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Genetic Behavior of some Agronomic Traits in Three Bread Wheat Crosses Using Five Population Model

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Cross Mark

ABSTRACT

The current research was performed at El-Gemmeiza Agricultural Research Station, ARC during 2015/16 to 2018/19 growing seasons, to investigate the mode of gene action and the inheritance pattern of plant height, No. of spikes plant⁻¹, spike length, No. of kernels spike⁻¹, 100-kernel weight and grain yield plant⁻¹ in three crosses of bread wheat, namely Gemmeiza 11 x Sakha 94, Gemmeiza 9 x Sakha 94 and Line 1 x Giza 168. The t-test showed a highly significant differences among parental genotypes of each cross for most studied traits. The obtained findings reported that additive, dominance and epistasis effects were important in the inheritance of the studied traits. The average degree of dominance proved that partial dominance was effective for controlling most of all studied traits with the exception of plant height in the 1st cross, 100-kernel weight in the 2nd cross and grain yield plant⁻¹ in both 1st and 3rd crosses which exhibited over-dominance gene effects. The heritability in both broad and narrow senses were moderate to high for most traits under the study except No. of kernels spike⁻¹ and 100-kernels weight in the 2nd cross and grain yield plant⁻¹ in the 3rd cross which showed low heritability narrow sense values. The values of expected genetic advance (Δg) were found to be correlated with heritability in narrow sense for most of studied crosses. Based on these results, crosses under this study would be of concern to wheat breeding program for genetic yield advancement with delaying the selection to later segregating generations.

Keywords: *Triticum aestivum* L. Genetic parameter, Components of variance, Heterotic effect, Heritability, Genetic gain.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most common and strategic crop of cereals in the world. Wheat is the most commonly adapted cereal food eaten in Egypt. Thus, the wheat breeders focus their attentions to increase the capacity of wheat yield by creating a new cultivars with favorable genetic composition to meet the future goals. Wheat grain yield is a complex character composed of the interactions of various components of yield and environments factors. Therefore, improving the grain yield by breeding (especially during the early generations) is difficult when grain yield is the only recorded factor, indicated that yield components traits can be used as yield improvement selection parameters. For this reason it is important to be aware of the genetic inheritance of yield components (Misra *et al.*, 1994). For this purpose, knowledge on genetic diversity and the relationships between breeding materials is important for plant breeders to improve this crop. Wheat breeders in Egypt are searching for sources of genetic diversity for grain yield and its components and other related agronomic characteristics.

Based on the evaluated genetic criteria, in the advanced generations selection for grain yield components could be efficient, due to dominance and epistatic effects (Erkul *et al.*, 2010). High estimates of heritability resulting in high genetic progression for wheat yielding components providing greater selection opportunities in early segregating generations (Memon *et al.*, 2005). However, A Low to high heritability estimates and genetic advances for yield components were reported (Afiah *et al.* 2000). Accordingly, heritability assessment play an important part for designing the breeding approach. A character's heritability defines the degree to which it is passed from generation to the next one

and it is an useful tool if used in combination with other criteria to estimate genetic benefit following the selection for that character (Ansari *et al.*, 2005). otherwise, estimates of heritability may suggest that certain morphological characters, which affect grain yield in wheat, are more heritable than yielding itself (Fethi and Mohamed, 2010). Heritability values are an indicator of the parents-offspring genetic connection. Therefore, considerable study was carried out to integrate the favorable genes in current wheat cultivars to improve the crop productivity (Memon *et al.*, 2007).

This research was carried out on three bread wheat crosses to obtain information on the genetic action, available genetic variation and heritability for grain yield and the associated traits. This information can be used to approve effective breeding strategies for improving wheat grain yield.

