

ESTIMATION OF SOME GENETIC PARAMETERS FOR GRAIN YIELD AND ITS COMPONENTS IN TWO BREAD WHEAT CROSSES

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ABSTRACT

Six populations (P_1 , P_2 , F_1 , BC_1 , BC_2 and F_2) of two bread wheat crosses namely *Misr-3 x Shandweel-1* and *Shandweel-1 x line-1* were produced and evaluated in a randomized complete block design with three replications during the three successive seasons of 2018/2019, 2019/2020 and 2020/2021 at El-Giza Agric. Res Station. The study aimed to know genetic parameters, heritability, and gene action for yield and its components of the studied genotypes using generation mean analysis. High degree of genetic variation was observed among generations for most of the studied traits. Most studied traits in both crosses were significant for at least one of the scaling test A, B, C, and D. It indicating the presence of non-allelic interaction (epistasis) and digenic model was adequate to explain the inheritance of the studied traits. Positive and highly significant heterotic effects relative to better parents were found by number of kernels/spike and grain yield/plant in both crosses, number of spikes/plant in the first cross and plant height in the second cross. Highly negative and significant heterotic effects relative to better parents were found by plant height in the first cross, number of spikes/ plant in the second cross and 100-kernel weight in both crosses. Additive gene effects were found to be significant for plant height, number of kernels/spike and grain yield/plant in the second cross. Dominance gene effects were significant for all traits except 100-kernel weight in the first cross. Additive x additive were significant for plant height and grain yield/plant in both crosses, number of kernels/spike in the first cross and number of spikes/plant in the second cross. Additive x dominance was significant for number of spikes/plant in both crosses, plant height and 100- kernel weight in the first cross and grain yield/plant and number of kernels/spike in the second cross. Dominance x dominance was significant for 100-kernel weight in both crosses, number of spikes/plant in the first cross, and for number of kernels/spike in the second cross. Moderate heritability was estimated in broad sense for most studied traits.

Key words: *Wheat, Genetic components, Six parameters model, Heterosis, Inbreeding depression, Heretability.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is a high-yielding crop with a wide range of adaptability; it is the main food in Egypt as it provides 20% of the total energy requirement in human food (Shewry, 2009). There is a gap between production and consumption of wheat in Egypt. Egypt import about 50% of requirements. Grain yield is a complex trait made up of the interaction between different yield components and environmental effects. Because of these complex interactions, it is difficult to improve yield through breeding (especially in the early generation) if yield is the only factor recorded, suggesting that component traits should also be used as selection criteria for yield improvement. This is the reason why it is necessary to know the genetic makeup of yield components (Chandra *et al* 2004). The choice of selection and breeding procedures for genetic

improvement of any crop is largely dependent on the knowledge of type and relative amount of genetic component and the presence of non-allelic interaction for different traits in the plant materials under investigation (Abd El-Rahman 2013 and Khaled 2013). Generation mean analysis belongs to the quantitative biometric methods based on measurements of phenotypic performances of certain quantitative traits on as many as possible plant individuals in basic experimental breeding generations (parental, filial, backcross and segregation generations). As it was outlined by (Singh and Pawar 2006), generation mean analysis is a useful technique in plant breeding for estimating main gene effects (additive and dominance) and their digenic (additive x additive, additive x dominance and dominance x dominance) interactions responsible for inheritance of quantitative traits. It helps us in understanding the performance of the parents used in crosses and potential of crosses to be used either for heterosis exploitation or pedigree selection (Singh *et al* 2004). For further progress, knowledge of breeding behavior, particularly of combining ability and type of gene action for the various traits, is necessary. Heterosis is a quicker method of improvement and increasing crop production. With a sufficient level of heterosis, commercial production of hybrid varieties will be justified, and heterotic studies can provide the basis for the exploitation of valuable hybrid combinations in breeding programs (Hassan *et al* 2006). One of the successful ways in breeding program and determining breeding methodology is information about the type of gene action involved in the inheritance of a trait in different wheat generations. Thus, the objectives of this study were

- i. Improving yield and its components for obtaining high yield genotypes.
- ii. To know the types of genetic variation studied genotypes.

