

II.6 GENERATION MEAN ANALYSIS FOR SOME QUANTITATIVE TRAITS IN BREAD WHEAT. I-AGRONOMIC CHARACTERISTICS

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Abstract

Six populations; P₁, P₂, F₁, F₂, BC₁ and BC₂ were used in the present study to determine genetic parameters for some quantitative traits such as earliness, and yield and its components. Means of the six generations were recorded for number of days to heading, number of days to maturity, grain filling period, grain filling rate, plant height, number of spikes plant⁻¹, number of kernels spike⁻¹, 100-kernel weight and grain yield plant⁻¹ in three crosses (Sakha 93 × Sakha 69, Sids 12 × Sids 13 and Sids 13 × Sakha 69) generated from four diverse parents. The experiment was conducted at Sakha Agric. Res. Station in 2010/2011, to 2012/2013 seasons. The t-test showed high significant differences among parental genotypes for most studied traits. The genetic analysis showed that the genetic variance among F₂ plants was different for all studied traits among the three wheat crosses. Results indicated that additive, dominance and epistatic effects were important in the inheritance of all traits in most cases in all crosses. The average degree of dominance indicated that partial dominance was important in controlling most studied traits in the three crosses. Meanwhile, days to heading, number of kernels spike⁻¹ in cross 2 and 100-kernel weight in cross 1 were controlled by over-dominance gene effect. The heritability in broad and narrow sense was moderate to high for most studied traits in most cases. The values of expected genetic advance (Δg) were moderate to high for most studied yield characteristics in the three studied crosses. Meanwhile, the values of (Δg) for number of days to heading, number of days to maturity and grain filling period in the three crosses were relatively low.

Keywords: *Triticum aestivum* L., six population analysis, scaling test, gene action, heritability.

INTRODUCTION

Wheat is the most important cereal crop in Egypt. However, the gap between the local production and consumption is wide due to increasing population and limited cultivated area. It has become necessary to develop genotypes characterized by superior performance (Shehab El-Din, 1993). Therefore, wheat breeders are dedicating their efforts to improve the yield potential of wheat to meet the future goals by developing new cultivars with desirable genetic makeup. Grain yield is a complex characteristic made up of the interaction among different yield components and environmental factors. So, it is difficult to improve yield through breeding (especially in the early generations) if yield is the only factor recorded, suggesting

that component characters should also be used as selection criteria for yield improvement. Therefore, it is necessary to know the genetic behavior of yield components (Misr et al., 1994). Consequently, information about genetic diversity and relationships among breeding materials are essential for plant breeders to improve this crop.

Understanding genetic factors controlling agronomic characteristics is a primary step for breeding studies. Generation mean analysis is a simple estimate but useful for estimating gene effects for a polygenic trait. Its greatest merit lying in the ability to estimate epistatic gene effects such as additive \times additive, dominance \times dominance and additive \times dominance effects (Mather and Jinks, 1982).

Based on the evaluated genetic parameters, selection in advanced generations might be effective for number of kernels per spike, kernel weight, fertile tillers number and grain yield, due to dominance and epistatic effects (Erkul et al., 2010). High heritability estimates resulting in high genetic advance for yield components in wheat offer better scope for selection of genotypes in early segregating generations (Singh and Chatrath, 1992 and Memon et al., 2005). The heritability values become a measure of the genetic relationship between parents and progeny; hence considerable research work has been carried out to incorporate the desirable genes in present wheat cultivars to increase the productivity of the crop (Memon et al., 2007).

The present study was carried out to obtain information about gene action, available genetic variability and heritability estimates for some agronomic traits in three bread wheat crosses. These information would be useful in the approval of efficient breeding strategies in wheat breeding.

MATERIALS AND METHODS

The materials used in this investigation included four bread wheat genotypes (*Triticum aestivum* L. Emend. Thell.), representing a wide range of diversity for several agronomic traits, names and pedigree of these parental genotypes are presented in Table 1.

Table 1. Name and pedigree of the four parental genotypes

Genotype	Pedigree
1- Sakha 93	SAKHA92/TR810328 S.8871-1S-2S-1S-0S
2- Sakha 69	Inia / RL 4220 // 7c / Yr "S" CM 15430 -2S-6S-0S-0S
3- Sids 12	BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CHAT"S"/6/MAY A/VUL//CMH74A.630/4*SX SD7096-4SD-1SD-1SD-0SD
4- Sids 13	KAUZ"S" //TSI / SNB"S" ICW94-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP-0AP-0SD

In 2010/2011 season, three different crosses were performed using four wheat genotypes. The established crosses were made as follows: Cross 1 = (Sakha 93 x Sakha 69), Cross 2 = (Sids 12x Sids 13) and Cross 3= (Sids 13 x Sakha 69).

