THE DETECTION OF THE DIFFERENT COMPONENTS OF VARIATION IN BREAD WHEAT (*Triticum aestivum* L.)

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ABSTRACT : *Six populations of the three wheat crosses i.e. Sakha 93 X Gemmieza 3, Sids 1 X Gemmieza 7 and Giza 170 X Gemmieza 7 were used to study (i) The potentiality of heterosis expression for grain yield and some of its components and (ii) Investigation of genetical behaviour, heritability and expected genetic advance under selection for grain yield and some of its components in the three wheat crosses.*

The obtained results can be summarized as follows

The genetic variances within F_2 populations were found to be highly significant for all traits studied in the three crosses under investigation. Highly significant useful heterosis was detected for heading date in the second cross Sids 1 X Gemmieza 7 and for 1000-grain weight in the first cross Sakha 93 X Gemmieza 3 (12.51%). Inbreeding depression values were found to be highly significant for mostly all traits studied in the three crosses under investigation. The F_2-deviation (E_1) found to be significant for all traits studied in the three crosses except number of productive tillers, main culm spike weight, main culm spike density, spike length and grain weight per spike in the second cross Sids 1 X Gemmieza 7 and main culm spike density and 1000-grain weight in the third cross Giza 170 X Gemmieza7. Backcross deviation (E_2) was found to be significant for number of both tillers and productive tillers per plant, number of grains per main culm spike, grain weight per main culm spike and grain weight per plant in the first and second cross and for heading date and main culm spike length in the first cross and for main culm spike weight in the second cross and 1000-grain weight in both second and third cross. The additive genetic effects (a) were found to be highly significant for mostly all traits studied in the three crosses under investigation. Dominance gene effects (d) were found to be highly significant in twenty three cases of the fourty two cases studied in the three crosses. Highly significant additive X additive (aa) were detected in twenty out of the fourty two cases studied. The epistatic type additive X dominance was found to be significant in seventeen cases of the fourty two cases studied. Dominance X dominance types of epistasis were detected to be significant in twenty seven cases of the fourty two cases studied in the three populations studied. Heritability estimates in both broad and narrow sense were found to be high in magnitudes for most traits studied in the three populations under investigation. High genetic advance under selection was found to be

associated with high narrow sense heritability estimates for main culm spike weight, main culm spike density, grain weight per spike and grain weight per plant in the three crosses studied and for plant height, number of productive tillers, main culm spike length, number of spikelets per main culm spike, grains per main culm spike, grain yield per main culm spike and spike length in the first cross and for plant height and spike length in the second cross and for number of productive tillers per plant, number of grains per main culm spike, grain yield per main culm spike and 1000-grain weight in the third cross.

Key words : Heterosis – gene action – wheat – heritability genetic advance under selection- six generations model

INTRODUCTION

Before the initiation of any breeding programme, the materials under investigation should be subjected to genetic analysis to find out the relative magnitude of various types of the genetic variances to formulate the most efficient breeding procedures to achieve quick and maximum improvement.

Improvement of yield in wheat through conventional breeding methods has reached a level at which phenomenal increase seem to be rather difficult. This warrant to think of some new breeding approach which might increase the yield considerably. The development of hybrid wheat is one way of increasing wheat production. Heterosis has long been observed in wheat, but to be of potential value, a hybrid should be more profitable than the best available commercial wheat varieties. The basic tools for hybrid wheat production, such as cytoplasmic male sterility, the fertility- restoring system and cross- pollination under field conditions are available (Wilson, 1968).

The objectives of the present study are to investigate the genetical behaviour using six generations model (Gamble 1962), heritability and expected genetic advance under selection for grain yield and some of its components in three selected crosses.

MATERIALS AND METHODS

The present experiment was carried out at the Experimental farm, Faculty of Agriculture, Minufiya University at Shebin El-Kom during the three successive seasons 2003/2004,2004/2005 and 2005/2006. Five common wheat varieties were used to establish the experimental materials for this investigation. Each two parents were crossed in 2003/2004 to obtain F_1 seeds of the three crosses. In 2004/2005 season, a part of the obtained hybrid seeds of the three crosses Sakha 93 x Gemmieza 3, Sids 1 x Gemmieza 7 and Giza 170 x Gemmieza 7, was sown and the rest being saved to the next season. F_1 plants were self-pollinated and backcrossed to both parents to obtain F_2 and backcross seeds. The six populations P_1, P_2, F_1, F_2, BC_1 and BC_2 were sown

using randomized complete block design with three replicates in 2005/2006 growing season. Each replicate comprised 25 rows of F_2, 10 rows of both BC_1 and BC_2 and 5 rows of any nonsegregated populations. The rows were 3 meters long with 20 cm. between rows and 10 cm. between plants within rows. Normal agricultural wheat practices were applied as usual for the ordinary wheat fields in the area. Heading date was recorded on an individual plant basis. At maturity, twenty guarded plants were randomly chosen from each row for subsequent measurements as follows:

Heading date, plant height, number of tillers per plant, number of productive tillers per plant, main culm spike length, number of spikelets per main culm spike, main culm spike weight, number of grains per main culm spike, grain weight per main culm spike, main culm spike density, spike length, grain weight per spike, grain yield per plant and 1000-grain weight.

