

## Genetic Analysis of Yield and Its Components in Some Bread Wheat Crosses (*Triticum aestivum* L.) using Five Parameters Model.

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### ABSTRACT

The present investigation was done at the Experimental Farm of Agronomy Department – Faculty of Agriculture Al-Azhar University, Nasr City, Cairo, Egypt during four successive seasons from 2012/2013 to 2015/2016. Four bread wheat varieties (parents) Misr1, Gemmeiza 9, Gemmeiza 10 and Gemmeiza 11 were chosen to form three bread wheat crosses; Misr1 × Gemmeiza 10, Gemmeiza 9 × Gemmeiza 11 and Gemmeiza10 × Gemmeiza 11. Five parameters model was used for measuring some important genetic parameters for yield and its component characters. These characters were number of spikes / plant, spike length (cm), grain weight/spike (gm), number of grains / spike, 100- grain weight (gm), grain yield / plant (gm) and harvest index %. Randomized complete block design (RCBD) with three replicates was used in the final experiment. Five populations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$ ) for each cross were used in this investigation. Results revealed that, the  $F_1$  population recorded the highest mean values compared with other populations for all characters in the three crosses except grain weight/spike in the third cross. The data also showed that, standard error estimates in  $F_2$  were larger than other populations. All studied traits in this investigation were controlled by both additive and non-additive genetic effects, but the values of dominance × dominance epistatic gene effects were greater than the other effects for most traits. Estimates of heterosis relative to mid-parent were positive and significant for number of spikes / plant, spike length, number of grains / spike and grain yield per plant in all crosses under study, while, the estimates of heterosis relative to better parent were positive and significant for number of spikes / plant and grain yield / plant in all crosses. Inbreeding depression percentage from  $F_1$  to  $F_2$  and  $F_3$  were positive and significant for most studied characters. Potence ratio revealed over dominance for most studied traits. Heritability in broad sense found to be moderate to high in most traits in three crosses, these estimates ranged from 0.56 for spike length in the second cross to 0.84 for 100- grain weight in cross 2, while the values of narrow sense heritability were low to moderate for all studied characters in the three crosses, these values were between 0.01 for number of spikes/plant in the second cross and 0.56 for number of grains/spike in the first cross.

**Keywords:** Gene effects, Heterosis, Inbreeding depression (ID), potence ratio, Heritability, Wheat.

### INTRODUCTION

Cereal crops have played an important role in the flourishing of human civilization. Wheat (*Triticum aestivum* L.) is a vital food crop in Egypt and all over the world which belongs to Poaceae (Gramineae) family. It is a staple food source for billions of people. The total world production of wheat in 2013 was about 713 million tons, so it became the third most- produced cereal after maize (1,016 million tons) and rice (745 million tons). FAO (2015).

The great important goal in any breeding program is yield and the ultimate aim of all plant breeders is to increase the yield. But grain yield is a polygenic trait and in relation with a number of component traits. The main yield contributing parameters in wheat are grains / spike, tillers / plant and 1000-grain weight (Sharma and Sain 2004). The select of plant breeding methods for improving the yield and its components greatly depends on how the reliable information on the type and magnitude of gene effects present in the population available. So it is important to know the gene action among the various components as well as the degree to which, different component characters are correlated with each other and with yield as well. Generation mean analysis is a simple but useful technique is to estimate gene effects such as additive × additive (aa), dominance × dominance (dd) and additive × dominance (ad) effects (Singh and Singh 1992).

In addition to type of gene action, breeders are eager to know how much of the variation in a crop is genetic and to what extent this variation is heritable, because the selection efficiency based greatly on

additive genetic variance, environmental effect and interaction between genotype and environment.

Hayman (1958) and Jinks and Jones (1958) developed the concept of generation mean analysis for the estimation of genetic components of variation. There are three models used to estimate gene effects and variances from generation means, viz., six parameters model, five parameters model and three parameters model based on the generations included in the study. This analysis provides the estimates of the main gene actions (additive and dominance) and their digenic and trigenic interactions, which help to understand the performance of the parental genotypes used and the crosses potential of either for heterosis exploitation or pedigree selection.

Generation mean analysis is a relatively simple and statistically reliable tool suitable for preliminary estimation of various gene effects (Mather and Jinks 1971).