MATERIALS AND METHODS

The experiment was conducted during the three successive seasons of 2018/2019, 2019/2020 and 2020/2021 at the experimental farm of the Giza Agricultural Research Station, Agricultural Research Center, Egypt. Three bread wheat genotypes (*Triticum aestivum* L.) were used in the present study on the basis of their genetic diversity presented in Table (1).

Table 1. Name, pedigree and origin of the three parental bread wheat genotypes.

Cross No.	Parent name	Pedigree	Origin
Cross 1	(Misr-3)	ATTILA*2/ABW65*2/KACHU CMSS06Y00258 2T-099TOPM-099Y- 099ZTM-099Y-099M-10WGY-0B-0EGY	Egypt
	(Shandweel-1)	SITE//MO/4/NAC/TH.AC//*3PVN/MIRLO/ BUC	Egypt
Cross 2	(Shandweel-1)	SITE//MO/4/NAC/TH.AC//*3PVN/MIRLO/ BUC	Egypt
	Line 1	BOW"S"/4/GIZA164/SAKHA61/5/MAI'S'/P J//ENU'S'/3/KITO/POTO//MO/JUP/4/K134/ VEE	Egypt

In the first season (2018/2019), the parental genotypes were crossed to obtain F₁ seeds for the following two crosses, Misr-3 x Shandweel-1, and Shandweel-1 x Line-1. In the second season (2019/2020), the hybrid seeds of the two crosses were sown to give the F₁ plants. The F₁ hybrid plants for each cross were backcrossed with both of its two parents to produce back cross seeds (BC₁ and BC₂). The rest of F₁ plants were self-pollinated to produce F₂ grains. Moreover, the same parents were crossed again to have enough F₁ seeds. In the third season (2020/2021) the obtained seeds of six populations P₁, P₂, F₁, BC₁, BC₂ and F₂ for each cross were evaluated in a randomized complete block design with three replications. Each plot consisted of 30 rows, ten rows for F₂ generation and four rows for each P₁, P₂, F₁ as well as BC₁ and BC₂ at Giza station. The rows were 3.0 m long spaced 20 cm apart and seeds were spaced 10 cm within row. Data was recorded on 10 individual guarded plants for P₁, P₂ and F₁, 30 plants for BC₁, BC₂ and 40 plants for the F₂ in each replicate. The studied traits were plant height (cm), number of spikes/plant, number of kernels/spike, 100-kernel weight (g) and grain yield/plant (g). All recommended field practices were adopted for wheat production.

Statistical and genetic analysis

To determine the presence or absence of non-allelic interaction, scaling test as outlined by Mather (1949) was used. The quantities A, B, C and D and their variances have been calculated to test the adequacy of the additive-dominance model in each case. The standard error of A, B, C and D was obtained by taking the square root of respective variances. T-test values were calculated upon dividing the effects of A, B, C and D by their respective standard errors. Type of gene effects was estimated according to Gamble (1962).

The standard error of a, d, aa, ad and dd is obtained by taking the square root of respective variances. T-test values were calculated upon dividing the effects a, d, aa, ad and dd by their respective standard error.

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 means 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 (SE). In addition, F_2 deviation (E1) and back-crosses deviation (E2) were measured as suggested by Mather and Jinks (1971). Broad-sense ($h^2_{b.s}$) and narrow-sense ($h^2_{n.s}$) heritability were estimated using Waner (1952) formulas. Furthermore the predicated genetic advance (Δg) from selection was computed according to (Johnson *et al* 1955) using 5% selection intensity. The genetic gain as percentage of the F_2 mean performance ($\Delta g\%$) was computed using the method of Miller *et al* (1958).

RESULTS AND DISCUSSION

Mean performance

Means and variances of the studied traits for P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of the two crosses are presented in Table (2). Generally, the differences between the parents in the two crosses were significant. The genetic variances within F_2 populations were also found to be significant for all studied characters for the two crosses. Consequently, the various genetic parameters were computed.

Table 2. Means and variances of the six populations (P₁, P₂, F₁, F₂, BC₁ and BC₂) for yield and its components of two bread wheat crosses.

