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Inheritance as A Base for Future Improvement of New Egyptian Bread Wheat Cultivars

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ABSTRACT

The main goals of that recent study were estimating the nature of the characters inheritance for three common wheat crosses. Six-parameters model was followed to achieve mention objectives. The scaling test proved significant values for all studied characters, except for the number of spikes. plant $^{-1}$. Additive and dominance effects controlled the number of spikes and grain yield. plant $^{-1}$ in cross I, along with, 100-grain weight in crosses I and II. The magnitude of heterosis was significant (P ≥0.01) for all characters of the three crosses, except for the number of grains. spike $^{-1}$ of cross I and III. Inbreeding had significantly affected 100-grain weight in any of the crosses and grain yield. plant $^{-1}$ in cross II. Over dominance toward the higher parent (P ≥0.01) had recorded for all wheat characters, except for the number of spikes. plant $^{-1}$ of cross II. Meanwhile, the values of over-dominance were towards the lower parent in the latter character. Heritability estimates ranged between 54.59% for (number of spikes. plant $^{-1}$) and 85.77% for (100-grain weight) in cross I and II respectively. Expected genetic advance from selecting the upper 5% were recorded high for cross I and III.

***Keywords**:* Expected genetic advance, Heterosis, grain yield, six parameters, Wheat crosses.

INTRODUCTION

Bread wheat "*Triticum astivum,* L." is a strategic food crop world-wide. Gap between production and consumption directed researchers in Egypt towards cultivars improvement. (Memon *et al*.,2007). The first step in Launching breeding program is to determine the nature of inheritance for yield and related characters. The effectiveness of selection program depends mainly on the existence of additive gene effects (Mather ,1949; Gamble ,1962; Peter and Frey 1966 and Mather and Jinks ,1971).

Generations means was proposed as an effective measure for gene effect and nature of inheritance (Khattab *et al*.,2001; Akhtar and Chowdhry ,2006; Khaled,2007; Farag,2009 and Abd-Allah and Hassan,2012).

The main objectives of that study were to estimate gene effect, heterosis, heritability of grain yield and related traits of bread wheat by using the six-parameters model (Gamble,1962).

MATERIALS AND METHODS

Four genotypes of bread wheat Table (1) were used to produce three different crosses during the winter seasons of 2018-2019 till 2020 -2021.The experimental site was the Experimental Farm of Alexandria University.

Table 1. Bread wheat genotypes, pedigree, and source.

Genotype	Pedigree	Source
MILAN	V"S"73.600/MRL/3/BOW/YR/TRF	CIMMYT
Gemmiza 10	MAYA 74"S"10N/1160-147/3/BB/g/LL/4/CHA7"S"/5/CROW"S"	EGYPT
Gemmiza 11	BOW"S"/KVZ117C/Seri82/3/Giza 168/Sakha61 CGM7892-2GM-1GM-2GM-OGM	EGYPT
Sids 12	BUC/7C/ALD/5MAYA7410N//1160.147/3/BB/GLL/4/C HAT"S"/6/MAYA/VUL//CMH74A.630/4*SX	EGYPT

In the first season of 2018/2019 crosses were obtained (Cross I: Gemmiza 10 × Milan, Cross II: Gemmiza 11 × Milan and Cross III: Gemmiza 11 × Sids 12). In the second season of 2019/2020, F_1 plants were selfed and backcrossed to parents to obtain the seed of F_2 and BC_1, BC_2 generations, respectively.

In the third season of 2020/2021, the six populations, that represent each cross (P_1, P_2, F_1, F_2, BC_1 and BC_2) were evaluated in a randomized complete block design (RCBD) with three replicates. Plot size for each population was as three rows for each of parents and F_1 ten rows for each of BC_1, BC_2 and F_2. Rows were three meters (m) long by 0.2 m apart. Measured samples were 30 plants for each non-segregating population, 150 plants for F_2 and 60 plants for backcrosses. Measured characters included: grain yield. plant $^{-1}$ (g), number of spikes. plant $^{-1}$, number of grains. spike $^{-1}$ and 100-grain weight (g).

Genetic parameters were estimated when F_2 variance was significant. Heterosis % relative to mid-parent (MP) or better parent (BP) was estimated according to (Bhatt, 1971).

Depression due to inbreeding (ID%) was calculated following (Mather and Jinks ,1971). Additivity of Scaling test model was tested according to (Mather and Jinks ,1982).

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Gambel ,1962 provided the method for portioning gene effect (additive (a), dominance (d), and epistatic (aa, ad, and dd). Deviation of the second filial generation from (E1) and deviation of backcross (E2) were estimated as shown by (Mather and Jinks ,1971). Potence-ratio was estimated as described by(Peter and Frey ,1966). Heritability (broad and narrow-sense) were calculated according to following (Mather ,1949). Expected gain (Δg) units and (Δg %) were estimated as represented by (Johnson *et al*., 1955).

