

## Genetical Analysis of some Quantitative Traits in Bread Wheat (*Triticum aestivum L.*)

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**Abstract:** Means of the six populations (P1, P2, F1, F2, BC1 and BC2) of the three wheat crosses; (1) Golan x Mexiback; (2) Sakha 202 x Wa 4767 and (3) Mexiback x Sakha 202 were used to estimate genetic parameters. Results revealed that epistatic gene effect cannot be ignored when establish a new breeding program to improve wheat populations for economic traits. The inheritance of all traits studied was controlled by additive and non-additive genetic effects, with greater values of dominance gene effect than the additive one in most cases. Heterosis relative to mid-parent and better parent was found to be significantly positive for grain weight /spike, no of grains /spike, grain yield / plant, biological yield and harvest index in the three crosses under study. The coincidence of sign and magnitude of heterosis and inbreeding depression was detected for most traits in the three crosses. The average degree of dominance as indicated by  $\sqrt{(H/D)}$  revealed existence of over-dominance towards the better parent for all traits except No. of spikes/plant in cross III. Narrow heritability sense estimates were generally found to be moderate in magnitudes in all cases. The highest estimates of narrow sense heritability associated with highest genetic advance for no of spikes / plant in the three crosses, grain weight/spike in crosses I and III indicated sufficient improvement of their traits variability.

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### 1. Introduction

The choice of selection and breeding procedures for genetic improvement of any crop is largely dependent on the knowledge of type and relative amount of genetic component and the presence of non-allelic inter-action for different characters in the plant materials under investigations.

Information of the type of gene action involved in the inheritance of a character is helpful in deciding the breeding procedures to be followed for plant improvement. To form a population with genetic variability for the characters studied, hybridization between genetically diverse parents must be done.

Plant breeders and geneticists frequently use generation mean analysis to obtain information of gene action controlling the economic traits in wheat (Nanda *et al.*, 1990; Gouda *et al.*, 1993; Moghaddam *et al.*, 1997; EL Hosary *et al.*, 2000 Khatab *et al.*, 2001; Esmail and Khatab, 2002; Akhtar and Chowdhry, 2006; Khaled, 2007 and Farag, 2009). Therefore, the present study was carried out to obtain information about gene action on yield and its components in the three wheat crosses. Introgression of desirable genes into Egyptian wheat following

backcross hybridization. Broaden the genetic germplasm base in Egyptian wheat.

### 2. Material and Methods

In the first season (2005-06), the four parental lines i.e, Sakha 202 and Mexiback (Egyptian varieties), Wa 4767/391/Ana and Golan (Syrian varieties) were intercrossed (by hand emasculation and pollination techniques) to produce three F1 crosses, (I) Golan x Mexiback; (II) Sakha 202 x Wa 4767 and (III) Mexiback x Sakha 202.

In the second season (2006-07), F1 plants of each cross were selfed and backcrossed to the two parents to obtain F2, BC<sub>1</sub> and BC<sub>2</sub> generations, respectively. Field experiments were carried out at the Experimental Farm of the National Research Center at shalkan EL-Kalyobia Governorate, Egypt.

Six generations 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> of the three wheat crosses were planted during the third season (2007-08) at Noubaria area in Al-Yashaa village (Al Behera Governorate, Egypt) under sprinkler irrigation in a randomized complete blocks design with three replicates in rows with 3m long and 20 cm apart with 10 cm between plants. Each parents

and  $F_{1,S}$  were represented by three rows, F2 and the two back cross generations ( $BC_1$  and  $BC_2$ ) by ten rows.

The data were recorded on twenty competitive plants randomly selected from each row of each replicate for the following eight traits:

Plant height (cm), no of spikes per plant, grain weight/spike (g), grains/spike, 100 grains weight (g), grain yield per plant (g), biological yield and harvest index.

