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GENETIC VARIATION IN GRAIN YIELD AND ITS COMPONENTS IN THREE BREAD WHEAT CROSSES

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ABSTRACT

Three experiments were carried out using the seven populations (P_1, P_2, F_1, BC_1, BC_1, F_2 and F_3) method to study the genetic make up of three crosses namely Gemmiza 9 x Dovin-2, Sids 1 x Sakha 93 and Sakha93 x Dovin-2. Results indicated significant positive heterosis effects for grain and biological yields/plant in all cross. Significant positive heterosis were also evident for plant height, no. of spikes/plant and kernel weight in the last two crosses. Heterosis was negative and insignificant for no. of spikes/plant, no. of kernels/spike and kernel weight. On the other hand, significant negative heterotic effect was found for plant height in the first cross. Heterotic increase were also evident for plant height, no. of spikes/plant and 100-kernels weight; no. of kernels/spikes and 100-kernels weight seemed to account for the heterotic yield response observed in the second and third crosses, respectively. Inbreeding depression was significant for all studied characters except 100-kernels weight in the first cross; and for plant height and biological yield/plant in the second cross and 100-kernel weight in the third one. Over dominance towards the higher parent for grain and biological yield/plant was observed in the first cross; for all characters except no. of kernels/spike in the second cross, and for no. of spikes/plant in the third one. However, partial dominance towards the lower parent was estimated for plant height in the first cross, while, partial dominance was found for no. of kernels/spike in the first and second crosses; and no. of spikes/plant in the third one. Meanwhile, complete dominance was found for no. of spikes/plant and 100-kernel weight in the first cross. F_2 deviation (E_1) and backcross deviation (E_2) were found to be significant for most of the characters under investigation. Moreover high to moderate values of heritability estimates were found to be associated with moderate and low genetic advance as percentage of F_2 and F_3 means in most characters.

The additive gene effect (d) in six parameter model and (d*) in five parameter model were found to be significant for all characters in all crosses except for plant height in first cross, and for biological yield/plant in the second cross (Model 1) and 100-kernels weight in the third one. (Model 2) Suggesting the potential for obtaining improvements of most characters studied. Both dominance and epistasis were found to be significant for most of the attributes under investigation. These obtained results indicated that selection for the studied characters could be used in the early generations but would be more effective if postponed to late ones.

Key words: ***Wheat, Crosses, Heterosis, Heritability, Inbreeding depression, Gene action.***

INTRODUCTION

Wheat (*T. asetivum* L. em. Thell) is the most important cereal crop in Egypt. Increasing wheat production to narrow the gap between production and consumption is considered the main goal in Egypt as well as in several countries all over the world. Wheat breeders are always looking for means and sources of genetic improvements in grain yield and its components and other agronomic characters.

The Egyptian wheat cultivars have some what narrow genetic background. Selection among these cultivars for increasing grain yield and its components would not be very effective. Hybridization between the Egyptian wheat cultivars and exotic materials was carried out to increase genetic variability.

Genetic diversity among crossed parents enables the breeder to develop, through genetic recombination, heritable variability upon which selection can be practiced. Knowledge of genetic relationship among parents is essential for planning crosses that may lead to developing more promising lines. Crumpacker and Allard (1962) indicated that efficiency in breeding of self-pollinating crops depends, first, on accurate identification of hybrid combinations that have the potentiality of producing maximum improvements and second, on identifying in early segregating generations, superior lines among the progeny of the most promising hybrids. Therefore, information on the genetics of breeding materials could ensure selection gains and more genetic improvements.

Mosaad *et al* (1990) found that additive genetic effects are the prevalent type controlling days to heading, plant height and spike length. Moreover, Abul-Naas *et al* (1991) and Al Kaddoussi *et al* (1994) reported that dominance played an important role in genetic control for number of spikes/plant, number of kernels/spike, 100-kernel weight and grain yield/plant. On the other hand, El-Hosary *et al* (2000), found that grain yield and its components in an eight durum wheat parent-diallel cross, were controlled by both additive and non-additive gene effects. In addition concerning the heritability estimates, Gouda *et al* (1993) indicated that heritability values ranged from 14 % to 71% for grain yield. Meanwhile, Moustafa (2002) and Hendawy (2003) reported that heritability in narrow sense estimates for plant height, heading date and yield components were medium to high (more than 50%), and El-Sayed (2004) and Abdel Nour, *et al* (2005) reported that heritability in narrow sense estimates for yield and its components were medium to high.