MATERIALS AND METHODS

Five genotypes of bread wheat were used in this study, covering a broad range of variation for many agronomic traits, to shape three crosses (Table 1). The experimental work was conducted over four successive seasons at El-Gemmeiza Agricultural Research Station, ARC, Egypt. In 2015/2016, three crosses were made using five bread wheat genotypes designated as follows, the 1st Cross (Gemmeiza 11 X Sakha 94), the 2nd Cross (Gemmeiza 9 X Sakha 94) and the 3rd Cross (Line 1 X Giza 168).

In 2016/2017 season, F₁ hybrid seeds were sown to produce the F₁ plants. Such F₁ plants were selfed to generate F₂ seeds. In 2017/2018 the F₁ and F₂ for each cross were grown in order to obtain F₂ and F₃ seeds, respectively. During the fourth season of 2018/2019 the seeds collected

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from the parental genotypes (P₁ and P₂) and different generations (F₁, F₂ and F₃) were evaluated using randomized complete block design (RCBD) with three replicates. Planting was done in rows 3 m long with 20 cm between rows, plants within rows were 10 cm apart allowing a total of 30 plants per row. Two rows were devoted to the studied parents and their F₁, 12 rows for each F₂ generation and F₃'s

bulk for each cross. Data were reported on 30 individual guarded plants from each of parents and F₁; 210 plants from F₂ generation and 180 plants from F₃ generation for the studied characters, plant height (cm), No. of spikes plant⁻¹, spike length (cm), No. of kernels spike⁻¹, 100-kernel weight (g) and grain yield plant⁻¹ (g).

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

parent	Name	Abbreviation	Pedigree and selection history
1	Gemmeiza 11	Gem. 11	BOWS/KVZS//7C/SER182/3/GIZA168/SAKHA61 GM7892-2GM-1GM-2GM-1GM-0GM
2	Sakha 94	S. 94	OPATA/RAYON//KAUZ CMBW90Y3180-OTOPM-3Y-010M-010M-010Y-10M-015Y-0Y-0AP-0S.
3	Gemmeiza 9	Gem. 9	Ald "S" / Huac // CMH74A. 30 / Sx CGM 4583-5GM-1GM-0GM
4	Line 1	L. 1	MILAN/MUNIA CMSS92M01740S-015M-0Y-0Y-050M-5Y-2M-0Y-4PZ-0Y-2PZ-0Y
5	Giza 168	G. 168	MRL / BUC // SERI CM93046-8M-0Y-0M-2Y-0B-0GZ

Statistical and genetic methods:

The collected data were analyzed to test the differences among parental genotypes for each cross using "t" test before starting the biometrical analysis.

The estimates of mean effect parameter (m), additive (d), dominance (h), dominance x dominance (l) and additive x additive (i) were measured using five parameters model illustrated by Hayman model according to Singh and Chaudhary (1985). Moreover, F₂ deviation (E₁) and F₃ deviation (E₂) were measured as obtained by Mather and Jinks (1982)

Heterosis was determined as the percent of deviation of F₁ hybrid over its mid parents (MP) or its better parents (BP) values. Inbreeding depression was obtained as the

average percentage decrease of the F₂ from the F₁ (Wynne et al., 1970). Heritability in both broad (H_{b,s}) and narrow (H_{n,s}) senses and mean degree of dominance (H/D)^{1/2} was estimated as obtained by Mather (1949). On the other hand, the genetic gain under selection reported as percentage of the F₂ means performance (Δg%) was calculated according to Miller et al. (1958).

RESULTS AND DISCUSSION

The choice of the appropriate parents are the most important problems facing the breeders to successfully cross breeding programs in them. The values of five populations means and variances for the tested traits of the three crosses are shown in Table 2.

Table 2. Values of means (x̄) and variances (s²) of five populations for the tested traits in the three bread wheat crosses.

