

DETERMINATION OF GENE EFFECTS AND VARIANCES IN THREE BREAD WHEAT CROSSES

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ABSTRACT

The present work was carried out at Etay-Elbaroud Research Station during four seasons from 2003 / 2004 to 2006/2007. Three crosses among six parents, namely Sids 1 x Gemmiza 7, Sakha 93 x Dophin 2 and Gemmiza 9 x Giza 168 were used. Five populations (P_1 , P_2 , F_1 , F_2 and F_3) for each cross were used in this investigation. Significant positive heterotic effects were found for all characters, except for number of spikes plant⁻¹ in the second and third crosses and number of kernels spike⁻¹ in the first and third crosses. Overdominance above the higher parent was detected for all characters, except for number of kernels spike⁻¹ in the first cross. The other types of dominance were also studied. Inbreeding depression estimates were found to be significant and positive for number of spikes plant⁻¹, number of kernels spike⁻¹ and grain yield plant⁻¹ in all crosses. Additive gene effects were positive and significant for number of spikes plant⁻¹, number of kernels spike⁻¹, and grain yield plant⁻¹ in the third cross. While, significant negative additive effects were obtained for number of spikes plant⁻¹, number of kernels spike⁻¹, grain yield plant⁻¹ in the second cross and 100-kernel weight in the first and second crosses. Dominance gene effects were found to be significant for all characters in all crosses, except the second cross for both number of spikes plant⁻¹ and grain yield plant⁻¹ and number of kernels spike⁻¹ in the first cross. Significant positive (E_1) were found for 100-kernel weight in the first and third crosses. Moreover (E_2) were found to be positive and significant for 100-kernel weight in the second and third crosses. High heritability estimates, in broad sense, were detected for all the studied characters, except number of spikes plant⁻¹ in the second cross. Narrow sense heritability estimates ranged from 33.82% for number of spikes plant⁻¹ to 82.20% for 100-kernel weight in the second cross. The parent-offspring regression heritability estimates ranged from 54.34% for number of spikes plant⁻¹ in the second cross to 88.68% for grain yield plant⁻¹ in the first cross. The expected and actual genetic advance were moderate for 100- Kernel weight and high for grain yield plant⁻¹ in all crosses.

Key words: Bread Wheat, Heterosis, Inbreeding Depression, Heritability Gene Action

INTRODUCTION

Wheat is one of the most important food crop in Egypt. The local consumption of wheat is increasing due to the continuous increase of populations. Wheat breeder faced with the difficulty of choosing the parental lines which when crossed would result in the highest proportion of desirable segregates and also with the difficulty in selecting the best genotypes from the progeny in early generations. The Egyptian wheat cultivars have relatively narrow genetic base, so, selection

among these cultivars for increasing grain yield and its components would be expected less effective. Hybridization between the local wheat cultivars and exotic materials would be the solution to increase genetic variability.

Information on the genetics and gene effect of breeding materials could ensure long term selection and better genetic improvements. Crumpacker and Allard (1962) reported that efficiency in breeding of self-

pollination crop plants depend, first, on accurate identification of hybrid combinations that have the potentiality of producing maximum improvements and, second, on identifying, in early segregating generations, of superior lines among the progeny of the most promising hybrids. Accordingly, the maximum progress in improving any character, in a selection program, would be expected when the additive gene action is the main component of genetic variance, whereas, the presence of non-additive gene action might suggest the use of hybridization program. To achieve this goal, many genetic models were proposed by Mather and Jinks (1971) for estimation of genetic variance components.

Al-Kaddoussi *et al.* (1994) reported that dominance component played an important role in genetic control for number of spikes plant⁻¹, number of kernels spike⁻¹, 100-kernel weight and grain yield plant⁻¹. Conversely, Ikram and Tanah (1991) indicated that additive and non-additive gene effects played equal roles in the inheritance of grain yield, number of spikes plant⁻¹, number of kernels spike⁻¹. Similarly, El-Hosary *et al.*

(2000), and Hamada and Tawfelis (2001) showed that additive and non-additive gene effects had important roles in controlling the genetic system for yield and its components. However, El-Hennawy (1992) revealed that additive and dominance gene effects were important for grain yield and number of kernels spike⁻¹.