This work was conducted to study the gene action, heritability and actual and predicated genetic gains from selection in three bread wheat crosses derived from four diverse bread wheat genotypes using seven populations of each cross.

MATERIALS AND METHODS

The three crosses used in the present study were derived from four widely diverse bread wheat cultivars. Names and pedigree of parental genotypes are given in Table (1). These genotypes were used to obtain the following three crosses: (1) Gemmiza 9 x Dovin-2, (2) Sids 1 x Sakha 93 and (3) Sakha 93 x Dovin-2.

Cultivar Dovin-2 from exotic materials (high yield and high bread quality) was crossed with the two local cultivars Gemmiza 9 and Sakha 93. Both are good yielders and have high number of spikes/plant and heavy kernel weight. Sids 1 (have high yield and high number of kernels/spike) was crossed with Sakha 93 (have high yield and high no. of spikes/plant).

The study was carried out at El-Giza Research Station during the four successive seasons from 2001/2002 to 2004/ 2005. In the first season (2001/2002), the parental genotypes were crossed to obtain F_1 seeds. In the second season (2002/2003), the hybrid seed of the three crosses were sown to give the F_1 plants. These plants were selfed to produce F_2 seeds. Crossing was repeated to ensure fresh hybrid seeds. The new hybrid seed and part of the F_2 seeds were stored under refrigeration for further use. In the third season (2003/2004), F_1, F_2 and parents seed were sown to produce more F_2 seeds, back cross seed (BC_1, BC_2) by crossing each F_1 to their respective parent F_2 plants were selfed to produce F_3 seeds.

In the fourth season (2004/2005) the seven populations P_1, P_2, F_1, BC_1, BC_2, F_2 and F_3 of each of the three crosses were evaluated using a randomized complete block design with three replications. Rows were 4 m long spaced 20cm. apart. The plants within rows were 10cm apart. Plot consisted of two rows for each parent, F_1 and backcross, five rows for F_2 generation and 20 rows for F_3 families selected from F_2 at season 2003/2004 from each cross. Data were recorded on individual guarded plants from each plot (50 plants from F_2, 40 plants from bulk F_3, 40 plants from each back crosses and 10 plants for parents and F_1) for plant height (cm), no. of spikes/plant, no. of Kernels /spike, 100-kernel weight (g), grain yield/plant (g) and biological yield/plant (g).

The amount of heterosis was expressed as the percentage increase of F_1 above better parent values. Inbreeding depression was calculated as the difference between the F_1 and F_2 means expressed as percentage of the F_1 mean. The T-test was used to determine the significance of these deviations where the standard error (S.E) was calculated as follows:

S.E for better parent heterosis
$\overline{F_1} - \overline{BP} = (V\overline{F_1} + V\overline{BP})^{1/2}$
and S.E for inbreeding depression
$\overline{F_1} - \overline{F_2} = (V\overline{F_1} + V\overline{F_2})^{1/2}$

In addition, F_2 deviation (E_1) and backcross deviation (E_2) were measured as suggested by Mather and Jinks (1971). Potence ratio (P) was also calculated according to Peter and Frey (1966).

Type of gene effects was estimated according to Gamble (1962) six parameters model and Singh and Chaudhary (1985) as follows:

The standard error of additive (d), dominance (h), additive x additive (i) additive x dominance (j) and dominance x dominance (l) were obtained by taking the squares root of respective variation 'T' test values are calculated upon dividing the effects of d, h, i, j and l by their respective standard error.

$m = \overline{F_2}$
$d = \overline{BC_1} - \overline{BC_2}$
$h = \overline{F_1} - 4\overline{F_2} - \frac{1}{2}\overline{P_1} - \frac{1}{2}\overline{P_2} + 2\overline{BC_1} + 2\overline{BC_2}$
$i = 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2}$
$j = \overline{BC_1} - \frac{1}{2}\overline{P_1} - \overline{BC_2} + \frac{1}{2}\overline{P_2}$
$l = \overline{P_1} + \overline{P_2} - 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2}$