RESULTS AND DISCUSSION

A- Mean performance:

Means, variances, and variances of the mean for characters of crosses six-populations are presented in Table (2). It was obvious that figures representing F_1 were superior to other populations in all studied characters, except for 100-grain weight and number of grains. spike^{-1} of cross I and III, respectively. The results indicate the presence of over-dominance. Number of grains. spike^{-1} of cross III was of lower value relative to F_1 along with higher value than mid-parent indicating partial dominance, (Zaaza *et al*., 2012 and Patel *et al*., 2018) had similar findings. Also, the non-additive gene effect was obvious in most studied crosses, since F_1 mean values were higher than F_2 mean values. Also, back-crosses presented means of higher value relative to parents.

Table 2. Mean performance ($\bar{x}$), variance (S^2) and variance of the mean ($S^2_{\bar{x}}$) of the six populations representing the studied wheat crosses.

Characters	Statistics	Cross I (Gemmiza 10 * Milan)						Cross II (Gemmiza 11 * Milan)						Cross III (Gemmiza 11 * Sids12)					
		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
No. of	$\bar{x}$	9.20	12.40	13.60	11.68	11.40	12.95	12.80	10.70	13.85	13.47	12.62	12.15	14.07	11.73	18.01	15.20	14.30	15.15
spikes	S^2	3.90	3.60	3.78	17.10	13.5	11.46	3.00	2.31	1.08	10.05	5.58	6.66	2.40	1.08	1.26	29.40	18.18	20.10
/plant	$S^2_{\bar{x}}$	0.130	0.120	0.126	0.114	0.225	0.191	0.100	0.077	0.036	0.067	0.093	0.111	0.080	0.036	0.042	0.196	0.303	0.335
No. of	$\bar{x}$	59.10	53.15	59.60	58.70	60.10	58.30	72.10	58.70	65.10	61.90	59.90	57.90	64.50	58.27	61.50	62.51	53.90	67.70
grains	S^2	19.38	20.58	13.59	125.70	79.80	92.88	11.19	8.19	13.08	180.0	119.88	109.80	13.29	14.19	8.40	160.8	100.08	95.70
/spike	$S^2_{\bar{x}}$	0.646	0.686	0.453	0.838	1.330	1.548	0.373	0.273	0.436	1.200	1.998	1.830	0.443	0.473	0.280	1.072	1.668	1.595
100-grain	$\bar{x}$	4.95	4.68	4.18	4.39	4.60	4.92	5.31	5.04	5.35	5.69	6.07	5.67	5.51	5.19	5.61	5.93	5.64	5.85
weight	S^2	0.09	0.06	0.09	0.45	0.36	0.42	0.03	0.030	0.03	0.45	0.24	0.24	0.06	0.06	0.03	0.60	0.300	0.42
(g)	$S^2_{\bar{x}}$	0.003	0.002	0.003	0.003	0.006	0.007	0.001	0.001	0.001	0.003	0.004	0.004	0.002	0.002	0.001	0.004	0.005	0.007
Grain	$\bar{x}$	22.60	28.30	42.10	32.80	37.60	41.80	34.20	30.10	37.20	39.10	31.95	30.80	36.20	34.62	37.80	36.50	39.60	39.10
Yield	S^2	13.50	13.20	13.05	87.60	64.08	61.02	4.95	4.29	3.84	100.50	47.82	70.38	8.19	6.75	3.93	99.00	67.86	69.66
/plant(g)	$S^2_{\bar{x}}$	0.450	0.440	0.435	0.584	1.068	1.017	0.165	0.143	0.128	0.670	0.797	1.173	0.273	0.225	0.131	0.660	1.131	1.161

$\bar{x}$, S^2 and $S^2_{\bar{x}}$: refer to Mean, Variance and Variance of mean of generation, respectively.

B- Heterosis and Inbreeding depression.

Data in Table (3) showed a positive significant estimate of heterosis relative to mid-parent in all studied wheat traits of the crosses, except for 100-grain weight in cross I and number of grains. spike^{-1} in cross II and III. Also, the estimates relative to better parent were significant for most studied traits, except for number of grains. spike^{-1} in all crosses and 100-grain weight in cross I. These results might indicate a valuable chance of using heterosis to improve yield and related traits of bread wheat (Memon,2010; Mousaa,2010; Zaazaa *et al*., 2012 and Alaa, 2014).

