Alex. J. Agric. Res. *Vol. 58, No.3, pp.183-195, 2013*

Estimation of Some Genetic Parameters through Generation Mean Analysis in Three Bread Wheat Crosses

Magda, E. Abd El-Rahman
Wheat Research Dept., Field Crops Research Institute, ARC, Egypt
E-mail: magdamoafi@yahoo.com

Received on: 29/8/2013 *Accepted: 7/10/2013*

ABSTRACT

The present investigation was conducted in 2009/10, 2010/11 and 2011/12 wheat growing seasons at Sakha Agric. Res. Station, Egypt. The analysis of gene effects used the means of six populations; P_1, P_2, F_1, F_2, BC_1 and BC_2 of the three bread wheat crosses to estimate genetic parameters. These crosses were Giza 168 × Sids 13, Gemmeiza 9 × Misr 2 and Sids 12 × Misr 2 generated from five diverse parents. Means of the six generations were recorded for seven characters, i.e. number of days to heading, days to physiological maturity, plant height, number of spikes per plant, number of kernels per spike, 100-kernel weight and grain yield per plant. Analyzed data revealed that there were variations among parental genotypes for all studied characters in all crosses except for number of kernels per spike in the first cross, days to physiological maturity and plant height in the second cross and grain yield per plant in the third cross. The genetic variance among F_2 plants was significant for all studied characters in the three crosses. Generation mean analysis using scaling test (A, B and C) indicated the presence of digenic epistasis for all studied characters in the three crosses except for kernel weight in the second cross. The additive, dominance and epistatic gene effects were important in controlling the inheritance of number of kernels per spike in the first cross, days to heading in the second cross and kernel weight in the third cross. Heterosis compared to mid-parent and better parent were found to be significantly positive for plant height in the first two crosses, number of spikes per plant in the second cross and grain yield per plant in the third one. The inbreeding depressions were highly significant and positive for all studied characters in the three crosses except for days to heading in the first cross. Heritability estimates in broad and narrow senses were generally moderate to high for most studied characters in the three crosses. Meanwhile, the values of heritability in narrow sense were low for number of kernels per spike, kernel weight and grain yield per plant in the cross Giza 168 × Sids 13. The expected genetic advance from selection estimates in the F_2 were low for number of kernels per spike and kernel weight in the first cross, days to heading in the second cross and days to physiological maturity in the third one. Variance component estimates revealed that additive genetic variance (σ^2 D) was larger than dominance variance (σ^2 H) for all characters in most crosses. The average degree of dominance as indicated by $(H_1/D)^{1/2}$ was less than unity for days to heading, plant height and grain yield per plant in the second cross as well as for kernel weight in the third one. Also, it was less than unity for days to physiological maturity in the first and third crosses, number of kernels per spike in the last two crosses and number of spikes per plant in the three crosses indicating the presence of partial dominance. On the contrary, the same parameter was more than unity for plant height, number of kernels per spike, kernel weight and grain yield per plant in the first cross as well as grain yield in the third cross indicating the presence of over- dominance. Based on these results, the second cross; Gemmeiza 9 × Misr 2 could be selected for obtaining plants having high grain yield. Moreover, the first cross; Giza 168 × Sids 13 is promising for selecting early mature plants.

Key words: Bread wheat, Generation mean analysis, Gene action, Heterosis, Heritability, Genetic advance, Variance Components.

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the most important widely adapted consumed food cereal in Egypt. Therefore, wheat breeders are concentrating 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 character 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 traits should also be used as selection criteria for yield improvement. This is the reason why it is necessary to know the genetic architecture of yield components (Misra *et al*., 1994). Therefore, information about genetic diversity and relationships among breeding materials is essential to plant breeders for improving this crop.

The information about gene effects including mean (m), additive and dominance gene effects (d and h) and the three types of non-allelic gene interactions, viz., additive x additive (i), additive x dominance (j) and dominance x dominance (l) are very important. Generation mean analysis is a simple but useful technique for estimating these genetic effects, and nature of epistasis is helpful in deciding breeding procedures to be adopted for the improvement of quantitative characters like yield

(Singh and Singh, 1992). 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). However Afiah *et al* (2000) reported low to high estimates of heritability and genetic advance for yield components. In this regard, heritability estimates play an important role for planning the breeding strategy. The heritability of a character determines the extent to which it is transmitted from one generation to the next and it is a valuable tool when used in conjunction with other parameters in predicting genetic gain that follows the selection for that character (Ansari *et al*., 2005). On the other hand, the heritability estimates may indicate that certain morphological traits, that influence grain yield in wheat are more heritable than yield itself (Fethi and Mohamed, 2010). 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 heritabilities for agronomic characters in three bread wheat crosses. These information would be used in the approval of efficient breeding strategies in wheat breeding.