The variances of these estimates were computed as follows:
and $V_m = V\overline{F_2}$
$Vd = V\overline{BC_1} + V\overline{BC_2}$
$Vh = V\overline{F_1} + 16V\overline{F_2} + \frac{1}{4}V\overline{P_1} + \frac{1}{4}V\overline{P_2} + 4V\overline{BC_1} + 4V\overline{BC_2}$
$Vi = 4V\overline{BC_1} + 4V\overline{BC_2} + 16V\overline{F_2}$
$Vj = V\overline{BC_1} + \frac{1}{4}V\overline{P_1} + V\overline{BC_2} + \frac{1}{4}V\overline{P_2}$
$Vl = V\overline{P_1} + V\overline{P_2} + 4V\overline{F_1} + 16V\overline{F_2} + 16V\overline{BC_1} + 16V\overline{BC_2}$

The standard error of additive – additive x dominance (d*), dominance (h), dominance x dominance (l) and additive x additive (I) is obtained by taking the squares root of respective variation 'T' test values are calculated upon dividing the effects of d*, h, l and i by their respective standard error.

$$m = \overline{F}_2$$
$$d^* = \tfrac{1}{2}\,\overline{P}_1 - \tfrac{1}{2}\,\overline{P}_2$$
$$h = 1/6\,(4\overline{F}_1 + 12\,\overline{F}_2 - 16\,\overline{F}_3)$$
$$l = 1/3\,(16\overline{F}_3 - 24\,\overline{F}_2 + 8\,\overline{F}_1)$$
$$i = \overline{P}_1 - \overline{F}_2 + \tfrac{1}{2}\,(\overline{P}_1 - \overline{P}_2 + h) - \tfrac{1}{4}\,l$$

and $V_m = V\overline{F}_2$

$$Vd^* = \tfrac{1}{4}\,(V\overline{P}_1 + V\overline{P}_2)$$
$$Vh = 1/36\,(16V\overline{F}_1 + 144V\overline{F}_2 + 256V\overline{F}_3)$$
$$Vl = 1/9\,(256\,V\overline{F}_3 + 576\,V\overline{F}_2 + 64V\overline{F}_1)$$
$$Vi = V\overline{P}_1 + V\overline{F}_2 + \tfrac{1}{4}\,(V\overline{P}_1 + V\overline{P}_2 + Vh) + 1/16\,Vl$$

Heritability in broad and narrow sense was calculated according to Mather (1949) and parent off-spring regression according to Sakai (1960). Furthermore, the predicted and actual genetic advance (Δg) from selection were computed according to Johanson *et al* (1955).

The genetic gain as percentage of the F_2 and F_3 mean performance (Δg %) was computed using the method of Miller *et al* (1958).

Table 1. The name, pedigree and origin of the four parental bread wheat cultivars.

Genotype	Pedigree	Origin
Gemmiza 9	Ald"S"/Huac"S"//CMH74A.630/SxcgM4583-5GM–1 GM - 0GM	Egypt
Dovin-2	CM84655-02Ap-300AP-300L-3AP-300L3AP-0L-0AP	ICARDA
Sids 1	HD21/Pavon"S"// 1158.57/MayA74"S"	Egypt
Sakha 93	Sakha92/TR81032658871-1S-2S-1S-0S	Egypt

RESULTS AND DISCUSSION

Varietal differences were significant in most characters under investigation. The F_2 genetic variances were also significant for all studied characters in the three crosses. Therefore, the different biometrical parameters used in this investigation were estimated. Means and variances of the seven populations P_1, P_2, F_1, BC_1, BC_2, F_2 and F_3 for the characters studied in the three crosses are presented in Table (2). Heterosis relative to the better parent, inbreeding depression percentage, potence ratio (P), E_1, E_2 and heritability estimates in each cross for the six studied characters are given in Table (3).

Significant positive heterosis was found for grain and biological yields/plant in the first cross; all characters except no. of kernels/spike in the second cross and no. of spikes/plant alone in the third one. Significant negative heterosis was found for plant height in the first cross. Similar results were reported by Gautam and Jain (1985), Moshref (1996), Hendawy (1998), El-Hosary *et al* (2000), Moustafa (2002), Hendawy (2003), El-Sayed *et al* (2004) and Abdel Nour, Nadya *et al* (2005).

Table 2. Means $(\bar{x})$ and variances (S^2) for some studied characters using the five populations (P_1, P_2, F_1, F_2 and bulk F_3 families) for three bread wheat crosses.

