

## Quantitative Traits Inheritance in Three Bread Wheat Crosses

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### ABSTRACT

Three field experiments were carried out, using the six populations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $Bc_1$  and  $Bc_2$ ) method to study the inheritance of some quantitative traits in three bread wheat (*Triticum aestivum* L.) crosses; namely, (1) Giza 168 × Sakha 94, (2) Irena × Giza 168 and (3) Irena × Gemmeiza 9, in three winter seasons (2009/ 2010, 2010/ 2011 and 2011/ 2012). Results indicated significant positive heterotic effects for all characters in the first cross, kernel weight in the second cross and grain yield/ plant in the third cross. On the other hand, significant negative heterotic effects were detected for number of spikes/ plant, number of kernels/ spike and kernel weight in the third cross, and grain yield/ plant in the second cross. Heterotic increases, also, were evident for number of spikes/ plant and number of kernels/ spike, which might be accounted for the heterotic response, observed in the first cross. Inbreeding depression was significant for all characters, except for number of kernels/ spike and kernel weight in the second cross.

There were overdominance effects towards the higher parent for all studied characters in the first cross, grain yield/ plant in the second and third crosses and kernel weight in the second cross. Meanwhile, overdominance towards the lower parent was found for number of kernels/ spike in the second cross. Complete dominance was found for both number of spikes/ plant and 100-kernel weight in the third cross, whereas, partial dominance was estimated towards the higher parent, for number of kernels/ spike in the third cross. Additive gene effects were positive and significant for number of kernels/ spike in the second and third crosses, and for grain yield/ plant in the three crosses, suggesting the potential for obtaining further improvements of studied characters. Both dominance and epistasis were significant for some of the attributes under investigation. Both  $F_2$  deviation ( $E_1$ ) and backcross deviation ( $E_2$ ) were significant for number of kernels/ spike, in first and third crosses, and grain yield/ plant in the second cross under investigation. Moreover, high to moderate values of heritability estimates, in the narrow sense, were associated with moderate and low genetic advance as a percentage of  $F_2$  means in most characters.

**Keywords:** Bread wheat, gene action, heritability, grain yield, yield components.

### INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the major winter crop in Egypt, where bread wheat production constitutes about 80% of the total wheat production area. Wheat breeders are concentrating to improve the grain yield potential of wheat by developing new cultivars with desirable genetic makeup in order to overcome the consumption pressure of ever increasing population (Memon *et al.*, 2005 and 2007).

High grain yield has been the main aim in wheat breeding, hence, it has been the subject of intensive studies (Sharma *et al.*, 2002 and Heidari *et al.*, 2005). Grain yield in wheat is a complex character resulting from the interaction among different grain yield components and environmental effects. Because of these complex interactions, it is difficult to improve grain yield through breeding (especially in the early generations) if grain yield is the only recorded factor. Hence, grain yield component traits, also, should be used as selection criteria for grain yield improvement. This is the reason why it is necessary to know the genetic architecture of grain yield components (Misra *et al.*, 1994).

Information about the type of gene action, involved in the inheritance of any studied character, is helpful in deciding the breeding procedures to be followed for improvement of that character. Improvement of a certain character necessitates the presence of adequate genetic variability for that character to facilitate selection, and that may be accomplished through hybridization among genetically diversified parents for that character.

Plant breeders and geneticists, frequently, use generation mean analysis to obtain information about gene action, controlling the economic traits in wheat (EL Hosary *et al.*, 2000; Khattab *et al.*, 2001; Esmail and Khattab, 2002; Akhtar and Chowdhry, 2006; Khaled, 2007 and Farag, 2009). Generation mean analysis is a simple and useful technique for estimating gene effects for polygenic traits, where its greatest merit lies in the ability to estimate epistatic gene effects, such as additive × additive (aa), dominance × dominance (dd) and additive × dominance (ad), (Singh and Singh, 1992). Conversely, Fethi and Mohamed (2010), reported that dominance and dominance × dominance epistatic effects were more important than additive effects and other epistatic components for grain yield.