Trait	Cross	Statis.	P ₁	P ₂	F ₁	F ₂	F ₃	t.test	
Plant height, cm	1	\bar{x}	118	116	120	111	122	**	
		s^2	3.23	12.18	10.79	172.43	132.90		
		\bar{x}	111	116	110	122	127		
	2	s^2	11.44	12.18	15.30	251.76	133.42	**	
		\bar{x}	105	132	121	107	107		
		s^2	1.36	1.94	2.49	85.30	64.40		
	No. of spikes plant ⁻¹	1	\bar{x}	16	10	12	10	13	**
			s^2	2.23	3.21	2.20	31.60	18.00	
			\bar{x}	10	16	11	12	13	
2		s^2	2.21	3.21	2.20	35.00	21.00	**	
		\bar{x}	8	10	11	12	12		
		s^2	12.19	13.28	12.21	42.02	30.00		
Spike length, cm		1	\bar{x}	16	19	15	12	14	**
			s^2	1.16	0.89	1.06	4.13	2.84	
			\bar{x}	19	19	15	13	14	
	2	s^2	0.93	0.89	1.87	3.74	2.90	N.S	
		\bar{x}	15	17	16	13	15		
		s^2	1.06	1.28	0.94	4.04	2.86		
	No. of kernels spike ⁻¹	1	\bar{x}	92	85	100	77	81	*
			s^2	107.89	100.78	127.56	331.26	259.64	
			\bar{x}	62	85	70	64	71	
2		s^2	90.32	100.78	105.44	242.24	201.03	**	
		\bar{x}	99	90	124	74	77		
		s^2	51.80	68.10	70.00	362.00	280.00		
100-kernel weight, g		1	\bar{x}	5.0	4.8	5.4	4.9	5.2	*
			s^2	0.08	0.11	0.10	0.30	0.22	
			\bar{x}	4.9	5.0	5.4	5.0	5.2	
	2	s^2	0.09	0.11	0.11	0.22	0.20	N.S	
		\bar{x}	5.0	5.3	5.4	4.6	4.7		
		s^2	0.10	0.12	0.11	0.32	0.25		
	Grain yield plant ⁻¹ , g	1	\bar{x}	31	23	30	44	49	**
			s^2	18.44	20.28	13.11	275.77	224.70	
			\bar{x}	51	23.00	56	46	47	
2		s^2	20.93	20.28	35.07	180.00	131.97	**	
		\bar{x}	26	21	26	49	49		
		s^2	32.22	42.26	31.98	318.14	265.32		

1stCross (Gemmeiza 11 X Sakha 94), 2ndCross (Gemmeiza 9 X Sakha 94), 3rdCross (Line 1 X Giza 168)

*and ** indicate significant at 0.05 and 0.01 levels of probability, respectively.

The t-test performed between parents of each cross (Table 2) showed significantly differences at most cases in all crosses under the study, except of spike length and 100-kernel weight in the 2nd cross (Gem. 9 X S.94). Therefore, a considerable amount of genetic variations were existed among the parents in this study. These results are in agreement with those reported by Sultan *et al.* (2011), Abd El-Rahman (2013) and Abd El-Hamid and El-Hawary (2015).

Gene effects

The five parameters were used to estimate the nature of gene action (Table 3). The determined F₂ mean effects (m), were found to be highly significant for all traits under the study in the all crosses, indicating the ability to enhance the performance of these traits by pedigree selection.

