents+hybrids) and included (10 parents and 45 individual hybrids). The experiment was arranged by using randomized complete block design (RCBD) with three replicates, cultivation was done at the fields of one of the farmers of the Kirkuk irrigation project at the agricultural season 2018-2019, the cultivation was done on lines, as the length of the line was 3 m, the distance between a plant and another was 0.25 meters, the distance between one line and another 0.70 m, watering was by sprinkler irrigation, the service operations were carried out for thinning and replanting. The compound fertilizer N.P.K was added as a single

Table 1: Genotypes used in the study.

1. Pedigree = 2000/DSO/0405-HBP/7005-2/B7/ DT Entry= PO6-OO1FB / FL	2. Pedigree = 2000/DSO/0405-HBP/7841/B7/ DT Entry= PO6-OO2FB / FL
3. Pedigree = 2000/DSO/0405-HBP/7106-1/B7/ DT Entry= PO6-OO3FB / FL	4. Pedigree = 2000/DSO/0405-HBP/7380/B7/ DT Entry= PO6-OO5FB / FL
5. Pedigree = Selection from ILB 1814 Entry= PO6-OO9FB / FL	6. Pedigree = 2000/DSO/0405-HBP/7038/B7/ DT Entry= PO6-O11FB / FL
7. Pedigree = 2000/DSO/0405-HBP/7486/B7/ DT Entry= PO6-O13FB / FL	8. Pedigree = 0405-SP80B(DS)/7986/B7/ DT Entry= PO6-O14FB / FL
9. Pedigree = ILB1814 Entry = Syrian Local large	10. Pedigree = ILB1266 Entry = Aguadolce

batch of 600 kg. h⁻¹ after tillage, Then, urea fertilizer 46% N was added at a rate of 200 kg h⁻¹ in one lot at the beginning of flowering. Data were collected from 10 plants for each line out of 12 plants, a traits of study were, nook length (cm), nook number. plant⁻¹, the number of seeds. nook⁻¹, weight 100 seeds (g), seed yield kg. ha⁻¹, the biological yield kg. ha⁻¹, harvest index (%).

Genetic Statistical Analysis

Statistical analysis was carried out according to the randomized complete block design (RCBD) with three replicates to determine the differences between Genotypes (Al-Rawi and Khalaf Allah, 1980). Estimate additional σ^2_A , dominant contrast σ^2_D , environmental variance σ^2_G and genetic variance phenotypic variance σ^2_p . The average degree of dominant (\bar{a}) was estimated for each attribute according to the following formula:

$$\bar{a} = \sqrt{\frac{2\sigma^2_D}{\sigma^2_A}}$$

$\bar{a} = 0$ = no dominant, $1 > \bar{a} > 0$ = partial dominant, $\bar{a} = 1$ = complete dominant, $1 < \bar{a}$ = superior dominant, inheritance percentage was estimated based on the following formula:

$$H^2(b.s) = \frac{\sigma^2_G}{\sigma^2_p} \quad H^2(n.s) = \frac{\sigma^2_A}{\sigma^2_p}$$

As:

$h^2_{b.s}$ = Inheritance ratio in the broad meaning.

$h^2_{n.s}$ = Inheritance ratio in the narrow meaning.

Inheritance was estimated in a broad meaning, according to the method of Hanson *et al.*, (1956) and by relying on the ranges shown by Ali (1999) and Muhammad (2000). Less than 40% (low), 40-60%

(medium), and more than 60% (high), the limits of the values of inheritance were adopted in the narrow sense mentioned by Al-Adhari (1987) as follows; Less than 20% (low), 20-50% (medium), and more than 50% (high). The expected genetic improvement for the traits was calculated from the following formula:

$$\Delta G = h^2 \cdot n \cdot s \cdot i \sigma p$$

h^2 . n . s = Narrow inheritance.

i = selection intensity 10%, at a value of 1.76.

σp = Phenotypic variance.

ΔG = Genetic improvement.

The ranges indicated by Robinson (1966), Agrwal, and Ahmad (1982) were based on the limits of expected genetic improvement. Less than 10% (low), 10 - 30% (medium), and more than 30% (high).