Heritability values are a measure of the genetic relationship among parents and progeny, hence, considerable research work has been carried out to incorporate the desirable genes in present wheat cultivars to increase the productivity of the crop (Memon *et al.*, 2007).

The aim of the present study was to investigate the inheritance of grain yield and its components in three specific bread wheat crosses. The information obtained from this study may assist in improving the efficiency of wheat breeding programs.

#### MATERIALS AND METHODS

The three crosses, used in the present study, were derived from four widely diversified bread wheat cultivars. Names and pedigrees of studied parental genotypes are given in Table (1). These genotypes were used to obtain the following three crosses: (1) Giza 168 × Sakha 94, (2) Irena × Giza 168 and (3) Irena × Gemmeiza 9.

The local cultivars, Giza 168 and Gemmeiza 9 (of high grain yield and number of kernels/ spike), were crossed with the introduced cultivar from Mexico (Irena).

The study started in the farm of Etay-Elbaroud Research Station, El-Behera Governorate, Agriculture Research Center, Egypt, for two successively growing winter seasons (2009/2010, 2010/2011) and the third season 2011/2012 was conducted in the farm of Kafr Al-Hamam Research Station, Al-Sharkia Governorate, Agriculture Research Center, Egypt. In the first season (2009/2010), three crosses were made to obtain  $F_1$  seeds. The next season, (2010/2011), each  $F_1$  and its two parents were grown in two rows. Part of the  $F_1$  plants were backcrossed to their respective parents to produce the first and second backcrosses ( $Bc_1$  and  $Bc_2$ ), while, the other part of  $F_1$  plants were selfed to obtain  $F_2$  seeds. Fresh seeds of  $F_1$ , from each cross, were obtained by crossing their two parents. At the end of this season, enough seeds from  $F_1$ ,  $F_2$ ,  $Bc_1$  and  $Bc_2$  were obtained from each of the three crosses. In the third season (2011/2012), the third experiment was carried out at Kafr Al-Hamam Research Station. Seeds of the six populations,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $Bc_1$  and  $Bc_2$  of the three crosses, were evaluated in three adjacent blocks. Each block

contained the six populations of each cross grown in rows of 300 cm in length, twenty cm apart with ten cm among plants. Each population was grown in three rows, except for  $F_2$ , which was represented by five rows. At harvest, random twenty plants were taken from each plot for the  $P_1$ ,  $P_2$ ,  $F_1$ ,  $Bc_1$  and  $Bc_2$  populations and fifty random plants from the  $F_2$  were taken from each block to study the following characters:

Number of spikes/ plant, number of kernels/ spike, 100-kernel weight (g) and grain yield/ plant (g).

Various biometrical parameters were calculated, only, if the  $F_2$  genetic variance was significant. The amount of heterosis was expressed as the percentage increase of  $F_1$  above the better parent values. Inbreeding depression was calculated as the difference between the  $F_1$  and  $F_2$  means expressed as percentage of the  $F_1$  mean. Genetic analysis of generation means for mean effect parameter ( $m$ ) and additive ( $a$ ) and dominance ( $d$ ) effects were obtained by the method illustrated by Gamble (1962). In addition,  $F_2$  deviation ( $E_1$ ) and backcross deviation ( $E_2$ ) were estimated following the method, suggested by Mather and Jinks (1971). Heritability was calculated, in both broad and narrow senses, according to Mather's procedure (1949). The genetic gain from selection, as an indication of the  $F_2$  mean performance, was obtained, according to Miller *et al.* (1958). The predicted genetic advance from selection was estimated using the formula presented by Johanson *et al.* (1955). Potence ratio, also, was calculated, according to Peter and Frey (1966).