Many investigators such as Abdel Nour, Nadya and Moshref (2006), Koumber and El-Gammaal (2012), Hamam (2013), Khaled (2013) and Abbasi *et al* (2014) used five parameters model to determine the type of gene action for which control the inheritance of yield and yield component characters in wheat (*Triticum aestivum* L.).

Knowledge of the degree of heterosis plays a decisive role towards the choice of breeding methodology. Exploitation of heterosis is considered to be one of the outstanding achievements of plant breeding. In a self-pollinated crops like wheat, the scope for utilization of heterosis depends mainly upon its direction and magnitude. Estimation of heterosis over the high-parent (heterobeltiosis) is useful in identifying

truly heterotic cross combinations (Sindhu and Singh, 1975).

Generally, the increased vigour of the  $F_1$  crosses over its parents is expressed as positive heterosis while that of decreased vigour is known as negative heterosis. Positive and negative estimates of heterosis are with great importance in plant improvement depending on the breeding objectives.

Inbreeding depression (ID) is mostly known as the lowered fitness or vigor of inbred individuals compared with their non-inbred counterparts. Its contrast is heterosis, the 'hybrid vigor' shown as increased size, growth rate or other parameters due to the increase in heterozygosity in  $F_1$  hybrids between inbred lines. Inbreeding depression, the depressive effect, is the expression of traits arising from increasing homozygosity (Allard, 1960).

The information about heritability helps the crop breeders in expecting the behavior of the following generations, making desirable selection and assessing the importance of genetic improvement by selection. Heritability, out of the variability, can also be used as a basis in determining the selection program. Selection in

early generations is done when heritability values are high; however, if lower, then the selection of the next generations will succeed because the chances of an increase uniformity in the population (Falconer, 1989).

The purpose of this work was giving information about type of gene action and available genetic variability such as heterosis, Inbreeding depression, potence ratio and heritability for yield and its components traits in some bread wheat crosses.

## MATERIALS AND METHODS

Four, bread wheat parental genotypes (varieties) Misr1, Gemmeiza 9, Gemmeiza 10, and Gemmeiza 11 were chosen to form three crosses, viz. Misr 1 × Gemmeiza 10 (cross 1), Gemmeiza 9 × Gemmeiza 11 (cross 2), and Gemmeiza 10 × Gemmeiza 11 (cross 3). Pedigree and origin of the four parents were presented in (Table 1). The experimental work was carried out at the Experimental Farm of Agronomy Department, Faculty of Agriculture, Al-Azhar University, Nasr City, Cairo, Egypt, during four successive seasons 2012/2013, 2013/2014, 2014/2015 and 2015/2016.

**Table 1. Pedigree and origin of the parental genotypes used.**

No.	Genotypes	Pedigree	Origin
1	Misr 1	OASIS/KAUZ//4*BCN/3/2*PASTO CMSS00Y01881T-050M-030Y-030M-030WGY-OOM-OY-OS	Egypt
2	Gemmeiza 9	ALD "S" /HUAC // CMH 74 A. 630/SX CGM 4583 - 5 GM - 1GM - OGM	Egypt
3	Gemmeiza 10	MAYA 74 "S" /ON //1160 - 147/3/BB/GLL/41 CHAT "S" /5CROW "S".CGM 5820 - 3GM - 1 GM - 2GM - OGM	Egypt
4	Gemmeiza 11	BOW"S"/KVZ"S"//7C/SERI 82/3/GIZA168/SAKHA61 CGM7892-2GM-1GM-2GM-1GM-0GM	Egypt

The experimental materials consisted of three crosses and five generations for each cross. The generations involved were  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$ . The generations were achieved during the years 2012-2016. In 2012/2013, the parental genotypes were crossed to obtain  $F_1$  seeds for each cross. In the second season 2013/2014, the hybrid seeds of the three crosses were sown to give the  $F_1$  plants. These plants were selfed to produce  $F_2$  and  $F_3$  seeds. Moreover, the same parental genotypes were crossed again to get enough  $F_1$  seeds. The new hybrid seeds and part of seeds obtained from  $F_1$  selfed plants ( $F_2$  seeds) were kept in refrigerator to be planted in the final experiment. In the third season 2014/2015 the  $F_1$  and  $F_2$  plants were selfed to produce  $F_2$  and  $F_3$  seeds, respectively. In the last season (2015/2016) the parental genotypes ( $P_1$  and  $P_2$ ) and different generations ( $F_1$ ,  $F_2$  and  $F_3$ ) of the three crosses were evaluated in the final experiment in a randomized complete block design (RCBD) with three replicates. Rows were 3 m long; spaces between the rows were 20 cm, and 15 cm between plants within rows. Two rows devoted for each parent and  $F_1$  progenies, 10 rows for  $F_2$  and  $F_3$  generations for each replication in the three crosses. Data were recorded on yield and its components traits (number of spikes / plant, spike length (cm), grain weight/spike (gm), number of grains / spike, 100- grain weight (gm), grain yield / plant (gm) and harvest index %).