The data were first subjected to test the differences between parental genotypes by applied "t" test for the studied characters before considering the biometrical analysis, as well as, the scaling test (A, B and C) were applied to detect the presence of epistasis according to Mather and Jinks (1982). Joint scaling test proposed by Cavalli (1952) as indicated by  $(\chi^2)$  was applied to test the adequacy of the genetic model controlling the studied characters. The simple genetic model (m, d, and h) was applied

when epistasis was absent, whereas in the presence of non-allelic interaction the analysis was proceeded to estimate the inter-action types involved using the six parameters genetic model i.e. (m, d, h, i, j, and l) according to Hayman (1958). Heterosis, inbreeding depression (%), F2 deviation (E1), backcross deviation (E2) heritability and genetic advance under selection were also estimated according to Miller *et al.* (1958).

### 3. Results and Discussion:

Table (1) shows the *t*-test and *f*-test of the three crosses under study. The range of performance for the various characters of the two parents was large except 100 grain weight,  $P_1$  excelled  $P_2$  in all characters. Genetic variance among F2 plants was found to be significant for all traits studied. Therefore, other parameters needed were estimated for all traits studied except 100 grain weight.

**Table (1): *f*-test and *t*-test in the three wheat crosses for all traits studied.**

Characters	Cross	<i>f</i> -test	<i>t</i> -test
Plant height	I	**	**
	II	**	**
	III	**	**
No of spikes per plant	I	**	**
	II	**	**
	III	**	**
Grain weight /spike	I	**	**
	II	**	**
	III	**	**
Grains/ spike	I	**	**
	II	**	**
	III	**	**
100 grains weight	I	NS	NS
	II	NS	NS
	III	NS	NS
Grain yield per plant	I	**	**
	II	**	**
	III	**	**
Biological yield	I	**	**
	II	**	**
	III	**	**
Harvest index	I	**	**
	II	**	**
	III	**	**

\* Significant at 0.05, \*\* significant at 0.01, N.S. = Insignificant.

Results of the scaling tests (A, B and C) and joint scaling test ( $\chi^2$ ) revealed the presence of non-allelic gene interaction for all traits studied in the three crosses except grain weight /spike in the cross 3, Table (2). Mather and Jinks (1982) reported that

significant results of scaling tests parameters indicate inadequacy of the additive - dominance model to interpret the gene effects involved in their materials i.e. epistatic contributions are important in the

inheritance of these traits in the particular materials investigated.

F2 epistatic deviation (E1), and backcross deviations (E2) were found to be significant for number of grains / spike and biological yield in the three crosses, plant height and grain yield per plant in cross I, grain weight /spike and harvest index in cross II, no. of spikes /plant and harvest index in cross III, indicating that the epistatic gene effects have a major

contribution in the inheritance of these attributes in these populations. The F2 deviations (E1) were accompanied by backcross deviations (E2) in most cases indicating the presence of epistasis and should require attention in wheat breeding programs. Insignificance of (E1 and E2) was found for grain weight/spike in cross III and harvest index in cross I indicating minor contribution of epistatic effects in the inheritance of these traits.

**Table (2): Estimates of epistatic deviation (E1 and E2), scaling tests and joint scaling test ( $\chi^2$ ), for all traits studied of the three wheat crosses.**

