

HETEROSIS, GENE EFFECT, HERITABILITY AND GENETIC ADVANCE IN BREAD WHEAT

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ABSTRACT: *Two crosses of bread wheat (Gemmeiza x Giza 164) and (RCB 70 x Glza 160), and their six populations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were tested for grain yield, some of yield components and some growth attributes. Significant positive heterotic effects were detected for all studied traits. Overdominance towards, the higher parent was found for plant height, and number of spikes/plant in both crosses; grain yield in the first cross and spike length, number of kernels/spike and 1000-kernel weight in the second cross. Significant positive values of inbreeding depression were detected for all studied characters. Significant epistatic effects, i.e., E_1 and E_2 were detected for most studied traits. Additive gene effects were significant in all traits. Dominance type of gene action was found to be significant for all traits, except for plant height and grain yield in the both crosses. Additive x additive types of gene action were found to be significant for all traits, except for number of spikes/plant and grain yield/plant in the second cross. Also, additive x dominance and dominance x dominance types of gene effects were significant for most traits. Heritability estimates, in broad sense were high to moderate in magnitude with values between 52.14% (for 1000-kernel weight) to 88.24% (for plant height). However, heritability estimates in narrow sense, were high to low in magnitude with values between 27.64% (for number of spikes/plant) to 79% (for no. of kernels/spike) in the second cross. The predicted genetic advance from selection was rather moderate for number of spikes/plant, number of kernels/spike and 1000-kernel weight in both crosses; spike length and grain yield in the second cross, but low for the remaining traits. These results indicated that Gemmeiza 3 x Giza 164 cross was superior to the second cross in grain yield and its components.*

Key words: *Wheat, gene effect, heritability and genetic advance.*

INTRODUCTION

High yielding ability cultivars in wheat could be achieved by introducing well adapted ones, or through hybridization and selection for one or more of its major yield components; i.e., plant height, number of spikes per plant, spike length, number of kernels/spike, grain yield/plant and 1000-kernel weight. Information about the type and magnitude of genetic variation and the relative importance of additive and non-additive gene action types would assist wheat breeders in carrying out the most suitable breeding programs

for wheat improvement. Accordingly, the maximum progress in improving any character would be expected in a selection program when the additive gene action was the main component of genetic variance. Whereas, the presence of non-additive gene action might suggest the use of an hybridization program (El-Hosary *et al.*, 2001). Number of grains per spike tended to show partial dominance, while grain weight showed over dominance (Narula, 1987). In dominance and dominance x dominance types of gene effects were more important and larger in magnitude than additive effects in the inheritance of grain yield per plants, spikes per plant and plant height. The dominance and additive x dominance epistatic type were larger in magnitude than the additive effects for only 1000-kernel weight (Mahdy, 1988). Additive and dominance effects for plant height, number of spikes per plant, grains per spike and yield per plant (Singh, 1990). Narrow sense heritability estimates, were high for plant height and spike length (Mosaad *et al.*, 1990). Also, the narrow sense heritability estimates in wheat, was high for spike length (77.83%) and number of grains per spike (56.39%) intermediate for number of spikelets per spike (45.49%) and 1000-kernels weight (Hassan and Abd El-Moniem, 1991).

In this study, the six populations, i.e, P₁, P₂, F₁, F₂, BC₁, and BC₂ were used for partitioning the genetic components, using the methods of Mather (1949), Gamble (1962), Hayman and Mather (1955) and Mather and Jinks (1971). The main objective of this investigation was to study the nature of gene action, heritability, genetic advance from selection and heterosis estimates for plant height, number of spikes/plant, spike length, number of kernels/spike, grain yield/plant and 1000-kernel weight.

MATERIALS AND METHODS

The present work was carried out at the Faculty of Agriculture, Minufiya University Shibin El-Kom, and in the Agricultural Research Station at Zarzora Farm, El-Bihera Governorate, during the three seasons, 1999/2000, 2000/2001 and 2001/2002. Four wheat cultivars or lines were used in making two crosses namely; Gemmeiza 3 x Giza 164, and Giza 160 x RCB 70 in this study. A brief description of these cultivars and lines is presented in Table (1). The experimental populations used in this study were derived from the two crosses among the parental material developed in 1999-2000 season in Shebin El-Kom.