The analysis was proceeded to estimate the various gene effects using the five parameters genetic model of Hayman [1958] and Kearsy and Pooni (1996) as follows:

$m$  = Mean effect.

$d$  = Additive gene effects.

$h$  = Dominance gene effects.

$i$  = Additive × additive epistatic gene effects.

$l$  = Dominance × dominance epistatic gene effects.

The magnitude to heterosis relative to mid and better parents ( $F_1$ ) and inbreeding depression (ID) ( $F_2$  and  $F_3$  generations) were calculated according to Turner (1953) and Hayes *et al.* (1956). The significance was tested using the formula suggested by Wynne *et al.* (1970).

The formula of Smith (1952) was used to calculate potence ratio (P). Complete dominance was indicated when  $P = \pm 1$ ; on the other hand, partial dominance is indicated when P value ranged from -1 to +1 except the value zero, which indicates absence of dominance effects. Over-dominance was considered when the value of potence ratio (p) exceeds  $\pm 1$ . The direction of dominance of either parent was indicated by the positive and negative signs.

Broad sense heritability ( $H^2$ ) was estimated by the formula of Allard (1960). Estimation of heritability from regression between parents and offspring by parent-offspring method was used to work out

heritability estimates in narrow sense according to Smith and Kinman (1965).

## RESULTS AND DISCUSSION

Mean performances and standard error for the five populations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$  and  $F_3$ ) for the seven studied characters in all crosses are presented in Table 2. Data on the cross 1 (Misr 1 × Gemmeiza 10) showed

that,  $P_1$  (Misr 1) recorded the highest mean values for spike length (11.53), grain weight/spike (3.12), number grains/spike (60.60) and 100- grain weight (4.70). while  $P_2$  (Gemmeiza 10) recorded the highest mean values for number of spikes/plant (10.03), grain yield/plant (24.70) and harvest index (35.46%). Similarly  $F_1$  for this cross was higher than parents,  $F_2$  and  $F_3$  generations for most studied traits.

**Table 2. Mean performances and standard error of five generations for studied traits in three wheat crosses.**

Traits	Crosses	$P_1$	$P_2$	$F_1$	$F_2$	$F_3$
Number of spikes/plant	1	9.87±0.09	10.03±0.15	13.63±0.26	9.11±0.30	10.06±0.04
	2	9.33±0.13	9.40±0.21	12.37±0.50	8.63±0.73	9.13±0.21
	3	10.30±0.10	9.93±0.12	14.07±0.15	9.70±0.23	9.75±0.15
Spike length (cm)	1	11.53±0.26	10.43±0.09	12.43±0.34	11.13±0.57	11.65±0.03
	2	12.30±0.06	12.97±0.17	13.40±0.15	12.24±0.20	12.77±0.02
	3	10.67±0.09	12.70±0.25	13.37±0.09	12.07±0.25	12.62±0.17
Grain weight/spike (gm)	1	3.12±0.02	2.89±0.04	3.08±0.06	3.03±0.07	3.08±0.01
	2	3.19±0.03	3.53±0.01	3.62±0.04	3.17±0.06	3.18±0.01
	3	3.02±0.05	3.48±0.02	3.45±0.05	3.03±0.08	3.14±0.01
Number of grains/spike	1	60.60±0.61	57.23±0.43	63.50±0.59	59.11±1.20	61.24±0.24
	2	62.63±0.97	65.70±0.72	67.57±0.22	61.44±1.51	62.77±0.44
	3	59.37±0.73	64.63±0.09	67.87±0.43	60.74±0.90	62.50±0.19
100-grain weight (gm)	1	4.70±0.02	4.59±0.05	4.73±0.01	4.65±0.08	4.60±0.03
	2	4.69±0.01	4.82±0.01	4.85±0.03	4.68±0.05	4.71±0.01
	3	4.57±0.05	4.84±0.02	4.86±0.03	4.68±0.09	4.62±0.03
Grain yield/plant (gm)	1	23.39±0.71	24.70±0.43	32.69±0.66	22.86±1.04	25.01±0.19
	2	24.12±0.78	26.38±0.53	33.85±0.54	22.71±1.03	23.91±0.23
	3	25.58±0.82	28.63±1.06	37.63±0.68	23.93±1.39	24.94±0.40
Harvest index %	1	35.07±0.66	35.46±0.31	37.36±0.41	34.47±0.97	35.81±0.39
	2	34.62±0.55	37.26±0.76	37.83±0.50	34.84±1.07	34.92±0.37
	3	33.37±0.72	36.08±0.47	38.00±0.11	35.93±0.85	36.04±0.74

