

INHERITANCE OF YIELD AND ITS COMPONENTS IN THREE BREAD WHEAT CROSSES USING FIVE POPULATION MODEL

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ABSTRACT

The present study was carried out at Sakha Agricultural Research Station, ARC, Egypt during four successive growing seasons from 2018/19 through 2021/22, to identify the mode of gene action and the pattern of inheritance for plant height, No. of spikes/plant, No. of kernels/spike⁻¹, 100-kernel weight and grain yield plant⁻¹ in three bread wheat crosses, namely Giza 171 x Line 1, Giza 171 x Sids 12 and Giza 171 x Line 2. For all studied traits, t-test revealed highly significant differences among parental genotypes of each cross. According to the findings, additive, dominance, and epistasis effects were relevant for the inheritance of the studied traits. The average degree of dominance showed that partial dominance was effective for controlling most of studied traits, with the exception of plant height in cross-1, No. of spikes/plant in cross-2 and cross-3, and No. of kernels/spike in cross-1 and cross-3, 100-kernel weight in cross-3, grain yield/plant in cross-2, which exhibited over-dominance gene effects. Most of the studied traits recorded moderate to high heritability values in both broad and narrow sense, with the exception of the number of kernels/spike⁻¹ in cross-2 and 100-kernel weight in cross-1, which demonstrated low heritability in narrow sense. In most cases of the studied traits, the values of expected genetic advance were shown to be connected with narrow sense heritability. Based on these findings, the investigated crosses in this work would be useful in the wheat breeding program for genetic yield advancement by delaying selection to later segregating generations.

Key words: Triticum aestivum L., Genetic Parameters, Components of variance, Heterosis, Heritability, Genetic gain.

INTRODUCTION

Wheat is the most often consumed cereal crop in Egypt. However, Egypt is the largest importer and consumer of wheat (FAO 2020). The overall wheat planted area in Egypt is about 1.4 million hectares, with a total output of 8.9 million tonnes (FAO 2020).

Wheat is a major challenge because of the huge gap between production and consumption, which costs the government an enormous amount of hard currency for wheat imports. As a result, increasing wheat production is a primary goal in Egypt in order to decrease the gap between wheat consumption and production.

To meet such a huge challenge, Egypt's wheat breeding program intends to introduce new cultivars with high grain yield potentiality. However, wheat grain yield is a complicated property made up of interactions between multiple yield components and environmental variables, hence direct selection is inefficient.

For this reason, it is critical to understand the inheritance of grain yield and its components (Misra *et al* 1994). Egyptian wheat breeders are

searching for genetic diversity in terms of grain yield, its component, and other agronomic traits.

The success of any breeding programme is determined by the genetic diversity and forms of gene action involved in the inheritance of various characters in the used materials. Mean generations analysis is a useful technique in plant breeding to estimate the main gene effects (additive and dominance) and their digenic interactions (additive \times additive, additive \times dominance and dominance \times dominance) which are responsible for the inheritance of the quantitative traits. It also helps wheat breeders to understand the performance of the parents used in crosses (Zaazaa *et al* 2012).

Biometrical studies (analyses) on different generations for agronomic characters in Egypt by Sultan *et al* (2011), Abd El-Hamid and El-Hawary (2015), El-Hawary (2016), Abd El-Hamid and Ghareeb (2018), Abdelkhalik (2019), Feltaous (2020), Gebrel *et al* (2020) and Mohamed *et al* (2021) identified the importance of both additive and dominance variances, they also added that heritabilities and predicted genetic advance from selection were found to be moderate to high. High heritability estimates paired with high genetic progress from selection can enhance the possibilities of cultivar improvement success through selection.

Therefore, three bread wheat crosses were applied to 1) ascertain the inheritance, gene action, and genetic variability for plant height, grain yield and its associated traits, and 2) estimate heterosis, heritability, and genetic progress from selection for such traits which can be utilized in improving the efficiency of wheat breeding efforts.

MATERIALS AND METHODS

Four bread wheat genotypes were used to create three crosses in this study (Table 1). At Sakha Agricultural Research Station, ARC, Egypt, the experiment was conducted over four successive seasons from 2018/2019 to 2021/2022. cross-1 (Giza 171 \times Line 1), cross-2 (Giza 171 \times Sids 12) and cross-3 (Giza 171 \times Line 2) were carried out in 2018/2019 using the four bread wheat genotypes.