Concerning the heritability estimates, Moustafa (2002), Hendawy (2003), El-Sayed (2004) and Abdel-Nour *et al.* (2005) reported that heritability estimates for yield and its components were moderate to high. In contrast, Tammam and Abd El-Gawad (1999) found that heritability, in broad and narrow senses, for number of spikes plant⁻¹, kernel weight and grain weight plant⁻¹ were high, while, the narrow sense heritability for number of kernels spike⁻¹ was low.

This work was conducted to study genetic variance, gene action, heritability, and actual and expected genetic gain in three bread wheat crosses to elucidate the breeding value of these crosses that could be utilized in breeding programs to improve wheat yield.

MATERIALS AND METHODS

Six bread wheat parents were chosen to form three crosses, *viz.* Sids 1x Gemmiza 7, Sakha 93x Dophin 2 and Gemmiza 9x Giza 168. Table (1) show names, pedigree and origin of parental genotypes.

The experimental work of the present study was carried out at Etay-Elbaroud Research Station during four successive seasons from 2003/2004 through 2006/2007. In the first season (2003 / 2004), the parental genotypes were crossed to obtain F₁ seeds, in the second season (2004 / 2005), the hybrid seeds were sown to give the F₁ plants. These plants were selfed to produce F₂ seeds. In the third season (2005/2006) the same parents were crossed to produce more hybrid seeds. Also, F₂ seeds were planted to produce F₃ seeds. In the fourth season (2006 / 2007) the seeds of the five populations P₁, P₂, F₁, F₂ and F₃ of the three crosses were evaluated using a randomized complete block design with three

replications. Rows were 3m long, spaced 20 cm apart, the plants within rows were spaced 10 cm apart. Two rows were devoted to each parent and F₁ plants, six rows to F₂ generation and 20 rows to F₃ families of each cross. Data were recorded on individual guarded plants for number of spikes plant⁻¹, number of kernels spike⁻¹, 100-kernel weight (g) and grain yield plant⁻¹(g).

Various biometrical parameters in this study were calculated when the F₂ genetic variance was found to be significant. Heterosis was expressed as the percentage deviation of F₁ mean performance from better parent values. Inbreeding depression was calculated as the difference between the F₁ and F₂ means expressed as percentage of the F₁ mean. The t-test was used to determine the significance of these deviations where the standard error (S.E) was calculated as follows:

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$$\overline{F_1} - \overline{BP} = \sqrt{VF_1 + VBP}$$

(S. E for better parent heterosis)

$$\overline{F_1} - \overline{F_2} = \sqrt{VF_1 + VF_2}$$

(S. E for inbreeding depression)

Potance ratio (P) was also calculated according to Peter and Frey (1966). In addition, F₂ deviation (E₁) and F₃ deviation (E₂) were measured as suggested by Mather and Jinks (1971).

Types of gene effects were estimated according to Hayman model as described by Singh and Chaudhary (1985) as follows:

$$m = \overline{F_2} \text{ (mean effect of } F_2)$$

$$d^* = \frac{1}{2} P_1 - \frac{1}{2} P_2 \text{ (additive effect)}$$

$$h = \frac{1}{6} (4\overline{F_1} + 12\overline{F_2} - 16\overline{F_3}) \text{ (dominance effect)}$$

$$L = \frac{1}{3} (16\overline{F_3} - 24\overline{F_2} + 8\overline{F_1}) \text{ (dominance x dominance)}$$

$$i = P_1 - \overline{F_2} + \frac{1}{2} (P_1 - P_2 + h) - \frac{1}{4} L \text{ (additive x additive)}$$

The variances of these estimates were computed as follows:

$$V_m = VF_2$$

$$V_{d^*} = \frac{1}{4} (V_{P_1} + V_{P_2})$$

$$V_h = \frac{1}{36} (16VF_1 + 144VF_2 + 256VF_3)$$

$$V_L = \frac{1}{9} (256VF_3 + 576VF_2 + 64VF_1)$$

$$V_i = V_{P_1} + VF_2 + \frac{1}{4} (V_{P_1} + V_{P_2} + V_h) + \frac{1}{16} V_L$$

The standard errors of additive (d*), dominance (h), dominance x dominance (L), and additive x additive (i) were obtained by taking the square root of respective variation. Also, "t" test values were calculated by dividing the effects of d*, h, L and I by their respective standard errors.