Cross 1 (Misr 1 × Gemmeiza 10), cross 2 (Gemmeiza 9 × Gemmeiza 11) and cross 3 (Gemmeiza 10 × Gemmeiza 11).

For the cross 2 (Gemmeiza 9 × Gemmeiza 11),  $P_2$  (Gemmeiza 11) was better than  $P_1$  (Gemmeiza 9) for all traits, while the mean values of the first filial generation  $F_1$  for this cross were higher than parents,  $F_2$  and  $F_3$  generations for most studied traits. In the cross 3 (Gemmeiza 10 × Gemmeiza 11),  $P_2$  (Gemmeiza 11) showed the highest mean values for all characters except number of spikes/plant while the  $F_1$  population recorded the highest mean values compared with other populations for all traits except grain weight/spike. The data also showed that, standard error estimates in  $F_2$  generation were larger than other populations ( $P_1$ ,  $P_2$ ,  $F_1$  and  $F_3$ ). The same results were obtained by Koumber and El-Gammaal (2012).

Type of gene action was estimated using the five parameters model. Data in Table 3 showed that, the estimates of  $F_2$  means were positive and with high significance for the seven characters in all crosses under study.

The estimates of additive gene effects, (d) were positive and significant for spike length, grain weight/spike and number of grains/spike, in the first cross, and also were positive and significant for number of spikes/plant in the third cross. These results revealed that, the inheritance of these traits were controlled by additive genetic effect, so the selection procedures in early generations will be effective. These results were harmony with those of El Hosary *et al.* (2000) and Khaled (2013).

The values of dominance gene effects, (h) were significantly positive for number of spikes/plant and grain

yield/plant in the third cross, and they were positive and significant for grain weight/spike in the second cross, indicating predominant role of dominant component of gene action in the inheritance of these traits, so the selection for these traits will be more useful in the later generations. The obtained results were in harmony with those obtained by Abdel Nour, Nadya and Moshref (2006) and Koumber and El-Gammaal (2012).

The values of additive × additive gene effects (i) were negative and non-significant for all studied traits in the three crosses except grain weight/spike and 100- grain weight in the first cross, which were positive and non-significant.

Data in Table 3 showed that, the estimates of dominance × dominance (l) gene effects were positive and significant for number of spikes/plant and grain yield/plant in the three crosses. Similar results were reported by Khaled 2013.

The values of dominance × dominance (l) gene effects were positive and significant in the second and third crosses for spike length and grain weight /spike; also, they were positive and significant for number of grains/spike in the first and third crosses. These results showed that, dominance × dominance gene effects control the inheritance of these traits. Khattab *et al* (2010) reported that, all studied yield and its component traits were controlled by additive and non-additive genetic effects, with greater estimates of dominance gene effects than the additive gene effects in most cases.