Table 1. Parental name, pedigree and selection history of four bread wheat genotypes.

Name	Abbrev.	Pedigree and selection history	Source
Giza 171	Gz.171	SAKHA 93 /GEMMEIZA9 Gz 2003-101-1Gz-4Gz-1Gz-2Gz-0Gz	Egypt
Sids 12	Sd.12	BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/ GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.63 0/4*SX SD7096-4SD-1SD-1SD-0SD	Egypt
Line 1	L.1	Giza158/5/CFN/CNO"S"//RON/3/BB/NOR67/4/ TL/3/ FN/TH//NAR59*2 S.10232-3S-2S-4S-5S-0S	Egypt
Line 2	L.2	CROC-1/AE.SQ(224)//OPATA-M- 85/3/PASTOR CMSS96Y02555S-040Y-020M-050SY-020SY- 6M-0Y	CIMMYT

To produce F₁ plants, F₁ hybrid seeds were sown in 2019/2020 season. F₂ seeds were produced by selfing these F₁ plants. Each of F₁ and F₂ seeds were planted in 2020/2021 to produce F₂ and F₃ seeds, respectively. Seeds from the parental genotypes (P₁ and P₂) and the three generations (F₁, F₂, and F₃) were evaluated in the field using a randomized complete block design (RCBD) with three replicates throughout the fourth seasons 2021/2022.

Planting was done in 3 m long rows with 20 cm between rows and 10 cm between plants within rows, resulting in a total of 30 plants per row. Two rows were dedicated for the parents and their F₁, 12 rows for each of F₂ generation, and F₃'s bulk.

The studied traits included plant height (PH, cm), no. of spikes/plant (SP^{-1}), no. of kernels/spike (KS^{-1}), 100-kernel weight (100KW, g), and grain yield/plant (GYP^{-1} , g).

Data were collected on 30 individual guarded plants from each parent and F_1 plants, as well as 210 plants from F_2 generation and 180 plants from F_3 generation.

Statistical and genetic methods

Before beginning the biometrical analysis, the collected data were evaluated to see if there were any variations in parental genotypes for each cross using the "t" test. According to Singh and Chaudhary (1985), the estimates of mean effect parameter (m), additive (d), dominance (h), dominance x dominance (l), and additive x additive (I) were assessed using a five-parameter model. Furthermore, F_2 deviation (E_1) and F_3 deviation (E_2) were calculated according to Mather and Jinks (1982).

Heterosis was calculated as the difference between the values of the F_1 hybrid and their mid parent (MP) and better parent (BP). The average reduction percentage of the F_2 from the F_1 was used to calculate inbreeding depression (Wynne *et al* 1970). Mather's (1949) method was used to estimate heritability in both broad ($H_{b,s}$) and narrow ($H_{n,s}$) sense, as well as average degree of dominance $(H/D)^{1/2}$. Alternatively, according to Miller *et al* (1958), the genetic gain under selection was estimated as a percentage of the F_2 mean performance ($\Delta g\%$).

RESULTS AND DISCUSSION

Choosing the correct parents is one of the most challenging issues that breeders face in order to develop effective crossing breeding programs. Table (2) displays the mean values of the five populations and their variances for the studied traits in the three crosses.

The t-test was performed among both parents of each cross (Table 2). It demonstrated significant differences for all studied cases. As a result, the parents in this study had a substantial amount of genetic variability. These findings are similar to those published by El-Hawary (2016), Abd El-Hamid and Ghareeb (2018), Gebrel *et al* (2020) and Mohamed *et al* (2021).

Table 2. Mean (\bar{x}) and variance (s^2) values of five populations for the studied traits in three bread wheat crosses.