Statistical analysis:

The t-test was used to examine the existence of genetic variance between parental means. Statistical procedures used herein would only be computed if the F_2 genetic variance was found to be significant. A one tail (F) ratio was used to examine the existence of genetic variance within the F_2 population. The degree of freedom for this test was considered as infinity. If calculated (F) ratio was equal to or larger than the tabulated ones, various biometrical parameters needed in this investigation would be computed. Heterosis (H), was expressed as percent increase of the F_1 mean performance above the respective better parent, i.e. $(F_1 - \overline{B.P})/ \overline{B.P}$ x 100. Inbreeding depression (I.d.) was measured as the average percent decrease of the F_2 from the $\overline{F_1}$. F_2 deviation (E_1), was calculated as the deviation of the F_2 mean performance from the average of F_1 and mid-parent value. Backcrosses deviation (E_2), was computed as the deviation of the two backcrosses performance from the F_1 and mid-parent performances. The validity of some estimates were examined by t-test. Nature of gene action was studied according to the relationships illustrated by Gamble (1962). In this procedure the means of the six populations of each cross were used to estimate six parameters of gene action. A test of significance of these parameters was conducted by the t-test. Heritability was estimated in both broad and narrow senses for F_2 generation, according to Mather's procedure (1949). The predicted genetic advance under selection (ΔG) was computed according to Johnson et al., (1955). This genetic gain represented as percentage of the F_2 mean performance was also obtained following (Miller et al., 1958).

RESULTS AND DISCUSSION

Varietal differences in response to their genetic background were found to be highly significant in most characters under investigation in each of the three crosses studied. The genetic variances within F_2 populations were also

found to be highly significant for all traits studied in the three crosses under investigation. Consequently, the various genetical parameters used in this investigation were estimated for all traits studied. The existence of the significant genetic variability in F_2 populations in spite of the insignificant differences between the parental cultivars for some characters in the three crosses, may suggest that the genes of like effects were not completely associated in the parental cultivars i.e. these genes are dispersed (Mather and Jinks , 1982). Means and variances of the six populations P_1, P_2, F_1, F_2, BC_1 and BC_2 for all traits studied in the three crosses are given in Table (1).

Heterosis was estimated as the percent increase of the F_1 mean performance above the respective better parent values. The expression of heterotic effects for all traits studied are presented in Table (2). Highly significant negative useful heterosis was detected for heading date only in the second cross Sids 1 X Gemmieza 7 which consider to be a potential advantageious materials in this concern. Highly significant useful heterosis was also detected by Hendawy (1994b), Hewezi (1996), EL-Sayed (1997), Hendawy (1998), Saad (1999), EL-Seidy and Hamada (2000), Comber (2001) and Seleem (2001). As for plant height, no useful heterotic effects were detected in the three crosses under investigation. Similar results were previously obtained by Hewezi (1996). As for 1000-grain weight, only Sakha 93 X Gemmieza 3 was found to exhibit highly significant useful heterosis which amounted to 12.51% over the respective better parent. Highly significant useful heterosis for 1000-grain weight was obtained by EL-Sayed (1997), Saad (1999), Afiah et al. (2000), EL-Hosary et al., (2000), Esmail and Kattab (2002), Hendawy (2003) and Seleem (2006).

Inbreeding depression is measured as the percent deviation of F_2 from F_1 mean performance. The estimates of inbreeding depression values are presented in (Table 2). Inbreeding depression values were found to be highly significant for nearly all traits in the three crosses under investigation. It is of interest to note that heterosis in F_1 generation should be followed by appreciable reduction in F_2 generation, since the two parameters are two sids of the same phenomena. The present results were found to agree with this expectation in most cases and that was previously obtained by Esmail and Kattab (2002), Darwish and Ashoush (2003) and Hendawy (2003). On the contrary, this expectation was not fulfilled in some cases, where significant heterosis and insignificant inbreeding depression were obtained. The contradiction between heterosis and inbreeding depression estimates could be due to the presence of linkage between genes in these materials (Van der Veen, 1959).

