

ESTIMATION OF EPISTASIS, ADDITIVE AND DOMINANCE VARIATION IN SOME BREAD WHEAT (*Triticum aestivum*, L) CROSSES

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ABSTRACT

A, B and C scaling test as well as 6-parameters model were used in order to assess the nature of gene effects for seven traits in three crosses of bread wheat viz. plant height, number of days to heading, number of days to maturity, number of spikes/plant, number of kernels /spike, 1000 kernel weight and grain yield /plant in three bread wheat crosses (*Triticum aestivum*, L). Analysis of variance indicated significant differences existed among generations for all studied traits. Non-allelic interactions were observed for all traits and crosses except in few cases in which the values did not reach the significant levels. In the 6-parameters model, the additive component (a) as well as dominance component (d) were significant in most cases. Additive X additive (aa) was significant for all cases except for plant height in cross III. Additive X dominance (ad) component was significant for plant height in cross II and days to maturity and spikes/plant in cross I. The dominance X dominance (dd) component was significant for all cases except

for days to maturity in cross II, and spikes/plant in cross I and cross III. Significant values of heterosis based on mid-parent values were obtained. Negative inbreeding depression was detected for some traits in some crosses whereas no inbreeding depression was observed for spikes/plant in cross I. High heritability values in broad sense were observed for all studied traits for all crosses. Narrow sense heritability ranged from 42.05 for kernels/spike to 74.30 for plant height in cross III. Genetic advance values were higher for spikes/plant in all crosses whereas those values were found to be very low for days to maturity in all crosses under study.

INTRODUCTION

Wheat is the main winter cereal crop in Egypt. It is used as a stable food grain for urban or rural societies and as a major source of straw for animal feeding. The total national wheat production reached about 6.8 million tons, which represents more than 55 % self sufficient of local needs Shehab El-Din *et. al.*, (2005).

The most important decision of plant breeder is the choice of the parents as a source of potential genetic variability. Parental selection is important because it determines the range and nature of the variability in the F₂ generation and a set of the potential limit for successful in the segregating generations. Mahdy, (1988) found that the selection based on grain yield per se was effective in improving grain yield itself and also, it was accompanied by a sizeable significant increase in number of spikes per plant and number of grains per spike.

In plant breeding programs, the priority of the breeding objectives normally determines the sequence of trait selection. In many programs

whereas yield is the primary objective, however, selection for yield follows selection for traits that had higher heritability such as disease resistance O'Brien et. al., (1978) and Makenzie and Dambert (1961), suggested that, selection for yield should be commence in the earliest possible generations.

In the recent years, plant breeding played an important role in improving yield of most crop plants. The essential information for the breeder is to assess and quantify the causes of variation. Estimates of genetic parameters have impacts on choosing the appropriate method of breeding and / or selection program. One of the most important problems, which convert the breeder is the direct selection for yield because it considered as a quantitative character. Thus, it highly influenced by the environmental fluctuation. Therefore, the direct selection for yield is misleading. Consequently, the main task for the breeder is to determine the highly heritable characters which contribute significantly to yield Hamada, et. al., (1997).

Heritability estimate is very useful for improving the efficiency of a breeding program through the development of appropriate selection strategies. Realized heritability is a useful tool in gouging the response to selection scheme. On the other hand, the significant level of heterosis, however, is still an open question since both positive and negative herterosis have been reported. Investigators evaluated their different hybrid combinations under different cultural practices. Thus, it is difficult to draw a general conclusion since herterosis found in hybrids derived from one group of parents in a particular location is not necessarily found under the other circumstances Mahrous, (1998).

The most daunting challenge confronting the production of hybrid wheat seed is the mass transport of wheat pollen, the expense of F₁ seed production and the presense of male sterility and fertility restoration genes. The existence of these factors would make hybrid wheat feasible.

MATERIALS AND METHODS

The present study was carried out at Sids Agric. Res. Station, ARC during the three successive seasons 2001/2002, 2002/2003 and 2003/2004. This study aimed to estimate, heterosis, heritability and type of gene action of some quantitative characters in some bread wheat crosses. Three hexaploid wheat, *Triticum aestivum*, L. were used for this study.

The pedigree of these hexaploid wheat are shown as followes .

