

## **ESTIMATION OF SOME GENETIC PARAMETERS FOR GRAIN YIELD AND SOME OF ITS COMPONENTS IN TWO BREAD WHEAT CROSSES**

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### **ABSTRACT**

*The present work was conducted at the Agric. Res. Station Farm, Faculty of Agric., Ain Shams Univ, at Shalakan, Kalubia Governorate during the three successive seasons 2004/2005, 2005/2006 and 2006/2007 using the six populations of two bread wheat crosses to estimate some genetic parameters for grain yield/plant and certain related characters. The first cross was between Giza<sub>168</sub> and IB<sub>18</sub> (Cross 1) and the second one between Sids<sub>1</sub> and IB<sub>18</sub> (Cross 2).*

*Results revealed that mean squares due to populations were highly significant for most studied characters in the two crosses, indicating that the six populations within each cross differed significantly for studied traits. Heterosis values were positive and significant relative to either mid parent or better-parent values in the two crosses for most of the studied characters, whereas heterosis values were negative and significant for days to heading in both crosses. Positive and significant inbreeding depression values were recorded for spike length in both crosses and for spikelets per spike in Cross 1, whereas negative significant values were obtained for days to heading in Cross 1 and 100-kernel weight in Cross 2. Over and complete dominance was recorded for all the studied characters except kernels/spike in Cross 1 as-well-as plant height and grain yield/plant in Cross 2.*

*Scaling tests (A, B, C and D) indicated the presence of non-allelic gene interactions for all studied traits in both crosses. Additive genetic variance was significant for each of days to heading, spikes/plant, grain yield/plant and spike length in both crosses as-well-as kernels/spike in Cross 2 and for plant height and 100-kernel weight in Cross 1. Dominance variance was significant for each of days to heading, plant height, spikes/plant, kernels/spike and spikelets/spike in both crosses. Epistasis effects were significant for most studied traits in the two crosses. Broad sense heritability estimates were relatively high and ranged from 77% to 93.83% in Cross 1 compared with values from 52.8% to about 93% in Cross 2. Narrow sense heritability percentages ranged between 41.38 and 81.59 in Cross 1 and between 41.25% and 77.58% in Cross 2 for the studied traits.*

*Key words: Bread wheat, Crosses, Heterosis, Inbreeding depression, Scaling tests, Additive effects, Dominance effects, Epistasis, Heritability, Genetic advance.*

### **INTRODUCTION**

An important objective in most wheat breeding programs is enhancing the genetic potential for grain yield through improving the main yield components. The understanding of genetic behavior of the major components determining grain yield/plant in wheat such as no. of spikes/plant, no. of kernels/spike and average kernel weight must be known

as the first step for breeding studies. The magnitude of both additive and non-additive effects is particularly useful to wheat breeders for developing high yielding varieties. To increase the selection efficiency, certain morphological and physiological traits measured on single plants in early segregating generations (as yield selection criteria) must be determined as important breeding goals.

Some investigators studied mode of gene action in wheat crosses using the generation mean analysis to determine the genetic behaviour of such major yield attributes. Additive gene effects were more important in the inheritance of days to heading and plant height (Mahgoub 2007, El-Sayed and El-Shaarawy 2006 and Abd El-Nour 2006b), for spike length (Khattab and Afiah 1998 and Darwish and Ashoush 2003), for no. of spikes/plant, no. of kernels/spike and 100-kernel weight (El-Sayed and El-Shaarawy 2006 and Khaled 2007) and for grain yield/plant (Abd-Allah 2007 and Khaled 2007). On the other side, non-additive gene effects were more important in the inheritance of days to heading, plant height, no. of kernels/spike, 100-kernel weight and grain yield/plant (Abd El-Aty *et al* 2005 and Abd Allah 2007), for spike length (Khattab and Afiah 1998) and for no. of spikes/plant (Khaled 2007).