Next season, the F_1 of each cross was back crossed to its respective parent to produce BC_1 ($F_1 \times P_1$) and BC_2 ($F_1 \times P_2$). The F_1 plants were selfed to produce F_2 seeds. In 2012/2013 season, the six populations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were studied in a final experiment. This experiment was designed in a randomized complete block design with three replications at Sakha Agric. Res. Stn., Kafer El-Sheikh Governorate. Each replicate consisted of 21 rows, one row for each of P_1 , P_2 and F_1 , 10 rows for F_2 , 3 rows for each of BC_1 and BC_2 as well as two border rows. Each row was 4-m long and 30-cm apart with 20-cm plant spacing. Twenty grains were manually drilled in each row on December 1, 2012. All other cultural practices were applied as recommended for wheat cultivation. The two outside plants from each row were excluded to avoid the border effect.

Studied traits

Data of the following traits were recorded on 10 random plants of each P_1 , P_2 , and F_1 ; 90 plants of F_2 and 30 plants on each of BC_1 and BC_2 in each replicate for: number of days to heading, number of days to maturity, grain filling period and grain filling rate, plant height, number of spikes plant⁻¹, number of kernels spike⁻¹, 100-kernel weight and grain yield plant⁻¹.

The collected data were analyzed to test the differences among parental genotypes for each cross using "t" test before the biometrical analysis. Moreover, "F" ratio was calculated to test the significance of genetic variance among F_2 plants according to Allard (1999).

Scaling test and gene action parameters: Simple scaling tests (A, B and C) were applied according to Mather and Jinks (1982) to test the presence of non-allelic interactions. According to Jinks and Jones (1958), the following notation for gene effects have been used: additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) effect. The type of epistasis was determined only when dominance (h) and dominance × dominance (l) effects were significant.

Genetic parameters: The genetic components; mean degree of dominance $(H/D)^{1/2}$, heritability in broad sense (h^2_{bs}) and narrow sense (h^2_{ns}), heterosis above better parent were calculated according to Mather and Jinks (1982) and genetic advance as percentage ($\Delta g\%$) of the F_2 mean were estimated as reported by Allard (1999).

RESULTS AND DISCUSSION

Generation mean

The t-test performed between parents of each cross (Table 2) showed significant or highly significant differences in most cases in the three studied crosses, except for grain filling period in cross 3, grain filling rate in cross 2, number of spikes plant⁻¹, 100-kernel weight and grain yield plant⁻¹ in cross 1. Therefore, a considerable amount of genetic variation existed among the parents, used in this study.

F-ratio and scaling test

The genetic variance among F_2 plants was genetically different for all studied traits in the three crosses (Table 3). These results assured the presence of enough variability in the material under study. Consequently, the various genetic parameters used in this investigation were computed for all studied traits.

Results of scaling test of the studied traits in the three wheat crosses are presented in Table 3. A and B scaling tests provide an evidence for the presence of i (additive × additive), j (additive × dominance) and l (dominance × dominance) gene interactions. The C scaling test provides test for l (dominance × dominance) epistasis. The calculated values of A, B and C scaling tests for all studied traits in the three crosses were significant, except for grain filling period in cross 2, number of spikes plant⁻¹ in cross 3 and 100-kernel weight in cross 1. These findings indicated that the six parameter model is valid to explain the nature of gene action for these traits. Meanwhile, non of A, B or C scaling tests were significant, indicating the adequacy of the three-parameter model to explain the type of gene action for grain filling period in cross 2, number of spikes plant⁻¹ in cross 3 and 100-kernel weight in cross 1. These

results are in general agreement with those obtained by Moussa (2010); Zaazaa *et al.* (2012) and Abd El-Rahaman (2013).

Type of gene action

The results in Table 4 indicated that the mean effect (m) was significant for all traits in the three crosses, except for grain filling rate and grain yield plant⁻¹ in cross 3, indicating that these traits are quantitatively inherited.

Additive gene effects (d) were significant or highly significant in most cases for all traits of the three crosses except for grain filling period in cross 3, grain filling rate in cross 2, number of spikes plant⁻¹, 100-kernel weight and grain yield plant⁻¹ in cross 1.

