

GENETIC STUDIES ON BREAD WHEAT CROSS UNDER UPPER EGYPT CONDITIONS

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ABSTRACT

The cross (Sids1 x Giza 168) of bread wheat was used. The analysis of gene effects was done using means of six populations, i.e. P₁, P₂, F₁, F₂, BC₁ and BC₂ on two sowing dates. The experiment was conducted at El -Mattaana Agricultural Research Station during three successive growing seasons (2017/2018, 2018/2019 and 2019/2020). For grain yield / plant, number of spikes/plant and 100-kernel weight, heterotic effects were significant and positive in the two sowing dates comparing with mid and better parent while No. of grains/spike was significant and positive in the first sowing date comparing with mid parent, as well as the biological yield/plant in the two sowing dates comparing with mid parent and in the second sowing date comparing with better parent. Significant and positive inbreeding depression was recorded for all studied characters in the two sowing dates except for the harvest index, these results for plant height can be utilized in breeding for semi-dwarfing. The additive type of gene action was significant and positive for the plant height, No. of spikes/plant and biological yield/plant in both sowing dates, No. of grains/spike in the second sowing date and grain yield / plant in the first sowing date, while dominance effects were significant and positive for plant height, No. of spikes/plant and biological yield/plant in both sowing dates, No. of grains/spike and grain yield / plant in the first sowing date. The (additive × additive) gene effects were significant for all studied characters, except for grain yield / plant in the second sowing date. The additive × dominance gene effects were significant for the plant height and harvest index in both sowing dates, No. of spikes/plant in the first sowing date and grain yield / plant in the second sowing date. The dominance × dominance gene effects were significant for the majority of traits, except for No. of spikes/plant and 100-kernel weight in the first sowing date. High to moderate heritability values in the broad and narrow sense were detected for all studied traits except No. of spikes/plant and biological yield/plant in the second sowing date and grain yield/plant in the first sowing date which had low values of heritability in narrow sense. The values of genetic advance as percent of the mean were high (25.78%) to moderate (19.99%) for all traits in both sowing dates except for the biological yield/plant in the late sowing date which was low (5.22%). These results showed the possible gain from selection as percent increase in the F₃ over the F₂ mean when the most desirable 5% of the F₂ plants are selected.

Key words: *Triticum aestivum*, Additive, Dominance, Heritability, Genetic advance.

INTRODUCTION

Wheat is one of the most important cereal crops in the world and in Egypt in particular. The aim of this study is to prepare a breeding program that avoids the negative impact of climate change, especially high temperatures in the case of late sowing in Upper Egypt, to obtain high-yielding varieties.

Since wheat is one of the most essential sources of food for a large number of people worldwide, its availability is crucial for most countries, especially developing ones, to ensure food security. Hossain *et al* (2021) reported that many studies had confirmed the damaging effect of heat on wheat. El-Maghraby *et al* (2016), Abd El-Rady (2018), Abdallah *et al*

(2019), Farhat (2020) and Mohiy *et al* (2021) reported that late sowing reduced plant height, number of spikes/m², number of kernels/spike, 1000-kernel weight and final grain yield. It has been discovered that wheat cultivars and lines differ genetically in their capacity to withstand heat. As a result, wheat geneticists and breeders need to keep creating high-yielding cultivars with the right genetic composition for a variety of settings. (Abdallah *et al* 2019, Raza 2019, Muazzam *et al* 2020, Sharshar and Genedy 2020, Attri *et al* 2021, Said and Hefny 2021 and Awaad *et al* 2023).

If the scaling tests A, B, C, and D are significant for at least one of the studied traits, they indicate the presence of non-allelic interaction (epistasis) and that the digenic model was sufficient to explain the inheritance of these studied traits (El-Said and Abd El-Zaher 2020, Kandil *et al* 2023 and El-Rashidy and El-Abedeem 2023).

A prerequisite for breeding programs is a thorough grasp of the genetic variables governing agronomic traits. In order to estimate the main gene effects (additive and dominance) and their interactions (additive × additive, additive × dominance, and dominance × dominance), generation mean analysis is a simple but crucial technique that is provided by the pattern inheritance of yield and other associated characters. (Sharshar and Esmail 2019, Haridy *et al* 2021, Kandil *et al* 2022 and Mohamed and Eissa 2022).