Heritability was calculated in both broad and narrow sense and parent off-spring regression according to Sakai (1960). The genetic gain, represented as percentage of the F₂ and F₃ mean performance ($\Delta g\%$) was estimated using the method of Miller *et al.* (1958).

Table (1): Commercial names, pedigree and origin of the parental genotypes.

Parent	Pedigree	Origin
Giza 168	MRL/Buc/SERI CM93046 - 8M - 0y - 0M - 2y - 0B	Egypt
Gemmiza 9	ALd "S"/Huac "S" // CMH 74A. 630 / SX CG M 4583 - 5G M- CGM 4583 - 5GM - 1 GM - 0GM	Egypt
Sids 1	HD 2172 / PAVON "S" // 1158.57/MAYA 74 "S" SD 46 - 4SD - 1SD - 0 SD	Egypt
Gemmiza 7	CMH 74A - 63015 X // SERI 82 /3/Agent CGM 4611 - 2GM - 3GM-1GM-0GM	Egypt
Sakha 93	Sakha 92 / TR 810328 S 8871 - 1S - 2S - 1S - 0S	Egypt
Dophin 2	DOVE "S"/INIA/4/4777(2)//FKN/GB/3/PVN CM84655-02AP-300AP-300L-3AP-OL-OAP	Mexico/Syria

RESULTS AND DISCUSSION

Parental differences, in response to their genetic background, were found to be significant in most characters under investigation. The F₂ genetic variances were also significant for all the studied characters in the three crosses. Means and variances of the five populations (P₁, P₂, F₁, F₂ and F₃) for the studied characters in the three crosses are presented in Table (2).

Heterobeltiosis, potance ratio (P), inbreeding depression percentage, F₂ deviation (E₁), F₃ deviation (E₂) and different gene actions for the four studied characters are given in Table (3).

Significant positive heterotic effects were found for all the studied characters, except a significant negative heterotic effect

for number of kernels spike⁻¹ in the third cross. Also, insignificant heterotic effect was found for number of spikes plant⁻¹ in the second and third crosses and number of kernels spike⁻¹ in the first cross. Heterotic effects in the first cross ranged from -1.4% for number of kernels spike⁻¹ to 10.3% for number of spikes plant⁻¹, while they ranged from 0% for number of spikes plant⁻¹ to 13.5% for number of kernels spike⁻¹ in the second cross. In the third cross, the heterotic effects ranged from

-15.3% for number of kernels spike⁻¹ to 8.3% for 100-kernel weight. Similar trends were reported by El-Hosary *et al.* (2000), Moustafa (2002), Hendawy (2003), El-Sayed (2004), Abdel-Nour *et al.* (2005) and Abd-Allah (2007). Number of spikes plant⁻¹, number of kernels spike⁻¹ and kernel weight are the main components of grain yield plant⁻¹. Hence, heterotic effect increase, if it found, in one or more of these attributes, would lead to favorable yield increase in a hybrid. The lack of significance in heterosis of number of spikes plant⁻¹ in the second cross could be due to the lower magnitude of the non-additive gene action. The absence of heterotic effect in the F₁ generation may be due to that some genes show dominance effect in one direction, while the others were in the other direction (Singh and Narayanan, 1993). These results are in agreement with El-Rassas and Mitkess (1985). The pronounced heterotic effect for 100-kernel weight in the three crosses would be of interest in a breeding program for high yielding ability. The first cross had higher number of spikes plant⁻¹, while the second cross had higher number of kernels spike⁻¹. Their heterotic effects were 10.3% and 13.5%, respectively.