Genetic analysis of generation means to give estimates of additive (a), dominance (d) and the three epistatic effects (aa), (ad) and (dd) were obtained according to relationships illustrated by Gamble (1962) and

presented in Table (2). The estimated mean effects parameter (m), which reflects the contribution due to the over-all mean plus the locus effects and interaction of the fixed loci, were found to be highly significant for all traits in the three crosses. The additive gene effects (a) were found to be highly significant for all traits in the three crosses studied except main culm spike length, number of spikelets per main culm spike, main culm spike weight, number of grains per main culm spike, grain weight per main culm spike, main culm spike density, spike length and grain weight per plant in the first cross. Also, the additive genetic effects did not reach the significant level in the second cross for heading date, plant height, number of spikelets per main culm spike, spike length, grain weight per spike and 1000-grain weight, however, in the third cross, the estimates of the additive genetic effects were found to be insignificant for number of grains per main culm spike, grain weight per spike and grain weight per plant. It is of interest to mention that the presence of the additive genetic effect in the inheritance of these traits would suggest the potential for obtaining further improvement of the characters which exhibited highly significant estimates of additive effects (a). Dominance gene effects (d) were found to be highly significant for heading date and main culm spike weight in the three crosses under examination. Also, the estimated values of dominance gene effects were detected to be highly significant for plant height, main culm spike length, main culm spike density, spike length, grain weight per spike and grain weight per plant in the first cross. In the second cross, dominance gene effects were found to be significant for plant height and number of spikelets per main culm spike. Dominance gene effects were also found to be highly significant in the second and third cross for number of productive tillers, number of grains per main culm spike and 1000-grain weight. However, in the third cross only, the estimated values of dominance gene effects were detected to be highly significant for number of tillers per plant, spike length and grain weight per plant.

Highly significant additive X additive (aa) epistatic type was found for heading date, main culm spike weight and 1000-grain weight in the three crosses studied. The estimated values of additive X additive epistatic type were detected to be significant for main culm spike length, spike length and grain weight per plant in the first and third cross and for number of tillers per plant, number of productive tillers per plant and number of grains per main culm spike in the second and third cross and for plant height, main culm spike density and grain weight per spike in the first cross and for plant height and grain weight per main culm spike in the second cross only. The estimated values of additive X dominance (ad) types of digenic epitasis were found to be significant for heading date, plant height, main culm spike length, grain weight per spike and 1000-grain weight in the first cross

Table (1): Means (X) and variances (S²) of P1, P2, F1, F2, BC1 andBC2 populations of the three crosses 1 (Sakha 93 X Gemmieza 3) , 11 (Sids 1 X Gemmieza 7) , 111 (Giza 170 X Gemmieza 7), for all traits studied .