So, the three basic gene effects—dominance, additive, and nonelelic interaction—determine the breeding strategy. Generation mean analysis is a regularly used tool in the study of quantitative trait inheritance, helping to determine the best breeding strategies for crop varieties with desired features. (Al-Naggar *et al* 2022 and Rady 2022). Application of generation mean analysis procedure is based on the hypothesis that the studied generations must arise from a cross involving two contrasting genotypes. The six parameters technique (Hayman 1958) was employed in this work to assess the wheat cross and calculate the generation means, gene action, and genetic variance components. The investigation of the direct genetic control of the features in such a random sample of bread wheat genotypes is made possible by the invention of the six parameters analysis as a technique for quantitative inheritance.

In order to help wheat breeders select the best breeding strategies, the goal of this study is to estimate the types of gene effects governing yield and yield components in the wheat cross (Sids1 x Giza168) under two sowing dates.

MATERIALS AND METHODS

This study was conducted at the Al-Mataana Agricultural Research Station at the Agricultural Research Center in Egypt during the successive growing seasons of 2017/2018, 2018/2019, and 2019/2020.

In the 2017/2018 season, hybridization was made between Sids1 x Giza 168 as the parents to produce F₁ hybrid seeds.

In the 2018/2019 season, some F₁ plants were crossed with both parents to produce backcrosses (BC₁ and BC₂). At the same time, some F₁ plants were grown to be self-pollinated to produce the F₂ generation. More crossing between parents was also done to produce more F₁ seeds.

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

Entry	Parent name	Pedigree	Origin
1	Sids-1	HD2172/PAVON''S''//1158.57/MAYA74''S''	Egypt
2	Giza 168	MRL/BUC//Seri82 CM 93046-8M-0Y-0M-2Y-0B	Egypt

In the 2019/2020 season, evaluation was done in two agricultural experiments under optimum sowing date (25th November) and late sowing date (25th December) for the six populations, namely P₁, P₂, F₁, F₂, BC₁, and BC₂ of the hybrid, in a randomized complete block design (RCBD) with four replications. Each replicate was planted with 45 seeds in three rows each for the two parents and the F₁ hybrid, 90 seeds in six rows for each of the backcrosses and 150 seeds in ten rows for the F₂ population. Plants were planted in rows 1.5 m long, 30 cm apart from each other and 10 cm apart within the rows. Recommended agricultural practices for wheat production were followed in all growing season.

Data were recorded on 25, 25, 60, 60 and 75 guarded plants of parents, F₁, BC₁, BC₂ and F₂ respectively, for each replicate in each experiment. The following traits were recorded: 1- Plant height (cm). 2- No.

of spikes/plant. 3- No. of grains/spike. 4- 100-kernel weight (g). 5- Grain yield/plant (g).

Statistical and genetic analysis

Scaling test

The A, B, C, and D scaling tests as outlined by Hyman and Mather (1955) were applied to test the presence of non-allelic interaction as follows:

$$A = 2\overline{B_1} - \overline{P_1} - \overline{F_1} \quad V_A = 4V(\overline{B_1}) + V(\overline{P_1}) + V(\overline{F_1})$$

$$B = 2\overline{B_2} - \overline{P_2} - \overline{F_1} \quad V_B = 4V(\overline{B_2}) + V(\overline{P_2}) + V(\overline{F_1})$$

$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2} \quad V_C = 16V(\overline{F_2}) + 4V(\overline{F_1}) + V(\overline{P_1}) + V(\overline{P_2})$$

$$D = 2\overline{F_2} - \overline{B_1} - \overline{B_2} \quad V_D = 4V(\overline{F_2}) + V(\overline{B_1}) + V(\overline{B_2})$$

The values of A, B, C and D should be equal to zero within the limits of this standard error. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction.

Genetic parameters

The analysis was proceeded to compute the interaction types involved the six parameters genetic model of Hayman (1958) according to as follows:

$$m = \overline{F_2} = \text{Mean}$$

$$d = \overline{B_1} - \overline{B_2} = \text{Additive effect}$$

$$h = \overline{F_1} - 4\overline{F_2} - (1/2)\overline{P_1} - (1/2)\overline{P_2} + 2\overline{B_1} + 2\overline{B_2} = \text{Dominance effect}$$

$$i = 2\overline{B_1} - \overline{B_2} - 4\overline{F_2} = \text{Additive X Additive type of gene interaction}$$

$$j = \overline{B_1} - 1/2\overline{P_1} - \overline{B_2} + 1/2\overline{P_2} = \text{Additive X Dominance type of gene interaction}$$

$$l = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{B_1} - 4\overline{B_2} = \text{Dominance X Dominance type of gene interaction}$$

m = Mean F_2 , d = Additive effect, h = Dominance effect, i = Additive X Additive type of gene interaction, j = Additive X Dominance type of gene interaction and l = Dominance X Dominance type of gene interaction.