Variable	Cross	Parameter	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
Plant height (cm)	C1	X ⁻	103.87±0.83	117.67±0.66	112.93±0.90	106.56±0.82	111.00±0.79	114.37±0.89
		σ ²	10.34	6.49	12.09	30.00	18.70	23.94
	C2	X ⁻	117.33±0.78	106.67±0.73	117.67±0.85	110.56±0.59	113.67±0.72	111.90±0.90
		σ ²	9.21	7.95	10.74	15.63	25.63	20.40
No. spikes/plant	C1	X ⁻	10.33±0.43	13.00±0.41	17.07±0.62	11.51±0.36	11.73±0.40	11.50±0.42
		σ ²	2.73	2.57	5.73	5.83	4.88	5.30
	C2	X ⁻	13.80±0.51	13.60±0.39	12.80±0.34	14.40±0.36	14.20±0.97	12.70±0.41
		σ ²	3.90	2.30	1.75	6.01	6.61	5.13
No. kernels/spike	C1	X ⁻	82.90±0.63	86.27±0.60	92.13±0.71	84.02±0.83	85.90±0.91	87.67±0.86
		σ ²	6.13	5.57	7.77	31.14	24.78	22.21
	C2	X ⁻	88.80±0.63	87.80±0.58	92.73±0.89	87.80±0.68	89.43±0.80	86.00±0.73
		σ ²	5.93	5.10	11.93	21.25	19.40	16.11
100-kernel weight (g)	C1	X ⁻	5.73±0.13	5.87±0.17	5.80±0.29	5.31±0.19	5.33±0.16	4.83±0.22
		σ ²	0.27	0.43	1.28	1.59	0.79	1.41
	C2	X ⁻	6.00±0.16	5.56±0.14	5.60±0.26	6.02±0.20	5.03±0.25	5.30±0.24
		σ ²	0.37	0.30	1.00	1.85	1.81	1.74
Grain yield/plant (g)	C1	X ⁻	55.09±0.46	55.50±0.53	56.59±0.39	52.67±0.54	54.38±0.64	56.44±0.61
		σ ²	3.11	4.16	2.33	13.24	12.44	11.39
	C2	X ⁻	57.09±0.50	45.89±0.44	58.47±0.23	48.50±0.64	57.05±0.70	47.32±0.67
		σ ²	3.80	2.94	0.82	18.43	14.91	13.39

Mode of gene action

As shown in Table (3) the scaling test (A, B, C and D) for the studied traits indicated that at least one of the scaling measures A,B, C and D had significant variations in both crosses for the studied traits. The results provide evidence for the failovers of a simple genetic model to explain its genetic mechanism controlling the traits indicating the presence of non-allelic interaction (epistasis) and digenic model is adequate to explain the inheritance of such traits. These results indicate the potentiality of improving the performance of these traits by using a pedigree selection program. Similar results were obtained by Abdel-Nour (2006), Abdel-Nour, and Hassan (2009) and El-Gabery *et al* (2009), Zaazaa *etal* (2012), Amin (2013), Abd El-Rahman (2013), Hamam (2014), El-Hawary (2016), Kumar *et al* (2017) and Abd El-Rady (2018).

Table 3. Estimates of scaling tests \pm standard error for the studied characters, using six population data in two bread wheat crosses.

Variable	Crosses	Scaling			
		A	B	C	D
Plant height (cm)	C1	5.20** \pm 1.20	-1.87** \pm 2.10	-21.18** \pm 3.87	-12.26** \pm 2.02
	C2	-7.67** \pm 1.88	-0.53 \pm 2.12	-17.11** \pm 3.09	-4.46** \pm 1.64
No. spikes/ plant	C1	-3.93** \pm 1.10	-7.07** \pm 1.12	-11.42** \pm 1.98	-0.21 \pm 0.82
	C2	1.80 \pm 1.12	-1.00 \pm 0.98	4.60** \pm 1.73	1.90** \pm 0.96
No. kernels/spike	C1	-3.23 \pm 2.06	-3.07 \pm 1.96	-17.34** \pm 3.73	-5.52** \pm 2.08
	C2	-2.67 \pm 1.94	-8.53** \pm 2.81	-10.87** \pm 3.38	0.17 \pm 1.75
100-kernel weight (g)	C1	-0.87 \pm 0.46	-2.01** \pm 0.54	-1.96* \pm 0.97	0.46 \pm 0.46
	C2	-1.53** \pm 0.58	-0.56 \pm 0.56	1.32 \pm 0.98	1.71** \pm 0.53
Grain yield/plant (g)	C1	-2.91* \pm 1.42	0.79** \pm 1.39	-13.07 \pm 2.41	-5.48** \pm 1.40
	C2	-1.48 \pm 1.51	-9.73** \pm 1.42	-25.95** \pm 2.69	-7.37** \pm 1.61