- 1- K134(60)/4/Top/Bman//Bb/3/Col/5/Chil/Buc/6/ Line # 11
- 2- K134(60)/4/Top/Bman//Bb/3/Col/5/Chil/Buc/6/ Kaus // Kaus / Star
- 3- Lines #11/3/ Kaus // Kaus / Star

During the season 2000/2001, seeds of the parental genotypes were sown under field conditions. Crosses combinations were made to obtain the F₁ seeds. In 2001/2002 season, F₁ plants were selfed to produce F₂ seeds and backcrossed to the respective parents to produce Bc₁ and Bc₂ seeds.

In 2002/2003 season, the six generations i.e., P₁, P₂, F₁, F₂, Bc₁ and Bc₂, were planted in a randomized complete block design in three

replications. Each cross was considered as a unit in the planting scheme. The Six populations were randomized with each block. Each replicate consisted of, four rows from each of the parents, F₁ and backcross and six rows from the F₂ populations. In each row seeds were sown by hand to ensure accuracy in spacing of 30 cm. between rows, plants within rows were 10 cm. apart and rows were 4 m., long. All recommended cultural practices in the area for wheat applied during the growing season. The number of plants used for each generation was 100 plants in P₁, P₂, F₁ and 250 plants in F₂ and 150 plants in BC₁ and BC₂.

Data were recorded on an individual guarded plants for the following characters.

- 1- Plant height (PH) at maturity, from soil surface to the top of the spike on the tallest culm (without owns.)
- 2- Number of days to heading (DHE), days from sowing to when the spikes were emerged from flag leaf sheath.
- 3- Number of days to maturity (DMA), days from sowing to the date of physiological maturity.
- 4- Number of spikes per plant (SP/PI).
- 5- Number of kernels per spike, average number of kernels from 10 main spikes (K/Sp).
- 6- kernels weight in grams (1000/KW).
- 7- Grain yield per plant in grams (GY/PI).

STATISTICAL AND GENETIC ANALYSIS

To determine the presence or absence of non-allalic interaction, four scaling tests as outlined by Mather (1949) were used. The quantities A, B, C, and D and their variances were calculated to test the adequacy of the additive - dominance model in each case where:

$$A = 2 \bar{Bc1} - \bar{P1} - \bar{F1}$$

$$B = 2 \bar{Bc2} - \bar{P2} - \bar{F2}$$

$$C = 4 \bar{F2} - \bar{F2} - \bar{P1} - \bar{P2}$$

$$D = 2 \bar{F2} - \bar{Bc1} - \bar{Bc2}, \text{ and}$$

The variance of these estimates were calculated as Follows :-

$$V(A) = 4 V(\bar{Bc1}) + V(\bar{P1}) + V(\bar{F1})$$

$$V(B) = 4 V(\bar{Bc2}) + V(\bar{P2}) + V(\bar{F1})$$

$$V(C) = 16 V(\bar{F2}) + 4 V(\bar{F1}) + V(\bar{P1}) V(\bar{P2})$$

$$V(D) = 4 V(\bar{F2}) + V(\bar{Bc1}) + V(\bar{Bc2})$$

The standard error of A, B, C and D is obtained by taking the square root of their respective variances. T-test values are calculated by dividing the effects of A, B, C, and D on their respective standard errors.

Type of gene effects were estimated according to Gamble (1962) as follows:

The standard error of a, d, aa, ad, and dd is obtained by taking the square root of their respective variances. T-test values are calculated by dividing the effects of a, d, aa, ad, and dd on their respective standard errors.

$$m = \bar{F}_2$$

$$a = \bar{Bc}_1 - \bar{Bc}_2$$

$$d = \bar{F}_1 - \bar{F}_2 - \frac{1}{2} (\bar{P}_1) - \frac{1}{2} (\bar{P}_2) + 2 (\bar{Bc}_1) + 2 (\bar{Bc}_2)$$

$$aa = 2 (\bar{Bc}_1) + 2 (\bar{Bc}_2) - (\bar{F}_2)$$

$$ad = \bar{Bc}_1 - \frac{1}{2} \bar{P}_1 - \bar{Bc}_2 + \frac{1}{2} \bar{P}_2$$

$$dd = \bar{P}_1 + \bar{P}_2 - 2 \bar{F}_1 + 4 \bar{F}_2 - (\bar{Bc}_1) - (\bar{Bc}_2), \text{ and } \sqrt{m} = \sqrt{F_2}$$