Dominance gene effects (h) were significant or highly significant for days to heading in cross 1 and cross 2, days to maturity in cross 2 and cross 3, grain filling period; grain filling rate and grain yield plant⁻¹ in cross 3, plant height and number of spikes plant⁻¹ in cross 2 and 100-kernel weight in cross 2 and cross 3.

Additive × additive gene effects (i) were significant for days to heading in cross 2, days to maturity in cross 2 and cross 3, grain filling rate in cross 3, plant height in cross 2, number of spikes plant⁻¹ in cross 2, number of kernels spike⁻¹ in cross 2 and cross 3, 100-kernel weight in cross 2 and cross 3 and grain yield plant⁻¹ in cross 3.

Additive × dominance gene effects (j) were significant or highly significant for days to heading in cross 3, days to maturity in cross 1 and cross 3, grain filling period in cross 1, grain filling rate in cross 1 and cross 3, plant height in the three crosses, number of spikes plant⁻¹ in cross 1, number of kernels spike⁻¹ in cross 2 and cross 3 and grain yield plant⁻¹ in cross 1 and cross 3.

Dominance × dominance gene effects (l) were significant or highly significant for days to heading in cross 1 and cross 2, days to maturity in cross 2 and cross 3, grain filling period in cross 3, grain filling rate in cross 2 and cross 3, plant height in cross 2, number of spikes plant⁻¹ in cross 2, number of kernels spike⁻¹ in cross 1 and cross 2, 100-kernel weight in cross 2 and grain yield plant⁻¹ in cross 3.

Duplicate epistasis was observed, as revealed by significance in signs of (h) and (l), which exhibited significant epistasis, while similar signs of (h) and (l) indicated complementary epistasis. These findings illustrated that duplicate epistasis was prevailing for all traits in the three crosses under this study, except for grain filling rate in cross 1 and grain yield plant⁻¹ in cross 2, where complementary epistasis prevailed, indicating that duplicate epistasis was greater and more important when compared with the complementary epistasis for these traits. These results are in

harmony with those reported by Abd El-Aty *et. al.* (2005), El-Hawary (2010) and Sultan *et. al.* (2010).

These results indicated that additive, dominance and epistasis were important for inheritance of most studied traits in the three crosses. These results are in accordance with those reported by El-Hawary (2010), Sultan *et. al.* (2011) and Abd El-Rahman (2013).

Genetic components of variance

The estimates of different variance components as well as the average degree of dominance are presented in Table 5. The results indicated that additive variance component was larger than dominance one for most studied traits in the three crosses, except for days to heading, number of kernels spike⁻¹ in cross 2 and 100-kernel weight in cross 1. Results also indicated that additive variance played the greatest and the most important role in inheritance of these traits, so that selection for these traits may be effective in early segregating generations. Similar results were previously reported by El-Hawary (2010), Sultan *et. al.* (2011) and Abd El-Rahman (2013).

The average degree of dominance (Table 5) was less than unity in most traits under the study, except for days to heading, number of kernels spike⁻¹ in cross 2 and 100-kernel weight in cross 1, where it exceeded the unity. These results are in agreement with those reported by Sultan *et. al.* (2010 and 2011) and Abd El-Rahman (2013).

Heterosis, heritability and expected genetic advance

The negative heterosis is desirable for days to heading, days to maturity and grain filling period. However, for grain filling rate, plant height, number of spikes plant⁻¹, number of kernels spike⁻¹, 100-kernel weight and grain yield plant⁻¹, the positive heterosis is the target of breeding programs. The results in Table 6 indicated that the positive significant heterosis over the mid-parent for grain filling rate was evident in the three crosses, number of spikes plant⁻¹ in cross 1, 100-kernel weight in cross 1, grain yield plant⁻¹ in cross 1 and cross 2. The results showed positive significant heterosis over the better parent for grain filling rate in cross 1 and cross 2, number of spikes plant⁻¹ in cross 1, 100 kernel weight in cross 1 and grain yield plant⁻¹ in cross 1 and cross 2. These results are in accordance with those reported by Sultan *et. al.* (2011), Abd El-Rahman (2013).

Results revealed that high significant positive inbreeding depression values were obtained for most studied traits in the three crosses as shown in Table 6. These

results are expected since the expression of heterosis in F_1 will be reduced in F_2 due to selfing and starting homozygosity. These results are in accordance with the findings of Moussa (2010), Zaazaa *et. al.* (2012) and Abd El-Rahman (2013).