Heritability estimates in wheat were reported by many investigators in broad and narrow sense. High broad sense percentages (more than 60%) were recorded for days to heading, plant height, no of spikes/plant, 100-kernel weight and grain yield/plant (Mahgoub 2007 and El-Shaarawy 2008), for spike length (El-Marakby *et al* 1994 and Ismail *et al* 2001) for no. of spikelets/spike (El-Marakby *et al* 1994) and for no. of kernels/spike (Khaled 2007 and Mahgoub 2007). Meantime, moderate (more than 40%) and relatively high (more than 50%) narrow sense heritability values were estimated for heading date, plant height, no. of spikes/plant, no-of kernels/spike, 100-kernel weight and grain yield/plant (Mahgoub 2007 and El-Shaarawy 2008) and for spike length and no. of spikelets/spike (El-Marakby *et al* 1994).

Positive and significant heterosis was obtained by several workers in wheat for no. of spikeletes/spike, no. of kernels/spike, spike length, 100-kernel weight and grain yield/plant (Salama 2000 and El-Hennawy 1996) for plant height and no. of spikes/plant (Ashoush 2006 and Dawwam *et al* 2007) and for heading date (Salama 2000 and El-Hennawy 1996). On the other side, negative and significant heterosis was reported by other investigators for days to heading, no-of spikes/plant, no. of kernels/spike, 100-kernel weight and grain yield/plant (Ahmed *et al* 2005) and for plant height and no. of spikeletes/spike (Abd El-Aty 2000 and Abd-Allah 2007).

The present investigation was carried out to determine the type of gene action and some genetic parameters using the six populations of two bread wheat crosses for grain yield/plant and some related attributes.

## MATERIALS AND METHODS

The field trails were started in 2004/2005 growing season in Agric. Res. Station Farm, Faculty of Agric., Ain Shams Univ. at Shalakan, Kalubia Governorate and lasted to 2006/2007 growing season. The materials used in this investigation comprised three parental bread wheat varieties (Table 1), two of which are local (Giza<sub>168</sub> and Sids<sub>1</sub>) and the third is introduced (IB<sub>18</sub>) from Syria.

**Table 1. Name, pedigree and origin of the three wheat parents used in this study.**

Name	Pedigree	Origin
Giza <sub>168</sub> (P <sub>1</sub> )	MRL/Buc// Seri CM93046-8M-oY-oM-2Y-oB	Egypt
Sids <sub>1</sub> (P <sub>2</sub> )	HD2172/Pavon "S"//1158.57/Maya 74 "S"- SD46-4SD-1SD-oSD	Egypt
IB <sub>18</sub> (P <sub>3</sub> )	ICW88-040b-OL-2AP-OL-OAP	Syria

In 2004/2005 season, hybridization between the introduced variety and both local ones was made to obtain the two crosses Giza<sub>168</sub> x IB<sub>18</sub> (Cross 1) and Sids<sub>1</sub> x IB<sub>18</sub> (Cross 2).

In 2005/2006 season, hybridization was made between the F<sub>1</sub> hybrid and its two respective parents to produce BC<sub>1</sub> and BC<sub>2</sub>. Some F<sub>1</sub> plants were selfed to produce the F<sub>2</sub> generation seed, meantime, some parental heads were selfed also to maintain parental purity. In addition, rehybridization between the parental varieties was made to obtain new hybrid F<sub>1</sub> seeds for each cross.

In 2006/2007 growing season, the six populations of each cross (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>) were sown on 20 Nov., 2006 to evaluate them and collect the data concerning each population in each cross. The experimental design used was the randomized complete blocks with 5 replicates. Each replicate consisted of single row for P<sub>1</sub>, P<sub>2</sub> and the F<sub>1</sub> populations, four rows for each backcross and ten rows for the F<sub>2</sub> populations in each cross. The length of the row was three meters with 20 cm apart between rows. Hills were spaced at 10 cm within the row and thinned at one plant per hill. The recommended cultural practices for wheat production were applied on the experimental materials throughout the growing period. Observations and measurements were recorded on 10 guarded plants from each row (making a total of 50 plants for P<sub>1</sub>, P<sub>2</sub> or F<sub>1</sub>). For each backcross population (BC<sub>1</sub> or BC<sub>2</sub>) in each cross, 25 guarded plants were randomly chosen from each replicate for data collection. Also, for each F<sub>2</sub> population, 50 guarded plants were randomly chosen from each replicate for data collection. The following readings and observations were recorded: days to heading, plant

height (cm), no. of spikes/plant, spike length (cm), no. of spikelets/spike, no. of kernels/spike, 100-kernel weight (g) and grain yield/plant (g).