The significance of the genetic components were tested using the "t" test values and calculated by dividing the effects of d , h , i , j and l on their respective standard errors as follows: $\pm t = \text{Effect}/(\text{variance effect})^{1/2}$.

Genetic variance

In the case of three – parameter model where the absence of non-allelic interactions as indicated by non- significance of scale test, the genetic components of variance for each character in the studied crosses were partitioned into additive (D), dominance (H) and environmental (E) genetic variances using Mather and Jinks (1982) formula as follows :-

$$E = 1/3 (VP_1 + VP_2 + VF_1),$$

$$D = 4 VF_2 - 2(VB_1 + VB_2) \text{ and}$$

$$H = 4 (VF_2 - 1/2 VD - VE).$$

Heritabilities % in broad and narrow sense were computed according to the formula:

$$H^2 \text{ Broad sense} = [(1/2 D + 1/4 H) / (VF_2)] \times 100$$

$$h^2 \text{ narrow sense} = [(1/2 D) / (VF_2)] \times 100$$

Heritability values are categorized as high (60% and above), moderate (30-60%) and low (0-30%) as stated by Robinson *et al.* (1949).

The expected genetic advance under selection (Δg): It was computed according to Johnson *et al.* (1955).

$$\Delta g = k \times \sqrt{VF_2} \times \frac{h^2 n}{100}$$

Where:

K = A constant value depends on the intensity of selection and equal to (2.06) in the case of selecting the highest (5%) of the F₂ generation plants.

$\sqrt{VF_2}$ = Standard deviation of F₂ generation.

$h^2 n$ = Narrow sense heritability.

Also, this expected gain was expressed as a percentage of F₂ mean ($\Delta g\%$) according to Miller *et al* (1958) as follows:

$$\Delta g\% = \frac{\Delta g}{\bar{X}} \times 100 \quad \text{Where: } (\bar{X}) = \text{mean of F}_2 \text{ population.}$$

Genetic advance as percent of mean is classified as high (>20%), moderate (10-20%) and low (<10%) as stated by Johnson *et al* (1955).

Heterosis: were calculated according to the following formulae proposed by Bhatt (1971).

I- Heterosis relative to mid-parent

$$\text{M.p. H} = (\overline{F_1} - \overline{\text{M.P.}}) / \overline{\text{M.P.}} \times 100$$

II- Heterosis relative to better parent (Heterobeltiosis)

$$\text{B.p. H} = (\overline{F_1} - \overline{\text{B.P.}}) / \overline{\text{B.P.}} \times 100$$

where:

$\overline{F_1}$ = Mean of a F_1 crosses.

$\overline{\text{M.P.}}$ = Mean of the two parents.

$\overline{\text{B.P.}}$ = Mean of the better parent.

Inbreeding depression (ID%): Inbreeding depression was calculated by Mather and Jinks (1971) as the difference between the means F_1 and F_2 and expressed as a percentage of the mean F_1 as follows:

$$\text{I.D\%} = (\overline{F_1} - \overline{F_2}) / \overline{F_1} \times 100$$

T-test was used to determine the significance of these deviations. The standard error (S-E) was calculated as follows:

$$\text{S-E} = (\sqrt{V_{F_1}} + \sqrt{V_{F_2}})^{1/2}$$

Genetic coefficient of variation (G.C.V) was calculated as follows:

GCV = standard deviation of genetic variance / mean of F_2 .

$$= [(\sqrt{V_{F_2}} - \sqrt{V_E}) / (\overline{F_2})] \times 100.$$

RESULTS AND DISCUSSION

Mean performance

The means, variances and standard errors of the studied traits on the two sowing dates for the six populations P_1 , P_2 , F_1 , F_2 , BC_1 , and BC_2 are presented in Table (2).

Table 2. Means (\bar{X}), variance (S^2) and standard errors (S.E.+) of six populations of the wheat cross (Sids 1 x Giza 168) in two sowing dates for the all studied traits .