The heritability values in broad sense (Table 6) were moderate to high for all studied traits in the three studied crosses revealing that most of the phenotypic variability in these traits was due to genetic effects. Simultaneously, the values of heritability in narrow sense were moderate to high for all traits in the three crosses under this study, except for days to heading in cross 2, number of spikes plant⁻¹ in cross 1 and 100-kernel weight in cross 1. These results reflect the importance of additive gene action in controlling these traits; therefore selection could be practiced in early segregating generations. Meanwhile, the remaining traits which had low ($h_{n,s}$) estimates, reflecting the role of environmental factors and dominance gene action in inheritance system of these traits. Similar results were obtained by Sultan *et. al.* (2010 and 2011) and Abd El-Rahman (2013).

As shown in Table 6, the values for expected genetic advance (Δg %) were low for number of days to heading, number of days to maturity and grain filling period in the three studied crosses. However, for grain filling rate, plant height, number of spikes plant⁻¹, number of kernels spike⁻¹, 100-kernel weight and grain yield plant⁻¹, moderate to high selection gains were obtained in the three crosses under this study. These results indicate the possibility of practicing selection in early segregating generation to enhance grain filling rate and hence selecting high yielding genotypes. These results are in agreement with those of El-Hawary (2010), Sultan *et. al.* (2011), Abd El-Rahman (2013) and Khaled (2013).

Table 2. Means (\bar{X}) and variances (S^2) of P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 populations of studied traits for three crosses of bread wheat.

Trait	Cross	Stat.	P_1	P_2	F_1	BC_1	BC_2	F_2	t. par.
Days to heading (day)	1	\bar{X}	89.36	92.18	92.03	92.59	93.31	92.90	**
		S^2	2.09	3.78	4.24	15.85	11.03	18.58	
	2	\bar{X}	92.43	95.04	95.04	95.30	97.00	95.35	**
		S^2	2.53	1.71	2.32	14.47	16.40	17.19	
	3	\bar{X}	95.04	92.18	94.60	93.81	97.08	95.93	**
		S^2	1.71	3.78	2.73	18.37	15.46	25.17	
Days to maturity (day)	1	\bar{X}	147.25	145.65	146.57	146.71	147.43	146.90	**
		S^2	3.82	5.49	5.50	11.05	9.44	13.73	
	2	\bar{X}	144.43	148.28	145.39	147.35	149.35	147.36	**
		S^2	1.07	2.71	3.16	11.77	6.78	15.72	
	3	\bar{X}	148.28	145.65	147.47	145.41	147.39	147.70	**
		S^2	2.71	5.49	3.91	15.62	11.55	18.14	
Grain filling period (day)	1	\bar{X}	57.89	53.47	54.53	54.12	54.11	54.00	**
		S^2	2.32	3.64	4.19	12.91	10.51	17.03	
	2	\bar{X}	52.00	53.24	50.35	52.05	52.33	52.03	*
		S^2	3.91	4.94	9.33	19.02	18.53	28.70	
	3	\bar{X}	53.24	53.47	52.87	51.61	50.32	51.77	NS
		S^2	4.94	3.64	3.09	30.95	29.73	46.08	
Grain filling rate (g/day)	1	\bar{X}	0.66	0.80	1.15	1.07	0.84	1.00	*
		S^2	0.04	0.08	0.16	0.27	0.19	0.32	
	2	\bar{X}	0.96	1.21	1.82	1.14	1.37	1.29	NS
		S^2	0.26	0.25	0.21	0.33	0.39	0.47	
	3	\bar{X}	1.21	0.80	1.04	1.35	1.50	1.16	**
		S^2	0.25	0.08	0.09	0.37	0.39	0.47	

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

NS = Not significant

Cross 1= Sakha 93 × Sakha 69 Cross 2 = Sids 12×Sids 13 Cross 3 = Sids 13×Sakha 69