In 2000/2001 season, at Zarzora, some of the resultant F₁ plants were crossed to each of their parents to produce BC₁ and BC₂, while some others were used to produce F₂ kernels. In 2001/2002 season, at Shebin El-Kom, two experiments consisted of randomized complete block designs, with three replicates, were conducted. Each experiment included P₁, P₂, F₁, BC₁ and BC₂ of each cross. Each plot consisted of four rows, Each row was three meters long and 30 cm apart. Plants within rows were 20 cm apart. Each replicate comprised eight plots for F₂, three plots for each of BC₁ and BC₂ and one plot

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for non-segregating populations. Data were recorded on guarded plants for plant height, number of spikes/plant, spike length, number of kernels/spike, 1000-kernel weight and grain yield/plant.

Table (1): The names and pedigrees of parental cultivars and/or lines evaluated.

No.	Cultivars and/or lines	Pedigree	Origin
1	Gemmeiza 3	Bb/7C*2/Y50/Kal*3//Skha8/4/prv/ww/5/3/Bg "S"//on CGM.424-1GM-13GM-2GM-OGM	Egypt
2	Giza 164	KV2/Buho"S"//Kal/Bb	Egypt
3	RCB (70)	Shi#4414/crow"s" Swm 11508-4-AP-2AP-IAP-2AP-OAP	Mexico
4	Giza 160	Chenab / Giza 155	Egypt

The genetic variance, within F_2 populations, was first evaluated. If that variance was significant, various genetic parameters were, then, derived. Estimation of the genetic statistics was made, according to the methods described by the following authors types of gene action (Gamble, 1962), heterosis relative to mid parent and inbreeding depression (Mather, 1949), estimation of heritability values in broad and narrow senses (Mather, 1949), and the predicted genetic gain from selection Δg (Johanson *et al.*, 1955).

RESULTS AND DISCUSSION

Number of plants, and mean and variance values of the six studied traits for parents, F_1 , F_2 , BC_1 and BC_2 are presented in Table (2). All studied characters showed significant genetic variance in F_2 plants in the two crosses and, therefore, other parameters were estimated.

Heterosis, inbreeding depression, potency ratio, F_2 deviation (E_1) backcross deviation (E_2) and gene action in the two crosses are presented in Table (3).

Almost highly significant positive heterosis were obtained for all studied traits in the two crosses. These results are in close harmony with Younis *et al.* (1988), Hendawy (1994), Darwish (1992), Ashoush (1996) and Darwish (1998).

Number of spikes/plant, number of kernels/spike, and 1000-kernel weight are the main components for grain yield/plant. Hence, heterotic increase, if shown in any of the three components may lead to considerable yield increase in hybrids, as shown in Table (3).

As to inbreeding depression, highly significant positive values were obtained for most of the studied traits in both crosses. This is logic since the expression of heterosis in F_1 will be followed by a considerable reduction in F_2 performance.

Table (2): Number of plants, mean (\bar{X}) and variance (S^2) values for six populations of the two bread wheat crosses.

Cross	Population	No. of plants	Plant height (cm)		Spike length (cm)		No. of spikes/plant		No. of kernels/spike		Grain yield/plant (g)		1000-kernel weight (g)	
			\bar{X}	S^2	\bar{X}	S^2	\bar{X}	S^2	\bar{X}	S^2	\bar{X}	S^2	\bar{X}	S^2
			Gemmelza 3 x Giza 164	P ₁	40	113.5	0.763	13.67	0.48	16.9	5.85	57.9	13.93	64.1
P ₂	40	119.3		0.565	13.36	0.22	19.4	3.90	65.5	22.6	58.6	1.21	41.4	7.89
F ₁	40	128.0		2.20	14.2	0.507	22.2	2.28	69.3	29.17	69.5	1.5	46.6	4.17
F ₂	460	126.3		6.20	13.43	1.06	18.7	13.99	58.4	92.1	66.2	9.19	43.1	14.3
BC ₁	150	121.3		3.52	14.1	0.682	19.4	11.63	59.8	62.68	65.2	5.6	45.5	10.49
BC ₂	150	123.3		4.33	13.8	0.73	21.4	5.24	67.8	52.68	63.3	4.26	43.36	5.17
Giza 160 x R.C.B. 70	P ₁	40	102.45	12.35	11.69	0.133	16.56	13.34	50.4	28.76	52.07	5.94	43.2	1.51
	P ₂	40	109.55	14.15	13.54	0.677	15.3	8.3	56.5	39.38	55.4	8.68	45.2	4.93
	F ₁	40	117.93	15.23	14.54	0.544	18.2	3.83	69.5	24.29	56.7	4.2	49.9	1.12
	F ₂	400	111.43	38.3	13.7	3.03	16.63	21.23	59.46	137.2	55.8	58.89	46.5	10.11
	BC ₁	150	104.53	27.69	12.5	1.304	17.9	16.87	57.8	24.85	54.2	16.71	46.2	2.12
	BC ₂	150	114.23	23.19	13.38	1.147	15.66	13.85	62.6	30.42	56.5	24.78	48.8	6.52