The variance values needed in this concern were obtained as follows:-

$$V_a = \bar{V} (\bar{Bc}_1/n) + \bar{V} (\bar{Bc}_2/n)$$

$$V_d = \bar{V} \bar{F}_1/n + 16 \bar{V} \bar{F}_2/n + \frac{1}{4} \bar{V} (\bar{P}_1/n) + \frac{1}{4} \bar{V} (\bar{P}_2/n) + 4 \bar{V} (\bar{Bc}_1/n) + 4 \bar{V} (\bar{Bc}_2/n)$$

$$V_{aa} = 4 \bar{V} (\bar{Bc}_1/n) + 4 \bar{V} (\bar{Bc}_2/n) + 16 \bar{V} (\bar{F}_2/n)$$

$$V_{ad} = \bar{V} (\bar{Bc}_1/n) + \frac{1}{4} \bar{V} (\bar{P}_1/n) + \bar{V} (\bar{Bc}_2/n) + \frac{1}{4} \bar{V} (\bar{P}_2/n)$$

$$V_{dd} = \bar{V} (\bar{P}_1/n) + \bar{V} (\bar{P}_2/n) + 4 \bar{V} (\bar{F}_1/n) + 16 (\bar{F}_2/n) + 16 \bar{V} (\bar{Bc}_1/n) + 16 \bar{V} (\bar{Bc}_2/n)$$

The amount of heterosis was expressed as the percentage deviation of F1 mean performance from mid-parent values. Inbreeding depression was calculated as the difference between the F1 and F2 means expressed as a percentage of the F1 mean. T-test was used to determine the significance of these deviation where the standard error (S.E) was calculated as follows:

S.E for mid-parent heterosis were calculated as follows :-

$$(\bar{F}_1 - \bar{MP}) = (\bar{V} \bar{F}_1 + \frac{1}{4} \bar{V} \bar{P}_1 + \frac{1}{4} \bar{V} \bar{P}_2)^{1/2}$$

and S.E for inbreeding depression were estimated as follows .

$$(\bar{F}_1 - \bar{F}_2) = (\bar{V} \bar{F}_1 + \bar{V} \bar{F}_2)^{1/2}$$

Heritability in both broad and narrow sense were estimated according to Mather (1949); predicted genetic gain from selection (Δg) were calculated according to Johanson *et al.*, (1955) and genetic coefficients of variation (G. C. V %) were estimated.

RESULTS AND DISCUSSION

Mean and variance of the seven studied traits in the three studied crosses for the six populations i.e., P1, P2, F1, F2, Bc and BC2 are presented in table (1).

Parental mean differences and genetic variance among F2 plants were calculated and tested for statistical significance. All studied characters showed significant genetic variance in F2 plants in the three crosses, therefore other needed parameters were estimated i. e., simple scaling test as outlined by Mather (1949) as the test of the presence of non-allielic interaction was estimated.

In general, the mean performance values of F2 plants were high in the three studied crosses for all studied traits except, crosses 2 and 3 for plant height, number of days to heading and number of kernels per spike in the three crosses. On the other hand, F2 variance had in magnitude, the highest value in the three studied crosses for all studied traits than the other studied populations.

The choice of the most efficient breeding procedures depends on a large extent on the knowledge of the genetic system contributing the characters to be selected because it is helpful in deciding the breeding procedures to be used for improvement of these characters. Therefore, the nature of gene action was also computed according to Gamble, (1962). The estimates of various types of gene effects contributing to the genetic variability are presented in Table (2).

Scaling test (A, B, C and D) as procedures by Mather, (1949) in Table (2) showed that all studied characters in the three crosses were significant except six values out of eighty four values. These results indicated the presence of non- allelic interaction for the significant values. On the other hand, it is clear that if scaling test A,B,C were significant this may be indicated the inadequacy of the simple model can be account for the differences between population means. These results were similar to those obtained by Amaya *et. al.* (1972) for plant height, number of days to heading and maturity and Hamada *et. al.* (1997) for number of days to heading, number of kernels per spike, grain yield per plant, 1000- kernel weight and number of spikes per plant .