Trait	Cross	Statistic.	P ₁	P ₂	F ₁	F ₂	F ₃	T-test
PH (cm)	1	\bar{x}	120.95	116.51	106.60	119.63	114.17	**
		s^2	10.47	9.29	11.79	323.21	256.37	
	2	\bar{x}	120.95	105.91	115.83	118.03	113.26	**
		s^2	10.35	5.89	6.25	510.96	365.69	
	3	\bar{x}	120.95	112.24	129.66	119.11	106.03	**
		s^2	10.47	11.22	14.84	331.95	281.24	
SP ⁻¹	1	\bar{x}	23.71	27.31	29.21	26.64	20.89	*
		s^2	26.49	55.67	69.19	174.70	147.70	
	2	\bar{x}	23.71	9.53	19.17	23.38	20.12	**
		s^2	26.49	21.29	36.77	89.82	60.99	
	3	\bar{x}	23.71	28.19	26.96	28.80	24.97	**
		s^2	26.49	45.66	53.10	153.99	105.80	
KS ⁻¹	1	\bar{x}	58.35	49.38	54.53	55.51	66.59	**
		s^2	130.36	136.75	86.82	336.39	261.45	
	2	\bar{x}	58.35	86.44	82.95	61.01	76.58	**
		s^2	130.36	120.59	137.73	346.21	309.26	
	3	\bar{x}	58.35	65.34	63.36	66.88	62.49	*
		s^2	130.36	94.14	117.49	382.36	261.45	
100KW (g)	1	\bar{x}	5.24	5.60	5.61	5.33	6.02	*
		s^2	0.26	0.32	0.32	0.86	0.76	
	2	\bar{x}	5.24	5.56	5.57	4.65	6.02	*
		s^2	0.26	0.18	0.16	0.87	0.74	
	3	\bar{x}	5.24	5.61	5.45	5.76	5.04	*
		s^2	0.26	0.32	0.38	0.82	0.66	
GYP ⁻¹ (g)	1	\bar{x}	64.48	57.88	71.36	49.93	59.56	**
		s^2	93.88	62.36	40.31	565.33	460.64	
	2	\bar{x}	64.48	49.17	50.77	48.65	56.17	**
		s^2	93.88	51.96	68.83	334.21	257.78	
	3	\bar{x}	64.48	69.83	72.63	64.70	58.11	*
		s^2	93.88	82.21	101.48	497.25	399.00	

Cross-1 = (Giza 171 x Line 1), Cross-2 = (Giza 171 x Sids 12), Cross-3 = (Giza 171 x Line 2) PH=Plant height, SP⁻¹=No. of Spikes Plant⁻¹, KS⁻¹=No. of Kernels spike⁻¹, 100KW=100-Kernel weight, GYP⁻¹=Grain yield plant⁻¹. * and ** indicate significant at 0.05 and 0.01 levels of probability, respectively.

Gene effects

The five parameters were used to estimate the type of gene action (Table 3). For all studied traits of the three crosses, the calculated F₂ mean effects (m) were found to be highly significant. These findings indicate that the studied traits are quantitatively inherited and indicate the importance of non-allelic interactions.

Table 3. The gene action parameters of the traits under study in the three bread wheat crosses.

Trait	Cross	m	d	h	l	i	E1	E2
PH (cm)	1	116.71**	2.17**	5.71	-62.27**	21.88**	6.79**	2.94
	2	115.15**	7.34**	10.97*	-30.53*	23.30**	3.32*	-2.66
	3	116.20**	4.25**	40.89**	-40.59**	36.64**	-3.93**	-33.37**
SP ⁻¹	1	25.99**	-1.76*	16.63**	-23.23*	9.51**	-0.70	-12.63**
	2	22.81**	6.92**	5.74**	-27.92**	17.09**	5.35**	4.35*
	3	28.10**	-2.19**	8.77**	-24.75**	3.42	2.29*	-2.90
KS ⁻¹	1	54.16**	4.38**	-29.47**	55.09**	-21.36**	1.28	24.19**
	2	59.52**	-13.70**	-26.23**	138.11**	-63.93**	-16.26**	-2.14
	3	65.25**	-3.41*	9.12*	-32.00*	0.83	4.18*	-0.21
100KW (g)	1	5.20**	-0.18*	-1.61**	4.29**	-2.14**	-0.18*	0.99**
	2	4.54**	-0.16**	-2.95**	9.47**	-3.43**	-0.81**	1.05**
	3	5.62**	-0.18**	1.67**	-4.53**	1.28**	0.32**	-0.77**
GYP ⁻¹	1	48.71**	3.22**	-11.13*	105.89**	-14.62**	-15.95**	-13.09**
	2	47.46**	7.47**	-18.19**	44.67**	2.66	-5.03**	4.63
	3	63.12**	-2.61*	22.31**	-13.65	11.75*	-5.07**	-23.00**