Table 2. Cont'd

Trait	Cross	Stat.	P ₁	P ₂	F1	BC1	BC2	F2	t. par.
Plant height	1	\bar{X}	91.43	107.94	102.83	103.24	97.36	100.79	**
		s^2	5.29	6.43	8.07	188.82	184.58	342.39	
	2	\bar{X}	97.14	106.60	97.61	101.63	99.09	96.87	**
		s^2	6.43	5.67	6.52	147.29	123.01	255.01	
	3	\bar{X}	106.60	107.94	106.83	107.13	95.13	98.69	*
		s^2	5.67	6.43	6.01	272.84	198.04	344.51	
Number of spikes plant ⁻¹	1	\bar{X}	32.32	30.47	35.27	40.59	30.66	34.04	NS
		s^2	55.19	54.39	89.37	198.37	105.53	181.66	
	2	\bar{X}	18.72	36.94	27.91	20.43	30.17	29.80	**
		s^2	53.08	53.18	47.90	90.35	145.60	165.04	
	3	\bar{X}	36.94	30.47	31.04	32.06	30.27	32.71	**
		s^2	53.18	54.39	36.65	169.89	123.04	202.93	
Number of kernels spike ⁻¹	1	\bar{X}	76.96	66.25	62.70	73.41	70.41	69.27	**
		s^2	119.21	112.33	128.84	199.65	218.62	296.13	
	2	\bar{X}	120.50	104.52	111.04	102.18	83.29	86.23	**
		s^2	90.55	81.93	102.68	449.61	593.40	663.54	
	3	\bar{X}	104.52	66.25	72.54	80.44	86.94	87.24	**
		s^2	81.93	112.33	149.86	259.87	301.00	399.66	
100 -kernel weight	1	\bar{X}	4.06	4.34	4.66	4.26	4.31	4.23	NS
		s^2	0.45	0.38	0.60	0.93	0.94	1.08	
	2	\bar{X}	6.23	4.77	3.94	5.31	4.26	4.02	**
		s^2	0.39	0.47	0.32	1.02	1.09	1.33	
	3	\bar{X}	4.77	4.34	3.46	4.06	3.84	4.17	*
		s^2	0.47	0.38	0.24	0.56	0.57	0.75	
Grain yield plant ⁻¹	1	\bar{X}	38.04	42.78	65.18	57.65	45.32	54.21	NS
		s^2	143.29	245.31	373.68	797.66	554.89	866.78	
	2	\bar{X}	51.16	67.24	88.50	59.78	74.20	66.29	**
		s^2	411.38	378.85	574.04	733.21	830.00	986.01	
	3	\bar{X}	67.24	42.78	55.21	67.86	73.96	58.08	**
		s^2	378.85	245.31	246.92	799.88	673.63	900.06	

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

NS = non significant

Cross 1= Sakha 93 × Sakha

Cross 2 = Sids 12×Sids 13

Cross 3 = Sids 13×Sakha 69

Table 3. F-ratio and scaling test for all studied traits in the three bread wheat crosses.

Trait	Cross	F ratio	A	B	C
Days to heading	1	**	3.79**	2.42**	6.01**
	2	**	3.12**	3.92**	3.83**
	3	**	-2.02*	7.38**	7.30**
Days to maturity	1	**	-0.40	2.64**	1.58
	2	**	4.87**	5.03**	5.93**
	3	**	-4.92**	1.67	1.92
Grain filling period	1	**	-4.19**	0.22	-4.43**
	2	**	1.75	1.08	2.18
	3	**	-2.89*	-5.70**	-5.38**
Grain filling rate	1	**	0.32*	-0.28*	0.22
	2	*	-0.51**	-0.29	-0.66*
	3	**	0.44**	1.15**	0.53*
Plant height	1	**	12.21**	-16.06**	-1.88
	2	**	8.50**	-6.03*	-11.49**
	3	**	0.82	-24.52**	-33.47**
Number of spikes plant ⁻¹	1	**	13.59**	-4.42	2.85
	2	**	-5.79*	-4.51	7.71
	3	**	-3.86	-0.98	1.36
Number of kernels spike ⁻¹	1	*	7.16	11.88**	8.48
	2	**	-27.18**	-48.99**	-102.18**
	3	**	-16.18**	35.08**	33.11**
100-kernel weight	1	*	-0.20	-0.37	-0.78
	2	**	0.43	-0.20	-2.82**
	3	*	-0.11	-0.10	0.65*
Grain yield plant ⁻¹	1	**	12.09	-17.32*	5.65
	2	*	-20.10*	-7.34	-30.22*
	3	**	13.28	49.94**	11.89

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

Cross 1 = Sakha 93 × Sakha 69 Cross 2 = Sids 12 × Sids 13 Cross 3 = Sids 13 × Sakha 69

Table 4. Types of gene action using generation means \pm standard errors for all studied traits in three bread wheat crosses.