Standard statistical procedures were used to obtain means and variance for each generation (Snedecor and Cochran 1980). The genetic variance in F<sub>2</sub> population was calculated first and so variance genetic parameters were then estimated. The studied genetic parameters included: heterosis expressed as the percentage increase or decrease of the F<sub>1</sub> mean over the mid-parent (M.P) values as-well-as the better-parent (B.P) values, inbreeding depression (I.D.) estimated as the decrease of F<sub>2</sub> mean compared with F<sub>1</sub> mean, potence ratio (P) calculated according to Smith (1952) and heritability in broad and narrow-sense were computed according to Warner (1952). The expected genetic gain after one cycle of selection (the best 5% of the F<sub>2</sub> generation plants) was calculated according to Frey and Horner (1957). The significance of additive, dominance and the three digenic epistasis effects were determined by generation mean analysis (GMA) using the method of Gamble(1962). Gene effects were based on six parameters model. The significance of the estimates were tested by the standard error of each of the six parameters.

## **RESULTS AND DISCUSSION**

### **Analysis of variance and mean performance**

The significance of mean squares for the studied traits of the six populations for the two bread wheat crosses are given in Table (2). All the studied traits showed highly significant variances among the various populations except number of kernels/spike in the first cross. These results indicated that the six populations within each cross are genetically differed from each other for most of the studied traits. Mean performance of the different characters for all populations and their standard errors are illustrated in Table (3).

### **Heterosis, inbreeding depression and potence ratio**

Heterosis, inbreeding depression and potence ratio estimates in the two crosses for all studied traits are presented in Table (4).The percentages of heterosis compared to mid-parent values are positive and significant for each of plant height (7.82% and 7.74%), number of spikes/plant (40.75% and 22.31%), spike length (7.8% and 7.69%), number of spikelets/spike (7.52% and 17.13%), 100-kernel weight (12.69% and 6.06%) and grain yield/plant (9.71% and 22.17%) in Cross 1 and Cross 2, respectively. Meantime, heterosis percentage was highly significant for number of kernels/spike (10.73%) in Cross 2 only. On the other hand, negative and highly significant mid-parent heterosis values were detected for days to heading (-7.37% and -3.23%) in crosses 1 and 2, respectively.

**Table 2. Mean squares for the studied characters, using the six populations data in two bread wheat crosses**

Source of variation	df	Mean squares							
		Days to heading	Plant height (cm)	No. of spikes/plant	Spike length (cm)	No. of spikelets/spike	No. of kernels/spike	100-kernel weight (g)	Grain yield /plant (g)
<b>Cross 1(Giza168xIB18)</b>									
Replications	4	1.95	5.12	0.31	0.05	0.17	6.97	0.06	2.81
Generations	5	65.627**	167.45**	9.287**	1.076**	3.085**	14.75	0.894**	9.608**
Error	20	0.39	4.52	0.40	0.05	0.15	6.21	0.03	1.85
<b>Cross 2 (Sidsi x IB18)</b>									
Replications	4	0.203	9.391	0.247	0.067	0.308	12.552	0.036	1.075
Generations	5	20.849**	57.665**	3.724**	1.545**	10.519**	60.984**	0.675**	27.561**
Error	20	0.634	5.854	0.419	0.055	0.136	7.505	0.038	2.392

\*\*\* Significant at 0.05 and 0.01 probability levels, respectively

**Table 3. Mean performance  $\pm$  standard error for the studied characteristics, using the six populations data in two bread wheat crosses**