#### RESULTS AND DISCUSSION

Varietal differences, in response to their genetic background, were found to be significant for most traits under investigation. The genetic variance, within  $F_2$  population, also, was found to be significant for all studied traits, in the three crosses, therefore, the different biometrical parameters, used in this investigation, were estimated. Means and variances of the six populations; i.e.,  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $Bc_1$  and  $Bc_2$  for the studied traits, in the three crosses, are presented in Table (2).

Table 1: Names, pedigrees and origin of parental cultivars and lines.

Parent	Pedigree	Origin
Giza 168	MRL/Buc/SERI CM93046-8M-0Y-0M-2Y-0B-0GZ	Egypt
Sakha 94	OPATA/RAYON//KAUZ CMBW90Y3180-OTOPM-3Y-010M-010M-010Y-10M-015Y-0Y-0AP-0S	Egypt
Gemmeiza 9	ALD"S"/HUAC"S"/CMH74A.630/SX GM4583-5GM-1GM-0GM	Egypt
Irena	BUC/FLKMYNA/VUL CM91575	Mexico

Table 2: Mean performance ( $\bar{X}$ ) and variances ( $S^2$ ) of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, Bc<sub>1</sub> and Bc<sub>2</sub> populations of the three wheat crosses for the studied traits.

Traits	Parameters <sup>(1)</sup>	Cross 1 (Giza 168 × Sakha 94)						Cross 2 (Irena × Giza 168)						Cross 3 (Irena × Gemmiza 9)					
		P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	Bc <sub>1</sub>	Bc <sub>2</sub>	P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	Bc <sub>1</sub>	Bc <sub>2</sub>	P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	Bc <sub>1</sub>	Bc <sub>2</sub>
No. of spikes/ plant	$\bar{X}$	21.5	17.82	25.61	20.91	22.33	24.10	21.32	26.05	23.45	21.29	17.95	16.99	20.50	24.9	24.80	22.90	17.72	20.45
	$S^2$	6.6	7.62	4.83	42.1	24.9	28.9	21.95	20.84	14.98	31.53	25.89	22.86	2.64	4.05	4.22	29.51	16.59	23.10
No. of kernels/ spike	$\bar{X}$	76.1	81.5	72.1	64.5	66.56	63.62	78.56	81.94	75.60	72.26	71.10	64.21	68.50	78.10	74.30	68.95	74.10	65.22
	$S^2$	20.53	26.1	21.1	113.9	89.45	76.55	59.10	74.43	55.90	182.57	150.62	99.24	15.65	16.80	21.15	194.60	99.92	142.20
100-kernel weight (g)	$\bar{X}$	4.38	4.40	5.08	4.61	4.71	5.11	4.42	4.42	4.87	4.67	4.71	4.74	5.022	4.50	5.015	5.02	4.51	5.17
	$S^2$	0.04	0.024	0.066	0.21	0.128	0.189	0.042	0.15	0.065	0.289	0.182	0.244	0.028	0.019	0.023	0.215	0.128	0.140
Grain yield/ plant (g)	$\bar{X}$	59.45	69.95	80.9	74.62	62.71	71.20	56.10	64.72	67.94	55.72	55.62	52.70	50.90	61.95	68.15	63.15	58.75	64.15
	$S^2$	42.70	58.75	29.51	158.92	127.55	110.15	78.90	86.99	120.32	289.92	242.15	235.29	16.25	26.95	31.15	369.50	163.95	285.59

<sup>(1)</sup>  $\bar{X}$ ,  $S^2$  = Generation mean and variance, respectively.