Character	Sowing dates	Statistical parameter	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
Plant height(cm)	I	\bar{X}	109.98	92.70	102.60	92.74	103.11	98.15
		S ²	24.59	13.51	40.81	382.74	207.23	263.39
		S.E.+	0.05	0.04	0.06	0.07	0.06	0.10
	II	\bar{X}	93.26	78.16	88.21	82.15	87.89	85.51
		S ²	14.47	26.23	41.34	260.43	144.81	162.72
		S.E.+	0.04	0.05	0.06	0.05	0.05	0.08
No. of spikes/plant	I	\bar{X}	11.81	9.97	13.20	9.61	12.23	10.08
		S ²	6.74	4.65	8.66	24.15	21.28	16.46
		S.E.+	0.03	0.02	0.03	0.02	0.02	0.03
	II	\bar{X}	9.18	8.32	10.80	8.28	9.88	9.10
		S ²	4.73	4.55	6.22	12.40	9.74	11.41
		S.E.+	0.02	0.02	0.02	0.01	0.01	0.02
No. of grains/spike	I	\bar{X}	58.43	50.41	57.23	34.62	44.11	42.41
		S ²	57.86	33.30	77.12	338.62	211.95	205.66
		S.E.+	0.08	0.06	0.09	0.06	0.06	0.09
	II	\bar{X}	52.82	42.66	46.72	37.80	43.34	38.83
		S ²	15.54	40.05	54.29	105.34	83.36	72.30
		S.E.+	0.04	0.06	0.07	0.03	0.04	0.05
100 KW(gm)	I	\bar{X}	4.94	4.90	4.97	4.13	4.44	4.55
		S ²	0.43	0.76	0.75	1.91	1.22	1.40
		S.E.+	0.01	0.01	0.01	0.005	0.005	0.01
	II	\bar{X}	3.91	4.01	4.18	3.92	3.79	3.77
		S ²	0.17	0.19	0.12	0.69	0.58	0.37
		S.E.+	0.004	0.004	0.003	0.003	0.003	0.004

Table 2. Cont.

Character	Sowing dates	Statistical parameter	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
Grain yield/plant (g)	I	\bar{X}	33.64	24.53	35.86	22.87	27.72	23.90
		S ₂	59.50	53.85	111.93	188.10	187.38	158.39
		S.E.+	0.08	0.07	0.11	0.05	0.06	0.08
	II	\bar{X}	16.77	14.04	17.08	14.65	14.22	14.49
		S ₂	20.11	13.73	27.68	37.96	31.17	31.26
		S.E.+	0.04	0.04	0.05	0.02	0.02	0.04
Biological yield/plant (g)	I	\bar{X}	98.90	70.89	103.74	69.14	91.01	74.43
		S ₂	556.08	301.32	691.99	1622.46	1351.95	1215.25
		S.E.+	0.24	0.17	0.26	0.13	0.15	0.23
	II	\bar{X}	59.63	46.88	65.26	48.74	58.39	54.11
		S ₂	201.49	160.72	338.42	484.16	470.66	470.47
		S.E.+	0.14	0.13	0.18	0.07	0.09	0.14
Harvest index%	I	\bar{X}	34.10	34.37	34.34	34.60	30.35	32.11
		S ₂	3.67	12.98	14.65	92.57	47.76	55.40
		S.E.+	0.02	0.04	0.04	0.03	0.03	0.05
	II	\bar{X}	28.12	30.31	26.11	31.18	24.60	27.65
		S ₂	8.24	16.32	12.08	43.38	23.32	33.13
		S.E.+	0.03	0.04	0.03	0.02	0.02	0.04

\bar{X} = Mean. ² = variance. S.E._± = Standard error

The analysis of variance indicated that there were significant differences among the studied generations in all traits under this study. Therefore, the required parameters were calculated.

In general, the average F₁ values are higher than the better parent for all traits except plant height, no. of grains/spike and harvest index in both sowing dates, where the values appear lower than the average of the parents. This is not desirable in the No. of grains/spike and harvest index but is required in the plant height trait to avoid lodging.

Gene action

Selecting the most efficient breeding methods depends on knowledge of the genetic system that controls the traits to be selected. Estimates of the different types of gene effects that contribute to genetic variation are shown in Table 3.

Table 3. Scaling test and gene action parameters of the wheat cross (Sids1 x Giza 168) in two sowing dates.