**Table 3. Gene effects for all studied traits of the three wheat crosses based on five parameters model.**

Traits	Crosses	<i>M</i>	<i>D</i>	<i>H</i>	<i>i</i>	<i>L</i>
Number of spikes/plant	1	9.11**	-0.08	0.50	-3.35	17.08**
	2	8.63**	-0.03	1.17	-1.90	12.60*
	3	9.70**	0.18*	2.78**	-0.80	11.89**
Spike length (cm)	1	11.13**	0.55**	-0.53	-0.88	6.27
	2	12.24**	-0.33	-0.63	-2.07	5.91**
	3	12.07**	-1.02	-0.61	-4.33	6.40**
Grain weight/spike (gm)	1	3.03**	0.12**	-0.08	0.08	0.36
	2	3.17**	-0.17	0.27*	-0.33	1.26**
	3	3.03**	-0.23	0.00	-0.66	1.65**
Number of grains/spike	1	59.11**	1.68**	-2.74	-3.96	23.02*
	2	61.44**	-1.53	0.54	-5.92	23.43
	3	60.74**	-2.63	0.04	-11.09	28.43**
100-grain weight (gm)	1	4.65**	0.05	0.17	0.20	0.00
	2	4.68**	-0.06	0.05	-0.17	0.58
	3	4.68**	-0.13	0.29	-0.13	0.14
Grain yield/plant (gm)	1	22.86**	-0.66	0.82	-9.13	37.68**
	2	22.71**	-1.13	4.24	-6.62	36.08**
	3	23.93**	-1.53	6.45*	-7.14	41.91**
Harvest index %	1	34.47**	0.001	-1.64	-3.53	14.84
	2	34.84**	-1.32	1.76	-2.76	8.43
	3	35.93**	-1.35	1.09	-4.88	6.02

Cross 1 (Misr 1× Gemmeiza 10), cross 2 (Gemmeiza 9× Gemmeiza 11) and cross 3 (Gemmeiza 10× Gemmeiza 11)

Heterosis for the economic traits in wheat crop such as yield and yield components is very important consideration in heterosis breeding.

Data on heterosis % as percentage from mid-parents and better-parent (in F<sub>1</sub> generation), inbreeding depression (in F<sub>2</sub> and F<sub>3</sub> generations) and potence ratio for the seven traits in all crosses are presented in Table 4.

Heterosis estimates as percentage from mid-parents were positive and significant for number of spikes/plant, spike length, number of grains /spike and grain yield/ plant in all crosses, also were positive and significant for grain weight/spike in the second cross, 100- grain weight in the third cross and for harvest index in the first and third crosses. The highest value of heterosis as percentage from mid-parents was recorded for number of spikes/plant in the third cross (39.04 %), while the lowest value of heterosis as percentage from mid-parents was recorded for 100-grain weight in the first cross (1.85%).

Thomas *et al* (2017) found that, the estimates of heterosis and heterobeltiosis were positive and significant for spike length, spike weight, 1000-grain weight and grain yield per plant in some wheat crosses.

Significant positive heterosis as percentage from better-parent was detected for number of spikes/plant and grain yield/ plant in the three crosses, for number of grains /spike in the first and third crosses, and for harvest index % in the third cross. The values of heterosis as percentage from better-parent ranged from (36.57%) for number of spikes/plant in the third cross to (-1.28%) for grain weight/spike in the first cross.

A high percentage of heterosis as percentage from mid and better-parent for grain yield per plant in wheat crosses were reported by Singh *et al.* (2013) and Garg *et al.* (2015). Yagdi and Karan (2000) observed significant heterosis and heterobeltiosis in spike length,

number of grains per spike, 1000-grain weight and grain yield per plant.

Inbreeding depression (ID) and heterosis are related phenomena of essential importance to evolutionary biology and applied genetics. Inbreeding depression (ID) refers to reduced fitness of progenies resulting from inbreeding (Stebbins, 1958 and Wright, 1977). In contrast, heterosis is referred to as the superiority of an F<sub>1</sub> hybrid over its parents (Stuber, 1994).

In this study, Inbreeding depression (ID) was found to occur in F<sub>2</sub> and F<sub>3</sub> generations for the most studied traits in the three crosses.

Inbreeding depression (ID) percentage from F<sub>1</sub> to F<sub>2</sub> and F<sub>3</sub> generations were estimated and presented in Table 4. Results indicated that, in F<sub>2</sub> generation the percentage of inbreeding depression was positive and significant for number of spikes/plant and grain yield/plant in the three crosses, and for spike length, grain weight/spike and number of grains/spike in the second and third crosses. The values of inbreeding depression percentage in F<sub>2</sub> generation ranged from (36.41%) for grain yield/plant in the third cross to (1.61%) for grain weight/spike in the first cross.