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

Trait	Cross	m	d	h	l	i	E1	E2
Plant height	1	111.00**	1.00**	-23.33**	82.67**	-24.33**	-7.50**	7.00**
	2	122.00**	-2.50**	-21.33**	-5.33	-22.83**	10.25**	30.50**
	3	107.00**	-13.50**	9.33**	37.33**	-20.17**	-12.75**	-25.50**
No. of spikes plant ⁻¹	1	10.00**	3.00**	-6.67**	21.33**	0.33	-2.50**	1.00
	2	12.00**	-3.00**	-3.33**	2.67	-7.33**	0.01	2.00**
	3	12.00**	-1.00*	-0.67	-2.67	-4.67**	2.00**	4.00**
Spike length	1	12.29**	-1.54**	-2.34**	15.92**	-3.32**	-3.86**	-4.56**
	2	12.97**	0.11	-0.77	10.03**	3.20**	-4.00**	-6.35**
	3	13.22**	-1.02**	-2.09**	16.77**	-4.27**	-3.07**	-3.01**
No. of kernels spike ⁻¹	1	76.73**	3.32*	4.47	85.39**	-0.90	-17.58**	-26.73**
	2	64.10**	-11.50**	-15.74**	55.08**	-35.24**	-7.65**	-0.54
	3	74.04**	4.29**	24.87**	152.45**	3.15	-35.40**	-64.18**
100-kernel weight	1	4.90**	0.10*	-0.46**	2.93**	-0.76**	-0.25**	0.10
	2	5.0**	-0.05	-0.26*	2.13**	-0.81**	-0.17**	0.05
	3	4.60**	-0.15**	0.26*	2.66**	-0.28	-0.67**	-1.15**
Grain yield plant ⁻¹	1	44.00**	4.00**	-22.67**	-10.67	-17.67**	15.50**	41.00**
	2	46.00**	14.00**	4.00	32.00**	13.00**	-0.50	1.00
	3	49.00**	2.50**	-15.33**	-61.33**	-12.83**	24.25**	48.50**

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

1stCross (Gemmeiza 11 X Sakha 94), 2ndCross (Gemmeiza 9 X Sakha 94), 3rdCross (Line 1 X Giza 168)

m=mean effect d=additive effect h=dominance effect
i=additive × additive effect l=dominance × dominance effect

The additive gene effects, (d) were found to be significantly positive for plant height, No. of spikes plant⁻¹, 100-kernel weight in the 1st cross (Gem. 11 X S.94), No. of kernels spike⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168), also, grain yield plant⁻¹ in the three crosses under the study. These findings obtained that selection using the pedigree method may be more effective in improving such characters. Otherwise, significant negative additive effects were recorded for plant height, No. of spikes plant⁻¹ in the 2nd cross (Gem. 9 X S.94) and the 3rd cross (L.1 X G.168), spike length in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168), No. of kernels spike⁻¹ in the 2nd cross (Gem. 9 X S.94) and 100-kernel weight in the 3rd cross (L.1 X G.168). These findings showed that the genetic materials that used in this research have decreasing alleles expressions. The present findings were greatly agreed with those obtained by El-Awady (2011), Hammad (2014), Al-Bakry *et al.* (2017) and Abd El-Hamid and Ghareeb (2018).

Regarding to the dominance gene effects (h), were significantly positive for plant height, No. of kernels spike⁻¹ and 100-kernel weight in the 3rd cross (L.1 X G.168). These results indicated that dominance gene effects were involved in the heredity of these traits. Meanwhile, the negative values of (h) were observed for plant height, No. of spikes plant⁻¹, 100-kernel weight in the 1st cross (Gem. 11 X S.94) and the 2nd cross (Gem. 9 X S.94), spike length, grain yield plant⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168) and No. of kernels spike⁻¹ in the 2nd cross (Gem. 9 X S.94). These findings reported that

the alleles responsible for less values of these traits were dominant over the alleles contributing high values. These findings are in general agreement with those obtained by Abd El-Rahman (2013), Hammad (2014), Al-Bakry *et al.* (2017) and Abd El-Hamid and Ghareeb (2018).