Cross-1 = (Giza 171 x Line 1), Cross-2 = (Giza 171 x Sids 12), Cross-3 = (Giza 171 x Line 2), PH=Plant height, SP⁻¹=No. of spikes Plant⁻¹, KS⁻¹=No. of Kernels spike⁻¹, 100KW=100-Kernel weight, GYP⁻¹=Grain yield plant⁻¹. *and ** indicate significant at 0.05 and 0.01 levels of probability, respectively., m=mean performance effect, d=additive effect, h=dominance effect, i=additive × additive effect, l=dominance × dominance effect, E1= F₂ deviation values , E2 = F₃ deviation values

The additive gene effects, (d) were found to be positive and significant for PH in the three crosses, SP^{-1} in cross-2 (Gz.171x Sd.12), KS^{-1} in cross-1 (Gz.171 x L.1), GYP^{-1} in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12). These results indicate that selection in the early generations could be effective for these traits since this inheritance pattern was controlled by additive gene effects. However, significant and negative additive effects were recorded for SP^{-1} in cross-1 (Gz.171 x L.1), cross-3 (Gz.171 x L.2), KS^{-1} in cross-2 (Gz.171 x Sd.12), cross-3 (Gz.171 x L.2), 100KW in the three crosses, GYP^{-1} in cross-3 (Gz.171 x L.2). These findings showed that there was decreasing alleles expression for these traits in the material under study, suggesting that selection to enhance these traits would be successful. The results of the current study were in agreement with those of Abd El-Hamid and Ghareeb (2018), Gebrel *et al* (2020) and Mohamed *et al* (2021).

Dominance gene effects (h), was significant and positive for PH in cross-2 (Gz.171 x Sd.12) and cross-3 (Gz.171 x L.2), SP^{-1} in the three crosses, KS^{-1} , 100KW and GYP^{-1} in cross-3 (Gz.171 x L.2). These findings suggest that the inheritance of these traits was influenced by dominance gene effects. Meanwhile, negative values of (h) were observed for KS^{-1} , 100KW and GYP^{-1} in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12). According to these results, the alleles responsible for less value of these traits were dominant over the high values of the contributing alleles. These results were generally in concurrent with those detected by Gebrel *et al* (2020) and Mohamed *et al* (2021).

The results indicated that both additive and dominance gene action have important contribution in the inheritance of the measured traits, suggesting that selection for desirable traits might be effective in the early generations. These findings are consistent with those reported by El-Hawary (2016) and Gebrel *et al* (2020).

The gene action pattern of dominance x dominance (l) was positive and significant for KS^{-1} , 100KW and GYP^{-1} in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12), confirming the important role of dominance x dominance gene interaction in the genetic system which controls these traits. In contrast, negative and significant value was detected for PH and SP^{-1} in

the three crosses and KS^{-1} , 100KW and GYP^{-1} in Cross-3 (Gz.171/L.2), suggesting the scope of heterosis breeding for developing superior populations. Moreover, significant positive values of additive×additive type of gene effects (i) were found for PH in the three crosses, SP^{-1} in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12), 100KW in cross-3 (Gz.171 x L.2) and GYP^{-1} in cross-3 (Gz.171 x L.2). So, in wheat breeding programs, early segregating generation selection in these materials may be successful for improving such traits. However, significant and negative values were detected for KS^{-1} and 100KW in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12) and GYP^{-1} in cross-1 (Gz.171 x L.1). These findings eliminate the possibility of improvement by early generations' selection. These findings are consistent with those obtained by Gebrel *et al* (2020) and Mohamed *et al* (2021).

According to Kearsey and Pooni (1996) type of epistasis can be determined when dominance (h) and dominance × dominance (l) gene effects were significant. When both effects have the same sign, the epistasis is complimentary, i.e. a symbol for high heterosis. Meanwhile, when the sign was different, the epistasis is duplicate.

Difference in signs for (h) and (l) was observed in the results for most cases, suggesting that duplicate type of epistasis was involved in controlling these traits, but complementary nonallelic gene interaction was also observed only for GYP^{-1} in cross-2 (Gz.171 x Sd.12). The results presented above are consistent with the findings of El-Hawary (2016), Abd El-Hamid and Ghareeb (2018), Abdelkhalik (2019) and Feltaous (2020).