The mean parameter (m) for all studied attributes which reflect the contribution due to the overall mean plus the locus effects and interactions of the fixed loci, reported highly significant.

Additive genetic estimates (a) in Table (2), are quite small in magnitude relative to the dominance gene effects .Additive gene effects were exhibited in all studied traits except; plant height in second cross, number of days to maturity in both first and second crosses and number of spikes per plant in the third cross. These results indicated that the potentiality of improving the performance of these traits using pedigree selection program may be more effective, Abul – Naas *et. al.*, (1993).

Table(1): Mean and variance of the six populations for Plant height(PLH), number of days to heading (DHE), number of days to maturity(DMA), number of spikes per plant(no. of sp./Pl), number of kernels per spike , 1000-kernel weight (1000/KW) and grain yield per plant(Gy/P) of the three studied crosses.

Traits	Cross (I)						Cross (II)						Cross (III)						
	\bar{P}_1	\bar{P}_2	\bar{F}_1	\bar{F}_2	\bar{Bc}_1	\bar{Bc}_2	\bar{P}_1	\bar{P}_2	\bar{F}_1	\bar{F}_2	\bar{Bc}_1	\bar{Bc}_2	\bar{P}_1	\bar{P}_2	\bar{F}_1	\bar{F}_2	\bar{Bc}_1	\bar{Bc}_2	
PLH	\bar{X}	106	105	116	100	104	94	96	107	109	114	114	97	95	97	106	107	104	104
	S^2	± 0.26	± 0.29	± 0.51	± 0.49	± 0.55	± 0.29	± 0.26	± 0.33	± 0.47	± 0.52	± 0.58	± 0.27	± 0.24	± 0.39	± 0.48	± 0.52	± 0.45	± 0.45
DHE	\bar{X}	6.80	8.20	15.20	64.30	35.80	45.63	8.2	6.8	10.6	55.2	41.2	7.5	5.6	15.3	56.8	41.2	30.2	30.2
	S^2	± 0.18	± 0.18	± 0.27	± 0.30	± 0.35	± 0.32	± 0.19	± 0.20	± 0.43	± 0.34	± 0.41	± 0.20	± 0.21	± 0.34	± 0.33	± 0.31	± 0.37	± 0.37
DMA	\bar{X}	3.3	3.4	7.2	22.6	18.6	15.4	4.1	18.6	31.5	17.3	25.3	4.1	4.3	11.6	27.3	14.2	20.3	20.3
	S^2	± 0.27	± 0.29	± 0.43	± 0.36	± 0.41	± 0.40	± 0.27	± 0.25	± 0.40	± 0.35	± 0.37	± 0.18	± 0.22	± 0.32	± 0.34	± 0.38	± 0.37	± 0.37
No. of Sp/PL	\bar{X}	7.2	8.2	18.6	32.2	25.6	23.8	7.1	6.3	15.8	26.3	18.3	3.2	4.9	10.2	28.3	21.3	20.3	20.3
	S^2	± 0.28	± 0.32	± 0.45	± 0.43	± 0.45	± 0.47	± 0.33	± 0.37	± 0.50	± 0.45	± 0.44	± 0.23	± 0.25	± 0.45	± 0.42	± 0.45	± 0.44	± 0.44
No. of Kernels/s	\bar{X}	8.1	10.2	20.3	46.3	30.1	32.5	10.8	13.5	24.6	40.9	30.2	5.1	6.3	20.5	43.5	30.1	29.6	29.6
	S^2	± 0.24	± 0.25	± 0.43	± 0.34	± 0.38	± 0.40	± 0.23	± 0.22	± 0.43	± 0.35	± 0.39	± 0.21	± 0.24	± 0.39	± 0.33	± 0.37	± 0.38	± 0.38
1000-KW	\bar{X}	5.6	6.4	18.9	29.6	31.3	23.9	5.1	4.8	18.7	30.2	25.4	4.3	5.6	15.6	27.8	20.6	21.5	21.5
	S^2	± 0.24	± 0.21	± 0.38	± 0.31	± 0.32	± 0.34	± 0.20	± 0.19	± 0.38	± 0.33	± 0.36	± 0.21	± 0.24	± 0.37	± 0.30	± 0.33	± 0.34	± 0.34
GYP	\bar{X}	5.6	4.5	14.2	24.6	15.3	17.8	4.2	3.5	14.6	27.8	19.1	4.3	5.6	13.8	22.6	16.3	17.4	17.4
	S^2	± 0.32	± 0.37	± 0.43	± 0.40	± 0.42	± 0.47	± 0.30	± 0.32	± 0.45	± 0.40	± 0.42	± 0.32	± 0.34	± 0.49	± 0.43	± 0.49	± 0.49	± 0.49
	\bar{X}	28.06	37.43	52.04	40.15	24.17	36	24.85	56.17	91.46	48.98	36.08	27.05	40.50	48.70	41.40	33.50	42	42
	S^2	± 0.32	± 0.37	± 0.43	± 0.40	± 0.42	± 0.47	± 0.30	± 0.32	± 0.45	± 0.40	± 0.42	± 0.32	± 0.34	± 0.49	± 0.43	± 0.49	± 0.49	± 0.49
	\bar{X}	10.5	13.5	18.6	40.2	26.4	32.6	9.2	10.5	20.4	39.5	26.3	10.2	11.8	23.6	46.3	35.4	36.2	36.2
	S^2	± 0.32	± 0.37	± 0.43	± 0.40	± 0.42	± 0.47	± 0.30	± 0.32	± 0.45	± 0.40	± 0.42	± 0.32	± 0.34	± 0.49	± 0.43	± 0.49	± 0.49	± 0.49