With respect to dominance x dominance (l) type of gene action was significant and positive for plant height in the 1st cross (Gem.11 X S.94) and the 3rd cross (L.1 X G.168), No. of spikes plant⁻¹ in the 1st cross (Gem. 11 X S.94), spike length, No. of kernels spike⁻¹, 100-kernel weight for the three crosses under the study and grain yield plant⁻¹ in the 2nd cross (Gem. 9 X S.94). However, negative significant value was detected for grain yield plant⁻¹ in the 3rd cross (L.1 X G.168).Meanwhile, additive × additive type of gene effects(i),were significant with positive values for spike length and grain yield plant⁻¹ in the 2nd cross (Gem.9 X S.94). So, selection in early segregation generation in wheat breeding program might be effective for these traits. However, significant negative values were detected for plant height in all crosses, No. of spikes⁻¹ plant in the 2nd cross (Gem. 9 X S.94) and the 3rd cross (L.1 X G.168), spike length and grain yield plant⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168), No. of kernels spike⁻¹ in the 2nd cross (Gem. 9 X S.94) and 100-kernel weight in the 1st cross (Gem. 11 X S.94) and the 2nd cross (Gem. 9 X S.94). These results makes selection to improve them in the early generations could not be successful. These findings are in agree with those previously obtained by Hammad (2014), Al-Bakry *et al.*

(2017), Zaazaa (2017) and Abd El-Hamid and Ghareeb (2018).

Significantly positive F_2 deviations (E_1) were detected for plant height in the 2nd cross (Gem. 9 X S.94), No. of spikes plant⁻¹ in the 3rd cross (L.1 X G.168), grain yield plant⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168). In the meantime, (E_1) was found to be significant and negative for plant height in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168); No. of spikes plant⁻¹ in the 1st cross (Gem. 11 X S.94) and spike length, No. of kernels spike⁻¹, 100-kernel weight in all studied crosses This may indicate that epistatic gene effects played a major role in the heredity of such traits. Moreover, insignificant F_2 deviation (E_1) was observed for No. of spikes plant⁻¹ and grain yield plant⁻¹ in the 2nd cross (Gem. 9 X S.94). which indicates that the effects of epistatic genes have a minor role in the heredity of such traits. Similar trend was obtained earlier by Koumber and El-Gammaal (2012).

F_3 deviation values (E_2) were significantly positive for plant height in the 1st cross (Gem. 11 X S.94) and the 2nd cross (Gem. 9 X S.94), No. of spikes plant⁻¹ in the 2nd cross (Gem. 9 X S.94) and the 3rd cross (L.1 X G.168), grain yield plant⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168). Otherwise, significant and negative (E_2) values were reported for plant height, 100-kernel weight in the 3rd cross (L.1 X G.168), spike length in the three crosses under the study, No. of kernels spike⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168). These findings would demonstrate the presence of epistasis gene effects to such an extent that a breeding program requires a great deal of attention. These results agree with those previously reported by Koumber and El-Gammaal (2012).

On general the obtained findings reported that the effects of additive, dominance and epistasis were important in the inheritance of most studied traits in the three crosses under the study. These findings in general agree with El-Hawary (2010), Sultan *et al.* (2011), Abd El-Hamid and El-Hawary (2015) and Abd El-Hamid and Ghareeb (2018).

Heterosis and inbreeding depression

Heterosis percentage relative to mid and better parents, inbreeding depression percentage for all traits in the three crosses under the study are presented in (Table 4). The possibility of creating hybrid cultivars of self-pollinated crops like wheat has been investigated by many plant breeders.

The results revealed significantly positive heterosis over mid-parents for both plant height and No. of kernels spike⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168), No. of spikes plant⁻¹ and spike length in the 3rd cross (L.1 X G.168), 100-kernel weight and grain yield plant⁻¹ in the three crosses under the study.

With respect to heterosis over the better parent, significantly positive values were detected for No. of spikes plant⁻¹ and No. of kernels spike⁻¹ in the 3rd cross (L.1 X G.168), 100-kernel weight in the 1st cross (Gem. 11 X S.94) and the 2nd cross (Gem. 9 X S.94) in addition to grain yield plant⁻¹ in the 2nd cross (Gem. 9 X S.94). These findings showed that the trend of dominance was across the best respective parent. The significant heterotic effect might be due to the dominance and/or dominance × dominance effects, confirming the previous results. These findings in general agree with Zaazaa *et al.* (2012), Abd El-Rahman (2013) and Abd El-Hamid and Ghareeb (2018). The feasibility of growing hybrid wheat cultivars mainly depends on the significant superiority of yield as well as the other contributing characters compared to the current commercial cultivars (Mahrous, 1998). thus, heterosis over better parent may be useful in identifying the best hybrid combinations (Prasad *et al.*, 1988).