Trait	Cross	M	d	H	i	j	l	Type of epistasis
Days to heading	1	90.57** \pm 1.53	-1.41** \pm 0.22	7.86** \pm 3.97	0.19 \pm 1.52	1.37 \pm 1.18	-6.4** \pm 2.58	Duplicate
	2	90.53** \pm 1.56	-1.3** \pm 0.19	14.76** \pm 4.1	3.21** \pm 1.55	-0.79 \pm 1.23	-10.24** \pm 2.64	Duplicate
	3	95.56** \pm 1.74	1.43** \pm 0.21	2.45 \pm 4.47	-1.95 \pm 1.73	-9.4** \pm 1.3	-3.41 \pm 2.84	Duplicate
Days to maturity	1	145.79** \pm 1.34	0.8** \pm 0.28	3.67 \pm 3.51	0.66 \pm 1.31	-3.05** \pm 1.11	-2.9 \pm 2.35	Duplicate
	2	142.39** \pm 1.34	-1.92** \pm 0.18	16.87** \pm 3.40	3.97** \pm 1.33	-0.15 \pm 0.98	-13.87** \pm 2.19	Duplicate
	3	152.13** \pm 1.53	1.32** \pm 0.26	-13.08** \pm 3.99	-5.17** \pm 1.51	-6.59** \pm 1.22	8.41** \pm 2.59	Duplicate
Grain filling period	1	55.22** \pm 1.45	2.21** \pm 0.22	-4.19 \pm 3.74	0.46 \pm 1.43	-4.42** \pm 1.11	3.5 \pm 2.43	Duplicate
	2	51.97** \pm 1.86	-0.62* \pm 0.27	1.86 \pm 4.78	-----	-----	-----	-----
	3	56.58** \pm 2.35	-0.12 \pm 0.27	-15.53** \pm 6	-3.22 \pm 2.33	2.81 \pm 1.73	11.82** \pm 3.77	Duplicate
Grain filling rate	1	0.91** \pm 0.2	-0.07* \pm 0.03	0.1 \pm 0.52	-0.18 \pm 0.2	0.59** \pm 0.16	0.14 \pm 0.35	complementary
	2	1.22** \pm 0.25	-0.12 \pm 0.06	-0.32 \pm 0.67	-0.13 \pm 0.24	-0.22 \pm 0.22	0.93** \pm 0.45	Duplicate
	3	-0.06 \pm 0.25	0.20** \pm 0.05	3.76** \pm 0.67	1.06** \pm 0.25	-0.71** \pm 0.21	-2.66** \pm 0.43	Duplicate

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

Cross 1 = Sakha 93 x Sakha 69 Cross 2 = Sids 12 x Sids 13 Cross 3 = Sids 13 x Sakha 69

m = mean effect d = additive effect h = dominance effect

i = additive x additive effect j = additive x dominance effect l = dominance x dominance effect

Table 4. Cont'd

Trait	Cross	m	d	H	i	J	L	Type of epistasis
Plant height	1	101.66**±6.08	-8.26**±0.31	-4.65±15.22	-1.97±6.07	28.27**±4.12	5.82±9.39	Duplicate
	2	87.9**±5.22	-4.73**±0.32	26.15*±13.03	13.97**±5.21	14.53**±3.52	-16.45*±8.03	Duplicate
	3	97.5**±6.44	-0.67*±0.32	-4.59±16.47	9.77±6.43	25.34**±4.62	13.93±10.26	Duplicate
Number of spikes plant ⁻¹	1	25.09**±5.02	0.93±0.96	25.66±13.26	6.31±4.93	18.01**±4.14	-15.48±8.96	Duplicate
	2	45.83**±4.6	-9.11**±0.94	-46.21**±11.96	-18**±4.5	-1.28±3.75	28.29**±7.85	Duplicate
	3	39.9**±5.09	3.24**±0.95	-19.88±13.21	-----	-----	-----	-----
Number of kernels spike ⁻¹	1	61.05**±6.17	5.36**±1.39	31.26±16.1	10.56±6.01	-4.72±5.13	-29.6**±10.81	Duplicate
	2	86.5**±9.33	7.99**±1.2	-25.61±24.31	26.01**±9.26	21.82**±7.22	50.16**±15.63	Duplicate
	3	99.59**±7.09	19.14**±1.27	-22.35±18.4	-14.2*±6.97	-51.26**±5.6	-4.7±12.24	Duplicate
100- kernel weight	1	3.99**±0.39	-0.14±0.08	0.3±1.04	-----	-----	-----	-----
	2	2.46**±0.42	0.73**±0.09	4.76**±1.11	3.05**±0.42	0.64±0.35	-3.28**±0.72	Duplicate
	3	5.42**±0.32	0.22**±0.08	-3.05**±0.84	-0.86**±0.31	-0.01±0.28	1.08±0.56	Duplicate
Grain yield plant ⁻¹	1	51.28**±11.6	-2.37±1.8	-2.21±28.07	-10.87±10.56	29.41**±8.55	16.1±18.83	Duplicate
	2	56.41**±11.6	-8.04**±2.57	7.43±30.62	2.78±11.31	-12.76±9.79	24.65±20.96	complementary
	3	3.68±11.14	12.23**±2.28	166.08**±29.29	51.33**±10.90	-36.66**±9.29	-114.55**±19.4	Duplicate