Significant and positive F_2 deviation (E_1) were detected for PH in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12), SP^{-1} in cross-2 (Gz.171 x Sd.12) and cross-3 (Gz.171x L.2), KS^{-1} and 100KW in cross-3 (Gz.171 x L.2). Meanwhile, (E_1) was observed to be negative and significant for PH in cross-3 (Gz.171 x L.2), KS^{-1} in cross-2 (Gz.171x Sd.12), 100KW in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12) and GYP^{-1} in the three crosses. This may suggest that epistatic gene effects significantly influenced the heritability of such traits. Moreover, non-significant F_2 deviation (E_1) was observed for SP^{-1} and KS^{-1} in Cross-1 (Gz.171 x L.1). So, it was suggested that the involvement of epistatic

genes in the heredity of such traits is not very important. Earlier studies found a similar pattern by Abd El-Hamid and Ghareeb (2018), Gebrel *et al* (2020) and Mohamed *et al* (2021).

F₃ deviation values (E₂) were significantly positive for SP⁻¹ in cross-2 (Gz.171 x Sd.12), KS⁻¹ in cross-1 (Gz.171 x L.1) and 100KW in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12). However, significant and negative (E₂) values were reported for PH in cross-3 (Gz.171 x L.2), SP⁻¹ in cross-1 (Gz.171 x L.1), 100KW in cross-3 (Gz.171 x L.2) and GYP⁻¹ in cross-1 (Gz.171 x L.1) and cross-3 (Gz.171 x L.2). These observations would reveal existence of epistasis gene action to such an extent that a breeding program would necessitate a great deal of focus. These findings support those previously reported by Abd El-Hamid and Ghareeb (2018), Gebrel *et al* (2020) and Mohamed *et al* (2021).

The acquired results generally indicated that the impacts of additive, dominance, and epistasis were significant in the inheritance of the majority of the studied traits in the three crosses. These results generally concur with El-Hawary (2016), Gebrel *et al* (2020) and Mohamed *et al* (2021).

Heterosis and inbreeding depression

Inbreeding depression % for all traits in the three crosses used in this study, as well as the heterosis percentage in relation to mid- and better-parents, are provided in (Table 4).

For all traits in the present study, positive heterosis is preferred. The findings showed that mid-parent heterosis values were significantly positive for PH in cross-2 (Gz.171 x Sd.12) and cross-3 (Gz.171 x L.2) in the direction of tallness, SP⁻¹ and 100KW in the three crosses, KS⁻¹ in cross-2 (Gz.171 x Sd.12) and GYP⁻¹ in cross-1 (Gz.171 x L.1) and cross-3 (Gz.171 x L.2).

PH in cross-3 (Gz.171 x L.2) had a significant and positive value of heterosis over the better parent. These results reveal a dominance trend among the better respective parent. These results are generally in agreement with those reported by Abd El-Hamid and Ghareeb (2018), Abdelkhalik (2019), Feltaous (2020), Gebrel *et al* (2020) and Mohamed *et al* (2021).

Reduction in the performance of F₂ generation in comparison to F₁ generation is a sign of inbreeding depression (Table 4). Negative inbreeding

depression is favorable for some studied traits, like plant height, days to heading and days to maturity.

Table 4. Heterosis, inbreeding depression percentage, components of variance and dominance degree for the studied traits in three bread wheat crosses.

Trait	Cross	Heterosis%		I.D	Component of variance			$(H/D)^{1/2}$
		MP	BP		E	D	H	
PH (cm)	1	-10.22**	-11.86**	-12.22**	10.26	174.65	130.42	1.16
	2	2.11**	-4.24	-1.90	7.32	207.72	283.46	0.86
	3	11.21**	7.20*	8.14**	11.88	213.03	98.94	1.47
SP ⁻¹	1	14.53**	6.98	8.81**	49.22	68.54	52.68	1.14
	2	15.33**	-19.15**	-21.98**	27.49	3.88	56.26	0.26
	3	3.89**	-4.36	-6.84**	40.73	15.48	94.02	0.41
KS ⁻¹	1	1.23	-6.55	-1.80	115.10	66.85	146.24	0.68
	2	14.58**	-4.03	26.45**	126.40	139.27	72.10	1.39
	3	2.44	-3.04	-5.57**	111.21	25.90	235.92	0.33
100KW (g)	1	3.50**	0.18	4.94**	0.29	0.35	0.20	1.32
	2	3.13**	0.18	16.39**	0.20	0.39	0.26	1.22
	3	0.57**	-2.74**	-5.64**	0.31	0.17	0.32	0.73
GYP ⁻¹	1	16.64**	10.67	30.03**	63.92	283.34	204.28	1.18
	2	-10.66**	-21.27*	4.18*	69.81	107.11	149.14	0.85
	3	8.15**	4.01	10.92**	90.26	203.16	191.70	1.03