Heterosis

Heterosis was estimated as the percent increase of the F_1 mean performance above its respective better parent value (Table 4). Highly significant and positive heterotic effects relative to better parents were found for number of kernels/spike and grain yield/plant in both crosses, plant height in the second cross and number of spikes/plant in the first cross. Highly negative and significant heterotic effects relative to better parent were found for plant height in the first cross, number of spikes/plant in second cross and 100-kernel weight in both crosses. Better parent heterosis values for grain yield/plant were highly significant and positive in both crosses, indicating that they could be considered as promising crosses in the wheat breeding program to produce hybrid wheat. Similar results were previously obtained by EI-Massry (2009).

Table 4. Heterosis, inbreeding depression and deviation in F_2 and BC in two bread wheat crosses.

Variables	Crosses	Heterosis Bp%	inbreeding depression (ID)%	E1 (F_2 deviation)	E2 (BC deviation)
Plant height (cm)	C1	-4.02**	5.65**	-4.73	6.38**
	C2	10.31**	6.04**	11.00**	7.11**
No. spikes/ plant	C1	31.28**	32.55**	4.07**	5.56**
	C2	-5.88**	-12.50**	-0.80	-1.60**
No. kernels/spikes	C1	6.80**	8.80**	5.87**	8.11**
	C2	5.62**	5.32**	4.93**	4.93**
100-kernels weight (g)	C1	-1.14**	8.43**	-0.07	0.49
	C2	-6.76**	-7.50**	-0.40	-0.42
Grain yield/plant (g)	C1	1.96**	6.92**	1.09**	3.91**
	C2	2.44**	17.07**	1.99**	9.98**

Inbreeding depression

Inbreeding depression measured as a reduction in performance of F₂ generation relative to F₁, is presented in Table (4). Highly significant and positive inbreeding depression (inbreeding gain) for most of the studied characters in both crosses, except for number of spikes/plant and 100-kernel weight in the second cross which recorded highly significant and negative inbreeding depression, this is a positive result, since the expression of heterosis in F₁ may be followed by a considerable reduction in F₂ performance. The information about inbreeding depression is useful to test the potentiality of F₂ seeds after reducing the heterosis in F₂ generation due to the reduction of heterozygosity caused by inbreeding.

Thus, it is logical expectation that the expression of heterosis in F₁ may be followed by reduction in F₂ performance for some of the studied traits especially those having high heterosis values. These results are in a harmony with those obtained by Abdel-Nour (2006), El-Gabery *et al* (2009), Yadav and Singh (2011), Hamam (2014) Said (2014) and El-Hawary (2016).

The data presented in Table (4) revealed that the F₁ generation should be followed by appreciable reduction in F₂ generation, since the two parameters are the two sides of the same phenomenon. The present results agreed with this expectation in most cases studied. However, these expectations are not fulfilled in some other cases, for instance number of kernels/spike and grain yield/ plant in both crosses, showed highly significant heterosis in the positive direction and positive and significant inbreeding depression. However, 100-kernel weight in the first cross showed significant and negative values. The present results are in accordance with those previously obtained by Esmail and Kattab (2002) and El-Nahas (2005).

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).

F₂ performance

F₂ mean performance was found to be deviated significantly with positive signs from the average of the F₁ and mid-parent value (EI) for

most of the studied traits in both crosses except 100-kernel weight in both crosses, plant height in the first cross and number of spikes/plant which exhibited negative value. Similar results are also reported by Esmail and Kattab (2002) and EI-Massry (2009).