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

Cross 1 = Sakha 93 × Sakha 69 Cross 2 = Sids 12 × Sids 13 Cross 3 = Sids 13 × Sakha 69

m = mean effect

d = additive effect

h = dominance effect

i = additive × additive effect

j = additive × dominance effect

l = dominance × dominance effect

Table 5. Type of gene action using generation variance for all studied traits in three crosses of bread wheat.

Trait	Cross	σ^2 ph	σ^2 E	σ^2 g	σ^2 D	σ^2 H	(H/D) ^{1/2}
Days to heading	1	18.58	3.37	15.21	10.29	4.93	0.69
	2	17.19	2.18	15.00	3.50	11.50	1.81
	3	25.17	2.74	22.43	16.51	5.92	0.60
Days to maturity	1	13.73	4.94	8.79	6.97	1.82	0.51
	2	15.72	2.31	13.41	12.89	0.52	0.20
	3	18.14	4.04	14.10	9.11	4.99	0.74
Grain filling period	1	17.03	3.38	13.65	10.65	3.00	0.53
	2	28.70	6.06	22.64	19.85	2.79	0.38
	3	46.08	3.89	42.19	31.47	10.72	0.58
Grain filling rate	1	0.32	0.10	0.22	0.19	0.03	0.40
	2	0.47	0.24	0.24	0.24	0.00	0.11
	3	0.47	0.14	0.33	0.19	0.15	0.88
Plant height	1	342.39	6.60	335.79	311.38	24.41	0.28
	2	255.01	6.21	248.81	239.73	9.08	0.19
	3	344.51	6.04	338.47	218.13	120.34	0.74
Number of spikes plant ⁻¹	1	181.66	66.32	115.34	59.42	55.92	0.97
	2	165.04	51.39	113.66	94.14	19.52	0.46
	3	202.93	48.07	154.85	112.92	41.93	0.61
Number of kernels spike ⁻¹	1	296.13	120.13	176.01	174.00	2.01	0.11
	2	663.54	91.72	571.83	284.07	287.75	1.01
	3	399.66	114.71	284.95	238.45	46.50	0.44
100- kernel weight	1	1.08	0.48	0.60	0.29	0.31	1.04
	2	1.33	0.40	0.93	0.55	0.38	0.83
	3	0.75	0.37	0.39	0.37	0.01	0.18
Grain yield plant ⁻¹	1	866.78	254.09	612.68	380.99	231.69	0.78
	2	986.01	454.76	531.25	408.80	122.45	0.55
	3	900.06	290.36	609.70	326.61	283.09	0.93

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

Cross 1= Sakha 93 × Sakha 69 Cross 2 = Sids 12×Sids 13 Cross 3 = Sids 13×Sakha 69

σ^2 ph = Phenotypic variance. σ^2 E = Environmental variance σ^2 g = Genotypic variance

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

Table 6. Heterosis over mid and better parent, inbreeding depression, heritability percentage in broad and narrow senses and expected genetic advance from selection for all studied traits in three bread wheat crosses.