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Table (3): Heterosis, inbreeding depression, potency ratio, F₂ deviation (E₁), backcross deviation (E₂) and gene action for characters studied in two crosses of bread wheat.

Character	Cross	Heterosis (%)	Inbreeding depression	Potency ratio	F ₂ deviation (E ₁)	BC deviation (E ₂)	Gene action (six parameters) (Gamble) ⁽¹⁾					m
							a	d	aa	ad	dd	
Plant height	I	9.96**	1.33**	4.0	4.1**	0.83*	-2.17**	-3.14	-14.74**	1.52*	13.08**	126.3**
	II	10.11**	5.50**	1.58	-0.535	-5.17**	-9.7**	3.73	-8.2*	-6.15*	18.54**	111.43**
Spike length	I	4.83**	4.00**	0.882	-0.428**	0.955*	0.3**	2.235**	2.08**	0.45*	-2.45**	13.43**
	II	7.63**	5.77**	1.04	0.1225**	-1.152**	0.88**	1.113*	-3.04**	0.05	5.59**	13.7**
No. of spikes/plant	I	22.71**	15.76**	1.62	-1.475**	0.45	-2.0**	11.3**	6.8**	-0.75	-7.7**	18.7**
	II	14.93**	8.63**	1.60	-0.435*	-0.57	2.24**	2.87*	0.6	1.67**	0.54	21.23*
No. of kernels per spike	I	12.31**	15.4**	1.0	-7.1**	-3.4*	-8.0**	29.2**	21.6**	-4.28**	22.4**	5.4**
	II	30.02**	17.32**	2.63	-4.01**	2.55*	-4.8*	27.01**	10.96**	-1.75	-5.86*	57.46**
Grain yield/plant	I	13.28*	4.74**	1.48	0.775*	-2.35**	1.9**	0.35	-7.8**	-0.85*	12.5**	66.2**
	II	5.52*	1.58*	0.89	0.483	0.065	2.3**	1.365	-1.8	-0.635	1.67	55.8**
1000-kernel weight	I	7.24**	7.51**	0.768	-1.9**	-1.190	1.14*	8.47**	5.32**	0.09	-2.94*	42.6**
	II	12.89**	6.8**	2.85	-0.55*	0.35	2.6**	9.7**	4.0**	-1.6	-5.8**	46.5**

I = The cross Gemmeiza 3 x Giza 164

II = The cross Giza 160 x RCB 70

* ** = significant at 0.05 and 0.01 levels, respectively.

(1) a = additive, d = dominance, aa = additive x additive, ad = additive x dominance, dd = dominance x dominance gene actions.

Overdominance, towards the higher parent was found for plant height and number of spikes/plant in both crosses, grain yield/plant in the first cross, and spike length, number of kernel/spike and 1000-kernel weight in the second cross. Similar results were reported by Tamam (1989) Abul-Nass *et al.* (1991) and Ashoush (1996).

Complete dominance towards the higher parent was found for number of kernels/spike in the first cross, while, partial dominance toward the higher parent was found for spike length and 1000-kernel weight in the first cross, and grain yield in the second cross. Blanco *et al.* (1982) Hassaballa *et al.* (1984) and Narulo (1987) found similar findings.

Significant F_2 deviation (E_1) were obtained for all studied traits, except for plant height, and grain yield in the second cross (Table 3). Significant backcross deviations (E_2) were found for plant height, spike length and number of kernels/spike, in both crosses, and grain yield/plant, in the first cross. This reveals that the epistatic gene effect might have a major contribution in the inheritance of these characters. The nature of gene action was studied according to Gamble (1962), as mentioned before.

For estimating various parameters of gene effects, the variety with a large mean value in each trait was usually considered as P_1 . In all traits, the mean effect of parameters (m) was almost highly significant (Table 3).