Backcross-performance

Backcross deviation (E2) as shown in Table (4) was found to be significant for the studied traits in both crosses, except number of spikes/plant in the second cross and 100-kernel weight in both crosses. Also, the F₂ deviation was accompanied by backcross deviation in most cases under study, indicating the presence of epistasis in such large magnitude as to warrant great deal of attention in the breeding program for improving these characters.

Nature of gene action

Genetic analysis of the nature of gene actions was performed according to Gamble (1962) which gives estimates of the six parameters model *i.e.* mean effect (m), additive (a), dominance (d) and the three epistatic types additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd) Table (5). The estimates of the mean effects (m) which due to the overall mean plus the locus effects and the interaction of the fixed loci, were found to be highly significant indicating that all studied characters were quantitatively inherited.

Additive gene effects (a) were found to be significant for plant height, number of kernels/spike and grain yield/plant in the second cross and number of spikes/plant in the first cross under investigation. Meanwhile, 100-kernel weight showed nonsignificant additive gene effect in the first cross while, plant height and grain yield/ plant exhibited negatively additive gene effect. These results would suggest the potential for obtaining further improvements for these traits.

The dominance gene effects (d) were found to be significant and highly significant for all studied characters except 100-kernels weight in the first cross, suggesting that the dominant factors playing a great role in the inheritance of these characters. Meanwhile, the negative values of (d) was obtained from number of spikes/plant in the second cross and 100-kernel weight in both crosses, which indicate that the alleles

responsible for less value were dominant over the alleles affecting high to value.

Table 5. Gene action parameters \pm standard error in two bread wheat crosses.

Variables	Crosses	Gene action parameters					
		m	a	d	aa	ad	dd
Plant height (cm)	C1	106.56 ^{**} \pm 0.82	-3.37 ^{**} \pm 1.19	26.68 ^{**} \pm 4.18	24.51 ^{**} \pm 4.04	3.53 ^{**} \pm 1.30	-27.8 ^{**} \pm 6.14
	C2	110.56 ^{**} \pm 0.59	1.77 ^{**} \pm 1.15	14.58 ^{**} \pm 3.44	8.91 ^{**} \pm 3.30	-3.57 ^{**} \pm 1.27	-0.71 \pm 5.55
No. Spikes/plant	C1	11.51 ^{**} \pm 0.36	0.23 [*] \pm 0.58	5.82 ^{**} \pm 1.97	0.42 \pm 1.85	1.57 [*] \pm 0.65	10.58 ^{**} \pm 3.06
	C2	14.40 ^{**} \pm 0.37	1.50 \pm 0.63	-4.70 [*] \pm 1.98	-3.80 [*] \pm 1.92	1.40 ^{**} \pm 0.70	3.00 \pm 3.05
No. kernels/spikes	C1	84.02 ^{**} \pm 0.83	-1.77 \pm 1.25	18.59 ^{**} \pm 4.25	11.04 ^{**} \pm 4.16	-0.08 \pm 1.33	-4.74 \pm 6.24
	C2	87.80 ^{**} \pm 0.96	3.43 ^{**} \pm 1.09	4.10 ^{**} \pm 3.64	-0.33 \pm 3.51	2.93 [*] \pm 1.17	11.53 [*] \pm 5.51
100-kernel weight (g)	C1	5.31 ^{**} \pm 0.19	0.50 \pm 0.27	-0.92 \pm 0.97	-0.92 \pm 0.93	0.57 [*] \pm 0.27	3.80 ^{**} \pm 1.49
	C2	6.02 ^{**} \pm 0.20	-0.27 \pm 0.34	-3.59 ^{**} \pm 1.10	-3.41 ^{**} \pm 1.10	-0.49 \pm 0.36	5.50 ^{**} \pm 1.69
Grain yield/plant (g)	C1	52.67 ^{**} \pm 0.54	-2.06 [*] \pm 0.89	12.24 ^{**} \pm 2.86	10.95 ^{**} \pm 2.81	-1.85 [*] \pm 0.96	-8.83 [*] \pm 4.30
	C2	48.50 ^{**} \pm 0.64	9.72 ^{**} \pm 0.97	21.74 ^{**} \pm 3.23	14.74 ^{**} \pm 3.21	4.12 ^{**} \pm 1.03	-3.54 \pm 4.72

Additive x additive (aa) epistatic type of gene effects were found to be significant for plant height and grain yield/plant in both crosses and number of kernels/spike in the first cross thus, selection in early generations for these traits might be effective. Negative and significant value (aa) for number of spikes/plant and 100-kernel weight were obtained in the second cross.