Heterosis, inbreeding depression, potence ratio and different gene action parameters in the three crosses for grain yield and its components are given in Table (3). Highly significant positive heterotic effects, compared to better parent, were found for all characters in the first cross, 100-kernel weight in the second cross and grain yield/ plant in the third cross. Moreover, significant or highly significant negative heterotic effects were found for number of spikes/ plant and number of kernels/ spike in the second cross. While, insignificant heterotic effect was found for number of spikes/ plant, number of kernels/ spike and 100- kernel weight in the third cross, and grain yield/ plant in the second cross. Similar results were reported by Esmail and Khattab (2002), Abdel-Nour (2006), Akhtar and Chowdhry (2006), Abd-Allah and Abd El-Dayem (2008), Abdel-Nour and Hassan (2009) and Abdel-Nour (2011).

Number of spikes/ plant, number of kernels/ spike and kernel weight are the main components of grain yield/ plant. Hence, heterotic increase, if found in one or more of these attributes with other attributes being constant, would lead to favourable grain yield increase in hybrids. The lack of significance in heterosis of 100-kernel weight, in the first and second crosses, could be due to the lower magnitude of the non-additive gene action. These results are in agreement with that of Amaya *et al.* (1972).

The pronounced heterotic effect, detected in number of spikes/ plant, number of kernels/ spike and 100-kernel weight in the first cross, would be a value in a breeding program for high yielding ability.

Inbreeding depression measured the reduction in the performance of  $F_2$  generations from their  $F_1$ 's in the three crosses due to inbreeding. Positive and highly significant values were found for all characters, in all three crosses, except for the number of kernels/ spike, in the second cross, and 100-kernel weight in both second third crosses. The obtained results, for most studied traits, were in harmony with those obtained by Abdel-Nour (2006), Abd-Allah and Abd El-Dayem (2008), Abdel-Nour and Hassan (2009) and Abdel-Nour (2011).

The potence ratio (P) indicated overdominance ( $P > 1$ ) towards the higher parent for all studied traits in the first cross, grain yield/ plant in the second and third crosses and 100-kernel weight in the second cross. Conversely, overdominance towards the lower parent for number of kernels/ spike was found in the second cross. Nearly complete dominance ( $P= 1$ ) was found for both number of spikes/ plant and 100-kernel weight in the third cross. Partial dominance towards the higher parent was recorded for number of kernels/ spike in the third cross. Overdominance for number of

spikes/ plant was reported by Abdel-Nour and Moshref (2006), Abd-Allah and Mostafa (2011), for number of kernels/ spike by Abdel-Nour (2011), for 100-kernel weight by Abdel-Nour and Moshref (2006), Abd-Allah and Mostafa (2011) and Abdel-Nour (2011), for grain yield/ plant by Abd-Allah and Abd El-Dayem (2008), Abd-Allah and Mostafa (2011) and Abdel-Nour (2011). Partial dominance, towards the higher parent for number of kernels/ spike, was reported by Abd-Allah and Abd El-Dayem (2008), Abd-Allah and Mostafa (2011) and Abdel-Nour (2011).

Nature of gene action (Table 3) was investigated, according to the relationships illustrated by Gamble (1962). The estimated mean effect parameter (m), which reflects the contribution due to the over-all mean plus the locus effect and interactions of the fixed loci, was found to be highly significant for all studied characters in all crosses. The additive gene effects (a) were found to be highly significant and positive for number of kernels/ spike in the second and third crosses, and for grain yield/ plant in the three studied crosses. That suggests the potential for obtaining further improvement of those traits, using pedigree selection program. Highly significant negative additive effect was obtained for number of spikes/ plant in the third cross and significant or highly significant for 100-kernel weight in the first and third crosses, indicating that the additive effects were less important in the inheritance of those traits.

Furthermore, dominance gene effects (d) were found to be or highly significant for number of spikes/ plant in the first and second crosses, respectively and highly significant for 100-kernel weight in the first cross. When dominance gene action is present, it would tend to favor the production of hybrids, while, the existence of the additive gene action, in the gene pool, encourages the improvement of the character through selection program. Besides, significant positive additive  $\times$  additive type of epistasis was detected for number of kernels/ spike and grain yield/ plant in the first cross. Additive  $\times$  dominance epistatic types were significant, or highly significant, and positive for number of spikes/ plant in the first and third crosses. Dominance  $\times$  dominance types of gene action were found to be positive and highly significant for number of kernels/ spike in the second and third crosses, for 100-kernel weight in the first cross and for grain yield/ plant in the third cross.