Characters	Cross	E1	E2	scaling test			$\chi^2$
				A	B	C	
Plant height	I	2.53	-3.85**	-5.0**	-2.7	10.1**	40.4**
	II	0.40	12.5**	-13.5**	-11.5**	1.6	85.0**
	III	-2.92**	0.75	-3.4	4.9*	-11.7**	35.1**
No. of spikes per plant	I	0.50	-0.20	-1.7*	1.3*	2.0*	18.2**
	II	1.35**	-0.7	-0.9	-0.05	5.4**	37.2**
	III	1.5**	2.10**	1.0	3.2**	6.0**	35.1**
Grain weight /spike	I	-0.28	-1.32**	-1.5**	-1.1**	-1.1	14.3**
	II	0.78**	1.31**	0.41	2.2**	3.13**	22.8**
	III	-0.22	-0.47	0.34	-1.27	-0.89	4.9
Grains/ spike	I	-2.95**	-23.1**	-36.9**	-9.3**	-11.8**	339.3**
	II	12.90**	13.30**	4.5	22.1**	51.8**	306.2**
	III	-4.20**	-6.90**	0.64	-14.5**	-16.8**	55.90**
Grain yield per plant	I	2.09**	3.99**	-1.67	9.64**	8.37**	111.4**
	II	4.15**	0.50	0.00	1.0	16.6**	94.70**
	III	1.99**	1.51	0.32	2.7*	7.96**	20.90**
Biological yield	I	16.35**	11.15**	4.7*	17.6**	65.5**	496.6**
	II	22.46**	27.72**	27.32**	28.12**	28.12**	772.4**
	III	18.95**	8.10**	-1.7	17.9**	17.9**	655.8**
Harvest index	I	-0.28	0.55	-3.9**	5.5**	-1.1	33.9**
	II	-5.15**	-13.1**	-14.8**	-11.2**	-20.6**	208.8**
	III	-3.55**	-3.90**	-0.3	-7.5**	-14.2**	63.7**

Cross (I) Golan x Mexiback; Cross (II) Sakha 202 x Wa 4767 and Cross (III) Mexiback x Sakha 202

\* Significant at 0.05, \*\* significant at 0.01

Results of types of gene action estimated by generation mean as genetic effects in six parameter model are presented in Table (3). Highly significance for the estimated values of mean effects (m) indicated that all the studied characters were quantitatively inherited. The additive gene effects (d) were significant and either positive or negative for all traits studied except no. of spikes/plant in all crosses, plant height and grain weight/spike in cross (I), grain yield /plant and harvest index in the crosses (II and III), suggesting the potential for obtaining further improvement of these traits by selection practice of their progenies.

The dominance gene effects (h) were found to be highly significant for most studied traits except

grain weight /spike in the three crosses, plant height and grain yield /plant in cross (III). The magnitude of additive gene effects (d) were small relative to the corresponding dominance effects (h) in most cases, suggesting that pedigree selection method is a useful breeding program for improving these populations. However, the negative value of (h) observed in most cases indicated that the alleles responsible for less value of the trait were dominant over the alleles controlling high value. These results are in harmony with those obtained by El-Hosary *et al.*, (2000), Esmail and Khattab (2002) and Salem (2006).

Significant epistatic additive x additive type of gene effects [i] was detected for plant height and biological yield in the three crosses; grain yield and

harvest index in crosses II and III; No. of spikes/plant and No. of grains/spike in the first and third crosses and grain weight/spike in cross I. Additive x dominance epistatic type of gene effects [j] was found to be significant for no. of grains / spike in all crosses under investigations ; no of spikes / plant,

biological yield and harvest index in the cross I and III; plant height in cross III and grain weight / spike in cross II. The negative sign of additive x dominance [j] interaction in most cases also suggested dispersion of genes in the parents.