Results and Discussions

The results of the analysis of variance are shown in table 2, the mean squares of genotypes, parents, parents vs. hybrids and hybrids were significant (Pd<0.05) in all traits studied, because of the genetic differences between parents and half hybrids, it may be due to the difference in genes, and that controls these studied traits, indicates that genetics differ between them genetically, the different hybrids resulting, this result was a good indicator of an important input for continuing the genetic, analysis of traits, estimate the components of genetic variation, the legacies controlling these traits, other researchers have obtained significant differences between the genotypes that included their studies, including Al-Shakarchi (2010) and Al-Jebouri (2016).

Table 3 refer to the mean genotypes and cross-hybrids for the studied traits, one of them is noted in the description of the nook length (cm), as this characteristic is more clear, genotypes vary in shape, size, length, and width of the nook, these specifications can be used as a main indicator in the diagnosis and classification of different items, a desirable production indicator for this

Table 2: Mean M.S squares for (genotypes of parents and parent vs. hybrids and hybrids).

S.O.V	Degree of freedom	Nook length (cm)	Nook number .plant ⁻¹	Number of seeds. nook ⁻¹	Weight 100 seeds (g)	Seed yield kg. ha ⁻¹	Biological yield kg. ha ⁻¹	Harvest index (%)
Replicates	2	2355.32	2245.33	2130.39	13553.12	280696953.48	76875476.30	33013.89
Genotypes	54	19.46**	23.04**	1.96**	1212.88**	1406843.05**	4475478.67**	148.76**
Parents	9	17.15**	7.96**	3.83**	83.38**	2721479.70**	6528794.02**	144.63**
Parent Vs. Hybrids	1	9.26**	227.84**	8.85**	1479.20**	8961741.46**	19593691.51**	403.24**
Hybrids	44	20.16**	21.46**	1.42**	1437.87**	966237.86**	3711886.60**	143.83**
Standard erroe	108	0.98	1.74	0.89	33.17	754198.53	457185.13	109.59

crop, either when using a green crop or to produce seeds, since the length of the nook (cm) was always linked to the increase in the number of seeds per nook. By comparing the averages for this trait, shows the highest value 22.867 cm for parent 5 followed by parents 7 and 2, with a non-significant difference of 22,000 cm and 22.300 cm respectively, while the lowest value for the average length of the nook (cm) was for the parent 10 and the rate 16.267 cm, as for the hybrids, they ranged between the highest rate 25.700 cm for the hybrid 2 x 7 and the lowest value for the hybrid 8 x 10, which was the lowest average length of the horn (cm) was 16.600 cm, the mean of the parents and the mean of hybrids were 20.18 and 20.79 cm, respectively. The general average for parents and hybrids was (20.68) cm, and this indicates the response of hybrids to the increase in this trait, agreed with Al-Hamdani, (2012) and AL-Jubory, (2016), so they noticed a significant difference between the genotypes used in their study of this trait. The number of nooks.plant⁻¹, we note the superiority of the parent 3 significantly and reached 21,100 nooks, while the parent 9 was the lowest value for this adjective of 16,500 nooks. As for hybrids, they ranged from hybrid 1×5, which gave a moral advantage, at an average rate of 26.267 nook, did not differ from hybrids 1×2, 2×8, 3×10, 4×9, 6×7, 7×9, 7×10, 8×9, 8×10, 9×10, reached 24.533, 24.567, 24.067, 24.100, 24.133, 24.367, 24.733, 25.467, 24.967 nooks respectively, and the hybrid (4x6) that gave the lowest averages and reached 17.167 nooks.

When comparing the mean of parents to the mean of hybrids, the hybrid were distinguished by a higher value, reached 21.61 nooks, whereas, the average of parents and the general average gave 18.57 and 21.06 nooks, respectively, the response of some parents and their hybrids increased in this trait, due to the adjective percentage of the *fruit* Set, which affected the increase in the number of nooks / plant, this positively affected the increase in the final crop, agreed with Al-Jebouri, (2016), note that a significant differences between the genotypes used in his study, therefore, obtaining high productivity, it is necessary to secure the use of genotypes possessing genetic susceptibility, gives a high rate in this capacity, which is considered an important component of the aggregate and qualifies it for higher production (Osman *et al.*, 2013). In the description of the number of seeds. nook⁻¹, we note the superiority of parent 2 significantly, reached 8.733 seeds, did not differ significantly from parents 4, 5 and 8 the lowest value for this trait, reached 7.000, 7,567 and 7,833 seeds, respectively, while the parent 3, who has the lowest value for this adult nook gave 5.033seed. As for hybrids, the ranged between hybrids 4