Characters		Cross 1						Cross2						Cross3					
		P_1	P_2	F_1	F_2	BC_1	BC_2	P_1	P_2	F_1	F_2	BC_1	BC_2	P_1	P_2	F_1	F_2	BC_1	BC_2
Heading date (days)	X	85.2	94.48	96.52	81.7	90.85	82.72	90.93	91.33	85.5	82.96	88.17	87.08	92.38	85.8	86.76	85.43	90.43	86.39
	S^2	6.71	5.12	0.973	35.18	21.72	28.72	2.13	4.19	2.74	23.39	20.72	17.91	2.74	3.82	2.19	22.36	15.02	14.78
Plant height (cm)	X	85.4	114.1	100.7	117.2	90.15	107.6	120.3	113.3	114.3	110.2	117.6	116.5	92.67	115.3	114.5	111.5	105.3	117.3
	S^2	6.32	7.27	14.96	125.6	62.69	73.03	5.15	4.85	7.83	149	67.5	127.1	12.37	8.27	6.95	88.78	45.45	85.9
Number of tillers per plant	X	4.1	4.63	4.77	6.93	5.8	6.75	7.6	5.37	5.97	6.18	7.78	6.18	5.83	5.9	5.37	7.07	6.49	4.92
	S^2	1.33	1.41	2.74	8.65	5.15	5.85	3.35	2.38	3.07	6.49	3.7	4.48	2.14	2.02	2.25	4.69	4.84	2.31
Number of productive tillers	X	3.87	4.63	4.27	6.36	5.37	6.17	6.8	4.87	5.53	5.51	7.08	5.78	5.47	5.4	5.07	6.95	5.73	4.62
	S^2	1.02	1.01	1.4	7.71	4.07	5.23	2.58	2.05	2.81	5.29	3.5	4.61	2.46	3.63	3.17	9.83	6.96	6.31
Main culm spike length (cm)	X	11.78	11.13	11.45	12.24	10.94	11.06	13.87	14.13	14.8	14.04	14.36	13.46	10.8	13.92	12.65	13.13	11.91	13.63
	S^2	0.309	0.344	0.144	2.12	1.2	1.34	0.447	0.926	0.683	1.661	1.18	1.57	0.66	0.519	0.441	1.51	1.52	0.603
No.of spikelets / main culm spike	X	20.43	20.67	20.57	21.38	21.15	21.23	23.07	24.13	24.07	23.26	23.28	23.78	21.85	24.57	23.17	23.69	22.73	24.2
	S^2	0.39	0.58	0.25	4.62	2.6	2.64	1.51	1.085	1.03	3.43	2.44	2.72	1.59	0.875	0.833	2.97	2.51	2.03
Main culm spike weight (gm)	X	3.13	3.32	3.45	4.13	3.62	3.45	4.53	5.3	4.71	4.89	5.44	6.08	4.01	5.09	4.32	4.64	4.12	4.55
	S^2	0.24	0.23	0.31	1.52	0.91	1.02	0.215	0.953	0.424	2.774	1.655	1.812	0.332	0.111	0.163	0.768	0.425	0.611
No.of grains per main culm spike	X	45.57	48.34	40.6	50.24	50.52	51.11	74.04	72.77	70.7	64.31	71.27	79.85	59.07	68.63	64.8	71.59	64.1	66.76
	S^2	53.29	54.24	53.83	317.9	198.6	182.9	78.52	110.2	82.42	191.9	207.6	106.6	31.86	33.76	32.17	137.7	95.09	83.15
Grain weight per main culm spike(gm)	X	2.45	2.44	2.45	3.08	2.97	2.91	3.8	4.39	3.55	3.5	4.06	5.06	2.81	3.86	3.31	3.56	3.45	3.72
	S^2	0.133	0.262	0.24	1.19	0.81	0.77	0.44	0.58	0.293	0.88	0.52	1.00	0.059	0.144	0.139	0.66	0.509	0.293
Main culm spike density	X	1.88	1.84	1.8	1.78	1.93	1.91	1.67	1.71	1.63	1.67	1.63	1.78	1.96	1.77	1.84	1.82	1.92	1.78
	S^2	0.013	0.003	0.001	0.042	0.021	0.028	0.007	0.008	0.004	0.024	0.018	0.013	0.026	0.004	0.009	0.031	0.012	0.003
Spike length (cm)	X	10.07	10.09	10.1	11.23	10.02	9.91	12.64	13.23	13.28	13.04	13	13.61	9.95	13.06	11.96	12.33	10.92	12.41
	S^2	0.595	0.335	0.329	2.68	1.53	1.8	0.88	0.65	0.66	2.38	1.4	1.76	0.51	0.562	0.554	1.301	1.42	0.665
Grain weight per spike (gm)	X	2.14	1.82	1.82	2.36	2.27	1.63	2.086	3.065	2.316	2.79	2.66	2.63	1.87	3.23	2.41	2.58	2.67	2.85
	S^2	0.126	0.153	0.153	0.85	0.63	0.59	0.598	0.71	0.84	2.62	1.71	1.83	0.054	0.186	0.138	0.74	0.571	0.347
Grain weight per plant (gm)	X	8.18	8.46	8.46	15.52	11.69	9.98	14.13	14.14	12.06	15.26	18.29	13.72	10.25	17.24	12.37	17.73	15.3	12.94
	S^2	4.52	12.21	12.21	102.2	62.63	69.04	17.42	16.19	15.7	52.18	35.04	37.13	11.09	24.73	27.02	76.55	48.4	62.72
1000 grains weight (gm)	X	53.96	53.71	60.71	60.76	58.66	54.8	47.38	59.98	50.23	55.9	61.45	63.96	46.86	56.12	50.97	50.43	54.25	57.34
	S^2	5.7	61.89	51.26	94.86	72.19	67.76	46.39	48.59	17.22	111.9	92.32	77.32	19.67	7.18	13.21	53.98	52.43	23.35

Table (2): Heterosis, inbreeding depression and gene action parameters in the three crosses 1 (Sakha 93 X Gemmieza 3) , 11 (Sids 1 X Gemmieza 7) , 111 (Giza 170 X Gemmieza 7) for all traits studied .