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

Trait	Cross	Heterosis		I.D	Component of variance			(H/D) ^{1/2}
		MP	BP		E	D	H	
Plant height	1	2.56**	1.69	7.50**	8.73	84.64	79.06	1.03
	2	-3.08	-5.17	-10.91	12.97	2.11	236.68	0.09
	3	2.11**	-8.33	11.57**	1.93	41.57	41.80	1.00
No. of spikes plant ⁻¹	1	-7.69	-25.00	16.67**	2.55	1.85	27.20	0.26
	2	-15.38	-31.25	-9.09	2.54	4.46	28.00	0.40
	3	22.22**	10.00**	-9.09	12.56	5.42	24.04	0.47
Spike length	1	-12.18	-19.38	18.61**	1.04	0.51	2.59	0.44
	2	-19.90	-20.37	14.05**	1.23	0.83	1.68	0.70
	3	0.96**	-4.99	19.24**	1.09	0.59	2.36	0.50
No. of kernels spike ⁻¹	1	13.58**	9.47	23.51**	112.08	75.94	143.24	0.73
	2	-4.76	-17.65	8.43**	98.85	60.97	82.42	0.86
	3	32.13**	26.38**	40.57**	63.30	134.70	164.00	0.91
100-kernel weight	1	10.20**	8.00*	9.26**	0.10	0.04	0.16	0.48
	2	9.09**	8.00*	7.41**	0.11	0.08	0.04	1.49
	3	4.85**	1.89	14.81**	0.12	0.06	0.15	0.66
Grain yield plant ⁻¹	1	11.11**	-3.23	-46.67	17.28	156.35	102.14	1.24
	2	51.35**	9.80*	17.86**	25.43	58.51	96.06	0.78
	3	10.64**	0.01	-88.46	35.49	177.01	105.64	1.29

1stCross (Gemmeiza 11 X Sakha 94), 2ndCross (Gemmeiza 9 X Sakha 94), 3rdCross (Line 1 X Giza 168)

I.D=Inbreeding depression E=Environmental variance D=Additive variance

H=Dominance variance (H/D)^{1/2}=Average degree of dominance

Inbreeding depression, estimated as a reductions in the performance of F_2 generation compared to F_1 generation are shown in (table 4). Significantly positive

inbreeding depression values were detected for plant height in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168), No. of spikes plant⁻¹ in the 1st cross (Gem.

11 X S.94), spike length, No. of kernels spike⁻¹, 100-kernel weight in all studied crosses and grain yield plant⁻¹ in the 2nd cross (Gem. 9 X S.94). These results agree with those previously reported by Zaazaa (2017) and Abd El-Hamid and Ghareeb (2018).

Components of variance and dominance degree

Estimates of components of variance and degree of dominance (H/D)^{1/2} are provided in Table 4. The obtained results reported that the dominance variance (H) was larger than additive variance (D) for all traits under the study in the three crosses, except for plant height in the 1st cross (Gem. 11 X S.94), 100-kernel weight in the 2nd cross (Gem. 9 X S.94) and grain yield plant⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168) which showed high values for additive variance. These results indicated that dominance variances played the greatest role in the heredity of most of the traits under the study. These findings are in good agreement with those reported by Sultan *et al.* (2011), Abd El-Rahman (2013) and Abd El-Hamid and Ghareeb (2018).