The values of depression in the studied traits following one generation of selfing are presented in Table (3). Such figures were reasonable when considered along with values of heterosis (Zaazaa *et al*., 2012; Alaa ,2014 and El-Said and Abd El-Zaher ,2020). Potence-ratio that indicates over-dominance (P≥1) relative to better parent had realized for number of spikes. plant^{-1}, 100-grain weight, and grain yield. plant^{-1} in crosses II and III, along with number of grains. spike $^{-1}$ in cross I. Contrary, over- dominance relative to lower parent were detected for number of spikes. plant^{-1}, 100-grain weight, and grain yield. plant^{-1} in cross I. Partial dominance, relative to parents was obvious for number of grains. spike $^{-1}$ in cross II and III.

Deviation of F_2 (E_1) and back-cross(E_2) were significant and positive for 100-grain weight of cross II and III, while, significant and negative for number of grains. spike^{-1} in cross II. These findings might be valuable for decision making and bread wheat breeding (Abd-Allah and Mostafa ,2011; Abdel-Nour, 2011; Alaa ,2014 and El-Said and Abd El-Zaher ,2020).

Table 3. Heterosis %, inbreeding depression%, Potence-ratio and deviation of F_2 (E_1) and back-cross (E_2) for bread wheat crosses.

Characters	Cross	Heterosis%		Inbreeding Depression	Potence Ratio	E_1	E_2
		MP	BP	(ID%)	(%)		
	I	25.92 **	9.67 **	-14.11 **	-1.75	-0.52 n.s	0.05 n.s
No. of spikes/plant	II	17.87 **	3.60 **	-2.74 **	2.00	0.67 *	-0.47 n.s
	III	39.61 **	28.00 **	-15.60 **	4.37	-0.26 n.s	-1.46 n.s
	I	6.19 **	0.16 n.s	1.51 n.s	1.16	0.83 **	2.77 n.s
No. of grains/spike	II	-0.46 **	-9.71 **	-4.91 **	-0.04	-3.35 **	-12.70 **
	III	0.19 n.s	-4.65 **	1.64 n.s	0.04	1.07 n.s	-1.29 n.s
	I	-13.09 **	-15.56 **	-5.02 **	-4.67	-0.10 n.s	0.53 **
100-grain weight (g)	II	3.48 **	0.75 **	-6.36 **	1.33	0.42 **	1.22 **
	III	4.85 **	1.81**	-5.70 **	1.63	0.45 **	0.53 **
	I	65.42 **	48.76 **	-22.09 **	-5.84	-0.97 n.s	11.85 **
Grain yield / plant (g)	II	15.70 **	8.77 **	-5.11 **	2.46	4.42 **	-6.60 **
	III	6.75 **	4.42 **	-3.43 **	3.03	-0.10 n.s	5.49 **

MP: Mid parents. BP: Better parent. E_1: F_2 deviation. E_2: Backcross deviation
***, **: Significant at 0.05 and 0.01 levels, respectively. n.s: Not significant**

The assumption of applying Hayman model Hayman,1958 was approved with obtaining significant scaling parameters (A, B and C) Table (4). Additive gene effect (a) was positive and significant for 100-grain weight of cross I. While a negative value was scored for the number of spikes. plant $^{-1}$, 100-grain weight and grain yield. plant^{-1} in cross I and number of grains. spike $^{-1}$ in cross III. A Significant dominance (d) effect was noticed for most studied traits, except for number of grains. spike $^{-1}$ in cross I.

The results might indicate dominance gene effect is more important in the inheritance of wheat characters relative to additive effect for number of spikes. plant $^{-1}$, specific 100-grain weight in cross I and II and grain yield. plant $^{-1}$ in cross I and III. Such characters might response to selection in late generations (Abd El-Aty and Katta; 2007; Abd-Allah and Mustafa 2011 and El-Said and Abd El-Zaher ,2020). Consequently, it might be advised to delay selection for such studied characters until late segregate generations to allow for better expression of additive gene effect (Petal *et al.*,2018).

Table 4. Scaling and gene effect parameters for bread wheat crosses.