Highly significant positive  $F_2$  deviations ( $E_1$ ) were detected for number of kernels/ spike in the first cross and 100-kernel weight in the third cross, while, highly significant negative values were obtained for number of kernels/ spike in the third cross and grain yield/ plant (g) in the second cross.

Table 3: Heterosis (B.P), Inbreeding depression, Potence ratio and Gene action parameters of the three wheat crosses for the studied traits.

Characters	Crosses	Heterosis (B.P)	Inbreeding depression	Potence ratio	Gene action parameters							
					m	a	d	aa	ad	dd	E <sub>1</sub> <sup>(2)</sup>	E <sub>2</sub> <sup>(3)</sup>
No. of spikes/ plant	I	19.12**	18.35**	3.234	20.91** <sup>(1)</sup>	1.77	15.17*	2.36	5.64*	-39.08*	1.725	1.16
	II	-9.98**	9.211**	-0.099	21.29**	0.96	15.515**	-18.40	8.00	59.00	-2.278	-12.195**
	III	-0.402	7.66**	0.955	22.90**	-2.73**	-13.16**	2.84	13.68**	13.72	-0.85	9.33**
No. of kernels/ spike	I	11.533**	10.54**	3.48	64.50**	2.94	-4.34	9.22*	-3.61	-11.54	10.95**	-20.72**
	II	-7.747*	4.418	-2.751	72.26**	6.89**	-23.07*	-15.28**	3.325	39.67**	-5.665	-20.54
	III	-4.87	7.20**	0.208	68.95**	8.88**	3.84	-15.26**	-0.53	33.92**	-4.85**	8.28**
100-kernel weight (g)	I	15.45**	9.25**	69.00	4.61**	-0.40*	1.89**	-30.66*	-3.24	54.04**	-0.125	0.35
	II	10.18**	4.11	∞	4.67**	-0.03	0.67	-6.20	7.20	46.0	0.025	0.16
	III	-0.139	-0.10	0.974	5.02**	-0.66**	-0.466*	-6.68	-0.275	10.03	0.132**	-0.0996
Grain yield/ plant (g)	I	15.65**	7.76**	3.086	74.62**	8.49*	-14.46	1.20*	-0.39*	-1.9*	1.82	11.69*
	II	4.98	17.99**	1.747	55.72**	2.92**	1.29	0.22	-0.03	-0.54	-8.455**	20.03**
	III	10.00**	7.38**	2.122	63.12**	5.40*	5.045	-0.72**	-0.921**	1.182**	0.833	1.675

<sup>(1)</sup> \*, \*\* significant at 0.05 and 0.01 probability levels, respectively.

<sup>(2)</sup> E<sub>1</sub> = F<sub>2</sub> deviation

<sup>(3)</sup> E<sub>2</sub> = backcross deviation

**Table 4: Heritability in broad and narrow senses ( $h^2b$  &  $h^2n$ ), genetic advance upon selection ( $\Delta g$ ) and genetic advance as percentage ( $\Delta g\%$ ) for the studied characters in the three wheat crosses.**

Characters	Crosses	Heritability		$\Delta g$	$\Delta g (\%)$
		$h^2b$	$h^2n$		
No. of spikes/ plant	I	81.47	50.96	11.204	17.37
	II	69.38	59.18	16.196	22.80
	III	89.13	77.24	22.196	32.19
No. of kernels/ spike	I	88.53	68.60	9.169	43.85
	II	52.49	31.82	3.681	17.29
	III	85.70	67.48	7.55	32.98
100-kernel weight (gm)	I	81.43	41.53	10.785	14.45
	II	58.50	43.92	15.41	27.65
	III	91.57	80.06	31.702	50.23
Grain yield/ plant (gm)	I	68.57	60.00	0.566	12.29
	II	77.51	45.43	0.503	10.77
	III	89.30	75.35	0.720	14.34

\*Selection intensity was 10%.