In autogamous crops i.e., wheat and barley, the breeder is normally aiming at isolating parental combinations that are likely to produce desirable homozygous segregants. The utility of attempts at identifying such pure lines is facilitated by the preponderance of additive genetic effects in self pollinating crops, Joshi and Dhawan, (1966).

Table (2): Scaling test and six-parameters model of the studied traits in the three crosses under study.

Trait	Cross	Scaling test				Six parameter					
		A	B	C	D	m	a	d	aa	ad	dd
PLH	I	5**	-3*	58**	36**	116**	-4**	-49**	-56**	4**	54**
	II	27**	25**	32**	28**	109**	0	32**	20**	1	72**
	III	20**	16**	38**	20**	106**	3**	-1	-2	2**	-34**
DHE	I	5**	2**	3*	5**	87**	2**	7.5**	4**	1.5**	-11**
	II	4**	11**	-7**	-11**	91**	-13**	14.5**	22**	-3.5**	-37**
	III	-7**	-20**	-35**	-7**	90**	-2**	18.5**	8**	6.5**	19**
DMA	I	12**	10**	18**	14**	151**	0	9**	4*	1	-26**
	II	2*	-7**	-11**	-3**	148**	-1*	8.5**	6**	4.5**	-1
	III	7**	-3**	0	8**	152**	0	12**	4*	5**	-8**
SP/PL	I	0	2	10**	10**	11**	-2**	-3	-8**	-1	6
	II	2	-17**	5**	7**	15**	2**	-15.5**	-20**	9.5**	35**
	III	5.6**	0	13.6**	5.6**	13**	0	-9.2**	-8**	2.8**	2.4
K/GSP	I	-12**	-16**	-66**	-62**	64**	9**	9**	38**	2**	-10**
	II	-56**	-25**	-97**	-39**	66**	4**	25.5**	16**	-15.5**	65**
	III	-41**	-8**	-71**	-37**	68**	-11**	20.5**	22**	-16.5**	27**
1000 KW	I	-15.61**	1.89*	10.08**	8.8**	55.59**	-4.72**	20.04**	-23.8**	-8.75**	37.52**
	II	-19.29**	-23.19**	-26.22**	2.22**	49.72**	7.41**	-0.93	-16.26**	1.95**	58.74**
	III	-3.88**	6.42**	22.22**	17.22**	51.84**	-4.16**	-13.57**	-19.68**	-5.15**	17.14**
GY	I	-31.76**	-17.47**	-8.97**	14.81**	40.15**	-11.83**	-20.97**	-40.26**	-7.15**	89.49**
	II	-44.19**	-96.07**	-68.02**	16.94**	48.98**	10.28**	-21.29**	-72.24**	-25.94**	212.5**
	III	-8.73**	-5.2**	0.69	15.27**	41.41**	-8.49**	0.31	-14.62**	-1.77*	28.55**