Character	Cross	Population					
		P <sub>1</sub>	P <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	BC <sub>1</sub>	BC <sub>2</sub>
Days to heading	1	124.4 $\pm$ 0.19	128.14 $\pm$ 0.23	116.96 $\pm$ 0.24	122.82 $\pm$ 0.25	123.94 $\pm$ 0.28	122.80 $\pm$ 0.25
	2	126.92 $\pm$ 0.23	128.14 $\pm$ 0.23	123.40 $\pm$ 0.23	123.59 $\pm$ 0.33	123.35 $\pm$ 0.36	124.78 $\pm$ 0.39
Plant height (cm)	1	97.34 $\pm$ 0.60	107.74 $\pm$ 0.65	110.56 $\pm$ 0.44	113.74 $\pm$ 1.02	102.88 $\pm$ 1.16	106.33 $\pm$ 1.07
	2	107.96 $\pm$ 0.68	107.74 $\pm$ 0.65	116.20 $\pm$ 0.75	112.64 $\pm$ 0.92	108.83 $\pm$ 1.19	109.07 $\pm$ 0.81
No. of spikes/plant	1	4.42 $\pm$ 0.25	5.64 $\pm$ 0.11	7.08 $\pm$ 0.26	8.11 $\pm$ 0.22	6.33 $\pm$ 0.25	7.62 $\pm$ 0.28
	2	6.46 $\pm$ 0.20	5.64 $\pm$ 0.11	7.40 $\pm$ 0.27	8.10 $\pm$ 0.18	6.52 $\pm$ 0.21	7.22 $\pm$ 0.21
Spike length (cm)	1	11.80 $\pm$ 0.08	11.72 $\pm$ 0.09	12.68 $\pm$ 0.09	11.51 $\pm$ 0.08	12.51 $\pm$ 0.10	12.12 $\pm$ 0.10
	2	12.46 $\pm$ 0.11	11.72 $\pm$ 0.09	13.02 $\pm$ 0.13	11.99 $\pm$ 0.07	12.30 $\pm$ 0.09	11.48 $\pm$ 0.09
No. of spikelets/spike	1	22.48 $\pm$ 0.12	22.2 $\pm$ 0.14	24.02 $\pm$ 0.13	22.48 $\pm$ 0.15	23.85 $\pm$ 0.17	23.42 $\pm$ 0.19
	2	21.00 $\pm$ 0.19	22.2 $\pm$ 0.13	25.30 $\pm$ 0.19	22.08 $\pm$ 0.17	22.26 $\pm$ 0.19	22.17 $\pm$ 0.19
No. of kernels/spike	1	53.54 $\pm$ 0.54	54.82 $\pm$ 0.63	56.76 $\pm$ 0.63	51.59 $\pm$ 1.09	54.90 $\pm$ 1.25	54.30 $\pm$ 1.22
	2	50.12 $\pm$ 0.57	54.82 $\pm$ 0.63	58.10 $\pm$ 0.65	50.51 $\pm$ 1.04	55.57 $\pm$ 1.20	50.84 $\pm$ 1.24
100-kernel weight (g)	1	4.14 $\pm$ 0.04	4.9 $\pm$ 0.04	5.11 $\pm$ 0.05	5.06 $\pm$ 0.06	5.05 $\pm$ 0.06	5.44 $\pm$ 0.07
	2	4.83 $\pm$ 0.04	4.9 $\pm$ 0.04	5.16 $\pm$ 0.06	5.70 $\pm$ 0.05	5.42 $\pm$ 0.07	5.63 $\pm$ 0.05
Grain yield/plant (g)	1	15.52 $\pm$ 0.28	17.5 $\pm$ 0.29	18.12 $\pm$ 0.34	17.74 $\pm$ 0.43	15.13 $\pm$ 0.58	18.38 $\pm$ 0.51
	2	13.93 $\pm$ 0.49	17.5 $\pm$ 0.29	19.20 $\pm$ 0.50	20.30 $\pm$ 0.53	16.50 $\pm$ 0.60	19.73 $\pm$ 0.62

**Table 4. Mid-parent and better parent heterosis (%), inbreeding depressing (I.D. %) and potence ratio (P) for the studied characteristics, using the six populations data in two bread wheat crosses**