The potance ratio (P) indicated that different types of dominance towards the higher parent were obtained for all characters, except for number of kernels spike⁻¹ in the first cross. Complete dominance towards the lower parent was found for number of kernels spike⁻¹ in the third cross, while complete dominance towards the higher parent was found for number of spikes plant⁻¹ in the second cross. Partial dominance towards the higher parent was found for number of kernels spike⁻¹ in the first cross. Overdominance was

obtained for number of spikes plant⁻¹ by Abdel-Nour and Moshref (2006), for number of grains spike⁻¹ by Al-Kaddoussi *et al.* (1994) and Abd-Allah (2007), for 100-kernel weight, by Al-Kaddoussi *et al.* (1994), Moustafa (2002), Abdel-Nour and Moshref (2006); for grain yield plant⁻¹ by Al-Kaddoussi *et al.* (1994), and Abd-Allah (2007). Partial dominance towards the lower parent was reported for number of kernels spike⁻¹ by Moustafa (2002).

With regard to inbreeding depression, significant positive values were found for number of spikes plant⁻¹ in the three crosses and number of kernels spike⁻¹ in the first and second crosses, 100-kernel weight in the third cross and grain yield plant⁻¹ in all crosses, except the third one. This is a valid result since the expression of heterosis in the F₁ may be followed by reduction in F₂ performance. The obtained results for most crosses were in harmony with those obtained by Khalifa *et al.* (1997). Significant heterosis and insignificant inbreeding depression were obtained for grain yield plant⁻¹ in the third cross only. Moreover, significant positive heterosis and significant negative inbreeding depression were detected for 100-kernel weight in the first and the second crosses. Heterosis and inbreeding depression coincided with the same particular phenomenon; therefore it is logic to anticipate that heterosis in the F₁ will be followed by an appreciable reduction in the F₂ performance. The contradiction between heterosis and inbreeding depression estimates could be due to the presence of linkage that exist between genes in the materials (Van der Veen, 1959).

Nature of gene action was determined using the five parameters model (Table 3). The estimated mean effect of F₂ (m), which reflects the contribution due to the overall mean plus the locus effect and interactions of fixed loci, was found to be highly significant for all the studied characters in all crosses. The additive gene effects (d*) were found to be significant and positive for number of spikes plant⁻¹ in the third cross, number of kernels spike⁻¹ in the first and third crosses and grain yield plant⁻¹ in the third cross. However, significant negative additive effect (d*) was

obtained for number of spikes plant⁻¹ in the first and second crosses, number of kernels spike⁻¹ in the second cross, 100-kernel weight in the first and third crosses. These results suggest the potential for obtaining further improvement for the former characters, i.e., that showed positive and significant values by using pedigree selection program. Dominance gene effects (h) were found to be significant for all characters of all crosses, except number of spikes plant⁻¹ in the second cross, number of kernels spike⁻¹ in the first cross and grain yield plant⁻¹ in the second cross. When dominance genes are 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 by selection program. Dominance x dominance (l) types of gene action were found to be negative and significant for number of spikes plant⁻¹ in the first and third crosses, number of kernels spike⁻¹ in the third cross, 100-kernel weight in the first and second crosses, and grain yield plant⁻¹ in the third cross. A significant and positive additive x additive type of epistasis (i) was detected for number of spikes plant⁻¹ in the third cross, number of kernels spike⁻¹ in the first and third crosses, 100-kernel weight in the first and second crosses, and grain yield plant⁻¹ in the third cross. A negative and significant additive x additive type of epistasis (i) was detected for number of spikes plant⁻¹ in the second cross, and 100-kernel weight in the third cross. The important roles of both additive and non-additive gene actions in certain studied characters indicated that selection procedures based on the accumulation of additive effects would be very successful in improving these characters. Similar findings were reported by Al-Kaddoussi *et al.* (1994), El-Hosary *et al.* (2000), Moustafa (2002) and Hendawy (2003).