These results may refer to the contribution of epistatic gene effects in the inheritance of these traits.

Backcross deviations ( $E_2$ ) were found to be positive and significant, or highly significant for number of spikes/ plant and number of kernels/ spike in the third cross, and for grain yield/ plant in the first and second crosses. On the other hand, highly significant negative ( $E_2$ ) was detected for number of spikes/ plant in the second cross and for number of kernels/ spike in the first one. However, insignificant backcross deviation ( $E_2$ ) values were detected for number of spikes/ plant in the first cross, number of kernels/ spike in the second cross, 100-kernel weight in the three crosses and grain yield/ plant only in the third cross. These results would ascertain the presence of epistasis in such magnitude as to warrant great attention in a breeding program.

Heritability in both broad and narrow senses and genetic advance under selection are presented in Table (4). Lush (1994) gave the term heritability to define the relation between genotypic and phenotypic variances as broad sense heritability, and the relation between additive and phenotypic variances as narrow sense heritability. Heritability values are important to the breeder since it quantifies the accepted improvement from selection. To achieve genetic improvement through selection, heritability must be reasonably high. In the present investigation, heritability estimates, in broad sense ( $h^2b$ ), were high to moderate, with values ranging between 91.57% for 100-kernel weight in the third cross to 52.49% for number of kernels/ spike in the second cross. Narrow sense heritability ( $h^2n$ ) estimates ranged from 80.06% for 100-kernel weight in the third cross, to 31.82% for number of kernels/ spike in the second cross. Similar results were obtained by EL-Sayed (2004), Abdel-Nour and Moshref (2006), Salem (2006), Khaled (2007), Abd-

Allah and Abd El-Dayem (2008), Abdel-Nour and Hassan (2009), Abd-Allah and Mostafa (2011) and Abdel-Nour (2011).

The expected genetic advance, as a percentage of  $F_2$ , ranged from (10.77%) for grain yield/ plant in the second cross, to (50.23%) for 100-kernel weight in the third cross. The highest estimates of narrow sense heritability were associated with the highest genetic advance for number of spikes/ plant and 100-kernel weight, in the third cross, and for number of kernels/ spike and grain yield/ plant in the first and third crosses, respectively.

These results indicated the possibility of practicing selection in early generations and obtaining high yielding genotypes. Therefore, selection in those particular populations could be effective and satisfactory for successful breeding purpose. These results were in harmony with those reported by Abd El-Fattah and Mohamed (2009), Khattab *et al.* (2010) and Abdel-Nour (2011).

The information obtained from the present study might be important for wheat breeders to increase grain yield potential, release new wheat genotypes and enhance Egyptian wheat germplasm.

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## الملخص العربى

## وراثة الصفات الكمية فى ثلاثة هجن من قمح الخبز

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أجريت ثلاث تجارب حقلية فى ثلاثة مواسم شتوية متتالية من ٢٠٠٩/٢٠١٠ وحتى ٢٠١١/٢٠١٢ حيث تم عمل التهجينات فى الموسم الأول للحصول على حبوب الجيل الأول وفى الموسم الثانى زرع جزء من الجيل الأول لعمل التهجين الرجعى وكلا الموسمين فى محطة بحوث إيتاى البارود بمحافظة البحيرة- مصر. ثم أجرى تقييم العشائر الستة فى الموسم الثالث فى محطة البحوث الزراعية بكفر الحمام بمحافظة الشرقية- مصر- لدراسة توارث بعض الصفات الكمية فى ثلاثة هجن من قمح الخبز بحيث كان لكل هجين ست عشائر هى الأبوان والجيلان الأول والثانى والجيلان الرجعيان.