Characters	Cross	Heterosis %	Inbreeding depression %	F2 deviation E1	Backcross deviation E2	Genetic action parameter					
						M	a	d	aa	ad	dd
Heading date (days)	1	13.29**	15.35**	-11.48**	--12.80**	81.7**	8.13**	826.98**	20.3**	12.77**	5.22
	2	-5.97**	2.97**	-5.36**	-1.38	82.96**	1.09	13.03**	18.66**	1.29	-15.9**
	3	1.12*	2.35*	-4.73**	0.97	85.43**	4.04**	9.59**	11.92**	-0.75	-13.86**
Plant height (cm)	1	17.95**	-16.37**	16.98**	-2.78	125.55**	-17.4**	-72.52**	-73.5**	-3.05*	79.1**
	2	0.618	3.34*	-5.2**	3.3	110.2**	1.07	24.61**	27.38**	-2.4	-33.98**
	3	30.66**	2.61**	2.28*	4.16	115.5**	-12.05**	9.75	-0.78	-0.75	-7.54
Number of tillers per plant	1	3.02	-0.453**	2.36**	3.41**	6.93**	-0.95*	2.41	-2.62	-0.68	-4.21
	2	-47.76**	-55.67	1.36**	4.32**	6.18**	1.6*	1.495	3.2*	-0.325	-11.83**
	3	-8.98	-31.66**	1.45**	0.175	7.07**	1.57**	-5.96**	-5.46**	1.61**	5.11**
Number of productive tillers	1	-7.78	-48.95**	2.1**	3.02**	6.36**	-0.8*	-2.35	-2.36	-0.42	-3.68
	2	-18.68**	0.362	-0.173	1.5*	5.51**	1.3**	3.38**	3.68**	0.335	-6.67**
	3	-7.31	-37.08**	1.7**	-0.155	6.95**	1.11*	-7.47**	-7.1**	1.08*	7.41**
Main culm spike length (cm)	1	-2.8*	-7.16**	0.818**	-0.91**	12.12**	-0.12	-5.085**	-5.08**	-0.445*	6.89**
	2	4.74**	5.14**	-0.36*	-0.98	14.04**	0.9**	0.28	-0.52	1.03**	2.48*
	3	-9.12**	-3.8**	0.625**	0.53	13.13**	-1.72**	-1.15	-1.44*	-0.16	0.38
No. of spikelets / main culm spike	1	-0.484	-3.94**	0.82**	1.26	21.38**	-0.08	-0.74	-0.76	0.04	-1.76*
	2	-0.249	3.37**	-0.575**	-0.61	23.26**	-0.5	1.55*	1.08	0.03	0.14
	3	-5.7**	-2.24*	0.5*	0.55	23.69**	-1.47**	-0.94	-0.9	-0.11	-0.2-
Main culm spike weight (gm)	1	3.92	-19.71**	0.793**	0.395	4.13**	0.17	-2.16**	-2.38**	0.265	1.59
	2	-11.13**	-3.82	0.078	1.9**	4.89**	-0.64**	3.28**	3.48**	-0.255	-7.27**
	3	-15.13**	-7.41**	0.205*	-0.2	4.64**	-0.43**	-1.45**	-1.22**	0.11	1.62*

Table (2) : Cont.

Character	Cross	Heterosis %	Inbreeding depression %	F2 deviation E1	Backcross deviation E2	Genetic action parameter					
						m	a	d	aa	ad	dd
No.of grains per main culm spike	1	-16.03**	-23.74**	6.46**	14.06**	50.24**	-0.59	-4.07	2.3	0.81	-30.42*
	2	-4.51	9.04**	-7.74**	7.02*	64.31**	-8.58**	42.3**	45**	-9.22**	-59.03**
	3	-5.58**	-10.48**	7.27**	2.21	71.54**	-2.66	-23.69**	-24.64**	2.12	20.22*
Grain weight per main culm spike (gm)	1	0	-25.71**	0.633**	0.985**	3.08**	0.06	-0.555	-0.56	0.055	-1.41*
	2	-19.13**	1.41	-0.323**	1.48**	3.5**	-1**	3.7**	4.24**	-0.705**	-7.19**
	3	-14.25**	-7.55**	0.24*	0.525	3.56**	-0.27*	0.075	0.1	0.255*	-1.15
Main culm spike density	1	-4.26**	1.11	-0.05*	0.18	1.78	0.02	0.5**	0.56**	0	-0.92**
	2	-4.68**	-2.45	0.01	0.09	1.67	-0.15**	0.08	0.14	-0.13**	-0.32**
	3	-6.12**	1.09	-0.033	-0.005	1.82	0.14**	0.095	0.12	0.045	-0.11
Spike length (cm)	1	0.099**	-11.19**	1.14**	-0.25	11.23**	0.11	-5.04**	-5.06**	0.12	5.56**
	2	0.378	1.81	-0.068	-0.605	13.04**	0.39	-0.595	-0.94	0.685**	2.15
	3	-8.42**	-3.09*	0.598**	-0.135	12.33**	-1.49**	-2.21**	-2.66**	0.065	2.93**
Grain weight per spike (gm)	1	-14.95**	-29.67**	0.46**	0.1	2.36*	0.64**	-1.8**	-1.64**	0.48**	1.44*
	2	-24.47**	-20.47*	0.344	0.395	2.79**	0.03	-0.84	-0.58	0.52*	-0.217
	3	-25.39**	-7.05	0.1**	0.56	2.58**	-0.18	0.58	0.72	0.5	-1.84**
Grain weight per plant (gm)	1	0	-83.45**	7.13**	4.89**	15.52**	1.71	-18.6**	-18.7**	1.85	8.96
	2	-14.71*	-26.53**	2.16*	5.82**	15.26**	4.57**	0.905	2.98	4.58**	-14.61**
	3	-28.25**	-43.33**	4.67**	2.13	17.73**	2.36	-15.82**	-14.44**	5.86**	10.19
1000 grains weight (gm)	1	12.51**	-0.082	3.49**	-1.09	60.76**	3.86*	-9.25	-16.1**	3.74**	18.29*
	2	-16.26**	-11.29**	3.95**	21.5**	55.9**	-2.51	23.77**	27.2**	3.79*	-70.22**
	3	-9.18**	1.06	-0.8	9.13**	50.43**	-3.09**	5.35**	21.46**	1.54	-39.72**

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

and for main culm spike length, number of grains per main culm spike, grain weight per main culm spike, main culm spike density, spike length, grain weight per spike, grain weight per plant and 1000-grain weight in the second cross and for number of tillers per plant, number of productive tillers per plant, grain weight per main culm spike and grain weight per plant in the third cross.