Significant and positive F₂ deviation (E₁) was found for 100-kernel weight in the three crosses, while negative values were obtained for number of spikes plant⁻¹ in the second cross, number of kernels spike⁻¹ in the three crosses, and grain yield plant⁻¹ in the first and second crosses. On the other hand, insignificant F₂ deviations were detected for

number of spikes plant⁻¹ in the first and third cross, and grain yield plant⁻¹ in the third cross. This may indicate that epistatic gene effects had major contribution in the inheritance of these traits.

F₃ deviation (E₂) was found to be positive and significant for 100-kernel weight in the second and third crosses. On the other hand, significant negative (E₂) values were detected for number of spikes plant⁻¹ and number of kernels spike⁻¹ in all crosses, 100-kernel weight, and grain yield plant⁻¹ in the first cross. While insignificant (E₂) values were detected for grain yield plant⁻¹ in the second and third crosses. These results would ascertain the presence of epistasis in such magnitude as to warrant great deal of attention in a breeding program.

Heritability estimates in broad and narrow senses, and between generations (parent off-spring regression), are presented in Table (4). Higher heritability values in broad sense were detected for all the studied characters that ranged from 75.8 % for number of spikes plant⁻¹ to 95.82% for grain yield plant⁻¹, while it was moderate estimate for number of spikes plant⁻¹ 75.8% in the second cross. Narrow sense heritability estimates ranged from 33.82% for number of spikes plant⁻¹ to 82.2% for 100-kernel weight in the second cross. The parent-offspring regression heritability was found to be of high to moderate and ranged from 54.34% for number of spikes plant⁻¹ in the second cross to 88.68% for grain yield plant⁻¹ in the first cross. The differences in magnitude of both narrow sense and parent-offspring regression heritability estimates for all the studied characters would ascertain the presence of both additive and non-additive gene effects in the inheritance of these characters. This conclusion was also reported by El-Sayed (2004), Abdel-Nour *et al.* (2005), and Abdel-Nour and Moshref (2006).

Table (4) shows the expected versus actual genetic gain for all the studied characters. The expected genetic advance ($\Delta g\%$ of F₂) and actual genetic advance ($\Delta g\%$ of F₃) was moderate for number of spikes plant⁻¹ and

number of kernels spike⁻¹ in the second cross, and 100-kernel weight in all crosses, while they were high for number of spikes plant⁻¹ and number of kernels spike⁻¹ in the first and third crosses, and grain yield plant⁻¹ in all crosses. These results indicated the possibility of practicing selection in early segregating generations to enhance these characters and hence selecting high yielding genotypes. Dixi *et al.* (1970) pointed out that high heritability is not always associated with high genetic advance, but in order to make effective

selection, high heritability should be associated with high genetic gain.

Generally, most of the significance biometrical parameters resulted from the first and third crosses and were higher in their values than those obtained from the second cross. Consequently, it could be concluded that the crosses (Sids 1 x Gemmiza 7) and (Gemmiza 9 x Giza 168) would be of interest in a breeding program for genetic improvement of wheat.

Table (2): Means (\bar{x}) and variances (S^2) for the studied characters Of the five populations (P_1, P_2, F_1, F_2 and bulk F_3 families) for three bread wheat crosses.