Character	Heterosis (%)				(I.D.) %		(P)	
	Cross 1		Cross 2		Cross 1	Cross 2	Cross 1	Cross 2
	Mid-parent	Better parent	Mid-parent	Better parent				
Days to heading	-7.37**	-5.98**	-3.23**	-2.77**	-5.01**	-0.15	-4.97	-6.77
Plant height (cm)	7.82**	2.61*	7.74**	7.63**	-2.87	3.06	1.54	75.90
No. of spikes/plant	40.75**	25.53**	22.31**	14.55*	-14.57	-9.45	3.36	3.29
spike length (cm)	7.80**	7.46**	7.69**	4.49**	9.21**	7.91*	24.15	2.51
No. of spikelets/spike	7.52**	6.85**	17.13**	13.96**	6.42*	12.72	12.00	6.16
No. of kernels/spike	4.76	3.53	10.73**	5.98**	9.10	13.06	4.03	2.39
100-kernel weight (g)	12.96**	4.22	6.06*	5.30*	1.05	10.46**	1.54	8.42
Grain yield/plant (g)	9.71*	3.5	22.17**	9.71**	2.08	-5.72	1.62	1.95

Better-parent heterosis values were positive and significant for each of plant height (2.61% and 7.63%), number of spikes/plant (25.53% and 14.55%), spike length (7.46% and 4.49%) and number of spikelets/spike (6.85% and 13.96%) for Cross 1 and Cross 2, respectively. In addition, positive and significant better parent heterotic effects were detected for number of kernels/spike, 100-kernel weight and grain yield/plant in Cross 2 only (5.98%, 5.3% and 9.71%, respectively). On the other side, negative significant heterosis values were revealed for days to heading (-5.98% and -2.77%) in Cross 1 and Cross 2, respectively. These pronounced heterotic effects estimated for the most studied characters indicated the importance of such crosses in wheat breeding programs for improving grain yield/plant and its main components. Similar findings were reported by Salama (2000), Ahmed *et al* (2005), Abd- Allah (2007) and Dawwam *et al* (2007).

As shown in Table (4), positive significant inbreeding depression values were obtained for each of spike length (9.21% and 7.91%) in Cross 1 and Cross 2, respectively as-well-as for number of spikelets/spike (6.42%) in cross I only. On the other side, negative and highly significant inbreeding depression values were obtained for days to heading (-5.01%) in Cross 1 and for 100-kernel weight (-10.46%) in Cross 2. The information about inbreeding depression is useful to test the potentiality of F<sub>2</sub> seeds after reducing the heterosis in F<sub>2</sub> generation due to the reduction of heterozygosity caused by inbreeding. Thus, it is logical expectation that the

expression of heterosis in  $F_1$  may be followed by reduction in  $F_2$  performance for some of the studied traits especially those having high heterosis values. These results are in close agreement with those obtained by Salem and Abd El-Dayem (2006), Abd- Allah (2007), Abd El-Nour (2006 a and b) and Khaled (2007).

Potence ratios given in Table (4), indicated that over dominance is revealed for each of days to heading towards the earlier parent in Cross 1 and towards the higher parent for no. of spikes/plant, spike length and no. of spikelets/spike in the two crosses as-well-as for 100- kernel weight in Cross 1 only. Complete dominance of the higher parent was revealed for plant height and grain yield/ plant in Cross 1 only. Meantime complete dominance towards the earlier parent was obtained for days to heading in Cross 1 whereas complete dominance towards the higher parent was detected for no. of kernels/spike and 100-kernel weight in Cross 2. These results are in harmony with those found by Abd El-Aty *et al* (2005), Abd El-Nour (2006a), Hendawy and Seleem (2007) and Mahgoub (2007).

#### **Mode of gene action**

As shown in Table (5) the scaling tests (A, B, C and D) for the studied characters indicated that at least one of the non-allelic interactions is significant for all the studied traits except no. of kernels/spike in Cross 1, indicating the adequacy of the six parameters model to explain the type of gene action controlling the traits in the two crosses. Nature of gene action was estimated for all the studied traits in both crosses according to Gamble (1962).

As presented in Table (5) additive gene effects appeared to be important in the inheritance of spike length in both crosses, days to heading in Cross1 and number of kernels/spike in Cross 2 revealing positive and highly significant estimates and suggesting the potential for obtaining further improvement of these traits *via* selection in early generations. These results are in agreement with those previously revealed by Abd El- Nour and Moshref (2006), El-Sayed and El-Shaarawy (2006), Abd Allah (2007), Khaled (2007), Mahgoub (2007) and El-Shaarawy (2008).