The estimates of dominance effects were significant for all studied traits except; plant height in the third cross, number of spikes per plant in first cross, 1000 – kernel weight in the second cross and grain yield per plant in the third cross. These results indicating the importance of dominance gene effects in inheritance of these traits. On the other hand, significant of (a) and (b) components indicated that both additive and dominance gene effects were important in the inheritance of these traits. Also, selecting desirable characters may be practiced in the early generations but it would be effective in the late one. Similar results were obtained by Bakheit *et al.*, (1989), Abul Naas *et al.*, (1991), AlKaddousi and Hassan (1991) Gouda *et al.*, (1993), Hendawy (1994), Hendawy (1998), Saad *et al.*, (1999), El Hosary *et al.*, (2000), Seleem (2001) Moustafa (2002) and Hendawy (2003).

Estimates for epistatic gene effects i.e. additive) x additive(aa), additive x dominance (ad) and dominance x dominance (dd) are presented in table (2). Significant estimates of epistatic gene effects for one or more of these three types of epistatic gene effects in the three crosses for all studied

traits were detected. Additive x additive (aa) gene effects were exhibited and significant for all studied traits except; plant height in the third cross. Additive x dominance was significant also for all studied traits except; plant height in the second cross, number of days to maturity in the first cross and number of spikes per plant in the first cross. Dominance x dominance gene effects were significant for all studied traits except; number of days to maturity in the second cross, number of spikes per plant in both first and third cross. These results were in agreement with those obtained by Bakheit *et. al.* (1989), Hendawy (1994), Hendawy (1998), Moustafa (2002) and Hendawy (2003).

The absolute relative magnitude of the epistatic gene effects to the mean effects were somewhat variable depending on the cross and trait studied. Generally, the absolute magnitude of the epistatic effects were large than additive or dominance effects. Therefore, it could be concluded that homozygot x homozygot and heterozygot x homozygot non- allelic interactions were more important than the heterozygot x heterozygot interaction in the inheritance of most studied traits. The study further revealed that epistatic gene effects was as important as additive and dominance gene effects for most of the traits. The failure to detect epistatic gene effects based on the generation mean analysis does not necessarily indicate that non-allelic interactions play no role in the determination of phenotypic value. Nighawan *et. al.*, (1969) have also reported the importance of all the three types of gene action. On the other hand, Ketata *et. al.*, (1976) postulated non-additive gene action of sizable amount for grain yield in wheat. Thus, the system of inbreeding employed in exploiting any character depends on the gene action involved in its expression for predicted gain in selection progress Abul Naas *et. al.*, (1993).

In self pollinated crops such as wheat, plant breeders have been investigated the possibility of developing hybrid cultivars. Thus, the utilization of heterosis in various crops through the world has tremendously increased the production either for human food or livestock feed. Heterosis is a complex phenomenon which depends on the balance of different combinations of genotypic effect as well as the distribution of plus and minus alleles in the parents. Heterosis is expressed as the percentage deviation of F1 mean performance from the better or mid parent of the trait. As it will be expected, better parent for plant height was the short one but may be the heterosis relative to the mid- parent value may be effective. On the other hand, a few days for both heading and maturity dates may be the best. In this concern, percentage of heterosis over the mid- parent values are presented in Table (3). Highly significant desirable heterotic effect relative to mid- parent value was observed for number of spikes per plant in the first and second crosses, but negative sign was detected for same trait in the third cross. No significant heterotic values were noted for the rest studied traits. These results were in agreement with those obtained by Mahrous (1998), Hamada *et. al.* (2002) and Hendawy (2003) and Moussa (2005).

Table (3): Heterosis (MP), inbreeding depression, Heritability (BS & NS), genetic advance and genetic coefficient of variability of the traits under study in the three crosses.