On the other hand, in F<sub>3</sub> population the percentage of inbreeding depression was positive and significant for number of spikes/plant, number of grains/spike and grain yield/plant in the three crosses. In case of spike length and grain weight/spike, inbreeding depression in F<sub>3</sub> was positive and significant in the second and third crosses, while it was positive and significant for 100-grain weight in the first and third crosses and for harvest index % in the second cross.

The estimates of inbreeding depression percentage in F<sub>3</sub> generation ranged from (33.73%) for grain yield/plant in the third cross to (0.23%) for grain weight/spike in the first cross.

**Table 4. Heterosis as percentage from mid-parents and better-parent, inbreeding depression%, potence ratio and heritability for all studied traits in the three crosses.**

Traits	Crosses	Heterosis %		Inbreeding depression %		Potence ratio	Heritability	
		MP	BP	F <sub>2</sub>	F <sub>3</sub>		h <sup>2</sup> b	h <sup>2</sup> n
Number of spikes/plant	1	37.02**	35.88**	33.15**	26.23**	46.00	0.64	0.18
	2	32.03**	31.56**	30.19*	26.18**	85.00	0.81	0.01
	3	39.04**	36.57**	31.02**	30.67**	-21.00	0.71	0.10
Spike length (cm)	1	13.20*	7.80	10.49	6.28	-2.63	0.80	0.37
	2	6.07*	3.34	8.67**	4.73*	2.28	0.56	0.33
	3	14.41**	5.25	9.69**	5.56*	1.66	0.59	0.07
Grain weight/spike (gm)	1	2.63	-1.28	1.61	0.23	-0.65	0.64	0.37
	2	7.83**	2.69	12.40**	12.09**	1.53	0.76	0.30
	3	6.05	-1.03	12.01*	9.03**	0.87	0.65	0.39
Number of grains/spike	1	7.78**	4.79*	6.91	3.56*	2.72	0.79	0.56
	2	5.30**	2.84	9.07*	7.10**	2.22	0.78	0.35
	3	9.46**	5.00**	10.50**	7.90**	2.23	0.70	0.30
100-grain weight (gm)	1	1.85	0.66	1.81	2.73*	-1.55	0.80	0.09
	2	2.04	0.72	3.48	2.98	1.46	0.84	0.22
	3	3.31*	0.45	3.73	5.07**	1.15	0.82	0.25
Grain yield/ plant (gm)	1	35.94**	32.32**	30.08**	23.50**	13.20	0.65	0.15
	2	34.06**	28.32**	32.91**	29.38**	7.61	0.63	0.18
	3	38.85**	31.45**	36.41**	33.73**	6.90	0.61	0.05
Harvest index %	1	5.94*	5.35	7.73	4.15	10.74	0.75	0.13
	2	5.26	1.53	7.90	7.68**	1.43	0.67	0.09
	3	9.43**	5.32*	5.76	5.43	2.41	0.66	0.23

Cross 1 (Misr 1× Gemmeiza 10), cross 2 (Gemmeiza 9× Gemmeiza 11) and cross 3 (Gemmeiza 10× Gemmeiza 11).

Hamam (2013) stated that, the inbreeding depression estimates were positive and significant for number of grains/spike and grain yield/plant in F<sub>2</sub> and F<sub>3</sub> generations. Khattab *et al* (2010) reported that, inbreeding depression percentage estimates were positive and highly significant for harvest index, grain weight/spike and number of grains / spike. On the other hand, significant negative values of inbreeding depression were detected for number of spikes /plant and grain yield/plant in some bread wheat crosses (Farag 2009).

Concerning potence ratio, data in Table 4 shows over dominance for all studied traits except spike length, grain weight/spike and 100- grain weight in the first cross, and for number of spikes/plant in the third cross. These results are in agreement with those obtained by Hendawy (2003).

Potence ratio estimates ranged from (85.00) for number of spikes/plant in the second cross to (-21.00) for number of spikes/plant in the third cross.

Data in Table 4 showed that, estimates of heritability in broad sense were moderate to high for all studied traits in the three crosses, these estimates ranged from 0.56 for spike length in the second cross to 0.84 for 100- grain weight in the second cross.

High values of heritability in broad sense were detected for 100- grain weight and number of grains/spike, indicating that superior genotypes for these traits could be identified from the expression and illustrate the importance of straight forward phenotypic selection for the improvement of these traits.

Heritability in narrow sense values were low to moderate for all traits in the three crosses, these values ranged from 0.01 for number of spikes/plant in the second cross to 0.56 for number of grains/spike in the first cross.