The estimates of parameter (a) are quite small in magnitude relative to parameter (d) in both crosses (Table 3). Additive gene effects (a) were almost highly significant for all studied traits in both crosses. These results indicated the potentiality of improving the performance of these traits by using pedigree selection program.

The dominance effect (d) and dominance x dominance (dd) epistatic effect played major roles in the inheritance of most studied traits. The estimates of dominance effects were either significant or highly significant for all studied traits in both crosses, except for plant height and grain yield. Moreover, the additive effect was more important and greater than the dominance effect (Table 3).

Dominance gene action would tend to favor the production of hybrids, while, for additive gene action, the significant standard selection procedures would be effective in bringing about advantageous changes in the characters.

The additive x additive (aa) epistatic type was almost highly significant for all traits, except for number of spikes per plant and grain yield in the second cross. Also, The additive x dominance gene effect (ad) was significant for plant height in both crosses, spike length, number of kernels/spike, and grain yield, in the first cross and number of spikes/plant in the second cross. Generally, significant one or more of the three types of epistatic gene effects were exhibited in both crosses for all studied traits (Table 3).

Blanco *et al.* (1982) found that additive and dominance gene effects were significant for plant height. Hassaballa *et al.* (1984) found that additive and

overdominance gene effects were important in the genetic system controlling the number of spikes/plant, while additive and partial dominance were more important in the genetic system of 1000-grain weight. Also, Narula (1987) found both additive and non-additive gene effects in a wheat diallel cross.

Lush (1949) gave the term, heritability, to define the relation between genotypic and phenotypic variances as broad sense heritability, and the relation between additive and phenotypic variance as narrow sense heritability. Heritability values are important to the breeder since it quantifies the expected improvement upon selection. To achieve genetic improvement through selection, heritability must be reasonably high. In the present investigation, heritability estimates, in broad sense (h^2) were high to moderate in magnitude with values ranging between 52.14%, for 1000-kernel weight, in the first cross, to 88.24% for plant height in the second cross. For plant height, number of kernels/spike and grain yield/plant, in both crosses, and spike length and 1000-kernel weight in the second cross, high estimates of broad sense heritability were detected. However, number of spikes/plant in both crosses and 1000-kernel weight in the first cross, moderate values in broad sense were obtained. Narrow sense heritability (h^2) estimates ranged between 27.64%, for number of spikes/plant in the second cross, to 79% for no. of kernels/spike in the second cross (Table 4). Such results agreed with those obtained from gene action studies (Table 3). Similar results were obtained by Mosaad *et al.* (1990), Hassan and Abd El-Moniem (1991) and El-Hosary *et al.* (2001).

Genetic coefficient of variation (G.C.V. %) showed moderate values for number of spikes/plant and number of kernels/plant, in both crosses, and spike length and grain yield in the second cross. The other traits had low values of G.C.V.% (Table 4). It is rather difficult to estimate the magnitude of heritable variation when the G.C.V. % is used alone, this will be easier when the heritability estimates and genetic gain are available (Swamp and Chayale, 1962).

The genetic advance under selection (Table 4) depends on the amount of genetic variability, the magnitude of masking effect of the environment and intensity of selection that is practiced. In terms of the progress expected, the effect in future generations, due to the non-additive variance, is included in the estimates. Therefore, the expected genetic advance for characters in this study was derived by using heritability in narrow sense.

The predicted genetic advance was rather moderate for number of spikes/plant, number of kernels/spike and 1000-kernel weight, in both crosses and spike length and grain yield in the second cross, but low for the remaining traits.

In the present investigation, moderate genetic heritability values were detected for number of kernels/spike, 1000-kernel weight and grain yield/plant in both crosses and spike length in the second cross. Therefore,

selection for these traits could be effective and satisfactory for successful breeding purposes.

The expected response to selection, which varies with the phenotypical standard deviation of population means, and which is a measure of the total variability of the trait, could therefore, reflects the total response that could be realized by breeding techniques.

Table (4): Heritability percentage ($h^2\%$) (in broad and narrow senses), genetic advance (G.S%) (as percent of the F_2 mean) and genetic coefficient of variability (G.C.V%) for characters studied in two bread wheat crosses.