Trait	Cross	Heterosis	ID%	Heritability		$\Delta g\%$	Δg	G.C.V %
		- M.P		Broad	Narrow			
PLH	I	7.14	-10.48**	84.34	73.36	10.45	12.12	6.35
	II	12.63	-1.87**	84.54	34.42	4.83	5.27	6.27
	III	1.04	-9.28	83.33	74.30	10.88	11.53	6.49
DHE	I	4.14	1.14**	79.57	49.56	5.58	4.85	4.87
	II	-7.77	-2.25**	72.28	64.76	8.23	7.49	5.24
	III	11.23	13.46**	75.58	73.83	8.81	7.92	5.05
DMA	I	3.47	-1.34**	64.80	46.58	3.61	5.45	3.03
	II	1.67	2.63**	62.99	53.23	3.80	5.62	2.75
	III	5.41	2.56**	78.45	53.0	3.82	5.81	3.10
SP/PL	I	83.33**	0	72.16	64.79	82.57	9.08	52.55
	II	39.13**	6.25**	60.15	55.50	48.75	7.31	33.70
	III	-11.76**	-44.44**	75.56	62.76	65.59	8.53	44.10
K/SP	I	-30.53	3.03**	65.20	47.30	8.28	5.30	6.86
	II	11.11	30.53**	68.43	42.05	7.21	4.76	6.89
	III	-1.73	20**	59.42	48.56	7.76	5.27	6.46
1000 KW	I	7.35	-1.16**	67.07	65.45	12.03	6.69	7.31
	II	31.54	22.24**	73.26	66.91	14.62	7.27	9.08
	III	14.13	-5.07**	65.05	50.88	9.61	4.98	7.4
GY	I	58.93	22.85**	94.68	63.53	17.32	6.95	12.70
	II	125.77	46.45**	66.16	53.54	16.80	8.23	10.44
	III	44.19	14.97**	67.17	45.36	15.35	6.36	13.47

Inbreeding depression measured the reduction in performance of the F2 generation due to inbreeding. The results in Table (3), showed that highly significant positive values were detected for; number of days to heading in first and third crosses, number of days to maturity in the second and third crosses, number of spikes per plant in the second cross, number of kernels per spike in all studied crosses, 1000 kernel weight in the second crosses and grain yield per plant in the three studied crosses. On the other hand, significant negative inbreeding values were detected for; plant height in both first and second cross, number of days to both heading and maturity in the second and first crosses, respectively and 1000- kernel weight in the first and third crosses. Significant effects for both heterosis and inbreeding depression were associated with number of spikes per plant in both first and second crosses Table (3) this seems logic since the expression of heterosis in F1 will be followed by considerable reduction in the F2 performance. Significant heterotic effect and significant inbreeding depression were obtained for the rest studied traits except, plant height and number of spikes per plant in the third cross. The contradiction between sings for dominance and epistatic effects of most parameters may be lead to the observed absence of heterosis effects, El-Hosary (1983). Also, they reported that the reduction in values of non- additive genetic components is logically caused by means of inbreeding depression. These results were in agreement with that obtained by Abul Naas *et. al.*, (1993) in barley, El-Seidy and Hamada (1997) and Hendawy (2003) .

Heritability value indicates the progress from selection for a plant character is relatively easy or difficult to make in a breeding program. A plant breeder, through experience, can perhaps rate a series of characters on their response to selection. Heritability gave a numerical description of this concept. An assessment of heritability of various traits is considerable importance in crop improvement programs, for example, to predict response to selection, Nyquist (1991) and to identify optimum environments for selection Allen *et. al.*, (1978). Heritability has been estimated in several experimental situations in literature. Standard errors of the estimates or the confidence intervals of heritability are reported for parent – offspring data by Falconer (1982) and others. Exact confidence intervals for heritability were obtained by Knapp *et. al.*, (1985) when the data were collected

On a progeny mean basis from several environments. The standard errors and confidence interval of response to selection have been given by Bridges *et. al* (1991). Singh *et. al* (1993) and Singh and Ceccarelli (1995) provided expression

for the standard errors of the estimates of heritability from the data generated in a randomized complete block design or incomplete blocks conducted in one environments (or single trial) and in several environments (or multi – location trials). Using a simulation technique, Singh *et. al.* (1993) found that, the distribution of heritability estimated close to normal distribution in their cases.

Heritability in broad sense for the studied traits was estimated and the obtained values are presented in Table (3). High heritability values were detected for all studied traits.