Dominance X dominance (dd) epistatic effect was found to be significant for number of grains per main culm spike and 1000-grain weight in the three crosses and for plant height, main culm spike length, grain weight per main culm spike and main culm spike density in the first and second cross and for heading date, number of tillers and number of productive tillers per plant in the second and third cross and for spike length and grain weight per spike in the first and third cross. However, dominance X dominance epistatic effects were detected to be significant for number of spikelets per main culm spike in the first cross only and for main culm spike weight and grain weight per plant in the second cross only. It is worth to mention that the three epistatic types aa, ad and dd were found to be accompanied by significant estimates of both E_1 and E_2 epistatic scales in most traits studied and that would ascertained the presence of epistasis in such large magnitude as to warrant great deal of attention in wheat breeding programs. Also, concerning the relative importance of both additive and dominance gene action, it was found that the later was greater in magnitude in all traits studied in the three crosses under investigation (Table 2). Consequently, it could be concluded that the presence of both additive and non-additive gene action in mostly all traits studied would indicate that selection procedures based on the accumulation of additive effects should be successful in improving all traits under investigation. However, to maximize selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variances are involved would be preferred. Similar results were previously reported by EL-Hennawy (1995) and Hendawy (1998) for heading date, EL-Hosary *et al.*, (2000) and Moussa (2005) for plant height, EL-Sayed and Moshref (2005) for number of productive tillers, Comber (2001) for main culm spike length, EL-Hennawy (1991) for number of spikelets per main culm spike, Hewezi (1996) for number of grains per main culm spike, Comber (2001) for grain weight per main culm spike , El-Seidy and Hamada (2000) and Shahid *et al.*, (2005) for spike length, Hewezi (1996) and Moussa (2005) for grain weight per spike, EL-Sayed and Moshref (2005) and Moussa (2005) for grain weight per plant and Hendawy (1994b), Hamada (2003) and Moussa (2005) and for 1000-grain weight.

Heritability in both broad and narrow sense and genetic advance under selection were computed and the obtained results are presented in Table (3). High heritability estimates in broad sense were found for all traits studied in the three crosses under investigation except for number of productive tillers, main culm spike length, number of grains per main culm spike and grain weight per main culm spike in the second cross and; number of tillers per plant and spike length in the third cross, where moderate estimates of broad sense heritability were detected for these characters. High estimates of narrow sense heritability were found for main culm spike weight, main culm spike density and grain weight per spike in the three crosses under examination and; plant height, spike length and grain weight per plant in the first and second cross and; heading date in the second and third cross. Also, in the first and third cross, high heritability estimates in narrow sense were found for number of productive tillers, main culm spike length, number of grains per main culm spike and grain weight per main culm spike and for tillers number per plant and number of spikelets per main culm spike in the first cross and for 1000-grain weight in the third cross only. Moderate narrow sense heritability estimates were found for the rest of the traits studied except for main culm spike length, number of grains per main culm spike and grain weight per main culm spike in the second cross where low estimates of narrow sense heritability were detected (Table 3). The differences in magnitudes of both broad and narrow sense heritability estimates were found for most traits under investigation would ascertained the presence of both additive and non-additive genetic variance in the inheritance of most traits in the three crosses under investigation as previously obtained from gene action parameters study. The same conclusion previously reached by Hendawy (1994a) and Moussa (2005) for heading date, EL-Hennawy (1995), EL-Hosary et al., (2000) and EL-Sayed and Moshref (2005) for plant height, Hendawy (1994b) and EL-Hennawy (1995), for number of productive tillers, Comber (2001) for main culm spike length, Hewezi (1996) for number of spikelets per main culm spike, Hewezi (1996) for number of grains per main culm spike, Comber (2001) for grain weight per main culm spike , Shahid et al., (2005) for spike length, Seleem (1993) and Moussa (2005) for grain weight per spike, EL-Hennawy (1991), Hendawy (1994c) and Moussa (2005) for grain weight per plant and Eissa et al, (1994), EL-Hosary et al., (2000) and Shahid et al., (2005) for 1000-grain weight.