The average degree of dominance (H/D)^{1/2} for most of the studied traits in the three crosses is less than unity (Table 4), except plant height in the 1st cross (Gem. 11 X S.94), 100-kernel weight in the 2nd cross (Gem. 9 X S.94) and grain yield plant⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168). These findings suggest the greatest role in regulating these traits with partial-dominance gene effects. Otherwise, (H/D)^{1/2} parameter was more than unity for plant height in the 1st cross (Gem. 11 X S.94), 100-kernel weight in the 2nd cross (Gem. 9 X S.94) and grain yield plant⁻¹ in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168). These results back up indicate the presence of over-dominance, suggesting that early selection might be improve such traits. These findings are in agreement with those obtained by Farooq *et al.* (2010) , Abd El Rahman (2013) and Abd El-Hamid and Ghareeb (2018).

Heritability and genetic advance

Assessment of heritability of various traits is evidence of a plant breeder predicting the action of successive generations and helping to estimate the response selection. The heritability values in broad sense were high and ranged from 51.41 to 97.74% for all traits in all studied crosses revealing that most of the phenotypic variability were due to genetic effects (Table 5).

The highest values of (H_{n.s}) were detected for plant height in the 2nd cross (Gem. 9 X S.94) being 94.01%, No. of spikes plant⁻¹ in all crosses under the study, spike length in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168), 100-kernel weight in the 1st cross (Gem. 11 X S.94) and grain yield plant⁻¹ in the 2nd cross (Gem. 9 X S.94) being 53.37% ensuring that most of the genetic variations of these traits is mainly due to the additive effects which makes efficient selection in the early segregation generations . However, moderate estimates of (H_{n.s}) were detected for plant height in the 1st cross (Gem. 11 X S.94) and the 3rd cross (L.1 X G.168) being 45.85 % and 49% respectively. Moreover, moderate (H_{n.s}) estimates were detected for spike length in the 2nd cross (Gem. 9 X S.94), No. of kernels spike⁻¹ in the both 1st (Gem. 11 X S.94) and 3rd (L.1 X G.168) crosses, 100-kernels weight in the 3rd cross (L.1 X G.168) and grain yield plant⁻¹ in the 1st cross(Gem. 11 X S.94) being 37.04 %.

Table 5. Heritability and percentage of genetic advance for the traits under the study in three crosses of bread wheat.

Trait	Cross	Heritability		Genetic advance	
		H _{bs}	H _{n.s}	Δ g	Δ g %
Plant height	1	94.94	45.85	12.40	11.17
	2	94.85	94.01	30.73	25.19
	3	97.74	49.00	9.32	8.71
No. of spikes plant ⁻¹	1	91.94	86.08	9.97	99.68
	2	92.74	80.00	9.75	81.25
	3	70.11	57.21	7.64	63.66
Spike length	1	74.90	62.60	2.62	21.34
	2	67.11	44.92	1.79	13.80
	3	72.94	58.42	2.42	18.30
No. of kernels spike ⁻¹	1	66.17	43.24	16.21	21.13
	2	59.19	34.02	10.91	17.02
	3	82.51	45.30	17.76	23.98
100-kernel weight	1	67.21	54.55	0.62	1.27
	2	51.41	16.00	0.15	0.31
	3	64.52	44.79	0.52	1.14
Grain yield plant ⁻¹	1	93.74	37.04	12.67	28.80
	2	85.87	53.37	14.75	32.06
	3	88.85	33.21	12.20	24.90

1st Cross (Gemmeiza 11 X Sakha 94),

2nd Cross (Gemmeiza 9 X Sakha 94), 3rd Cross (Line 1 X Giza 168)

Low values of (H_{n.s}) were recorded for both No. of kernels spike⁻¹ and 100-kernels weight in the 2nd cross (Gem. 9 X S.94) being 34.02 and 16.0, respectively. Moreover, grain yield plant⁻¹ showed also low values of (H_{n.s}) being 33.21 % in the 3rd cross (L.1 X G.168). Which makes selection for these traits would be of less effectiveness in these crosses. It could be concluded that the differences in the estimated heritability values in the studied traits may be due to the presence of both additive and non-additive genetic variances in these heredity. Similar findings were obtained by Sultan *et al.* (2011), Abd El-Hamid and El-Hawary (2015) and Abd El-Hamid and Ghareeb (2018).