Cross-1 = (Giza 171 x Line 1), Cross-2 = (Giza 171 x Sids 12), Cross-3 = (Giza 171 x Line 2), PH=Plant height, SP⁻¹=No. of Spikes Plant⁻¹, KS⁻¹ = No. of Kernels spike⁻¹, 100KW = 100 Kernel weight, GYP⁻¹ = Grain yield plant⁻¹. I.D = Inbreeding depression, E = Environmental variance, D =Additive variance, H = Dominance variance, $(H/D)^{1/2}$ = Average degree of dominance, MD = Mid parent, BP= Better parent.

Significant and negative inbreeding depression values were detected for PH in cross-1 (Gz.171 x L.1), SP⁻¹ in cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12), KS⁻¹ and 100KW in cross-3 (Gz.171 x L.2). On the other hand, Significant and positive inbreeding depression values were detected for

PH in cross-3 (Gz.171 x L.2), SP^{-1} in cross-1 (Gz.171 x L.1), KS^{-1} in cross-2 (Gz.171 x Sd.12), 100KW in both cross-1 (Gz.171 x L.1) and cross-2 (Gz.171 x Sd.12) and GYP^{-1} in the three crosses. These findings support the earlier findings of Abd El-Hamid and El-Hawary (2015), Abdelkhalik (2019), Feltaous (2020), Gebrel *et al* (2020) and Mohamed *et al* (2021).

Components of variance and dominance degree

Table 4 provides estimates of the variance components and degree of dominance $(H/D)^{1/2}$. The findings revealed that the additive variance (D) was larger than dominance one (H) for PH in cross-1 (Gz.171 x L.1) and cross-3 (Gz.171 x L.2), SP^{-1} in cross-1 (Gz.171 x L.1), KS^{-1} in cross-2 (Gz.171 x Sd.12), 100KW in cross-1 (Gz.17 x L.1) and cross-2 (Gz.171 x Sd.12) and GYP^{-1} in cross-1 (Gz.171 x L.1) and cross-3 (Gz.171 x L.2). According to these findings, additive variance was the most important in the heredity of these traits. However, dominance variance was larger than additive variance for PH in cross-2 (Gz.171 x Sd.12), SP^{-1} in cross-2 (Gz.171 x Sd.12) and cross-3 (Gz.171 x L.2), KS^{-1} in cross-1 (Gz.171 x L.1) and cross-3 (Gz.171 x L.2), 100KW in cross-3 (Gz.171 x L.2) and GYP^{-1} in cross-2 (Gz.171 x Sd.12). These findings suggested that dominance variances also played an important role in the inheritance of these cases. These results concur well with those obtained by Feltaous (2020), Gebrel *et al* (2020) and Mohamed *et al* (2021).

The average degree of dominance $(H/D)^{1/2}$ was less than unity for PH in cross-2 (Gz.171 x Sd.12), SP^{-1} in cross-2 (Gz.171 x Sd.12) and cross-3 (Gz.171 x L.2), KS^{-1} in cross-1 (Gz.171 x L.1) and cross-3 (Gz.171 x L.2), 100KW in cross-3 (Gz.171 x L.2) and GYP^{-1} in cross-2 (Gz.171 x Sd.12). This result indicates that partial-dominance gene effects play the most important role in influencing such traits. Further, $(H/D)^{1/2}$ parameter was greater than unity for PH in cross-1 (Gz.171 x L.1) and cross-3 (Gz.171 x L.2), SP^{-1} in cross-1 (Gz.171 x L.1), KS^{-1} in cross-2 (Gz.171 x Sd.12), 100KW in cross-1 (Gz.171x L.1) and cross-2 (Gz.171x Sd.12) and GYP^{-1} in cross-1 (Gz.171x L.1) and cross-3 (Gz.171x L.2). These findings support the existence of over-dominance, showing that late selection could be effective in improving such traits. These findings are consistent with those found by El-Hawary (2016), Gebrel *et al.* (2020) and Mohamed *et al.* (2021).