Characters	parameter	Gemmiza 9 x Dovin-2						
		P_1	P_2	F_1	BC_1	BC_2	F_2	$F_{3\ bulk}$
Plant height (cm)	X	110.4	113.8	110.8	106.9	108.9	108	105.4
	S^2	15.55	10.63	18.27	81.88	94.85	128.05	34.29
No. of spike s/plant	X	20.0	25.0	24.9	17.69	20.36	23.0	21.57
	S^2	5.53	4.17	4.31	12.37	22.99	29.66	19.38
No. of kernels /spike	X	68.8	78	74.1	74.06	64.79	68.87	72.5
	S^2	15.75	16.7	20.94	99.43	140.75	193.94	121.41
100-kernel weight (g)	X	5.02	4.5	5.01	4.52	5.16	5.02	4.21
	S^2	0.029	0.018	0.024	0.129	0.142	0.214	0.133
Grain yield/plant (g)	X	50.8	61.88	68.2	58.63	63.71	62.93	59.71
	S^2	16.17	27.77	31.12	132.64	288.3	361.67	173.83
Biological yield/plant (g)	X	186	193.75	222	183.75	215	213.33	187.86
	S^2	46.32	50.54	58.95	188.29	460.15	572.71	292.45
		Sids 1 x Sakha 93						
Plant height (cm)	X	119.8	106.6	125.2	124.7	116.53	124.3	124.19
	S^2	6.72	7.56	6.7	92.41	59.04	132.7	119.53
No. of spike s/plant	X	18.5	22.5	24.5	17.28	20	22	18.06
	S^2	4.7	5.83	7.84	14.47	54.19	59.2	23.1
No. of kernels /spike	X	80.75	72.58	79.2	75.33	62	72.4	72.19
	S^2	14.28	10.86	20.91	111.12	191.89	256.35	156.99
100-kernel weight (g)	X	4.19	4.47	4.76	4.65	4.91	5.25	4.17
	S^2	0.056	0.042	0.032	0.099	0.298	0.317	0.135
Grain yield/plant (g)	X	52	60.25	65.05	53.72	59.8	56.5	54.38
	S^2	7.04	11.67	12.89	140.77	235.3	344.14	184.04
Biological yield/plant (g)	X	191.25	164.17	227	178.33	174.67	216	195.63
	S^2	89.67	77.54	106.32	823.04	1579.28	1916.78	1771.76
		Sakha 93 x Dovin-2						
Plant height (cm)	X	106.6	133.8	122.7	94.8	122	111.52	114.5
	S^2	7.56	10.06	15.17	119.05	124.97	171.07	147.42
No. of spike s/plant	X	22.5	25	24.5	19.33	22.58	21.32	22.85
	S^2	5.83	6.53	5.68	11.85	22.91	24.22	21.98
No. of kernels /spike	X	72.58	81.4	93.2	76	70.17	70.2	67.25
	S^2	10.86	27.41	18.6	126.48	97.99	190.31	170.82
100-kernel weight (g)	X	4.46	4.57	4.94	4.73	5.39	5.23	4.77
	S^2	0.042	0.062	0.08	0.314	0.302	0.426	0.254
Grain yield/plant (g)	X	60.25	64.82	71.2	63.92	71.67	62.76	62.72
	S^2	11.67	23.01	30.06	304.58	373.11	444.67	278.67
Biological yield/plant (g)	X	164.17	194	228	186.67	214.17	176	193
	S^2	77.54	88.42	101.1	797.2	832.98	1175.84	1113.89

Table 3. Heterosis, potence ratio, inbreeding depression and heritability for studied characters of three bread wheat crosses.