Genetic advance under selection which are given in (Table 3) show the possible gain from selection as percent increase in the F_3 over the F_2 mean when the most desirable 5% of the F_2 plants are selected. Genetic advance under selection ($\Delta G\%$) was found to be high in magnitude for number of tillers per plant, number of productive tillers per plant, main culm spike weight, number of grains per main culm spike, grain weight per main culm

Table (3):Heritability estimates, genetic advanced (Δg) and genetic advance expressed as a percent of F₂ means (Δg%) for all characters studied in the three crosses under investigation .

CHARACTERS	CROSS	HERITABILITY		GENETIC ADVANCE	
		Broad sense	Narrow sense	Δg	ΔG%
Heading date (days)	1	87.86	56.91	6.95	8.51
	2	90.07	72.89	7.26	8.75
	3	86.96	66.73	6.5	7.61
Plant height (cm)	1	92.42	91.9	21.21	18.09
	2	96.01	69.45	17.47	15.85
	3	89.64	52.05	10.1	9.06
Number of tillers per plant	1	78.84	72.83	4.41	63.64
	2	61.94	54.39	2.85	46.12
	3	54.23	47.55	2.12	29.99
Number of productive tillers	1	85.21	79.38	4.54	71.38
	2	53.11	46.61	2.21	40.11
	3	68.60	65.01	4.2	60.43
Main culm spike length (cm)	1	87.49	80.19	2.41	19.65
	2	58.74	34.62	0.919	6.55
	3	64.24	59.40	1.5	11.42
No.of spikelets / main culm spike	1	91.20	86.58	3.83	17.91
	2	64.73	49.48	1.89	8.13
	3	62.99	47.14	1.678	7.05
Main culm spike weight (gm)	1	82.08	73.03	1.86	45.04
	2	80.87	75.02	2.57	52.56
	3	73.70	65.10	1.18	25.43
No.of grains per main culm spike	1	83.08	79.99	29.38	52.51
	2	52.90	36.29	10.36	16.11
	3	76.32	70.52	17.05	23.82
Grain weight per main culm spike (gm)	1	82.21	67.23	1.51	49.03
	2	50.27	27.27	0.527	15.06
	3	82.73	78.49	1.31	36.8
Main culm spike density	1	86.51	83.33	0.352	19.78
	2	73.61	73.83	0.226	13.54
	3	74.51	68.63	0.249	13.68
Spike length (cm)	1	84.34	75.75	2.56	22.8
	2	69.33	67.32	2.14	16.41
	3	58.34	47.43	1.12	9.08
Grain weight per spike (gm)	1	83.06	56.47	1.07	45.34
	2	72.67	64.89	2.16	77.42
	3	82.97	75.95	1.35	52.17
Grain weight per plant (gm)	1	90.56	71.18	14.82	95.49
	2	68.50	61.69	9.18	60.16
	3	72.67	54.84	9.88	55.75
1000 grains weight (gm)	1	58.24	52.47	10.53	17.33
	2	66.57	48.19	10.5	18.78
	3	75.26	59.62	9.02	17.89

spike, main culm spike density, grain weight per spike, grain weight per plant and 1000-grain weight in the three crosses studied and; main culm spike length, number of spikelets per main culm spike and spike length in the first cross only and for spike length in the second cross and plant height in the first and second cross. Relatively low genetic advance were obtained for the rest of the traits studied (Table 3). Johnson *et al.* (1955) reported that heritability estimates along with genetic gain upon selection were more valuable than the former alone in predicting the effect of selection.

On the other hand, Dixit *et al.* (1970) pointed out that high heritability is not always associated with high genetic advance, but in order to make effective selection, high heritability should be associated with high genetic gain. In the present investigation, high genetic gain was found to be associated with high narrow sense heritability estimates for main culm spike weight, main culm spike density, grain weight per spike and grain weight per plant in the three crosses studied and for plant height, number of productive tillers, main culm spike length, number of spikelets per main culm spike, number of grains per main culm spike, grain weight per main culm spike and spike length in the first cross and for plant height and spike length in the second cross and for number of productive tillers per plant, number of grains per main culm spike, grain weight per main culm spike and 1000- grain weight in the third cross only. Therefore, selection for these traits in these three populations should be effective and satisfactory for successful breeding purposes, however, selection for the rest of the characters studied could be of less effectiveness.

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تقدير مكونات التباين المختلفة في قمح الخبز

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الملخص العربى

أجري هذا البحث في مزرعة كلية الزراعة بشبين الكوم جامعـة المنوفيـة بهـدف دراسة كل من قوة الهجين والسلوك الوراثي و درجة التوريث و التحسين الـوراثي المتوقـع بالانتخاب لصفات محصول الحبوب و بعض مكوناته .