Heritability and genetic advance:

Plant breeders can choose the best breeding strategy by estimating heritability, either in broad or in narrow sense. According to Robinson *et al* (1949) heritability is classified into three categories: low (0 - 30), moderate (30 - 60), and high (≥ 60).

High broad-sense heritability estimates (Table 5) were obtained for all the studied traits in the three crosses which ranged from 61.25 to 98.53, indicating a greater role of the genetic factors (additive + dominance + interaction) influencing the traits.

Table 5. Heritability and genetic advance from selection for the studied traits in three bread wheat crosses.

Trait	Cross	Heritability		Genetic advance	
		H (b.S)	H (n.S)	Δg	$\Delta g\%$
PH (cm)	1	96.75	41.36	15.13	12.96
	2	98.53	56.86	26.15	22.71
	3	96.33	30.55	11.33	9.75
SP ⁻¹	1	71.12	30.91	8.31	31.98
	2	68.63	64.20	12.38	54.28
	3	72.89	62.58	15.80	56.23
KS ⁻¹	1	64.93	44.56	16.63	30.70
	2	62.58	21.35	8.08	13.58
	3	70.19	63.24	25.16	38.56
100KW (g)	1	65.48	23.81	0.45	8.64
	2	76.86	30.59	0.58	12.80
	3	61.25	40.00	0.74	13.11
GYP ⁻¹	1	88.41	37.04	17.92	36.79
	2	78.59	45.74	17.01	35.85
	3	81.39	39.52	17.93	28.41

Cross-1 = (Giza 171 x Line 1), Cross-2 = (Giza 171 x Sids 12), Cross-3 = (Giza 171 x Line 2), PH = Plant height, SP⁻¹ = No. of Spike Plant⁻¹, KS⁻¹ = No. of Kernels spike⁻¹, 100KW = 100- Kernel weight, GYP⁻¹ = Grain yield plant⁻¹., H (b.s) = heritability in broad sense, H (n.s) = heritability in narrow sense and ($\Delta g\%$)= F2 mean performance.

A high heritability estimate of narrow sense was obtained for SP^{-1} in cross-2 (Gz.171 x Sd.12) and cross-3 (Gz.171 x L.2) in addition to KS^{-1} in cross-3 (Gz.171 x L.2) which ranged from 64.20 to 62.58% assuring that the majority of the genetic variation in these traits is linked to additive effects, allowing for effective selection in the early segregating generations. However, moderate estimates of ($H_{n.s}$) were detected for PH in the three crosses, SP^{-1} in cross-1 (Gz.171 x L.1), KS^{-1} in cross-1 (Gz.171 x L.1), 100KW in both cross-2 (Gz.171 x Sd.12) and cross-3 (Gz.171 x L.2) and GYP^{-1} in the three crosses which ranged from 30.55 to 56.86%. While, low values of (H^2_n) were recorded for KS^{-1} in cross-2 (Gz.171 x Sd.12) and 100KW in cross-1 (Gz.171 x L.1) being 21.35 and 23.81%, respectively. As a result, selection for such traits would be less successful in the early generations in such cases.

It is possible to conclude that discrepancies in estimating heritability values for the examined traits are owing to the existence of both additive and non-additive genetic variances influencing the inheritance of these traits. Similar results were found by El-Hawary (2016), Abdelkhalik (2019), Feltaous (2020), Gebrel *et al* (2020) and Mohamed *et al* (2021).

The percentage of expected genetic progress from selection indicated the potential gain through selection as a percentage increase in the F_3 over F_2 mean when the most desirable 5% of the F_2 plants were selected. The genetic advance estimates are helpful in identifying the mode of gene action involved in the inheritance of different polygenic traits. High genetic advance values suggested additive gene action, whereas low values indicated non-additive gene action (Singh and Narayanan 1993).