The highest broad senesce heritability was obtained for grain yield per plant in the first cross (94.68). Meanwhile, the lowest value was resultant for number of kernels per spike in the third cross.

Heritability in narrow sense was estimated using the F2 and backcross data and the obtained results are presented in Table (3). Low heritability were obtained for 'plant height in the second cross (34.42) and the highest value was obtained for the same trait but in the third cross (74.30).

The results revealed that the genetic variance was mostly attributed to the additive effects of genes for the other studied traits. This confirmed the previous results found by means of gene action estimates of additive genetic portion, which was mostly predominant. These results were in harmony with those obtained by Al- Kaddoussi (1996) EL-Seidy and Hamada (1997), El-Hosary *et al.* (2000), Moustafa (2002), Hamada *et al.* (2002) and Hendway (2003).

The genetic advance as a percentage of the F2 mean for the studied characters is presented in Table (3). Genetic advance (Δ g%) was detected for; number of spikes per plant and grain yield per plant in all studied crosses. Relatively low genetic advance was obtained in the other cases. Heritability estimates along with the genetic gain were reported by Johanson *et. al.*, (1955) to be more variable than the former alone in predicting the effect of selection. For number of spikes per plant and grain yield plant that mentioned above, high genetic advance was found to associate with heritability in

narrow sense Table (3). Therefore, the selection for these traits could be effective and satisfactory for successful breeding purpose.

Heritability estimates with genetic gain upon selection would be more valuable than the former alone in predicting the effect of selection. In the present investigation, high genetic gain was found to be associated with high narrow sense heritability for number of spikes per plant, 1000- grain weight and grain yield per plant in almost of the three studied crosses, therefore selection for these traits should be effective and satisfactory.

It could be concluded that the presence of the additive effects would suggest the potentiality for obtaining further yield and yield components improvements.

Also, selection procedures would be successful in improving these characters and the presence of the non- additive effects would be suggest the using of the breeding procedures which will be effective when both additive and non additive effects are involved

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تقدير التباين المتفوق والتجميعي والسيادي في بعض هجن قمح الخبز

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أجرى هذا البحث بهدف تقدير ودراسة طبيعة الفعل الجيني ونظام التحكم الوراثي والتمردح الوراثي المتناسق لدراسة عدد من الصفات وهي : تاريخ طرد السنابل وتاريخ النضج وطول النبات وعدد السنابل في النبات الواحد و عدد الحبوب في السنبلة ووزن الألب حبة ووزن محصول النبات الواحد لثلاثة هجن من قمح الخبز .

وقد دلت النتائج المتحصل من تحليل التباين عليها وجود اختلاف معنوية بين العشائر الوراثية تحت الدراسة لجميع الصفات في جميع الهجن الثلاثة. كما تلاحظ وجود تباين غير الأبلي لجميع القيم ماعدا بعض القيم. حيث كانت قيم الفعل الجيني المصيف وكذلك السيادي معنوية لمعظم القيم ماعدا بعض الحالات القليلة. كان التفاعل الجيني التقوي من نوع المضيف X المصيف معنوية لجميع القيم ماعدا صفة طول النبات للهجين الثالث. كما لوحظ أن التفاعل الجيني التقوي من نوع المضيف X السيادي كان معنويا لصفة طول النبات للهجين الثاني و تاريخ النضج وعدد السنابل للصفات الواحد في الهجين الأول. وقد اظهرت النتائج أن التفاعل الجيني التقوي من النوع السيادي X السيادي كان معنويا لجميع القيم ماعدا تاريخ النضج للهجين الثاني وعدد السنابل للصفات الواحد في الهجين الأول والثالث.

أوضحت النتائج وجود قوة هجين معنوية منسوبة لمتوسط الأبوين في معظم الصفات في الهجن الثلاثة. لم يلاحظ وجود أي أثر لمعامل التربية الداخلية ماعدا لصفة عدد السنابل في النبات الواحد للهجين الأول.

كانت قيم كفاءة التوريث بالمعنى الرابع عالية لجميع الصفات في جميع الهجن تحت الدراسة. أما قيم كفاءة التوريث بالمعنى الضيق تتراوح بين ٤٢,٠٥ لعند الحبوب في السنبلة حتى ٧٤,٣٠ لطول النبات للهجين الثالث.