Characters	Cross	h^2 broad (%)	h^2 narrow (%)	G.S.	G.S. (%)	G.C.V. (%)
Plant height	I	81.03	36.76	0.661	0.523	0.642
	II	88.24	78.49	6.31	5.66	4.432
Spike length	I	62.04	44.78	0.949	7.06	6.04
	II	85.00	59.60	2.135	15.60	11.72
No. of spikes/plant	I	71.34	39.74	3.06	16.37	16.89
	II	60.00	27.64	2.62	15.77	21.46
No. of kernels/plant	I	76.37	37.94	7.50	12.84	14.34
	II	82.00	79.00	14.20	33.44	17.95
Grain yield/plant	I	85.2	46.35	2.895	4.37	4.403
	II	88.17	64.77	10.239	18.34	13.75
1000-kernel weight	I	52.14	45.24	3.524	8.17	6.33
	II	75.06	57.00	3.730	8.03	5.924

Hence, the moderate genetic advance detected for number of spikes/plant in the second cross, in spite of their low heritability estimates, might be ascribed to a relative range of variability in this cross. Therefore, selection would be effective in breeding purposes. Relatively low genetic advance was associated with low heritability values in the remaining cases. It could be concluded that selection for these traits would be less successful than the former previous cases.

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قوة الهجين والتأثير الجيني ومعامل التوريث والتحسين الوراثي في قمح الخبز

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الملخص العربي

أجرى هذا البحث بمزرعة كلية الزراعة - جامعة المنوفية بشبين الكوم والمزرعة البحثية بزرزورة بمحافظة البحيرة على هجينين من قمح الخبز. الأول "جميزه ٣ × جيزه ١٦٤" والثاني "جيزه ١٦٠ × RCB70" وشملت الدراسة في كل منهما ست عشائر هي الأبوان والجيلان الأول والثاني وجيلا الهجينين الرجعيين لصفات ارتفاع النبات، وطول السنبله، وعدد السنابل للنبات، وعدد الحبوب بالسنبله ومحصول الحبوب للنبات ووزن ألف حبة.

ويمكن تلخيص أهم النتائج كالتالي:

- كانت قوة الهجين معنوية وموجبة لكل الصفات تحت الدراسة.
- بالنسبة لدرجة السيادة فقد كانت السيادة فائقة في اتجاه الأب الأعلى وذلك لصفات ارتفاع النبات وعدد السنابل بالنبات لكلا الهجينين، ومحصول الحبوب بالنبات في الهجين الأول، وطول السنبله وعدد الحبوب بالسنبله، ووزن الألف حبة في الهجين الثاني.
- بالنسبة لمعامل التربية الداخلية فقد أظهر نقصا موجبا معنويا لكل الصفات المدروسة.
- كانت قيم الانحراف الرجعي إلى التفاعل الجيني E_1 , E_2 معنوية لمعظم الصفات المدروسة.
- بالنسبة لطبيعة فعل الجينات كان أثر فعل الجينات من النوع المضيف معنويا لكل الصفات المدروسة، بينما كان فعل الجينات من النوع السيادي معنويا لكل الصفات عدا ارتفاع النبات ومحصول الحبوب للنبات في كلا الهجينين.
- كان فعل الجينات من النوع التفوقي (المضيف × المضيف) معنويا لكل الصفات عدا عدد السنابل بالنبات ومحصول الحبوب بالنبات في الهجين الثاني، وأيضا كان فعل الجينات من النوع (المضيف × السيادي) أو (السيادي × السيادي) معنويا لمعظم الصفات المدروسة.

- كانت قيم معامل التوريث بمعناها الواسع عالية إلى متوسطة وتراوحت من ٨٨,٢٤% لصفة ارتفاع النسب في الهجين الثاني إلى ٥١,١٤% لصفة محصول الحبوب بالنبات في الهجين الأول. بينما كانت قيم معامل التوريث بمعناها الضيق عالية إلى منخفضة وتراوحت ما بين ٧٩% لصفة عدد السنابل للنبات إلى ٢٧,٤٦% لصفة عدد الحبوب بالسنبل في الهجين الثاني.
- كانت النسبة المئوية للتحسين الوراثي المتوقع متوسطة لصفات عدد السنابل للنبات وعدد الحبوب بالسنبل ومحصول الحبوب بالنبات (في كلا الهجينين) وطول السنبل في الهجين الثاني بينما كانت منخفضة في الحالات الأخرى.
- من النتائج السابقة يمكن ملاحظة تفوق الهجين (جميزه ٣ × جيزه ١٦٤) على الهجين (جميزه ١٦٠ × RCB70). في محصول الحبوب ومكوناته.