Character	Sowing dates	Scaling test				Gene action parameters					
		A	B	C	D	m	D	h	i	j	l
Plant height	I	-6.36*	0.99	-36.92*	-15.77*	92.74*	4.96*	32.81*	31.55*	-3.68*	-26.18*
	II	-5.69*	4.65*	-19.23*	-9.09*	82.15*	2.38*	20.68*	18.18*	-5.17*	-17.13*
No. of spikes/Plant	I	-0.56	-3.01*	-9.74*	-3.08*	9.61*	2.15*	8.48*	6.17*	1.23*	-2.60
	II	-0.21	-0.93	-5.98*	-2.42*	8.28*	0.79*	6.89*	4.84*	0.36	-3.70*
No. of grains/spike	I	-27.44*	-22.00*	-84.82*	-17.28*	34.62*	1.70	37.37*	34.56*	-2.31	15.70*
	II	-12.87*	-11.73*	-37.73*	-6.57*	37.80*	4.51*	12.12	13.14*	-0.57	11.46*
100 KW	I	-1.07*	-0.76*	-3.26*	-0.71*	4.13*	-0.13	1.47	1.43*	-0.16	0.40
	II	-0.52*	-0.66*	-0.61*	0.28*	3.92*	0.02	-0.34	-0.57*	0.07	1.74*
Grain yield/plant	I	-14.06*	-12.59*	-38.40*	-5.87*	22.87*	3.82*	18.52*	11.74*	-0.73	14.91*
	II	-5.41*	-2.13*	-6.35*	0.60	14.65*	-0.27	0.48	-1.19	-1.64*	8.74*
Biological yield/plant	I	-20.61*	-25.78*	-100.72*	-27.16*	69.14*	16.58*	73.17*	54.33*	2.58	-7.94
	II	-8.10*	-3.92	-42.07*	-15.02*	48.74*	4.29*	42.05*	30.04*	-2.09	-18.02
Harvest index%	I	-7.74*	-4.49*	1.26	6.75*	34.60*	-1.76*	-13.39*	-13.49*	-1.62*	25.72*
	II	-5.02*	-1.11	14.10*	10.11*	31.18*	-3.05*	-23.33*	-20.23*	-1.96*	26.36*

* indicate significant at 0.05 level of probability.

m = Mean F₂, d = Additive effect, h = Dominance effect, i = Additive X Additive type of gene interaction, j = Additive X Dominance type of gene interaction and l = Dominance X Dominance type of gene interaction.

The scaling test A, B, C and D in Table (3) showed that all the traits studied in the two sowing dates were significant except for eight out of fifty six estimates. The findings demonstrated the existence of non-allelic interaction, or epistasis, by demonstrating that at least one of the four scales is significant for each of the traits under investigation. The digenic model or the six parameters model can adequately explain the nature of gene action in this case. (Feltaous 2020)).

The six parameters, i.e. mean (m), additive (d), dominance (h), additive \times additive (i), additive \times dominance (j), and dominance \times dominance (l) were estimated to give a clear view of the type of genetic influences controlling studied attributes. These results are consistent with those reported by (Soliman 2018, Abdallah et al 2019, Koubisy 2019, and El-Rashidy and El-Abedeem 2023).

The mean parameter (m) was significant for all studied traits for the two sowing dates, which reflects the contribution of the general average in addition to spatial effects and interaction between fixed sites. These results are consistent with the results of (Sharshar and Genedy 2020), Haridy et al 2021, Swelam et al 2022 and Kandil et al 2023).

Additive gene effect (d) was positive and significant for plant height, number of spikes /plant and biological yield/plant at the two sowing dates, grain yield/plant at the first sowing date, and number of grains/spike at the second sowing date. These findings show that selection for these qualities in more developed generations is influenced by the additive gene effect.

The estimates of dominance effects (h) were positive and significant for plant height, No. of spikes/plant and biological yield/plant in the first and second sowing dates, No. of grains/spike and grain yield/plant in the first sowing date. These results indicate the importance of dominance gene effects in the inheritance of these traits. On the other hand, the importance of additive (d) and dominance (h) components indicated that the effects of additive and dominant genes were important in the inheritance of these traits. Similar results were reported by (Abdallah *et al* 2019, Raikwar 2019, Raza 2019, Mohamed and Eissa 2022 and Sandhu *et al* 2023).

Additive \times additive (i) gene effects were positive and significant for plant height, No. of spikes/plant, No. of grains/spike and biological

yield/plant in the first and second sowing dates ,100-kernel weight and grain yield / plant in the first sowing date, indicating that selection for the development of these traits could be effective. These results are in agreement with those of (Rady 2022).

Data concerning the epistatic gene effects, additive x dominance (j) revealed different were positive and significant for No. of spikes/plant in the first sowing date, while plant height in the first and second sowing date was negative and significant. These results indicate that the inheritance of these traits was affected by the duplication effect of epistatic genes. Similar results were obtained by (Kandil *et al* 2022).

The dominance x dominance (l) gene effects differed according to different sowing dates and traits. For No. of grains/spike, grain yield/plant and harvest index in the two sowing dates they were positive and significant. For plant height in the two sowing dates they were as negative and significant. Positive or negative and significant results confirm the important role of dominance x dominance gene interactions in the genetic system controlling these traits. These results are in agreement with those of (Hossain *et al* 2021).