On the other hand, negative and significant additive effect was obtained for plant height in Cross 1 only. Negative and highly significant additive effects were estimated for each of no. of spikes/ plant and grain yield/ plant in both crosses and for days to heading in Cross 2 only as-well-as for 100- kernel weight in Cross 1 only.

As presented in Table (5), positive significant dominance effects were detected for spike length in Cross 1 only and for no. of spikelets/spike and no. of kernels/spike in both crosses. Meantime, negative significant dominance effects were revealed for days to heading, plant height and no. of spikes/ plant in both crosses, and for grain yield/plant in Cross 2 only. From

**Table 5. Estimates of scaling tests and gene effects for the studied characteristics, using the six populations data in the two bread wheat crosses (1 and 2)**

Character	Crosses	Scaling test				gene effect					
		A	B	C	D	M	a	d	aa	ad	dd
Days to heading	1	-6.51**	-0.50	-4.80**	-1.10	122.81**	1.13**	-7.10**	2.20**	6.01**	-9.22**
	2	3.62**	1.98**	7.50**	-0.95**	123.59**	-1.43**	-2.23**	1.90**	-1.64**	3.70**
Plant height (cm)	1	2.14	5.64*	-28.76**	18.27**	113.74**	-3.44*	-28.52**	-36.54**	3.50	44.32**
	2	6.50**	5.80**	-2.46**	7.38**	112.64**	-0.24	-6.41**	-14.76**	-0.70*	27.06**
No. of spikes/plant	1	-1.15*	-2.52**	-8.22**	2.27**	8.11**	-1.29**	-2.49*	-4.54**	-1.37*	0.86
	2	0.82**	-1.40**	-5.50**	2.46**	8.10**	-0.70**	-3.57**	-4.92**	-2.22**	4.34**
Spike length (cm)	1	-0.55*	0.16**	2.83**	-1.61**	11.50**	0.39**	4.13**	3.22**	0.71*	-3.60**
	2	0.88**	1.78**	2.26**	0.20	11.99**	0.82**	0.53	-0.40*	0.90**	3.06**
No. of spikelets/spike	1	-1.19**	-0.61	2.81**	-2.31**	22.47**	0.43	6.30**	4.62**	0.58	-6.43**
	2	1.78**	3.16**	5.48**	-0.27	22.08**	0.09	4.24**	0.54**	1.38**	4.40**
No. of kernels/spike	1	0.50	2.97	15.51**	-6.01*	51.59**	0.59	14.61**	12.03**	2.46	-8.55
	2	-2.92**	11.24**	19.10**	-5.39**	50.51**	4.73**	16.41**	10.78**	14.16**	-2.46**
100-kernel weight (g)	1	-0.84**	-0.87*	-0.95**	-0.37*	5.05**	-0.39**	1.34	0.75**	-0.02	-2.47**
	2	-0.85**	-1.20**	-2.75**	0.35	5.70**	-0.21	-0.40	-0.70**	-0.35	-1.35
Grain yield/plant (g)	1	3.38*	-1.12	-1.69	1.97	17.74**	-3.24**	-2.35	-3.95	-4.51**	6.21**
	2	0.13	-2.76**	-11.37**	4.37**	20.30**	-3.23**	-5.25**	-8.74**	-2.89**	6.11**

\*\*\* significant at 0.05 and 0.01 probability levels, respectively

m = mean

a = additive effect

d = dominance effect

aa = additive × additive Interaction

ad = additive × dominance Interaction

dd = dominance × dominance Interaction



the previous results it could be concluded that the dominance gene effects had significant contribution in the inheritance of some traits under study and the selection should be achieved in advanced generations as homozygosity become fixable.

Positive and highly significant additive x additive type of epistasis was detected for each of days to heading, no. of spikelets/spike and no. of kernels/spike in the two crosses and for spike length and 100- kernel weight in Cross 1 only.

Negative significant additive x additive epistasis effects were estimated for each of plant height and no. of spikes/plant in the two crosses and for spike length, 100-kernel weight and grain yield/ plant in Cross 2 only.