Additive x dominance (ad) type of digenic epistasis was found to be significant for number of spikes/plant in both crosses, number of kernels/spike and grain yield/plant in the second cross, plant height and 100-kernel weight in the first cross.

Meanwhile, the epistatic type dominance x dominance (dd) was detected to be significant for number of spikes/ plant in the first cross, number of kernels/spike in the second cross and 100-kernels weight in both crosses the (dxd) epistatic effect in the first cross for plant height and grain yield/plant were relatively high in the direction of lower plant height and grain yield/plant. It is worth to mention that the three epistatic types aa, ad and dd were accompanied by significant estimates of both EI and E2 epistatic scales in most of studied traits and that would ascertain the presence of epistasis in such large magnitude as to warrant great deal of attention in wheat breeding programs. The presence of both additive and non additive gene actions in most of studied traits would indicate that selection procedures based on the accumulation of additive effect would be successful in improving such traits.

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.

A great deal of attention of epistasis was reported in wheat by Darwish and Ashoush (2003), Bayoumi, (2004), Heidari *et al* (2006), Dawwam *et al* (2007), EI-Shaarawy (2008), EI-Massry (2009), Hendawy *et al* (2009) and Dawwam *et al* (2010).

Heritability and genetic advance

Heritability is one of the most important parameters for determination the genetic behavior of a metric trait. It is expressed as the proportion of the variance attributed to the average effect of genes. However, the most important function of the heritability in the genetic study of quantitative traits as its predictive role. It expresses the reliability of the phenotypic value as a guide to the breeding value. The possible advance through selection based on phenotypic value can therefore, be predicted only from knowledge of the degree of correspondence between phenotypic value and breeding value. The degree of correspondence is measured by heritability estimates. The heritability estimates enter into almost every formula connected with breeding methods and many practical decisions about the techniques followed depends on its magnitude.

Heritability in both broad and narrow sense and genetic advance under selection were calculated and the obtained results are presented in Table (6). The difference between h^2b and h^2n indicated that the dominance was found in the genetics of these traits. Heritability values are categorized as high (60% and above), moderate (30-60%) and low (0-30%) as stated by Robinson *et al.* (1949).

Table 6. Heritability in broad and narrow sense (bs, ns), genetic advance and genetic advance percentage in two bread wheat crosses.

Variable	Crosses	Heritability %		Genetic advance	
		$h^2bs\%$	$h^2ns\%$	\hat{g}	$\hat{g}\%$
Plant height (cm)	C1	68.93	57.84	6.53	6.12
	C2	64.03	60.45	6.3	5.2
No. spikes/plant	C1	41.39	25.63	1.28	11.08
	C2	58.38	4.40	0.22	1.54
No. kernels/spike	C1	79.61	49.06	5.64	6.71
	C2	66.55	32.94	3.13	3.56
100-kernel weight (g)	C1	66.74	61.95	1.61	30.33
	C2	74.05	8.11	0.23	3.77
Grain yield/plant (g)	C1	76.51	20.04	1.50	2.85
	C2	88.66	46.48	4.11	8.48

High to moderate heritability estimates in broad sense were observed for most of the studied traits. Meanwhile, high to moderate narrow sense heritability values were detected for plant height and number of kernels/spike in both crosses, 100-kernel weight in the first cross and grain yield/plant in the second cross.