Characters	Cross	Heterosis % over B.P	Potence ratio (P)	Inbreeding depression %	E1	E2	Heritability %		
							Broad sense	Narrow sense	Parent-off spring regression
Plant height (cm)	1	-2.64*	-0.754	2.53*	-3.445**	-7.08**	85.73	64.83	76.71
	2	4.55**	1.828	0.719	5.118**	2.89*	94.95	85.65	90.19
	3	7.82**	3.465	9.11**	-4.925**	-16.06**	91.13	59.84	76.72
No. of spikes/plant	1	-0.4	0.96	7.63**	-0.7	-9.355**	87.64	82.96	85.3
	2	8.89**	2.00	10.2**	-0.5	-7.722**	89.66	84.01	86.83
	3	2.0	0.6	12.98**	-2.805**	-6.334**	76.55	55.14	65.16
No. of kernels/spike	1	-5.0	0.152	7.06**	-4.883**	-8.651**	89.2	77.78	84.3
	2	-1.92	0.62	8.59**	-5.533**	-18.537**	91.85	83.96	88.99
	3	14.49**	3.677	24.68**	-14.896**	-24.025**	90.23	81.86	85.95
100-kernel weight (g)	1	-0.26	0.95	-0.16	0.132**	-0.097	88.88	73.33	81.2
	2	6.61**	3.169	-10.27**	0.705**	0.466**	89.91	71.29	78.86
	3	8.23**	8.52	-5.75**	0.497**	0.66**	81.22	59.86	72.77
Grain yield/plant (g)	1	10.22**	2.142	7.73**	0.661	-2.199	93.04	85.25	89.14
	2	8.71**	2.273	13.74**	-4.31**	-8.103**	96.93	91.49	94.21
	3	9.84**	3.791	11.85**	-4.108*	1.85	93.24	49.5	72.32
Biological yield/plant (g)	1	14.58**	8.29	3.91**	7.393**	-13.125**	90.93	88	89.47
	2	18.69**	3.64	4.85	13.645**	-51.709**	94.45	75.46	85.35
	3	17.53**	3.28	22.81**	-27.54**	-6.24	91.41	62.38	77.41

* and ** significant at 0.05 and 0.01 probability levels respectively .

Number of spikes/plant, number of kernels/spike and kernel weight are the main components of grain yield/plant. Hence, heterotic increase if found in one or more of these attributes with others attributes being constant would lead to favorable yield increase in hybrids. The lack of significant in heterosis of no. of kernels/spike in the first cross and no. of spikes/plant in the second one could be due to the lower magnitude of the non-additive gene action. These results are in agreement with Amaya *et al* (1972), Ketata *et al* (1976) and El-Rassas and Mitkees (1985).

The pronounced heterotic effect detected for no. of spikes/plant and kernels weight in the second cross (Sids 1 x Sakha 93); and no. of krnels/spike and kernels weight in the third one (Sakha 93 x Dovin-2) would be of interest in a breeding program for high yielding ability.

The potence ratio indicated over-dominance towards the higher parent for grain and biological yield/plant in the first cross and for all characters except no. of kernels/spike in the second cross and except no. of spikes/plant in the third one. Complete dominance was found for no. spikes/plant and kernels weight in the first cross. There were partial dominance towards the higher parent for no. of Kernels/spike in the first and second crosses, and no. of spikes/plant in the third one. Meanwhile, partial dominance towards the lower parent was found for plant height in the first cross. These results are in harmony with those obtained by Ketata *et al* (1976), Jatasra and Paroda (1980), Rady *et al* (1981), Mosaad *et al* (1990), Abul-Naas *et al* (1991), Al-Kaddoussi *et al* (1994), Moustafa (2002) and Hendawy (2003).

Significant inbreeding depression was found for all characters except kernel weight in the first cross; plant height, kernel weight and biological yield/plant in the second cross and kernel weight in the third one. However, significant negative inbreeding depression (inbreeding gain) was detected for kernel weight in the three crosses. This is a valid result, since the expression of heterosis in F_1 may be followed by considerable reduction in F_2 performance. The obtained results for most cases were in harmony with those obtained by Gautam and Jain (1985) and Khalifa *et al* (1997).

Significant heterosis and insignificant inbreeding depression were obtained for plant height in the second cross. Moreover, significant positive heterosis and significant negative inbreeding depression for kernel weight in the second and third crosses were detected. 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).

Significant positive F_2 deviation were indicated for kernel weight and biological yield/plant in the first cross, for plant height, kernel weight and biological yield/plant in the second cross and for kernel weight in the third one. Meanwhile, significant negative values were obtained for plant height and no. of kernels/spike in the first cross, for no. of kernels/spike and grain yield/plant in the second cross and for all characters except 100-kernel weight in the third one. These results may refer to the contribution of epistatic gene effects in the performance of these characters.

On the other hand, significant F_2 deviations were detected for no. of spikes/plant in the first and second crosses; and for grain yield/plant only in the first one. This may indicate that the epistatic gene effects have minor contribution in the inheritance of these characters.

Backcross deviations (E_2) was significant for all characters in all crosses except for kernel weight and grain yield/plant in the first cross; and for grain and biological yields/plant in the third one. These results would ascertain the presence of epistasis in such large magnitude as to warrant great deal of attention in breeding programs.