In the contest, Johnson *et al* (1955) classified genetic advance (Δg) into three categories as high (more than 20 percent), moderate (between 10% and 20%) and low (less than 10%). According to our findings in the current study (Table 5), high expected genetic gain (Δg) was obtained for PH in cross-2 (Gz.171 x Sd.12), SP^{-1} in the three crosses, KS^{-1} in cross-1 (Gz.171 x L.1) and cross-3 (Gz.171x L.2), GYP^{-1} in the three crosses which ranged from 22.71 to 54.88%. While, moderate (Δg) was recorded for PH in cross-1 (Gz.171 x L.1), KS^{-1} in cross-2 (Gz.171 x Sd.12) and 100KW in cross-2 (Gz.17 x Sd.12) and cross-3 (Gz.171 x L.2) which ranged from

12.80 to 13.58%. On the other hand, low (Δg) was recorded for PH in cross-3 (Gz.171 x L.2) and 100KW in cross-1 (Gz.171 x L.1) being 9.75 and 8.64%, respectively.

The largest expected genetic gain was shown to be connected with moderate or high heritability in narrow sense in all studied traits. As a result, selection becomes more effective. This result is consistent with the findings of Hassan (2009), who stated that traits with high expected genetic improvement and high heritability might be regarded or selected based on the significant impacts of additive gene action. Similar results were reported by, El-Hawary (2016), Abdelkhalik (2019), Feltaous (2020), Gebrel *et al* (2020) and Mohamed *et al* (2021).

In general, the main biometrical measures had high values for the majority of the traits studied. As a result, it should be recognized that such crosses are critical to the wheat breeding program for genetic yield progression.

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وراثة المحصول و مكوناته لثلاث هجن من قمح الخبز باستخدام نموذج العشائر الخمس

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تم تنفيذ هذه الدراسة في المحطة البحثية بسخا - كفر الشيخ، مركز البحوث الزراعية، خلال أربعة مواسم زراعية متتالية من ٢٠١٨/٢٠١٩ إلى ٢٠٢١/٢٠٢٢ و ذلك لدراسة تأثير الفعل الجيني ونمط التوريث لصفات طول النبات، عدد السنابل للنبات، عدد حبوب السنبل، وزن المائة حبة ومحصول الحبوب للنبات كمؤشرات للانتخاب للإنتاجية العالية لمحصول الحبوب لثلاث هجن من قمح الخبز وهي (جيزة ١٧١ × السلالة ١) و(جيزة ١٧١ × سدس ١٢) و (جيزة ١٧١ × السلالة ٢) باستخدام نموذج العشائر الخمسة وهم (الأبوين ، الجيل الأول، الجيل الثاني والجيل الثالث). وقد أشارت نتائج اختبار المعنوية إلى وجود فروق معنوية بين الأبوين لكل هجين في جميع الصفات المدروسة للثلاثة هجن تحت الدراسة. كانت التأثيرات الجينية المضيفة والسيادية والتفوقية مهمة في توارث معظم الصفات المدروسة للهجن الثالث. وقد أشارت درجة السيادة إلى تحكم السيادة الجزئية في كل الصفات للهجن الثالث تحت الدراسة ما عدا في (صفة طول لنبات في الهجين الأول، عدد السنابل للنبات في كل من الهجينين الثاني والثالث، عدد حبوب السنبل في كلا الهجينين الأول والثالث، وفي وزن المائة حبة للهجين الثالث و محصول حبوب النبات للهجين الثاني). كذلك أشارت النتائج إلى أن تقديرات كفاءة التوريث بالمعنى الواسع والضيق كانت متوسطة إلى مرتفعة في كل الصفات المدروسة للهجن الثالث ما عدا صفة عدد حبوب السنبل للهجين الثاني و وزن ١٠٠ حبة للهجين الأول حيث سجلا قيماً منخفضة تتراوح ما بين ٢١,٣٥ - ٢٣,٨١% لدرجة التوريث بالمعنى الضيق. و قد سجلت تقديرات التحسين الوراثي المتوقع من الانتخاب قيماً تراوحت بين متوسطة إلى مرتفعة في معظم الصفات للهجن الثالث المدروسة. بناء على هذه النتائج، تصبح هذه الهجن الثالث موضع اهتمام في برامج التربية للتحسين الوراثي لمحصول القمح مع مراعاة تأخير الانتخاب للأجيال النعزالية المتأخرة.

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