و لتحقيق هذه الأهداف الثلاثة تم استخدام خمسة أصناف من القمح العادي و تم عمل التهجين بين كل صنفين منهم في موسم ٢٠٠٣/٢٠٠٤ و تم الحصول على العشائر الـستة المتمثلة في الأبوين والجيلـين الأول و الثاني و الجيلـين الـرجعيين و ذلـك فـي موسـم ٢٠٠٤/٢٠٠٥ لعدد ثلاثة هجن هي الأول سخا ٩٣ x جميزة ٣ و الثاني سدس ١ x جميزة ٧ و الثالث جيزة ١٧٠ x جميزة ٧ و قد تم تقييم هذه العشائر الستة لكل من الهجن الثلاثة فـي موسم ٢٠٠٥/٢٠٠٦ في تصميم قطاعات كاملة العشوائية في ثلاثة مكررات و قد تـم تحليـل البيانات باستخدام طريقة جامبل (١٩٦٢) لتقدير طبيعة الفعل الجيني في العشائر الستة و تـم دراسة كل من الصفات التالية :تاريخ طرد السنابل – طول النبات – عدد الفروع الجانبية علـى النبات – عدد الفروع المنتجة على النبات – طول سنبلة الساق الرئيسية – عدد السنيبلات في سنبلة الساق الرئيسية – وزن سنبلة الساق الرئيسية – عدد الحبوب في سنبلة الساق الرئيسية – وزن الحبوب في سنبلة الساق الرئيسية – كثافة سنبلة الساق الرئيسية – طول الـسنبلة – وزن حبوب السنبلة – محصول النبات الفردي – وزن الألف حبة و يمكـن تلخـيص النتـائج المتحصل عليها كما يلي :

وجود اختلافات وراثية معنوية في عشائر الجيل الثاني لكل الصفات المدروسـة فـي الهجن الثلاثة. كانت قوة الهجين مفيدة و عالية المعنوية لصفة ميعاد طرد السنابل في الهجـين الثاني و صفة وزن الألف حبة في الهجين الأول (٢١,٥١%). كان تأثير التربيـة الداخليـة

معنويا لمعظم الصفاتَ تحت الدراسة. كانت انحرافات الجيل الثاني معنوية لجميع الصفات فــي الهجن الثلاثة المستخدمة فيما عدا صفات عدد الفروع المنتجة ووزن سنبلة الساق الرئيسية و كثافة سنبلة الساق الرئيسية و طول السنبلة ووزن الحبوب في السنبلة في الهجيــن الثــاني و صفات كثافة السنبلة الرئيسية ووزن الألف حبة في الهجين الثالث جيــزة ١٧٠ x جميــزة ٧. كانت انحرافات الهجن الرجعية معنوية لصفات عدد الفروع و عدد الفـروع المنتجــة و عــدد الحبوب في سنبلة الساق الرئيسية ووزن الحبوب في سنبلة الساق الرئيسية و محصول النبات الفردي في الهجينين الأول و الثاني و كذلك لصفات ميعاد طرد السنابل و طول ســنبلة الــساق الرئيسية في الهجين الأول و لصفة وزن سنبلة الساق الرئيسية في الهجين الثاني ووزن الألف حبة في الهجينين الثاني و الثالث. كان فعل الجينات من النوع المضيف عالي المعنوية لمعظــم الصفات المدروسة في الهجن الثلاثة تحت الدراسة و كان تأثير الجينات من النــوع الــسيادي عالي المعنوية في ثلاثة و عشرون حالة من الاثنين و الأربعون حالة المدروسة فــي الهجــن الثلاث و كان فعل الجينات من النوع التفوقي (المضيف x المضيف) عالي المعنويــة فــي عشرون حالة كما كان الفعل الجيني التفوقي (المضيف x السيادي) معنويا في سبعة عشرة حالة و كذلك الفعل الجيني التفوقي (السيادي x السيادي) معنويا في سبعة و عشرون حالــة من الاثنين و الأربعون حالة المدروسة في العشائر الثلاثة المستخدمة في الدراسة . كانت قــيم الكفاءة الوراثية بمعناها العام و الدقيق عالية لمعظم الصفات المدروسة في العشائر الثلاثة تحت الدراسة. كانت القيم العالية للتحسين الوراثي المتوقع بالانتخاب مرتبطة مع التقديرات العاليــة لدرجة التوريث بمعناها الدقيق و ذلك في صفات وزن سنبلة الساق الرئيسية – كثافــة ســنبلة الساق الرئيسية – ووزن حبوب السنبلة و محصول النبات الفردي في الهجن الثلاثة المستخدمة في الدراسة و كذلك لصفات طول النبات ، عدد الفروع المنتجة ، طول سنبلة الساق الرئيسية ، عدد السنيبلات في سنبلة الساق الرئيسية ، عدد حبوب سنبلة الساق الرئيسية ، محصول سنبلة الساق الرئيسية و طول السنبلة في الهجين الأول و كذلك صفات طول النبت و طول السنبلة في الهجين الثاني و كذلك صفات عدد الفروع المنتجة ، عدد حبوب ســنبلة الــساق الرئيــسية ، محصول حبوب سنبلة الساق الرئيسية ووزن الألف حبة في الهجين الثالث.