x 8, which gave significant superiority, at an average of 9,000 seeds, did not differ significantly from hybrids 1x5, 1x6, 1x10, 3x5, 3x7, 6x9 and 9x10, they reached 8.133, 8.133, 8,100, 8,167, 8,033, 8,133 and 8,200 seeds, respectively, and the hybrid 6×7 that gave the lowest rate of 5.833 seeds, when comparing the average of parent to the mean of hybrid, The hybrid was characterized by a higher value of 7.27 seeds, whereas, the mean of the parents and the mean were 6.67 and 7.16 seeds, respectively, agreed with Osman *et al.*, (2013), found significant differences between the genotypes, it is necessary to use genotypes possessing genetic susceptibility, to give high output, as this trait was an important component of the quotient, Which contains a large amount of seeds, the genotypes in which there are sufficient quantities of dry matter during the stage of formation and development of nooks, may increase the ratio between reducing sterile and abortive flowers and fertile flowers, this increases the number of seeds in the nook, which may have a positive effect on the plant's output, parents and superior hybrid genotypes can be utilized in crossbreeding programs, to improve future cereal yield or utilization (Altin, 2010).

The attribute the weight of 100 seeds, parent 2 was significantly superior, reaching 148.767 g, parents 1, 4, 5, 7 and 8 followed by a non-significant difference, reached 140,700, 142,967, 147,433, 147,600 and 145,833 g respectively, compared to other parents, different from parent 9, gave the lowest value for this adjective 134.767 g.

As for hybrids, they ranged between hybrids 5x8, which gave a significant superiority and an average of 163,833 g, did not differ from hybrids 1×4, 1×8, 2×4, 2×5, 4×5, 4×6, 4×7, 4×9, 5×6, 5×7, 2×10, 3×7, 4×5, 4×6, 4×7, 4×9, 5x6, 5x7, 5x9, 5x10 and 6x7, reached 157.467, 151.167, 154.867, 158.600, 156.967, 151.100, 157.933, 157.800, 162.100, 158.433, 158,833, 158,800, 150,200, 156,700 and 157,200 g consecutively, and the hybrid 3×9, which gave the lowest rate was 86,600 g. The average of parent and hybrids with a rate of 141.95 g for parent and 134.18 g for hybrid, while the general average gave an average of (135.60) grams. The reason for the superiority of these parent and hybrid was due to the description of the duration of the seed filling (days), as we note these parents and hybrids are superior in this trait, the longest time to reach physiological maturity, which reflected positively on the average weight of the seed, therefore it is reflected positively on the final quotient, the superiority of parent and hybrids may be due to their superiority in the description of the leaf area, led to the transfer and representation of manufactured materials

Table 3: Parents' performance averages (the 10 genotypes and their interchangeable hybrids) for the studied traits.