Heterosis

The heterosis compared to the mid and better parent values are presented in Table 4. Significant and positive effects were obtained for the number of spikes/plant, weight of 100 grains, grain yield/plant at both sowing dates, as well as the plant height and biological yield/plant at the second sowing date compared to the mid parents (MP), and the better parent (BP). Likewise, at the first sowing date, plant height was significant and positive compared to the better parent as well as the number of grains/spike and biological yield/plant compared to the mid parents. These results are in agreement with those reported by (El-Said and Abd El-Zaher 2020 and El-Rashidy and El-Abedeen 2023).

Inbreeding depression

The results in Table (4) showed that the inbreeding depression values were significantly positive for the number of spikes/plant, the number of grains/spike, the weight of 100 grains, the grain yield/plant and biological yield/plant in the first and second sowing dates. Plant height was

significantly positive in the first sowing date, while in the second sowing date it was negatively significant. Harvest index was negatively significant in the second sowing date. Significant and positive inbreeding depression values for both heterosis and inbreeding depression seem logical since the expression of heterosis in F_1 is followed by a significant decrease in F_2 performance. Results revealed a harmony with what have been previously reported by (Khatab et al 2020, Sharshar and Genedy 2020 and Ahmad 2021).

Table 4. Heterosis, inbreeding depression and genetic variance for cross (Sids 1 x Giza 168) in two sowing dates.

Character	Sowing dates	Heterosis%		Inbreeding depression %	Genetic variance			
		MP	BP		H	D	E	(H/D) ^{1/2}
Plant height	I	1.24	10.68*	9.61*	246.32	589.72	26.30	0.65
	II	2.92*	12.86*	6.87*	79.01	426.67	27.35	0.43
No. of spikes/plant	I	21.21*	11.77*	27.20*	27.64	21.12	6.68	1.14
	II	23.43*	17.65*	23.33*	14.35	7.30	5.16	1.40
No. of grains/spike	I	5.16*	-2.05	39.51*	91.55	519.28	56.10	0.42
	II	-2.14*	-11.55*	19.10*	54.79	110.02	36.63	0.71
100 KW	I	0.94*	0.50*	16.85*	0.27	2.38	0.65	0.34
	II	5.63*	4.21*	6.32*	0.37	0.87	0.16	0.65
Grain yield/plant	I	23.29*	6.61*	36.22*	330.26	60.89	75.09	2.33
	II	10.83*	1.81*	14.19*	15.85	26.97	20.51	0.77
Biological yield/plant	I	22.20*	4.90	33.36*	1713.08	1355.46	516.46	1.12
	II	22.54*	9.44*	25.31*	893.75	54.35	233.54	4.06
Harvest index%	I	0.30	-0.10	-0.77	0.62	163.96	10.43	0.06
	II	-10.62*	-13.85*	-19.44*	3.43	60.62	12.21	0.24

* indicate significant at 0.05 level of probability.

D= additive genetic variance, H= dominance genetic variance, E= environmental variance and $(H/D)^{1/2}$ = The average degree of dominance genetic variances.

Genetic variance of three -parameters model

The components of genetic variation and the effects of additive genes (D) and dominance genes (H) in Table (4) showed that the additive genetic variation was higher than dominance in plant height, number of grains/spike, weight of 100 grains and harvest index in the two sowing dates, and grain yield/plant at the second sowing date, which indicates however, the effects of the additive genes play the main role in the inheritance of these traits, while the dominance gene effects were more important in the genetic system controlling the remaining traits.

The average degree of dominance $(H/D)^{1/2}$ given in Table (4) revealed that partial dominance gene effect was presented for plant height, number of grains/spike, weight of 100 grains and harvest index in the two sowing dates, and grain yield/plant in at the second sowing date, exhibited partial dominance in the genetic system controlling them. Over dominance gene effects were observed in the inheritance of grain yield/plant in the first sowing date, as well as No. of spikes /plant and biological yield/plant in the two sowing dates. These results indicate that the genetic systems controlling these traits in the two sowing dates are additive and non-additive gene effects. Similar results were reported by (Said and Hefny 2021, Haridy *et al* 2021 and Swelam *et al* 2022).

Genetic coefficient of variation (GCV), Heritability and genetic advance:

Table 5 displays the genetic coefficient of variation (G.C.V.), broad and narrow sense heritability, and genetic advance. These estimates are useful in the possibility of selection in these materials because they show the presence of the desired genetic variation that is transmitted from generation to generation and the percentage of the degree of heritability in the broad sense (additive and dominance) and in the narrow sense (additive) To reach the goal of this research, which is to estimate the genetic advance that can be obtained.