**Table (3): Estimates of six parameter genetic models for all traits studied of the three wheat crosses.**

Characters	Cross	Gene effects					
		m	d	h	i	j	l
Plant height	I	105.5**	0.9	-28.4**	-17.8**	-1.2	25.5**
	II	114.5**	-4.5**	-26.0**	-26.6**	-1.0	51.6**
	III	101.3**	-6.2**	5.2	13.2**	-4.2**	-14.7**
No of spikes per plant	I	6.3**	-0.4	-4.4**	-2.4*	-1.5**	2.8
	II	7.2**	-0.4	-5.3**	-6.8**	-0.2	8.2**
	III	6.9**	-0.7	-1.6	-1.8	-1.1*	-2.4
Grain weight /spike	I	3.71**	-0.45	-0.49	-1.54*	-0.22	4.18**
	II	3.92**	-1.02*	0.19	-.052	-0.89*	-2.09
	III	3.90**	1.32**	1.85	-0.04	0.81	0.97
Grains/ spike	I	75.9**	-10.4**	-13.7**	-34.4**	-13.8**	80.6**
	II	80.3**	-17.0**	-12.7**	-25.2**	-8.8**	-1.4
	III	73.9**	13.67**	41.14**	2.94	7.57**	10.92
100 grains weight	I	4.76**	-0.02	0.41	0.52	0.48	0.26
	II	5.05**	-0.22	0.85	0.12	-.036	-2.37*
	III	4.96**	0.27	1.59*	1.14	-0.41	-1.37
Grain yield per plant	I	15.36**	-4.38**	3.59*	-0.4	-5.65**	-7.57*
	II	19.1**	-1.2	-7.1**	-15.6**	-0.5	14.6**
	III	15.87**	-1.19	2.82	-4.94*	-1.19	1.92
Biological yield	I	61.4**	-6.4**	-33.1**	-43.2**	-6.45**	20.9**
	II	64.1**	-2.0	-11.7*	-34.4**	-0.4	-21.0**
	III	59.7**	-5.2**	-44.7**	-59.6**	-9.8**	43.4**
Harvest index	I	29.9**	-2.3**	4.85*	2.2	-4.45**	-3.3
	II	30.9**	-1.7	-4.9*	-5.4*	-1.8	31.4**
	III	31.0**	-1.0	12.9**	6.4**	3.6**	1.4

Cross (I) Golan x Mexiback; Cross (II) Sakha 202 x Wa 4767 and Cross (III) Mexiback x Sakha 20

\* Significant at 0.05, \*\* significant at 0.01

Concerning the third type of epistatic effect i.e. dominance x dominance [l], highly significant effects were detected for plant height and biological yield in all crosses; grain weight /spike , no of grains /spike and grain yield /plant in cross I, no of spikes /plant ,grain yield /plant and harvest index in cross II. These results are in agreement with those obtained by Khattab *et al.*,(2001), Esmail and Khattab (2002), Mahgoub and Hamed (2006) , Khaled (2007) and Farag (2009).

The signs of (h) and (L) were opposite in most cases suggesting duplicate type of non-allelic interaction in these traits, while complementary epistasis type of gene effects gave similar signs of (h) and (L) for all other traits in the three crosses.

Results obtained here revealed the importance of epistatic types of gene effects in the inheritance of all traits studied, and cannot be ignored when establish a new breeding program to improve wheat populations for economic traits. The inheritance of all traits studied was controlled by additive and non-additive genetic effects, with greater values of dominance gene effect than the additive one in most cases. Farag (2009) reported that among the epistatic components, the dominance × dominance was greater in magnitudes than additive × additive and additive × dominance in most studied traits. When additive effects are larger than the non-additive, it is suggested that selection in early segregating generations would be effective, while, if the non-additive portion are larger than additive, the

improvement of the characters needs intensive selection through later generation.

Heterosis was expressed as the percentage deviation of F1 mean performance from the better or mid parent of different traits. Heterosis relative to mid-parent and better parent Table (4) was found to be significantly positive for grain weight /spike, no of grains /spike, grain yield / plant, biological yield and harvest index in the three crosses under study, and no. of spikes / plant in cross II, while, it was negative for plant height and no. of spikes / plant in crosses I and III. Moghaddam *et al.*, 1997; Khattab *et al.*, 2001; Esmail and Khattab, 2002; Akhtar and Chowdhry, 2006. found similar results. Positive heterotic effects relative to the mid parent and better

parent were found for most of the studied traits except for, plant height Farag (2009).