MATERIALS AND METHODS

Plant materials:

Field experiment was conducted at the Experimental Farm of Sakha Agric. Res. Station A.R.C., Egypt, during the three successive seasons of 2009/10, 2010/11 and 2011/12. Five bread wheat cultivars were used. The name and pedigree of these cultivars (parents) are presented in Table (1).

In 2009/10 growing season, the parental genotypes were crossed to produce the three F_1's. The crosses were designated as follows:-

I- Cross 1 : Giza 168 × Sids 13
II- Cross 2: Gemmeiza 9 × Misr 2
III- Cross 3: Sids 12 × Misr 2

In 2010/11 growing season, a part of seed obtained from each parent and the F_1's seeds were sown. Each was crossed with its two respective parents to produce backcrosses (BC_1 and BC_2).

In 2011/12 growing season, the six generations; P_1, P_2, F_1, F_2, BC_1 and BC_2, of each of the three crosses, were planted in the field in three replicates using randomized complete block design. Each plot consisted of two 3 m long rows spaced 30 cm apart and 10 cm among plants within row. All cultural practices were conducted during the growing season according to the recommended package of technology. Data on thirty randomly selected plants from each parent and F_1 generation, 90 plants from each backcross (BC_1 and BC_2) and 300 plants from F_2 generation were recorded to calculate the studied characters.

Evaluation of some morpho-physiological and agronomic characters:

Days to heading (DH), days to physiological maturity (DM), plant height (PH), number of spikes per plant (SP^{-1}), number of kernels per spike (KS^{-1}), 100-kernel weight (KW) and grain yield per plant (GYP^{-1}) for all populations of the three crosses were recorded.

Statistical and genetic methods:

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

Table 1: Name and pedigree of the studied parental bread wheat cultivars.

parent	Name	Pedigree
1	Giza 168	Mrl / Buc // Seri CM 93046-8M-0Y-0M-2Y-0B
2	Gemmeiza 9	Ald “S” / Huac // C74A. 630 / Sx CGM 4583-5GM-1GM-0GM
3	Sids 12	BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CHAT"S"/6/ MAYA/VUL//CMH74A.630/4*SX SD7096-4SD-1SD-1SD-0SD
4	Sids 13	ALMAZ- 19= KAUZ "S" // TSI/SNB "S". ICW94-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP-0AP-0SD
5	Misr 2	SKAUZ / BAV92 CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S

The analysis was proceeded to estimate the various gene effects as well as the scaling test (A, B and C) to detect the presence of nonallelic interactions (epistasis) according to the six parameters genetic model of Mather and Jinks (1982) as follows:
m = Mean effects.
d = Additive gene effects.
h = Dominance gene effects.
i = Additive × additive epistatic gene effects.
j = Additive × dominance epistatic gene effects.
l = Dominance × dominance epistatic gene effects.

Heritability in both broad and narrow senses and mean degree of dominance $(H/D)^{1/2}$, heterosis above mid and better parents and inbreeding depression (%) were estimated according to Mather and Jinks (1982). Genetic advance as percentage of the F_2 mean were estimated as reported by Allard (1999).

RESULTS AND DISCUSSION

Generation means:

Generation means of the six populations, "t" test and F test for agronomic traits are presented in Table 2. Data revealed highly significant differences among parental genotypes for all studied traits in all crosses except for number of kernels per spike in the first cross, days to physiological maturity and plant height in the second cross and grain yield per plant in the third cross indicating the presence of insufficient genetic variability.