Characters	Cross	Scaling. Parameters test			Gene effect parameter					
		A	B	C	m	a	d	aa	ad	dd
No. of spikes/plant	I	0 n.s	-0.10 n.s	-2.08 n.s	11.68 **	-1.55 *	4.78 *	1.98 n.s	0.05 n.s	-1.88 n.s
	II	-1.41 *	-0.25 n.s	2.68 *	13.47 **	0.47 n.s	-2.24 n.s	-4.34 *	0.58 n.s	6.00 **
	III	-3.48 **	0.56 n.s	-1.02 n.s	15.20 **	-0.85 n.s	3.21 n.s	-1.90 n.s	-2.02 *	4.82 n.s
No. of grains/spike	I	1.50 n.s	3.85 n.s	3.35 n.s	58.70 **	1.80 n.s	5.47 n.s	2.00 n.s	-1.17 n.s	-7.35 n.s
	II	-17.4 **	-8.00 **	-13.40**	61.90 **	2.00 n.s	-12.30 *	-12.00 n.s	-4.70 *	37.40 **
	III	-18.2 **	15.63 **	4.27 n.s	62.51 **	-13.80 **	-6.72 n.s	-6.84 n.s	-16.91 **	9.41 n.s
100-grain weight (g)	I	0.07 n.s	0.98 **	-1.43 **	4.39 **	-0.32 *	0.84 **	1.48 **	-0.840 **	-2.53 **
	II	1.48 **	0.95 **	1.71 **	5.69 **	0.4 **	0.89 **	0.72 n.s	0.265 **	-3.15 **
	III	0.16 n.s	0.09 n.s	1.80 **	5.93**	-0.21 n.s	-0.48 n.s	0.74 *	-0.370 **	-0.32 n.s
Grain yield / plant (g)	I	10.5 **	13.20 **	-3.90 n.s	32.80 **	-4.20 *	44.25 **	27.60 **	-1.350 n.s	-51.30 **
	II	-7.50 **	-5.70 *	17.70 **	39.10 **	1.15 n.s	-25.85 **	-30.90 **	-0.90 n.s	44.10 **
	III	5.20 *	5.78 **	-0.42 n.s	36.50 **	0.50 n.s	13.79 **	11.40 **	-0.290 n.s	-22.38 **

***, **: Significant at 0.05 and 0.01 levels, respectively.**
n.s: Not significant

C- Heritability and Genetic advance.

Table (5) illustrated the estimate of heritability's (broad and narrow- sense) along with expected advance from selection for the studied wheat crosses. The relative magnitude of broad-sense estimates emphasized the role of non-additive gene effect (Hammad ,2003 and El-diasty *et al.*, 2008). The value of expected advance supposes that the responsive characters to selection might be 100-grain weight and number of spikes. plant^{-1}. These findings match true with those reported by (Darwish and Ashoush, 2003 and Aboshosha and Hammad, 2009).

Table 5. Estimates of heritability (h^2_b and h^2_n %) and expected genetic advance(Δg) for the studied wheat crosses.

Characters	Cross	h^2_b %	h^2_n%	Δg	Δg%
No. of spikes /plant	I	78.01	54.04	4.60	39.38
	II	78.81	78.21	5.09	37.79
	III	94.63	69.79	7.71	50.72
No. of grains /spike	I	85.79	62.63	14.32	24.39
	II	93.98	72.40	19.89	32.13
	III	92.56	78.25	20.38	32.60
100-grain weight (g)	I	82.22	26.67	0.36	8.20
	II	93.33	93.33	1.29	22.67
	III	90.00	80.00	1.28	21.59
Grain yield / plant (g)	I	84.87	57.16	10.99	33.51
	II	95.62	82.39	16.93	43.29
	III	93.65	61.09	12.50	34.35

h^2_b %: Heritability in broad- sense. Δg: Expected advance.
h^2_n%: Heritability in narrow- sense. Δg %: Expected advance%.

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الوراثة كقاعدة للتحسين المستقبلي لاصناف قمح الخبز المصري الجديد .

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الملخص

تهدف الدراسة الي تقدير طبيعة وراثة الصفات لثلاث هجن من قمح الخبز العادي. حيث استخدم موديل العشائر الستة لتحقيق تلك الأهداف. أثبت اختبار SCALING وجود قيم معنوية لجميع الصفات المدروسة باستثناء صفة عدد السنابل لكل نبات ، كما ظهر تأثير للفعل الجيني المضيف والسيادي في صفات عدد السنابل ومحصول الحبوب لكل نبات في الهجين الأول ، مع وزن 100 حبة في الهجين الأول والثاني. كان حجم التغاير معنوياً (P ≥0.01) لجميع صفات الهجن الثلاثة ، باستثناء صفة عدد الحبوب. سنبلة -1 للهجين الأول والثاني. كانت قيم التربية الداخلية معنويا في صفة وزن 100 حبة في كل من الهجن تحت الدراسة ومحصول الحبوب لكل نبات. سجلت سيادة فائقة تجاه الاب الأعلى (P ≥0.01) لجميع صفات القمح ، باستثناء صفة عدد السنابل لكل نبات في الهجين الثاني . وفي الوقت نفسه ، ظهرت قيم للسيادة الفائقة تجاه الاب الأدنى في الصفات الأخيرة.تراوحت تقديرات معامل التوريث بين 54.59٪ لصفة (عدد السنابل لكل نبات) و 85.77٪ لصفة (وزن 100 حبة) في الهجين الأول والثاني على التوالي.كما سجلت أيضا أعلي قيم للتحسين الوراثي المتوقع من انتخاب اعلي 5% في الهجين الاول والثالث.