Traits \ Parents	Nook length (cm)	Nook number .plant ⁻¹	Number of seeds. nook ⁻¹	Weight 100 seeds (g)	Seed yield kg. ha ⁻¹	Biological yield kg. ha ⁻¹	Harvest index (%)
1	16.300	18.000	6.167	140.700	2092.221	7298.367	27.996
2	22.000	20.067	8.733	148.767	4393.766	9717.067	44.307
3	19.300	21.100	5.033	136.433	1567.483	7500.633	20.989
4	21.733	19.600	7.000	142.967	2821.766	9472.233	28.796
5	22.867	17.633	7.567	147.433	2924.295	9410.467	29.993
6	19.567	16.300	5.567	138.500	1587.602	6499.333	24.142
7	22.300	18.267	6.500	147.600	2428.525	9669.233	23.897
8	21.700	20.300	7.833	145.833	3693.089	9491.567	37.331
9	19.767	16.500	6.500	134.767	1969.714	6343.733	30.309
10	16.267	17.900	5.800	136.467	1652.572	6546.367	25.318
1×2	16.800	24.533	6.767	143.033	3553.147	7876.533	44.012
1×3	23.100	19.033	7.900	126.533	3455.989	8415.800	40.344
1×4	23.467	20.567	6.633	157.467	2867.463	9534.100	29.202
1×5	24.067	26.267	8.133	120.800	4568.218	10363.900	42.956
1×6	18.700	20.233	8.133	121.167	3116.683	8466.200	35.364
1×7	24.300	19.533	7.133	148.633	3197.850	9888.933	31.212
1×8	24.267	21.633	6.000	151.167	2450.688	9684.700	24.439
1×9	20.267	19.900	7.267	118.067	2489.064	8465.767	28.300
1×10	17.600	20.400	8.100	108.833	2943.459	8122.633	34.228
2×3	20.133	23.333	6.367	143.100	2973.826	8940.167	31.708
2×4	20.633	18.767	6.867	154.867	2812.129	9507.600	28.753
2×5	23.533	17.567	7.400	158.600	3060.185	10786.600	27.603
2×6	19.533	23.233	6.400	144.067	2920.064	8335.067	33.674
2×7	25.700	23.933	7.867	113.900	3430.048	10893.267	30.150
2×8	21.067	24.567	6.567	117.200	2641.359	9594.133	26.759
2×9	19.067	22.533	7.800	120.967	3216.760	8387.400	37.602
2×10	20.767	23.367	6.533	156.967	3364.414	7978.267	38.844
3×4	20.267	21.267	6.833	148.067	3081.085	9462.467	30.255
3×5	23.500	19.033	8.167	143.800	3476.011	9200.767	35.505
3×6	18.933	16.867	7.200	115.400	2018.895	7430.567	26.249
3×7	19.133	17.200	8.033	151.100	3224.202	8466.200	36.317
3×8	24.067	23.900	7.167	117.267	3082.126	10542.267	27.470
3×9	17.800	23.500	7.733	86.600	2542.520	8618.033	28.523
3×10	20.000	24.067	6.900	106.467	2556.220	8465.767	29.257
4×5	23.667	20.300	7.067	157.933	3269.392	12484.700	23.707
4×6	20.300	17.167	6.467	157.800	2355.667	8466.200	26.330
4×7	19.533	18.067	7.300	162.100	3046.223	8875.600	33.314
4×8	23.633	20.833	9.000	121.867	3874.189	12097.233	30.291
4×9	17.967	24.100	7.233	158.433	4228.301	8032.433	49.350
4×10	19.167	22.533	7.200	109.300	2717.074	7389.300	35.168
5×6	23.867	18.000	6.567	158.833	2504.005	9787.967	24.867
5×7	24.300	17.400	7.533	158.800	3035.360	10248.000	29.028
5×8	23.467	18.867	6.867	163.833	2942.833	10166.767	28.211
5×9	18.033	23.300	7.667	150.200	4053.487	8281.100	48.970

Table 3 contd....

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Traits \ Parents	Nook length (cm)	Nook number .plant ⁻¹	Number of seeds. nook ⁻¹	Weight 100 seeds (g)	Seed yield kg. ha ⁻¹	Biological yield kg. ha ⁻¹	Harvest index (%)
5×10	16.733	22.900	6.267	156.700	3038.429	8338.067	35.084
6×7	18.000	24.133	5.833	157.200	2871.651	8536.467	32.096
6×8	23.367	21.567	7.600	109.500	2942.132	8319.533	34.695
6×9	16.767	22.500	8.133	108.600	3144.582	7998.900	37.537
6×10	20.067	21.500	7.000	110.400	2416.676	8520.867	27.605
7×8	22.700	19.300	7.567	117.267	2590.778	8150.200	30.990
7×9	19.833	24.367	7.467	109.100	3021.847	9668.500	30.247
7×10	23.033	24.733	7.767	99.567	3143.830	9321.567	32.285
8×9	18.900	25.467	6.667	147.067	3673.933	9014.033	39.619
8×10	16.600	24.967	7.867	146.000	4873.695	8675.633	56.115
9×10	19.100	25.367	8.200	103.700	3494.035	9175.767	37.004
Parent mean	20.18	18.57	6.67	141.95	2513.10	8194.90	29.31
Hybrid mean	20.79	21.61	7.27	134.18	3117.34	9088.35	33.36
Parent and hybrid mean	20.68	21.06	7.16	135.60	3007.48	8925.91	32.62
L.S.D _{0.05}	1.604	2.134	1.529	9.321	1405.5	1094.3	16.943

from the Source to the downstream Sink at seed storage sites, reflected positively on this trait, therefore it reflects positively on the final quotient.