The magnitude and direction of heterosis varied from cross to another (Table 2). In the first cross, the F_1 mean plant height exceeded the better parent. Also, in the second cross for number of days to heading, number of spikes per plant and kernel weight. Similarly, in the third cross for plant height. These results indicated that over-dominance of genes were controlling these characters. On the contrary, the mean values were lower than that of the two parents for number of kernels per spike in the second and the third cross indicating the presence of partial dominance. These results are in accordance with those obtained by Abd El-Rahman and Hammad (2009) for number of days to physiological maturity, number of spikes per plant, kernel weight and grain yield per plant, and Zaazaa *et al.* (2012) for number of spikes per plant, number of kernels per spike, kernel weight and grain yield per plant.

The variance among F_2 plants was found to be significant for all studied characters in the three crosses. Therefore, other parameters needed were estimated for all studied characters. The mean values of the F_2 populations comparing with their parents were higher than the highest parent for days to physiological maturity in the first two crosses and plant height in the three crosses indicating appreciable amount of genetic variability for these characters in the corresponding crosses.

Scaling test:

Significant results of scaling tests parameters indicate inadequacy of the additive- dominance model to interpret the gene effects involved in the materials. Epistatic contributions are important in the inheritance of these traits in the particular materials investigated (Mather and Jinks, 1982).

Table 3. illustrates the scaling test parameters (A, B, and C) estimated for studied characters in the three studied crosses. The computed permeates of scaling test for all studied characters in the three crosses were statistically significant except for kernel weight in the second cross. These findings indicated that the six parameter model is valid to explain the nature of gene action for these characters. Meanwhile, A, B or C scaling tests were non significant ones, indicating the interactive model failed to explain the type of gene action in this case. These results are similar to those reported by Zaazaa *et al* (2012) for number of spikes per plant, number of kernels per spike and grain yield per plant and Moussa (2010) for days to heading, days to physiological maturity and plant height.

Genetic effects for agronomic characters:

Estimates of the six parameters, i.e. additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l) and F_2 means (m) are presented in Table 4. The results indicated that the mean effects (m) were highly significant for all studied characters in the three wheat crosses, indicating that these traits are quantitatively inherited.

The additive gene effects (d) were positive and significant for plant height and days to maturity in the first cross, for days to heading and grain yield per plant in the second cross and for number of kernels per spike and kernel weight the three crosses. The obtained results indicated that selection could be effective for these characters in early generations. Meanwhile, negative and significant values were detected for grain yield per plant in the first cross, days to physiological maturity and plant height in the third cross, days to heading in the first and the third cross and for number of spikes per plant in the three crosses. These results indicated that the materials used in this study have decreasing alleles for these characters and selection to improve it could be effective except for plant height if shorter cultivars are desired. The results for all studied characters are in accordance with the previous findings of El-Shaarawy (2012).

With regard to the dominance gene effects (h), were found to be positive and highly significant for number of kernels per spike in the first cross, days to heading in the second cross.

Table 2: Means, t'' test, F test, standard errors and variances for studied characters in three crosses.

Character	Cross	Static.	P_1	P_2	BC_1	BC_2	F_1	F_2	t test	F ratio
DH	C1	$\overline{X}$ ± S.E.	101.23±0.18	106.73±0.17	102.76±0.31	105.52±0.40	102.57±0.16	104.67±0.32	**	**
		S^2	0.94	0.89	8.66	14.34	0.74	29.82		
	C2	$\overline{X}$ ± S.E.	110.30±0.12	108.87±0.11	110.58±0.34	109.38±0.31	108.20±0.16	109.30±0.21	**	**
		S^2	0.42	0.40	10.61	8.69	0.79	13.44		
	C3	$\overline{X}$ ± S.E.	100.30±0.11	106.93±0.14	101.97±0.15	104.61±0.30	102.93±0.14	103.06±0.25	**	**
		S^2	0.36	0.62	1.94	8.13	0.62	19.01		
DM	C1	$\overline{X}$ ± S.E.	159.37±0.22	157.83±0.17	158.07±0.37	156.76±0.30	158.20±0.18	156.08±0.24	**	**
		S^2	1.41	0.90	12.56	8.03	0.92	17.36		
	C2	$\overline{X}$ ± S.E.	158.70±0.18	159.00±0.17	158.90±0.20	158.91±0.21	158.33±0.15	158.03±0.17	NS	**
		S^2	0.98	0.90	3.75	3.92	0.64	8.40		
	C3	$\overline{X}$ ± S.E.	155.30±0.13	158.63±0.13	155.94±0.29	155.78±0.42	155.57±0.15	153.44±0.27	**	**
		S^2	0.49	0.52	7.42	16.00	0.67	22.35		
PH	C1	$\overline{X}$ ± S.E.	99.50±0.28	96.33±0.41	99.50±1.88	103.22±1.50	102.00±0.45	102.17±1.03	**	**
		S^2	2.33	5.06	318.01	203.55	6.21	320.88		
	C2	$\overline{X}$ ± S.E.	116.33±0.41	116.50±0.43	111.94±0.74	115.33±0.83	116.33±0.41	117.33±0.59	NS	**
		S^2	5.06	5.43	49.27	62.25	5.06	105.24		
	C3	$\overline{X}$ ± S.E.	101.83±0.45	106.50±0.43	94.11±1.27	109.61±1.54	112.50±0.46	113.93±1.13	**	**
		S^2	6.01	5.43	144.14	214.73	6.47	385.11		