Positive and highly significant dominance x dominance type of epistasis was detected for plant height and grain yield/plant in the two crosses and for days to heading, no. of spikes/plant, spike length and no. of spikelets/spike in Cross 2 only.

On the other side, negative and highly significant dominance x dominance effects were revealed for some characters in both crosses.

Positive significant additive x dominance type of epistasis was detected for spike length in the two crosses and for days to heading in Cross 1 only as well-as for no. of spikelets/ spike and no. of kernels/ spike in Cross 2 only. Meantime, negative significant additive x dominance type of epistasis was obtained for no. of spikes/ plant and grain yield/ plant in both crosses and for each of days to heading and plant height in Cross 2 only. Similar results were recorded by Abd El Aty *et al* (2005), El- Sayed and El-Shaarawy (2006), Abd Allah (2007) and El- Shaarawy (2008).

As presented in Table (6) broad sense heritability estimates were relatively high for most studied traits which ranged from 77.06% for spike length to 93.83% for no. of kernels/spike in Cross I and from 52.81% for spike length to 92.98% for no. of kernels/spike in Cross II. High broad sense heritability values were also reported by El-Marakby *et al* (1994). El- Sherbeny *et al* (2000), Ismail *et al* (2001), Hamada *et al* (2002), Mahgoub (2007).

As shown in Table (6), moderate to high narrow sense heritability percentages were estimated for most studied characters which ranged from 41.38% for grain yield/ plant in Cross 1 to 81.59% for days to heading in the same cross. Regarding Cross 2, narrow sense heritability estimates ranged from 41.25% for spike length to 77.58% for plant height. These results are in accordance with those reported by El-Marakby *et al* (1994), El- Sherbeny *et al* (2000), Ismail *et al* (2001), Abd El-Aty and katta (2002), Hamada (2003), Abd El- Nour (2006 a) and Khaled (2007).

The expected genetic advance upon selection as a percentage of the F<sub>2</sub> generation mean ( $\Delta g$  %) was calculated and presented in Table (6). The predicted genetic gain percentages are high for most studied traits ranging from 5.49% for days to heading to 79.70% for no. of spikes / plant in Cross 1

**Table 6. Heritability estimates in broad and narrow sense and predicted genetic gain from one cycle of selecting the highest 5% of the F<sub>2</sub> population for the studied characters, using the six populations data in the two bread wheat crosses**

Characters	Heritability %				Genetic response			
	Cross 1		Cross 2		Cross 1		Cross 2	
	Broad sense	Narrow sense	Broad sense	Narrow sense	Absolute	% of F <sub>2</sub> mean	Absolute	% of F <sub>2</sub> mean
Days to heading	83.52	81.59	89.93	68.33	6.74	5.49	9.68	7.83
Plant height (cm)	93.79	81.23	88.60	77.58	26.92	23.67	9.70	8.61
No. of spikes/plant	78.88	48.80	72.85	59.65	6.46	79.70	3.75	46.36
Spike length (cm)	77.06	47.56	52.81	41.25	1.30	11.34	0.97	8.17
No. of spikelets/spike	85.55	60.80	78.80	66.48	3.03	13.77	4.58	20.76
No. of kernels/spike	93.83	70.79	92.98	62.98	25.33	49.10	21.64	42.84
100-kernel weight (g)	88.30	74.11	81.09	61.19	1.53	30.36	0.56	9.83
Grain yield/plant (g)	89.84	41.38	86.95	66.82	2.15	12.16	14.54	71.64

compared to a range of 7.83% for days to heading and 71.64% for grain yield/plant in Cross 2. These results are in harmony with those obtained by Khattab and Afiah (1998), EL-Sayed and El-Shaarawy (2006), Abd El-Nour (2006 a) and Abd- Allah (2007).

These results indicated that selection could be effective in early generations when the additive gene effects play an important role in the inheritance of the characters under study while the selection will be more effective in the late segregating generations if the dominance gene effects had the greatest contribution of the inheritance of the desired characters and the selection procedure based on the accumulation of additive effects may be very successful in improving of these characters.