From the foregoing, we notice that the quality of the weight of 100 seeds (g) was of great importance, as an indication of the efficient transmission and representation of manufactured materials from Source to downstream Sink at seed storage sites, It is also an important component of the quotient, agreed Mille *et al.*, (2005) Who indicated that the difference between genotypes in the seed weight rate, may be due to the difference in the number of nooks / plant and the number of seeds / nook, due to the difference in the length of the nooks with plants, which is determined by the amount of photosynthesis products from the source to the estuary.

The study evaluated the mathematical averages of parent and hybrid in seed yield, we notice that the father 2 produced the highest mean average of 4393.766 kg. ha⁻¹, while the parent 3 produced the lowest mean for this trait was 1567.483 kg. ha⁻¹, while the hybrid values ranged between hybrids 8×10, the highest rate was 4873.695 kg. ha⁻¹, which did not differ significantly from hybrids 1x5, 4x9 and 5x9, reached 4568.218, 4228.301 and 4053.487 kg. ha⁻¹, respectively, to the hybrid 3×6 which gave the least yield of 2018.895 kg. ha⁻¹. The mean of hybrid was significantly higher than the average of parent 3117.34 kg. ha⁻¹, the average of parents and the general average was 2513.10 and 3007.48 kg. ha⁻¹ respectively. The parent and hybrids in the seed quotient, as a result of its excellence in the components of the

quotient, which was positively reflected on the final quotient, the differences between parents and parent were in the seed quotient, it may be due to the difference in the increase of photosynthesis and the accumulation of the dry matter of the seeds during the flowering phase and the duration of the seed full, which reflected positively on the final quotient, from the foregoing, it is noted that the quality of the seed yield is the final result of most phenotypic and physiological trait of the plant, as the increase of this trait and its components is an important achievement for plant breeders, agreed with Al-Hamdani (2012), indicated that there were significant differences between the genotypes.

As for the biological yield, it is noted that the father 2 produced the highest mean average of 9717.067 kg. ha⁻¹, parents 4, 5, 7 and 8 followed by a non-significant difference, reached 9472.233, 9410.467, 9669.233, and 9491,567 kg. ha⁻¹ compared to the rest of the parents, while the parent 9 produced the lowest mean for this trait was 6343,733 kg. ha⁻¹, while the values of hybrids ranged between 4×5 hybrids, which showed the highest rate of 12484,700 kg. ha⁻¹, did not differ significantly from hybrids 1x5, 2x5, 2x7, 3x8, 4x8, 5x7 and 5x8, reached 10363,900, 10786,600, 10893,267, 10542,267, 12097,233, 10248,000, and 10166,767 kg. ha⁻¹ Sequentially, to the hybrid 4x10 which gave a lower yield of 7389,300 kg. ha⁻¹, the mean of hybrid was significantly higher than the average of parent 9088.35 kg. ha⁻¹, the average of parents and the overall mean were 8194.90 kg. ha⁻¹ and 8925.91 kg. ha⁻¹ respectively, this indicates that the accumulation of dry matter and the net photosynthesis increase, it has

Table 4: Genetic parameters of the characteristics of the studied values.

Genetic P. \ Traits	Nook length (cm)	Nook number .plant ⁻¹	Number of seeds. nook ⁻¹	Weight 100 seeds (g)	Seed yield kg. ha ⁻¹	Biological yield kg. ha ⁻¹	Harvest index (%)
$\sigma^2 A$	32.754	19.348	0.798	1578.371	1472879.530	9099534.968	107.322
$\sigma^2 D$	4.508	7.279	0.703	327.316	415449.267	880237.971	48.774
$\sigma^2 E$	0.328	0.580	0.298	11.058	251399.511	152395.042	36.531
$\sigma^2 G$	37.262	26.627	1.500	1905.687	1888328.797	9979772.939	156.096
$\sigma^2 P$	37.590	27.207	1.798	1916.746	2139728.308	10132167.981	192.626
\hat{A}	0.0916	0.1972	1.4862	0.0162	0.00061	0.00014	0.09202
$H^2_{B.s}$	0.9912	0.9786	0.8344	0.9942	0.8825	0.9849	0.81035
$H^2_{n.s}$	0.8713	0.7111	0.4436	0.8234	0.6883	0.8980	0.55715
GA	9.4025	6.5283	1.4036	2777.93	2592267.973	16015181.54	13.61

positively reflected the biological yield of these genotypes, Al-Jebouri (2016) emphasized that there are significant differences between the genotypes used in his study of this trait. From the foregoing, we understand that the biological yield is the accumulation of carbon dioxide representation during the growing season, This depends on the balance between photosynthesis and respiration (Al-Mugheer, 2012).