Genetic coefficient of variation (GCV)

The results in Table (5) showed that the highest genetic coefficient of variation (GCV) was for the number of grains/spike (48.55%), while the lowest estimate was for plant height (20.36%) at the first sowing date, while

at the second sowing date the highest genetic coefficient of variation (GCV) was (32.49%) for the number of spikes/plant and the lowest value for the harvest index (17.90%). The average of all studied traits for the genetic coefficient of variation (GCV) was (37.19 and 25.78%) at the first and second sowing dates, respectively. The highest values of the genetic coefficient of variation (GCV) were obtained for most of the studied traits at both sowing dates, and this is useful in selecting for these traits of this hybrid. (Ahmad 2021 and Haridy *et al* 2021).

Table 5. Genetic coefficient of variation (GCV), Heritability and genetic advance for cross (Sids 1 x Giza 168) for the all studied characters in two sowing dates.

Character	Sowing dates	GCV%	Heritability%		Genetic advance	
			H ² (Broad)	h ² (Narrow)	△ g	△ g%
Plant height	I	20.36	93.13	77.04	31.05	33.48
	II	18.58	89.50	81.92	27.23	33.15
No. of spikes/plant	I	43.49	72.33	43.72	4.43	46.05
	II	32.49	58.36	29.43	2.13	25.78
No. of grains/spike	I	48.55	83.43	76.68	29.07	83.96
	II	31.93	65.23	52.22	11.04	29.21
100 KW	I	27.17	66.07	62.50	1.78	43.04
	II	18.56	76.54	63.13	1.08	27.59
Grain yield/plant	I	46.48	60.08	16.19	4.57	19.99
	II	28.50	45.97	35.53	4.51	30.77
Biological yield/plant	I	48.10	68.17	41.77	34.66	50.13
	II	32.48	51.76	5.61	2.54	5.22
Harvest index%	I	26.19	88.73	88.56	17.55	50.73
	II	17.90	71.85	69.87	9.48	30.40

Heritability

Heritability estimates were based on the amounts of the additive and dominance genetic variance components (Table 5).The values of broad-

sense heritability were high (greater than 60%) for all studied traits in the two sowing dates, except for No. of spikes/plant, grain yield/plant and biological yield/plant under the second sowing date which were moderate (between 30-60%) by values (58.36, 45.97 and 51.76%), respectively. The maximum percentages were shown for plant height in the two sowing dates (93.13 and 89.50%), respectively, while the minimum values were for grain yield/plant at the two sowing dates (60.08 and 45.97%), respectively.

The values of narrow sense heritability, as estimated using F_2 and backcrosses, were high (greater than 60%) for all studied traits in the two sowing dates, except No. of spikes and biological yield/plant which were moderate in the first sowing date and low (between 0-30%) in the second sowing date, No. of grains/spikes which was moderate in the second sowing date and grain yield/plant which was low in the first sowing date and moderate in the second sowing date. grain yield/plant in the first sowing date and biological yield in the second sowing date which recorded minimum values (16.19 and 5.61%), respectively, and maximum values in harvest index in the first sowing date and plant height in the second sowing dates (88.56 and 81.92%), respectively.

In the case of plant height, 100 KW and harvest index in both sowing dates, as well as No. of grains/spikes in the first sowing date, the results demonstrated that additive genetic variation was important in the presence of variation in these traits.

In cases of the No. of spikes/plant in the two sowing dates, No. of grains/spike in the second sowing date, as well as grain yield/plant and biological yield/plant in both sowing dates, the results ascertained that both additive and non-additive genetic variance were important in these cases. These results are in agreement with those reported by (Shehab-Eldeen 2020, Farhat 2020, Akbari *et al* 2020, Al-Naggar *et al* 2022 and Mohamed *et al* 2022).

Genetic advance under selection

The expected genetic advance (Δg) from selection (Table 5) ranged from (1.78 and 1.08) for 100-kernel weight under both sowing dates to (34.66 and 27.23) for biological yield/plant in the first sowing date and plant height in the second sowing date, respectively. These results indicate that

low values of genetic advance although the heritability values were high could be due to low values of genetic coefficient of variation or *vice versa*, as each of them contributes to the genetic advance.

High to moderate values of genetic advance for plant height and number of grains/spike at the two sowing dates, as well as biological yield/plant and harvest index in the first sowing date. The use of early selection in the F₂ population for these traits could be permitted and would be effective in this cross.