Heritability in both broad and narrow senses, and between generations (parent off-spring regression) are presented in Table (3). High heritability values in broad sense were detected for all studied characters except for plant height in the first cross; no. of spikes/plant and 100-kernels weight in the third cross where moderate broad sense heritability estimates were detected.

High to moderate estimates of narrow sense heritability and parent offspring regression was found for all studied characters in all crosses. The differences in magnitude of both broad and narrow sense and parent offspring regression heritability estimates for all studied characters would ascertained the presence of both additive and non-additive gene effects in the inheritance of these characters. This conclusion was also confirmed by estimates of gene action parameter. Similar results were obtained by Jatasra and Paroda (1980), Mosaad *et al* (1990), Gouda *et al* (1993), Moshref (1996), El-Sayed (2004) and Abdel Nour *et al* (2005).

Table (4) shows the predicted versus actual gain for all studied characters. The actual genetic advance (actual gain Δg %) regard from moderate to high for all studied characters in all crosses (Table 4). These results indicate the possibility of practicing selection in early generations to enhance these characters and hence selecting high yielding genotypes.

Table 4. Predicted and actual gain from selection for all characters in three bread wheat crosses.

Character	Cross	Predicted gain		Actual gain	
		g	% of F_2	g	% of F_3
Plant height (cm)	1	15.11	13.99	9.25	8.78
	2	20.32	16.35	20.31	16.36
	3	16.12	14.46	19.19	16.76
No. of spikes/plant	1	9.308	40.47	7.74	35.86
	2	13.31	60.52	8.6	47.59
	3	5.59	26.22	6.29	27.54
No. of kernels/spike	1	22.313	32.40	19.13	26.39
	2	27.69	38.25	22.97	31.82
	3	23.263	33.14	23.14	34.41
100-kernel weight (g)	1	0.699	13.94	0.61	14.5
	2	0.827	15.75	0.597	14.32
	3	0.805	15.4	0.756	15.86
Grain yield/plant (g)	1	32.76	52.05	24.21	40.54
	2	43.96	61.88	26.33	48.41
	3	21.503	34.26	24.87	39.64
Biological yield/plant (g)	1	43.38	20.34	31.52	16.78
	2	68.057	31.51	74.01	37.83
	3	44.06	25.04	53.22	27.5

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.

Nature of gene action was determined according to Gamble (1962) six parameters model (Table 5). The estimated mean effect parameter (m), which reflects the contribution due to the over all mean plus the locus effect and interactions of the fixed loci, was found to be highly significant. The additive gene effect (d) was significantly positive for plant height and biological yield/plant in the second cross and for no. of kernels/spike in all crosses. These results suggest the potential for obtaining further improvement for these characters by using pedigree selection program. Similar results were obtained by Amaya *et al* (1972), Hendawy (1998), El-Hosary *et al* (2000), Moustafa (2002), Hendawy (2003), El-Sayed (2004) and Abdel Nour *et al* (2005). On the other hand significant negative additive effect (d) was obtained for all characters except for no. of kernels/spike in the first and third crosses and for no. of spikes/plant, kernel weight and grain yield/plant in the second one. Dominance gene effects (h) was significant for no. of spikes/plant, kernel weight and biological yield/plant in the first and second crosses and for no. of kernels/spike, grain yield/plant and biological yield/plant in the third one.

Table 5. Gene action parameters by using two models for all studied characters in three crosses of bread wheat.