As for the harvest evidence index, it is superior to parent 2 significantly, gave the highest value of 44.307%, while the parent gave 3 the lowest value of 20.989%, the hybrid 8x10, gave the highest value 56.115%, did not differ significantly from hybrid 4x9 and 5x9, reached 49.350 and 48.970 %, respectively, to the hybrid 1x8 which gave the lowest value of 31.009%, the mean of parents and hybrid, the average hybrid showed an average of 33.36%, it is greater than the average of parents 29.31%, the general average for parent and hybrid was 32.62%, the reason for the high value of the harvest index for parent and hybrid, it is mainly due to what the value of the seed yield constitutes due to the biological yield, this indicates the response of crosses to the increase in the proportion of harvest index, harvest index was an inherited genetic trait, because it is of great importance in biological and genetic studies, it is also evidence of the ability of genotype to perform well (Shukla and Singh, 1999).

From the above, we note with regard to parents, parent 2 outperformed other parents, it was distinguished as the number of seeds. nook⁻¹ and weight of 100 seeds (g), seed yield (kg. ha⁻¹), biological yield (kg. ha⁻¹) and yield index (%), and the parent 5 in the description of the spike length (cm), and the parent 9 for the nook number. plant⁻¹.

The the hybrid 2x7 was distinguished from the other hybrids, exceeds the length of the pod (cm), hybrid 8x10 seed yield (kg. ha⁻¹) and yield index%, a hybrid 4x5 biological yield (kg. ha⁻¹), a hybrid 1x5 in the nook number. plant⁻¹, a hybrid 4x8 number of seeds. nook⁻¹, a hybrid

5x8 for 100 seeds trait.

In order to obtain high-productivity hybrids in the properties of the product and components, therefore, genetically separated genotypes were important factors, if the genetic distance increases, the genetic differences between the parents increase, this works to collect good and desired genes in the resulting hybrid, this also increases the chances of an increase in the compatibility (Al-Taweel, 2009; Al-Sawaf, 2012 and Al-Jebouri, 2016).

Table 4 shows estimates of additional variance $\sigma^2 A$, dominant $\sigma^2 D$, and environmental $\sigma^2 E$ for all studied traits, the values of additional genetic variance were greater than dominant genetic variation in all traits, the traits in which the values of additional genetic variation were greater than the values of dominant variance, the additional gene action was more important in controlling the inheritance of these traits, therefore, the most appropriate method of breeding was the pure breed or total selection.

While a trait the values of dominant genetic variation are greater than the values of additional genetic variation, the dominant genetic action was more effective than the additional genetic action in controlling the inheritance of these traits. Therefore, the most appropriate breeding method adopted to improve these traits, to produce varieties by crossbreeding.

The values of environmental variance were lower than the values of additional and dominant variance and for all studied traits, as for genetic variance $\sigma^2 G$, the value of genetic variation has increased for all traits compared to the values of environmental variance, so, the increased genetic variance of any of these characteristics, led to a decrease in environmental variability, as for phenotypic variation values $\sigma^2 P$, we notice high phenotypic variances and all traits compared to genetic and environmental variations, agreed with Al-Hamdani (2014) and Al-Jebouri (2016).

The degree of dominance, it is noted that all traits

were less than one value, except for the adjective the number of seeds. nook^{-1} , this indicates that there is dominance in this trait, this is evidence of the possibility of benefiting from the phenomenon of hybrid strength, to obtain superior hybrids from this study within the breeding materials used, it surpasses parents involved in the hybrid compared to the best parents, the rest traits given less than one, indicates the existence of partial dominance, thus, benefit from the method of selection in breeding programs, agreed with Al-Jebouri, (2016). As for the *heritability*, it is the degree of inheritance of the quantitative trait from the selected parents to the offspring, or the amount of the quantitative trait from one generation to another, or the degree of similarity in the characteristic between parents and offspring, or the ratio of hereditary variances to the sum of the heterogeneity of the trait (Sahuki *et al.*, 1983). Inheritance values in the broad and narrow meaning were high in all studied traits, while the expected genetic improvement was low in characteristic length of nook (cm), number of nook. plant^{-1} , number of seeds. nook^{-1} and yield index (%), high in 100 seed weight (g), seed yield (kg. ha^{-1}) and biological yield (kg. ha^{-1}).

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