Concerning inbreeding depression, measured as reduction in performance of F2 generation due to inbreeding (Table-4) positive and highly significant values were obtained for harvest index in the three crosses, grain weight/spike and no of grains / spikes in crosses I and III. However, it was significantly negative in the three crosses for biological yield and number of spikes /plant. Significant negative inbreeding depression values were detected for plant height and grain yield/plant in cross 2; number of spikes/plant in cross 1, Farag (2009).

**Table (4): Estimates of Heterosis over better parent(BP%) and mid parent( MP%)Inbreeding depression (ID%),Degree of dominance( $\sqrt{H/D}$ ) Heritability in narrow sense(  $h^2 n$ ) and Genetic advance under selection (GS%) for all traits studied in the three wheat crosses.**

Characters	crosses	Parameters					
		BP%	MP%	ID%	$\sqrt{H/D}$	( $h^2 n$ ) %	GS%
Plant height	I	-11.4**	-9.75**	-7.98**	1.39	47.1	3.09
	II	2.5**	0.60	-0.09	1.69	37.3	1.98
	III	9.2**	-7.4**	-1.1	1.38	46.7	2.94
No. of spikes per plant	I	-39.2**	-29.4**	31.3**	1.02	51.4	17.3
	II	24.5**	29.4**	-9.1	1.12	48.5	16.7
	III	-3.5	3.8	-25.5**	0.93	53.6	17.0
Grain weight /spike	I	22.2**	30.3**	17.7**	1.21	38.7	11.9
	II	19.9*	25.3*	-12.3	1.59	29.6	9.4
	III	27.4**	59.7**	23.1**	1.27	38.3	12.7
Grains/ spike	I	24.1**	30.2**	14.9**	1.87	33.6	2.1
	II	6.2**	20.5**	-9.1**	1.99	31.1	3.1
	III	49.3**	64.7**	23.9**	1.69	37.8	2.7
Grain yield per plant	I	21.6**	35.3**	-0.7	1.94	29.8	6.6
	II	68.4**	79.4**	0.5	1.29	48.0	10.8
	III	77.6**	77.6**	10.6**	1.94	29.4	6.2
Biological yield	I	25.3**	25.4**	-22.6**	1.35	49.0	6.7
	II	66.1**	74.9**	-20.9**	1.56	42.0	7.4
	III	27.2**	44.7**	-23.9**	1.36	47.7	6.1
Harvest index	I	1.6	9.2**	5.1**	1.55	39.7	4.5
	II	1.1	1.4	14.9**	1.05	56.9	6.3
	III	5.3**	20.8**	17.9**	1.65	36.7	4.2

\* Significant at 0.05, \*\* significant at 0.01

The average degree of dominance as indicated by  $\sqrt{H/D}$  revealed existence of over-dominance towards the better parent for all traits except no. of spikes /plant in cross III. Esmail and Khattab (2002), Mahgoub and Hamed (2006) found the same results.

Heritability estimates in narrow sense were moderate for all studied traits in all crosses, ranged from 29.4% for grain yield/plant in cross III to 59.9% for harvest index in cross II indicating that these characters greatly affected by non-additive and environmental effects. These results were coincident with those reported by Abdel-Nour *et al.* (2005), El-Sayed and El-Shaarawy (2006), Salem (2006) and Khaled (2007).

The expected genetic advance as percent of F2 ranged from (1.98%) for plant height in cross II to (17.3%) for no of spikes/plant in cross1. The highest estimates of narrow sense heritability associated with highest genetic advance for no of spikes / plant in the three crosses, grain weight /spike in crosses I and III indicated sufficient improvement of their variability traits. These results indicated the possibility of practicing selection in early generations and obtain high yielding genotypes. Therefore, selection in those particular populations should be effective and satisfactory for successful breeding purposes. Abd El-Fattah and Mohammad (2009) found that genetic advance under selection as a percentage recorded 0.15 by biological yield (ton/ha.) character.

This information is of importance for wheat breeders to improve yield potential, release new wheat genotypes and enhancement of Egyptian wheat germplasm.

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