Genetic advance as percent of mean is classified as high (>20%), moderate (10-20%) and low (<10%) as stated by Johnson *et al* (1955). Based on this, the expected genetic advance which is given in Table (6) showed 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, and that heritability estimates along with genetic gain upon

selection were more valuable in predicting the effect of selection than the former alone. Also, Dixit *et al* (1970) pointed out that high heritability is not always associated with high genetic advance, but in order to make your selection more effective, high heritability should be associated with high genetic gain. In the present study, high genetic gain was found to be associated with high to moderate narrow sense heritability for plant height number of kernels/spike in both crosses, number of spikes/plant and 100-kernel weight in the first cross and grain yield/plant in the second cross. Therefore, selection for these traits could be effective and satisfactory for successful breeding purposes. While, the remaining traits, selection would be effective, but probably of less success.

CONCLUSION

The traits examined in the present study showed complex genetic behavior. The genetic analysis based on the present investigation revealed that both additive and non-additive components of genetic variance are important. Results also showed that all studied traits were controlled by additive as well as non-additive genetic effects. Type of gene action differed among crosses for the same trait. Selection in early generation will be effective in the crosses which were controlled by additive effect while, delaying selection to later generation will be more effective in the other crosses. So, it is suggested that modified pedigree/bulk and selected bulk of selection are recommended methods for breeding these traits in wheat.

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تقدير بعض المعيار الوراثية لظنك لمصول ومكونته في هجينين من قح لخن

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تم اجراء البحث في محطة البحوث الزراعية في الجيزة خلال ثلاث مواسم زراعية (٢٠١٨-٢٠١٩)، (٢٠١٩-٢٠٢٠) و (٢٠٢٠-٢٠٢١) وذلك لتقدير المعايير الوراثية وقوة الهجين والفعل الجينى للمحصول ومكوناته لهجينين من قمح الخبز وهما (مصر ٣ × شندويل ١) و (شندويل ١ × سلالة ١) باستخدام طريقة العشائر الستة وهى الاب الأول و الأب الثانى و الجيل الأول والجيل الثانى والجيل الرجعى الأول والجيل الرجعى الثانى وكان ذلك بهدف الحصول على تراكيب وراثية ذات محصول عالى لانتاج سلالات عالية المحصول ومعرفة التباينات الوراثية داخل هذه التراكيب . اظهر تحليل التباين ان هناك فروق معنوية بين الأجيال للصفات المدروسة في الهجينين، وكانت النتائج المتحصل عليها كالتالى: يوجد قوة هجين موجبة عالية المعنوية مقارنة بالأب الأفضل في عدد حبوب السنبله ومحصول الحبوب للنبات لكلا الهجينين، وعدد السنابل للنبات في الهجين الأول وارتفاع النبات في الهجين الثانى. كما وجد قوة هجين سالبة ومعنوية بالنسبة لارتفاع النبات في الهجين الاول و عدد السنابل للنبات في الهجين الثانى ووزن ١٠٠-حبة في كلا الهجينين. كان تأثير السيادة معنويا لجميع الصفات المدروسة لكلا الهجينين ماعدا وزن ١٠٠-حبة معنويا في الجيل الأول. أظهر تحليل *scaling test* وجود واحد على الأقل *A, B, C, D* بصورة معنوية في كلا الهجينين مما يدل على وجود تفاعل غير أليلى (تفوق) لتفسير وراثه الصفات تحت الدراسة. تأثير الفعل الجينى مضيف X مضيف كان معنويا لصفات طول النبات ومحصول الحبوب/نبات في الهجينين وكان معنويا لصفات عدد السنابل/نبات في الهجين الثانى وعدد حبوب السنبله في الهجين الأول. وكان تأثير مضيف X سيادى معنويا لصفة عدد السنابل للنبات في كلا الهجينين ومحصول الحبوب/نبات وعدد الحبوب للسنبله في الهجين الثانى وزن ١٠٠-حبة في الهجين الاول. وكان تأثير الفعل الجينى سيادى X سيادى معنويا لصفة عدد السنابل للنبات في الهجين الأول، وعدد حبوب السنبله في الهجين الثانى وزن ١٠٠-حبة في كلا الهجينين. كانت قيم كفاءة التوريث بمعناها الواسع متوسطة الى عالية المعنوية لمعظم الصفات المدروسة.

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