وأوضحت النتائج أن:

- ١- قوة الهجين فى الجيل الأول - بالنسبة للأب الأعلى- كانت معنوية وموجبة لكل الصفات المدروسة بالنسبة للهجين الأول، ولصفة وزن المائة حبة فى الهجين الثانى وصفة محصول الحبوب/ النبات فى الهجين الثالث، بينما كانت قوة الهجين معنوية وسالبة لصفة عدد السنابل/ النبات وعدد الحبوب/ السنبل فى الهجين الثانى.
- ٢- كان تأثير التربية الداخلية موجباً ومعنوياً لكل الصفات المدروسة ما عدا عدد الحبوب/ السنبل ووزن المائة حبة فى الهجين الثانى.
- ٣- أظهرت دراسة طبيعة التوارث وجود سيادة فائقة تجاه الأب الأعلى لكل الصفات المدروسة للهجين الأول، محصول الحبوب/ النبات فى الهجين الثانى والثالث ووزن المائة حبة فى الهجين الثانى. بينما ظهرت سيادة فائقة تجاه الأب الأقل لصفة عدد الحبوب/ السنبل فى الهجين الثانى، كذلك وجود سيادة تامة لكل من صفتى عدد الحبوب/ السنبل ووزن المائة حبة فى الهجين الثالث، وكذلك ظهرت سيادة جزئية تجاه الأب الأعلى لصفة عدد الحبوب/ السنبل فى الهجين الثالث.
- ٤- كان التأثير المضيف معنوياً وموجباً لصفة عدد الحبوب/ السنبل فى كل من الهجين الثانى والثالث، وصفة محصول الحبوب/ النبات للهجن الثلاثة، بينما كان التأثير المضيف معنوياً وسالباً لصفة عدد السنابل/ النبات فى الهجين الثالث وصفة وزن المائة حبة لكل من الهجين الأول والثالث، كذلك كان التأثير السىادى معنوياً لصفة عدد السنابل/ النبات لكل من الهجين الأول والثانى ووزن المائة حبة فى الهجين الأول. بينما كان نوع التفاعل (المضيف × المضيف) معنوياً وموجباً لصفة عدد الحبوب/ السنبل ومحصول الحبوب/ النبات فى الهجين الأول، كما كان للتأثيرات الوراثية غير المضيفية دوراً هاماً فى وراثه معظم الصفات المدروسة.

- ٥- كانت انحرافات الجيل الثانى ( $E_1$ ) معنوية وموجبة لكل من صفة عدد الحبوب/ السنبله فى الجيل الأول ووزن المائه حبه فى الهجين الثالث. بينما كانت ( $E_1$ ) معنوية وسالبة لصفة عدد الحبوب/ السنبله فى الهجين الثالث وصفة محصول الحبوب فى الهجين الثانى.
- ٦- كانت انحرافات الأجيال الرجعية ( $E_2$ ) معنوية وموجبة لكل من صفتى عدد السنابل/ النبات وعدد الحبوب/ السنبله فى الهجين الثالث، وصفة محصول الحبوب/ النبات فى الهجين الأول والثانى. بينما كانت ( $E_2$ ) معنوية وسالبة لصفة عدد السنابل/ النبات فى الهجين الثانى وصفة عدد الحبوب/ السنبله فى الهجين الأول.
- ٧- أظهرت كفاءة التوريث- بمعناها الواسع- قيماً عالية لمعظم الصفات، كما أظهرت كفاءة التوريث- بمعناها الضيق- قيماً متوسطة مرتبطة بنسبة تحسين وراثى مرتفعة إلى متوسطة فى معظم الصفات المدروسة. وقد أرتبطت قيم التحسين الوراثى المنخفضة والمرتفعة بمثيلتها لمعامل التوريث بمعناه الضيق فى جميع الهجن المدروسة.