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## تقدير بعض الثوابت الوراثية لمحصول الحبوب وبعض مكوناته في هجينين من قمح الخبز

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تم إجراء التجارب الخاصة بهذه الدراسة في محطة للتجارب والبحوث الزراعية لكلية الزراعة جامعة عين شمس بشلقان - محافظة القليوبية خلال ثلاث مواسم زراعية 2004/2005 و 2005 / 2006 و 2006 / 2007 بهدف دراسة قوة الهجين والانخفاض النشئي عن التربية الذاتية ونوع ودرجة السيادة مع تحديد طبيعة الفعل الجيني للعوامل الوراثية المتحكم في وراثية صفة المحصول لنبات القمح وبعض الصفات المؤثرة عليه مع تقدير المكافئ الوراثي والتقدم الوراثي المتوقع بالانتخاب في هجينين من قمح الخبز .

في هذه الدراسة تم استخدام العشائر الستة (الآباء، هجن  $F_1$ ،  $F_2$ ، الهجن الرجعية) لهجينين من قمح الخبز وتم أخذ القراءات والقياسات على صفات ميعاد طرد السنابل، ارتفاع النبات ، عدد السنابل / نبات ، طول السنبل ، عدد السنبلات / سنبل ، عدد الحبوب / سنبل ، وزن الـ 100 حبة، محصول النبات الفردي من الحبوب لهجينين من القمح هما الهجين الأول بين الصنف المحلي جيزة 168 والصنف المستورد IB18 (2) الهجين الثاني بين الصنف المحلي سدس 1 ونفس الصنف المستورد IB18 .

أظهرت النتائج ان متوسط مجموع مربعات التباين كان عالي المعنوية لجميع الصفات تحت الدراسة ماعدا صفة عدد الحبوب / السنبل في الهجين الأول (جيزة 168 X IB18) . كما اوضحت النتائج وجود قوة هجين موجبة ومعنوية بالنسبة لمتوسط الأبوين وكذلك للأب الأيمن لمعظم الصفات المدروسة بينما كانت قوة الهجين سالبة ومعنوية بالنسبة لصفه عدد الأيام حتى طرد السنابل في كلا الهجينين .

كما اشارت النتائج ايضا الى وجود نقص ناتج عن التربية الذاتية في صفه طول السنبل وكذلك عدد السنبلات بالسنبل في الجيل الثاني مقارنة بالجيل الأول .

أظهرت النتائج وجود سيادة فائقة وتامة لكل الصفات تحت الدراسة ماعدا عدد الحبوب بالسنبلة في الهجين الأول وارتفاع النبات ومحصول الحبوب للنبات في الهجين الثاني.

أكدت النتائج وجود تفاعل غير اليئي في جميع الصفات تحت الدراسة مما يدل على ان النموذج الوراثي ذو الستة مقاييس كاف تصاب تباين الصفات الستة وأشارت النتائج الى ان التأثير المضيف كان معنوياً وكثير اهمية لصفات ميعاد طرد السنابل ، طول السنبلة وعدد الحبوب/السنبلة بينما كان التأثير الميادي معنوياً و مهما لصفات طول السنبلة وعدد السنبيلات بالسنبلة وعدد الحبوب بالسنبلة . وكذلك كان التفوق (التفاعل غير الاليسى) بين الجينات المتحركة في كل صفة معنوياً في معظم الصفات تحت الدراسة.

وقد تراوحت تقديرات قيم المكافء الوراثي بالمعنى الواسع من ٧٧,٠٦% لصفة طول السنبلة الى ٩٣,٨٣% لصفة طول النبات في الهجين الأول وتراوحت من ٥٢,٨١% لصفة طول السنبلة الى ٩٢,٩٨% لصفة عدد الحبوب بالسنبلة في الهجين الثاني بينما تراوحت قيم المكافء الوراثي بالمعنى الضيق من ٤١,٣٨% لصفة محصول الحبوب بالنبات الى ٨١,٥٩% لصفة ميعاد طرد السنابل في الهجين الأول وتراوحت من ٤١,٢٥% لصفة طول السنبلة الى ٧٧,٥٨% لصفة طول النبات في الهجين الثاني و كان التقدم الوراثي المتوقع نتيجة انتخاب احسن ٥% من عشيرة الجيل الثاني عاليا في معظم الصفات تحت الدراسة .

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