Selection in early generations will be the most suitable for the traits which scored the higher values of heritability while, selection in the next generations will succeed for the traits which scored the lower values of heritability such as most traits in this study.

The difference in magnitude of heritability in broad and narrow sense measurements for all studied characters would ascertain the presence of both additive and non-additive gene effects in the inheritance of these characters. These results are in harmony with those obtained by Abd-Allah, Soheir *et al.* (2008), Abdel-Nour, Nadya and Hassan, Manal (2009), Koumber and El-Gammaal (2012), Hamam (2013) and Khaled (2013).

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## التحليل الوراثي للمحصول ومكوناته في بعض هجن قمح الخبز باستخدام نموذج العشائر الخمسة

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أجريت هذه الدراسة في مزرعة قسم المحاصيل بكلية الزراعة - جامعة الأزهر بالقاهرة (مدينة نصر) - جمهورية مصر العربية. وذلك خلال أربع مواسم زراعية هي 2012/2013, 2013/2014, 2014/2015 و 2015/2016 م. واستخدم في هذه الدراسة أربعة أصناف مصرية من القمح هي مصر 1, جميزة 9, جميزة 10 وجميزة 11 لعمل ثلاث هجن هي (مصر 1×جميزة 10), (جميزة 9×جميزة 11) و (جميزة 10×جميزة 11) لتقدير بعض المقاييس الوراثية لصفات المحصول ومكوناته, وكانت الصفات المدروسة هي: عدد السنابل/النبات, طول السنبل/السنبلة, وزن الحبوب/السنبلة بالجرام, عدد الحبوب/السنبلة, وزن 100- حبة بالجرام, وزن محصول النبات الفردي بالجرام, ودليل الحصاد كنسبة مئوية. وأجريت التجربة باستخدام تصميم القطاعات الكاملة العشوائية في ثلاث مكررات. وتم استخدام خمس عشائر في هذه الدراسة وهي الأب الأول, الأب الثاني, الجيل الأول, الجيل الثاني والجيل الثالث وذلك لكل هجين من الهجن الثلاث. وأوضحت النتائج أن الجيل الأول سجل أعلى متوسط وكان متوسط الجيل الأول أعلى من متوسطات باقي العشائر (الأب الأول, الأب الثاني, الجيل الثاني والجيل الثالث) في كل الصفات المدروسة في الثلاث هجن ماعدا وزن حبوب السنبل في الهجين الثالث. - أوضحت النتائج أيضا أن تقديرات الخطأ المعياري للجيل الثاني والجيل الثالث. وتحكم التباين المضيف وغير المضيف في وراثية كل الصفات تحت الدراسة ولكن كانت قيم التباين السيادة × السيادة هي الأعلى مما يدل على وجود سيادة فائقة تتحكم في وراثية معظم الصفات المدروسة. - كانت تقديرات قوة الهجين بالنسبة لمتوسط الأبيون موجبة ومعنوية بالنسبة لعدد السنابل/النبات, طول السنبل/السنبلة, عدد الحبوب/السنبلة ووزن محصول النبات الفردي بالجرام في الهجن الثلاث. بينما كانت تقديرات قوة الهجين بالنسبة لأفضل الأبيون موجبة ومعنوية بالنسبة لعدد السنابل/النبات ووزن محصول النبات الفردي بالجرام في الهجن الثلاث. وأظهرت تقديرات درجة سيادة فائقة لمعظم الصفات المدروسة في الثلاث هجن حيث كانت معظم التقديرات أعلى من الواحد الصحيح. - كانت تقديرات درجة التوريث بمعناها العام (الواسع) متوسطة إلى مرتفعة في معظم الصفات المدروسة وتراوحت هذه التقديرات بين (0.56) بالنسبة لصفة طول السنبل في الهجين الثاني إلى (0.84) بالنسبة لصفة وزن 100- حبة بالجرام في الهجين الثاني. - كانت تقديرات درجة التوريث بمعناها الضيق منخفضة إلى متوسطة في معظم الصفات المدروسة في الهجن الثلاث وتراوحت من (0.01) بالنسبة لصفة عدد السنابل/النبات في الهجين الثاني إلى (0.56) بالنسبة لصفة عدد الحبوب على السنبل في الهجين الأول.