Trait	Cross	Heterosis %		Inbr. Dep.	Heritability percentage		Expected genetic advance (Δg)%
		M.P	B.P		$h_{b,s}$	$h_{n,s}$	
Days to heading	1	1.40**	2.99**	0.94*	81.87	55.36	5.29
	2	1.39**	2.82**	0.32	87.29	20.37	1.82
	3	1.06**	2.63**	1.40**	89.12	65.60	7.07
Days to maturity	1	0.08	0.63	0.23	64.04	50.76	2.64
	2	-0.66	0.66	1.35**	85.28	81.97	6.69
	3	0.34	1.25*	0.16	77.74	50.23	2.98
Grain filling period	1	-2.06	1.99**	0.98*	80.13	62.51	9.84
	2	-4.32	-3.18	3.34**	78.89	69.16	14.67
	3	-0.92	-0.70	2.08**	91.56	68.30	18.45
Grain filling rate	1	58.23**	44.14**	13.53**	69.68	59.95	70.24
	2	67.89**	50.91**	29.31**	50.26	49.63	54.78
	3	4.12**	-13.35	10.68**	70.45	39.75	48.79
Plant height	1	3.16**	-4.73	1.99	98.07	90.94	34.39
	2	-4.18	-8.43	0.76	97.57	94.01	31.93
	3	-0.41	-1.03	7.63**	98.25	63.32	24.53
Number of spikes plant ⁻¹	1	12.33**	9.11**	3.46	63.49	32.71	26.68
	2	0.29	-24.44	6.76**	68.86	57.04	50.65
	3	-7.90	-15.97	5.38**	76.31	55.65	49.92
Number of kernels spike ⁻¹	1	-12.44	-18.53	10.48**	59.44	58.76	30.07
	2	-1.30	-7.85	22.34**	86.18	42.81	26.34
	3	-15.05	-30.60	20.27**	71.30	59.66	28.16
100- kernel weight	1	10.95**	7.41**	9.12**	55.74	26.74	13.50
	2	-28.37	-36.75	1.93**	70.20	41.47	24.51
	3	-24.15	-27.62	20.62**	51.32	49.66	21.30
Grain yield plant ⁻¹	1	61.29**	52.37**	16.83**	70.69	43.96	49.18
	2	49.50**	31.62**	25.09**	53.88	41.46	40.46
	3	0.37	-17.89	5.20	67.74	36.29	38.62

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

Cross 1 = Sakha 93 × Sakha 69 Cross 2 = Sids 12 × Sids 13 Cross 3 = Sids 13 × Sakha 69

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٦-٢ دراسة بعض الصفات الكمية في قمح الخبز باستخدام تحليل متوسطات الأجيال. I- الصفات المحصولية

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تم استخدام ست عشائر ($BC_2, BC_1, F_2, F_1, P_2, P_1$) لتقدير بعض الصفات الوراثية لبعض الصفات الكمية كالتبكير والمحصول ومكوناته. وقد تم قياس متوسطات تلك العشائر بالنسبة لعدد الأيام حتى طرد السنابل وحتى النضج الفسيولوجي، فترة امتلاء الحبوب، معدل امتلاء الحبوب، ارتفاع النبات، عدد السنابل/نبات، عدد الحبوب/سنبله، وزن ١٠٠ حبة ومحصول الحبوب للنبات الواحد لثلاثة هجن من قمح الخبز ناتجة من أربعة آباء وهي سخا ٩٣ × سخا ٦٩، سدس ١٢ × سدس ١٣ و سدس ١٣ × سخا ٦٩. وقد تم قياس التباين في الست عشائر لكل هجين لجميع الصفات السابق ذكرها. وقد أجريت التجربة في ثلاثة مواسم زراعية وهي ٢٠١١/٢٠١٠، ٢٠١١/٢٠١٢ و ٢٠١٢/٢٠١٣ في محطة البحوث الزراعية بسخا. أشارت نتائج اختبار "ت" إلي وجود اختلافات معنوية بين الأبوين لكل هجين في معظم الصفات للثلاثة هجن تحت الدراسة. وقد أظهرت النتائج المتحصل عليها أن التباين الوراثي بين نباتات الجيل الثاني كان مختلفاً لكل الصفات تحت الدراسة للثلاثة هجن. كانت التأثيرات الجينية المضيئة والسيادية والتفوقية مهمة في توارث معظم الصفات للهجن الثلاثة. كما أشارت درجة السيادة إلي تحكم السيادة الجزئية في معظم الصفات للهجن الثلاثة تحت الدراسة ماعدا صفات عدد الأيام حتى طرد السنابل وعدد الحبوب/سنبله للهجين الثاني ووزن ١٠٠ حبة للهجين الأول. كما أشارت النتائج إلي أن تقديرات كفاءة التوريث بالمعنى الواسع والضيق كانت متوسطة إلي مرتفعة لمعظم الصفات للهجن الثلاثة تحت الدراسة. وقد كانت تقديرات التحسين الوراثي المتوقع من الانتخاب في الجيل الثاني متوسطة إلي مرتفعة لكل الصفات للهجن الثلاثة ماعدا صفات عدد الأيام حتى الطرد وعدد الأيام حتى النضج الفسيولوجي وفترة امتلاء الحبوب حيث كان معدل التحسين الوراثي بالانتخاب لها منخفضاً.