The genetic advance as percent of the mean of grain yield/plant under stress (the late sowing date) was higher than that under normal conditions (the optimal sowing date), which indicates that selection for the grain yield/plant under the late sowing date (heat stress) is better.

Finally, the most important thing in this study, the values of genetic advance as percent of the mean were high (>20%) to moderate (10-20%) for all traits at both sowing dates, except for biological yield/plant in the second sowing date and these results showed the possible gain from selection as percent increase in the F₃ over the F₂ mean when the most desirable 5% of the F₂ plants are selected and which would be effective in a breeding program aimed at improving these traits. Similar results have been reported by (Abdel-Latif 2018, Sharshar and Esmail 2019, Ahmad 2021 and El-Rashidy and El-Abdeen 2023).

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دراسات وراثية على هجين لقمح الخبز تحت ظروف مصر العليا

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تم استخدام هجين قمح الخبز (سدس 1 × جيزة 168). و تحليل الفعل الجيني باستخدام متوسطات ستة عشائر منه عبارة عن الأب الأول، والأب الثانى، والجيل الأول للهجين، والجيل الثانى للهجين، والتهجين الرجعى للهجين مع الأب الأول، والتهجين الرجعى للهجين مع الأب الثانى في موعدين للزراعة (25 نوفمبر و 25 ديسمبر). أجريت التجربة بمحطة البحوث الزراعية بالمطاعة خلال ثلاثة مواسم زراعية متتالية (2017/2018، 2018/2019، 2019/2020). بالنسبة لمحصول الحبوب/نبات، وعدد السنابل/نبات، ووزن 100 حبة كانت قوة الهجين موجبة معنوية في كل من موعدي الزراعة مقارنة مع متوسط الأبوين والأب الأفضل، بينما عدد حبوب/السنبله كان موجبا ومعنويا في موعد الزراعة الأول مقارنة مع متوسط الأبوين، وكذلك المحصول البيولوجي/نبات في موعدي الزراعة مقارنة مع متوسط الأبوين وفى موعد الزراعة المتأخر مقارنة مع الأب الأفضل. تم الحصول على انخفاض معنوي موجب ناتج من التربية الداخلية من الجيل الأول للجيل الثانى لجميع

الصفات المدروسة في مواعدي الزراعة ما عدا صفة دليل الحصاد ويمكن الاستفادة باستخدام هذه النتائج بالنسبة لصفة طول النبات في التربية للحصول على نباتات قصيرة. كان نوع الفعل الجيني المضيق معنوياً وموجباً في كل من الصفات الآتية طول النبات، وعدد سنابل/النبات والمحصول البيولوجي/نبات في مواعدي الزراعة، وعدد الحبوب/سنبل في الموعد المتأخر، ومحصول حبوب/النبات في الموعد الأمثل، بينما كانت تأثيرت السيادة معنوية و موجبة لطول النبات، وعدد السنابل/نبات والمحصول البيولوجي/نبات في مواعدي الزراعة، وعدد حبوب/السنبل ومحصول حبوب/النبات في الموعد الأول. وكان فعل الجين (المضيق × المضيق) معنوياً لجميع الصفات المدروسة ما عدا محصول حبوب/النبات في الموعد الثاني. وكانت فعل الجين (المضيق × السيادة) معنوياً في طول النبات ودليل الحصاد في كلا الموعدين، وعدد سنابل/النبات في الموعد الأول، ومحصول حبوب/النبات في الموعد الثاني. وكانت تأثيرات الجين(السيادي × السيادة) معنوية في أغلب الصفات باستثناء عدد سنابل/النبات، ووزن ١٠٠ حبة في الموعد الأول. كانت قيم كفاءة التوريث من عالية إلى متوسطة بالمعنى الواسع والضيق لجميع الصفات المدروسة باستثناء عدد سنابل/النبات والمحصول البيولوجي/نبات في موعد الزراعة المتأخر ومحصول حبوب/النبات في موعد الزراعة الأمثل فكانت كفاءة قيم التوريث بالمعنى الضيق منخفضة. تراوحت قيم العائد الانتخابي كنسبة مئوية من عالية عن (٢٥،٧٨%) إلى متوسطة بقيمة (١٩،٩٩%) لجميع الصفات في كلا مواعدي الزراعة ما عدا صفة المحصول البيولوجي/نبات في موعد الزراعة المتأخر فكانت منخفضة بقيمة (٥،٢٢%) وأظهرت هذه النتائج الزيادة المتوقعة من الانتخاب كنسبة زيادة في الجيل الثالث على متوسط الجيل الثاني عند شدة انتخاب ٥% من نباتات الجيل الثاني.

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