Sids 1 x Gemmiza 7						
Characters	Parameters	P_1	P_2	F_1	F_2	F_3 bulk
No. of spikes plant ⁻¹	\bar{x}	18.45	22.57	24.9	22.1	18.07
	S^2	4.65	5.89	7.95	59.4	43.21
No. of kernels spike ⁻¹	\bar{x}	80.5	72.9	79.4	73.1	72.25
	S^2	14.1	10.99	21.2	259.4	157.5
100 Kernel weight(g)	\bar{x}	4.18	4.48	4.78	5.35	4.18
	S^2	0.057	0.043	0.033	0.309	0.199
Grain yield plant ⁻¹ (g)	\bar{x}	52.2	60.93	65.6	57.1	54.9
	S^2	7.07	11.83	12.92	309.25	185.5
Sakha 93x Dophin 2						
No. of spikes plant ⁻¹	\bar{x}	22.6	24.9	24.9	21.15	22.73
	S^2	5.97	6.35	5.82	24.05	19.87
No. of kernels spike ⁻¹	\bar{x}	72.92	82.01	93.1	71.05	68.1
	S^2	10.97	28.1	18.4	185.4	151.51
100 Kernel weight(g)	\bar{x}	4.51	4.62	4.93	5.24	4.82
	S^2	0.043	0.063	0.07	0.425	0.261
Grain yield plant ⁻¹ (g)	\bar{x}	60.3	64.9	71.18	62.45	62.81
	S^2	11.72	24.0	30.09	439.9	277.5
Gemmiza 9 x Giza 168						
No. of spikes plant ⁻¹	\bar{x}	21.5	20.15	22.45	21.05	18.72
	S^2	5.92	3.9	5.18	33.28	24.01
No. of kernels spike ⁻¹	\bar{x}	80.24	67.95	67.95	67.81	63.51
	S^2	20.1	16.92	18.5	251.5	172.3
100 Kernel weight(g)	\bar{x}	4.47	5.04	5.46	5.31	5.71
	S^2	0.04	0.03	0.033	0.24	0.141
Grain yield plant ⁻¹ (g)	\bar{x}	55.8	52.15	60.25	58.1	55.38
	S^2	19.1	18.09	16.75	292.37	182.5

Table (3): Heterosis, potance ratio, inbreeding depression and gene action parameters for the three bread wheat crosses.

Characters	Cross	Heterosis% over B.P	Potance ratio (P)	Inbreeding depression %	Gene action parameters						
					m	d*	h	l	i	E ₁	E ₂
No. of Spikes plant ⁻¹	1	10.32**	2.131	11.44**	22.1**	-2.06**	12.613**	-14.027*	4.103	-0.605	-9.27**
	2	0.00	1.00	15.06**	21.15**	-1.15**	-1.713	18.427**	-5.164*	-3.175**	-3.19**
	3	4.419	2.407	6.236*	21.05**	0.675*	7.147**	-8.693*	6.872**	-0.588	-5.835*
No. of Kernels spikes ⁻¹	1	-1.366	0.711	7.93**	73.1**	3.8**	6.467	12.267	11.367*	-4.95**	-11.6**
	2	13.523**	3.44	23.68**	71.05**	-4.545**	22.567**	43.067**	-2.158	-14.233**	-34.365**
	3	-15.32**	-1.0	0.206	67.81**	6.145**	11.56**	-22.56*	29.99**	-3.213**	-15.025**
100-Kernel weight (g)	1	6.7**	3.00	-11.92**	5.35**	-0.15**	2.74**	-7.76**	1.99**	0.795**	-0.75**
	2	6.71**	6.636	-6.288**	5.24**	-0.055	0.913**	-3.067**	0.438**	0.493**	0.145*
	3	8.33**	2.474	2.75*	5.31**	-0.285**	-0.967**	2.533**	-2.242**	0.203**	1.205**
Grain yield plant ⁻¹ (g)	1	7.66**	2.07	12.96**	57.1**	-4.365**	11.533*	10.933	-6.231	-3.98**	-12.365**
	2	9.68**	3.73	12.26**	62.45**	-2.3**	4.86	25.2	-8.32	-4.44**	-8.16
	3	7.975**	3.438	3.568	58.1**	1.825**	8.687*	-8.773	6.062*	0.988	-3.465

*and** indicate significant at 0.05 and 0.01 level of probability, respectively.

Table (4): Heritability and expected versus actual gain for all the studied characters in three crosses of bread wheat.