Characters	Cross	Six parameters model							Five parameters model			
		m	d	h	i	j	l	m	d*	h	i	l
Plant height (cm)	1	108**	-2.05	-1.67	0.38	0.34	14.54*	108**	-1.71**	8.907**	6.777*	-6.613
	2	124.3**	8.189**	-2.655	-14.69**	1.604	8.91	124.3**	6.585**	0.901	2.037	1.797
	3	111.52**	-27.17**	0.09	-12.42*	-23.56**	44.54**	111.52**	-3.61**	-0.493	-20.224**	45.707**
No. of spikes/plant	1	23**	-2.669**	-13.51**	-15.91**	-0.169	34.62**	23**	-2.5**	5.08**	-2.321	-2.555
	2	22**	-2.722**	-9.444**	-13.444**	-0.722	28.888**	22**	-2.0**	12.165**	-3.0	-14.331*
	3	21.32**	-3.25**	-0.698	-1.448	-2.0**	-14.116**	21.32**	-1.25**	1.96	-3.01*	16.64**
No. of kernels/spike	1	68.867**	9.277**	2.93	2.23	13.877**	15.072	68.867**	-4.6**	-6.199	-16.099**	33.331**
	2	72.4**	13.33**	-12.407	-14.94*	9.247**	52.013**	72.4**	-4.084**	5.099	10.732*	17.003
	3	70.2**	5.833**	27.742**	11.534*	10.241**	36.515**	70.2**	-4.408**	23.2**	-1.83	45.6**
100-kernel weight	1	5.015**	-0.652**	-0.473*	-0.72**	-0.912**	0.914**	5.015**	0.26**	2.144**	2.417**	-4.32**
	2	5.25**	-0.253**	-1.488**	-1.886**	-0.117	0.954**	5.25**	-0.136**	2.559**	1.856**	-7.071**
	3	5.226**	-0.654**	-0.242	-0.668*	-0.604**	-0.652	5.226**	-0.05	1.04**	0.514**	-3.216**
Grain yield/plant (g)	1	62.93**	-5.089*	4.82	-7.042	0.449	11.439	62.93**	-5.548**	12.08*	-5.608	-24.075
	2	56.5**	-6.078**	10.419	1.044	-1.953	15.162	56.5**	-4.125**	11.653*	-5.972	12.693
	3	62.76**	-7.75**	28.793**	20.128*	-5.465*	-23.826	62.76**	-2.285**	5.653	-7.582	22.453
Biological yield/plant (g)	1	213.33**	-31.25**	-23.695*	-55.82**	-27.375**	82.07**	213.33**	-3.875**	73.7**	33.825**	-112.72**
	2	216**	3.666	-108.709**	-158**	-9.876	261.417**	216**	13.542**	61.667**	-0.208	79.333*
	3	176**	-27.5**	146.596**	97.68**	-12.584**	-85.193**	176**	-14.916**	-11.333	90.416**	232**

The significance of these components indicate that both additive and dominance gene effects are important in the inheritance of these characters. Therefore, selecting desired characters could be practiced in the early generations but would be more effective in late ones (Sheab El-Din 1993).

Additive x additive) type of epistasis (i) was detected to be significant for no. of spikes/plant, kernel weight and biological yield/plant in the first cross, and for all characters in the other two crosses except for grain yield/plant and for no. of spikes/plant in the second and third crosses, respectively.

Significant additive x dominance (j) appeared for all characters in the third cross, for no. of kernels/spike, kernel weight and biological yield/plant in the first cross and for no. of kernels/spike in the second one. Dominance x dominance (l) type of gene action was significant for all characters except for no. of kernels/spike and grain yield/plant in the first cross, for plant height and grain yield/plant in the second cross and kernel weight and grain yield/plant in the third one.

Nature of gene action investigated using the five parameters analysis (Hayman's model) according to Singh and Chaudhary (1985) was presented in Table (5). The estimated mean effect parameter (m), which reflects the contribution due to the over all mean plus the locus effect and interactions of the fixed loci, was highly significant. The parameter (d*) was significantly positive for plant height and biological yield/plant in the second cross and for kernel weight in the first and the third crosses.

Meanwhile, (d*) was significantly negative for all characters in all crosses. The dominance effect (h) was significant for no. of kernels/spike in the first cross, for all characters in the first two crosses, except no. of kernels/spike in the third cross and plant height and no. of kernels/spike in the second cross and were significant for no. of kernels/spikes and 100-kernels weight in the third one, indicating the importance of dominance gene effects in the inheritance of all characters. Meanwhile, (i) was significant for all characters in the first cross except for no. of spikes/plant and grain yield/plant. It was also significant for no. of kernels/spike and kernel weight in the second cross and for all characters except no. of kernels/spike and grain yield/plant in the third one. Moreover, (l) was significant for kernel weight and biological yield for all crosses, for plant height, no. of spikes/plant and no. of kernels/spike in the third cross. no. of spikes/plant in the second cross and no. of kernels/spikes in the first one.

The important roles of both additive and non-additive gene action in most studied characters indicated that selection procedures based on the accumulation of additive effects would be very successful in improving these characters. Similar results were reported by Gouda *et al* (1993), Al-Kaddoussi *et al* (1994), Hosary (2000), Moustafa (2002) and Hendawy (2003).