The findings of the present study reported that the expected genetic gain (Δ g) was ranged from 9.32 to 30.73 for plant height, 7.64 to 9.97 for No. of spikes plant⁻¹, 1.79 to 2.62 for spike length, 10.91 to 17.76 for No. of kernels spike⁻¹, 0.15 to 0.62 for 100-kernels weight and from 12.20 to 14.64 for grain yield plant⁻¹ (Table 5). The highest expected genetic gain was found to be correlated with high heritability in narrow sense estimated in all studied characters. Which makes selection more effective. This conclusion coincide with the findings of Manal (2009) pointed out that, traits with predicted genetic improvement and high heritability could be basically considered or making selection for these traits were mainly affected by the major effects of additive gene action. Meanwhile, Dixit *et al.* (1970) noted that, high genetic gain is often not correlated with high heritability, but high genetic advance should be correlated with high heritability in order to allow efficient selection.

Generally, the most biometrical parameters had high values for most of the studied traits. therefore, it could be noted that such crosses are important to wheat breeding program for genetic yield advancement.

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السلوك الوراثي لبعض الصفات المحصولية باستخدام نموذج العشائر الخمس في ثلاثة هجن من قمح الخبز عصام معوض علي جبريل ، محمد نبيل عوض الهواري و محمد يوسف المصري قسم بحوث القمح - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية - مصر

أجريت هذه الدراسة في محطة البحوث الزراعية بالجميزة ، مركز البحوث الزراعية، خلال أربعة مواسم من 2015/2016 إلى 2018/2019 بهدف دراسة طبيعة الفعل الجيني ونمط التوريث لصفات طول النبات، عدد السنبال للنبات، طول السنبل، عدد حبوب السنبل، وزن المائة حبة و محصول الحبوب للنبات لاستخدامها كمؤشرات للانتخاب للإنتاجية العالية لمحصول الحبوب لثلاث هجن من قمح الخبز و هي جميزة 11× سحا 94 ، جميزة 9 × سحا 94 و السلالة 1 × جميزة 168 باستخدام نموذج العشائر الخمس (الأبوين ، الجيل الأول، الجيل الثاني و الجيل الثالث). و قد أشارت نتائج اختبار "ت" إلي وجود اختلافات معنوية بين الأبوين لكل هجين في معظم الصفات المدروسة للثلاث هجن تحت الدراسة. كانت التأثيرات الجينية المضيفة والسيادية و التوقيه مهمة في توارث معظم الصفات المدروسة للهجن الثلاث. كما أشارت درجة السيادة إلي تحكم السيادة الجزئية في كل الصفات للهجن الثلاث تحت الدراسة ما عدا صفة طول النبات في الهجين الأول، و وزن المائة حبة في الهجين الثاني و محصول الحبوب/نبات في الهجين الأول و الثالث. كما أشارت النتائج إلي أن تقديرات كفاءة التوريث بالمعنى الواسع والضيق كانت متوسطة إلي مرتفعة لمعظم الصفات المدروسة للهجن الثلاث تحت الدراسة. و قد كانت تقديرات التحسين الوراثي المتوقع من الانتخاب في الجيل الثاني متوسطة إلي مرتفعة في معظم الصفات للهجن الثلاث تحت الدراسة. بناء على هذه النتائج، تصبح هذه الهجن الثلاث موضع اهتمام في برامج التربية للتحسين الوراثي لمحصول القمح مع مراعاة تأخير الانتخاب للأجيال اللاحقة المتأخرة.