Characters	Cross	Heritability %			Expected gain		Actual gain	
		Broad sense	Narrow sense	Parent-offspring regression	G.S	Δg % of F ₂	G.S	Δg % of F ₃
No. of spikes plant ⁻¹	1	86.62	57.52	73.57	7.76	35.11	8.46	46.84
	2	75.80	33.82	54.34	2.90	13.72	4.32	18.99
	3	84.44	55.71	70.34	5.62	26.72	6.03	32.22
No. of kernels spike ⁻¹	1	91.83	80.79	87.42	22.77	31.15	19.20	26.57
	2	90.08	36.15	62.91	8.61	12.12	13.55	19.90
	3	92.64	62.98	77.81	17.48	25.78	17.87	28.14
100-kernel weight (g)	1	89.00	67.64	76.70	0.660	12.30	0.599	14.32
	2	86.12	82.20	84.12	0.938	17.9	0.752	15.603
	3	86.25	81.96	83.83	0.703	13.24	0.551	9.65
Grain yield plant ⁻¹ (g)	1	95.82	80.78	88.68	24.86	43.57	21.14	38.50
	2	93.16	75.69	85.35	27.78	44.48	24.88	39.61
	3	93.85	74.74	84.29	22.36	38.49	19.93	35.98

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تقدير التأثيرات الجينية وتبايناتها في ثلاثة هجن من قمح الخبز باستخدام نموذج العشائر الخمس

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أجرى هذا البحث بمحطة البحوث الزراعية -إيتاي البارود في أربعة مواسم متتالية من ٢٠٠٣/٢٠٠٤ إلى ٢٠٠٦/٢٠٠٧ على ثلاثة هجن من قمح الخبز ناتجة من ستة أباء وهي: سدس X١ جميزه٧، سخا X٩٣، دوفن ٢، جميزه X٩ جيزة ١٦٨ واشتملت الدراسة على الأبوين والأجيال الأولى والثاني والثالث لكل هجين. أوضحت النتائج أن قوة الهجين في الجيل الأول معنوية وموجبة لكل الصفات ماعدا صفة عدد الحبوب بالسنبلة التي كانت معنوية وسالبة في الهجين الثالث بينما كانت قوة الهجين غير معنوية لصفة عدد السنابل/النبات في كل من الهجينين الثاني والثالث وعدد الحبوب بالسنبلة في الهجين الأول. أوضحت دراسة طبيعة التوارث أن درجة السيادة كانت فائقة تجاه الأب الأعلى لجميع الصفات ماعدا صفة عدد الحبوب بالسنبلة في الهجين الأول، كما أظهرت سيادة تامة تجاه الأب الأقل لصفة عدد الحبوب بالسنبلة في الهجين الأول وتجاه الأب الأعلى لصفة عدد السنابل/نبات في الهجين الثاني -كذلك وجدت سيادة جزئية تجاه الأب الأعلى لصفة عدد الحبوب بالسنبلة للهجين الأول. وكان تأثير التربية الداخلية في الجيل الثاني موجبا ومعنويا لصفة عدد السنابل/نبات، عدد الحبوب بالسنبلة ومحصول الحبوب/نبات لجميع الهجن ماعدا عدد الحبوب بالسنبلة ومحصول النبات في الهجين الثالث. بينما كان تأثير التربية الداخلية معنويا وسالبا لصفة وزن المائة حبة في كل من الهجينين الأول والثاني. أظهرت التأثيرات الوراثية المضيفة وكذلك الفعل الجيني غير المضيف دورا هاما في وراثة معظم الصفات المدروسة.

كانت انحرافات الجيل الثاني (E_1) وانحرافات الجيل الثالث (E_2) معنوية لمعظم الصفات في الهجن تحت الدراسة مما يوضح أهمية الفعل الجيني التوقفي في وراثة الصفات. وقد أظهرت كفاءة التوريث بمعناها الواسع قيما عالية لمعظم الصفات، كما أظهرت كفاءة التوريث بمعناها الضيق وكذلك الكفاءة الوراثية المحسوبة من الانحدار بين الأجيال قيما عالية إلى متوسطة مرتبطة بنسبة تحسين وراثي متوسط في معظم الصفات المدروسة.

والخلاصة أنه يمكن الاستفادة من الهجين الأول والثالث في برامج تربية القمح للحصول على سلالات جديدة متفوقة في المحصول. كما أن النتائج المتحصل عليها تدل على أن الانتخاب في الأجيال الإنزالية المبكرة قد يكون مفيدا ولكن سوف يكون أكثر كفاءة إذا تم تأجيله إلى الأجيال الإنزالية المتأخرة