Generally, the most biometrical parameters resulted from the first and second crosses were higher in magnitude than those obtained from the third one. Consequently, it could be concluded that the crosses (Gemmneiza 9 xDovin-2) and (Sids 1 x Sakha 93) would be of interest in a breeding program for bringing about the maximum genetic improvement.

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التباين الوراثي للمحصول ومكوناته في ثلاثة هجن من قمح الخبز

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البرنامج القومي لبحوث القمح – معهد بحوث المحاصيل الحقلية مركز البحوث الزراعية

أجرى هذا البحث في محطة بحوث الجيزة في أربعة مواسم متتالية من 2002/2001م إلي 2004 /2005م على ثلاثة هجن من قمح الخبز وهي (1) جميزة 9 × دوفن-2، (2) سدس1 ×سخا93 و (3) سخا 93 × دوفن-2

واشتملت الدارسة على كل من الأبوين والجيل الأول والجيلين الرجعيين والجيلين الثاني والثالث وكانت النتائج كما يلي :

1) ***كانت قوة الهجين في*** F_1 ***معنوية وموجبة بالنسبة لمحصول الحبوب ووزن النبات الكامل في الهجن الثلاثة. وكذلك أظهر الهجينان الثاني والثالث قوة هجين موجبة ومعنوية في كل من طول النبات ووزن الحبوب ، أما بالنسبة لقوة الهجين في عدد السنابل / نبات فقد ظهرت في الهجين الثاني فقط.***
2) ***تأثير التربية الداخلية في*** F_2 ***كان موجبا ومعنوياً في كل من عدد السنابل/نبات ، عدد حبوب / سنبلة ووزن المحصول في الثلاثة هجن وكذلك كانت موجبة ومعنوية بالنسبة للهجين الأول والثاني في صفتي طول النبات ووزن النبات الكلي بينما كانت قيماً سالبة ومعنوية في الهجينين الثاني والثالث لصفتي المحصول ووزن الحبوب .***

٣) أوضحت دراسة طبيعة التوارث أن درجة السيادة كانت كاملة في الهجين الأول لصفتي عدد السنابل/ نبات ووزن الحبوب بينما ظهرت السيادة الفائقة تجاه الأب الأعلى في جميع الصفات المدروسة في الهجينين الثاني والثالث ماعدا صفة عدد حبوب السنبلة في الهجين الثاني وعدد السنابل /نبات في الهجين الثالث ، كما ظهرت سيادة تامة تجاه الأب الأعلى لصفتي عدد السنابل /نبات ووزن الحبوب في الهجين الأول كذلك أمكن تحديد سيادة جزئية نحو الأب الأعلى في صفة عدد حبوب السنبلة في الهجين الأول والثاني وعدد السنابل /نبات في الهجين الثالث .

٤) كانت انحرافات الجيل الثاني (E_1) وانحرافات الأجيال الرجعية (E_2) معنوية لمعظم الصفات في الهجن تحت الدراسة مما يوضح أهمية الفعل الجيني التفوقي في وراثة هذه الصفات .

٥) أظهرت كفاءة التوريث بمعناها الواسع قيماً عالية لمعظم الصفات كما أظهرت كفاءة التوريث بمعناها الضيق وكذلك الكفاءة الوراثية من الانحدار بين الأجيال قيماً عالية إلي متوسطة مرتبطة بنسبة تحسين وراثي مرتفع إلي متوسط في معظم الصفات المدروسة .

٦) كانت قيم التحسين الوراثي الفعلي المتحصل عليها بصفة عامة متطابقة مع القيم المتنبأ بها لتحسين المحصول ومكوناته من خلال الانتخاب ، ومن ثم يمكن للمربي الاعتماد على القيم المتنبأ بها في الانتخاب لتحسين الصفات المحصولية .

٧) أظهرت التأثيرات الوراثية المضيفة وكذلك الفعل الجيني غير المضيف دوراً هاماً في وراثة معظم الصفات المدروسة .

٨) يمكن الاستفادة من الهجين الأول والثاني في برامج تربية القمح للحصول على سلالات جديدة متفوقة في المحصول .

٩) النتائج المتحصل عليها تدل على أن الانتخاب في الأجيال الانعزالية المبكرة قد يكون مفيداً ولكن سوف يكون أكثر كفاءة إذا تم تأجيله إلي الأجيال الانعزالية المتأخرة .