** = significant at 0.01 level of probability.

Cross 1= Giza 168× Sids 13 Cross 2 = Gemmeiza 9 × Misr 2 Cross 3 = Sids 12 × Misr 2

Cont Table 2:

Character	Cross	Static.	P_1	P_2	BC_1	BC_2	F_1	F_2	t test	F ratio
SP^{-1}	C1	$\bar{X}$ ± S.E.	20.80±0.36	24.30±0.20	19.42±0.42	22.88±0.47	23.03±0.33	19.90±0.29	**	**
		S^2	3.82	1.25	15.91	19.73	3.34	25.62		
	C2	$\bar{X}$ ± S.E.	17.07±0.24	20.57±0.34	16.39±0.46	19.31±0.46	21.33±0.37	18.41±0.30	**	**
		S^2	1.79	3.43	19.18	18.78	4.02	26.85		
	C3	$\bar{X}$ ± S.E.	8.53±0.37	22.43±0.34	11.10±0.42	16.92±0.49	18.40±0.45	14.25±0.30	**	**
		S^2	4.19	3.43	15.53	21.26	6.11	27.31		
KS^{-1}	C1	$\bar{X}$ ± S.E.	72.87±0.47	71.60±0.43	71.40±1.39	73.03±1.27	73.53±0.38	67.27±0.76	NS	**
		S^2	6.67	5.56	173.55	144.98	4.40	173.50		
	C2	$\bar{X}$ ± S.E.	79.40±0.41	69.73±0.42	61.48±1.76	66.47±1.45	64.37±0.42	65.05±1.17	**	**
		S^2	5.01	5.24	279.49	189.87	5.41	409.16		
	C3	$\bar{X}$ ± S.E.	98.03±0.34	74.27±0.40	80.84±1.98	71.70±1.72	78.53±0.39	71.79±1.27	**	**
		S^2	3.41	4.89	352.94	266.57	4.53	480.31		
KW	C1	$\bar{X}$ ± S.E.	4.50±0.07	4.15±0.06	3.99±0.05	4.19±0.06	4.20±0.02	4.06±0.03	**	**
		S^2	0.15	0.11	0.24	0.29	0.01	0.29		
	C2	$\bar{X}$ ± S.E.	5.05±0.06	4.45±0.10	4.92±0.06	4.61±0.06	5.08±0.08	4.80±0.04	**	**
		S^2	0.12	0.29	0.34	0.33	0.20	0.54		
	C3	$\bar{X}$ ± S.E.	5.42±0.07	4.92±0.06	6.14±0.11	5.00±0.07	5.40±0.04	5.16±0.07	**	**
		S^2	0.17	0.10	1.13	0.47	0.04	1.42		
GYP^{-1}	C1	$\bar{X}$ ± S.E.	49.38±0.68	53.11±0.68	42.42±1.61	48.21±1.55	51.79±0.61	42.61±0.93	**	**
		S^2	13.92	13.78	232.02	216.00	11.28	260.80		
	C2	$\bar{X}$ ± S.E.	52.65±0.70	36.60±0.65	40.01±1.54	42.28±1.76	51.98±0.61	43.87±1.15	**	**
		S^2	14.68	12.71	213.87	279.43	10.99	398.58		
	C3	$\bar{X}$ ± S.E.	46.73±0.69	46.27±0.70	45.46±1.54	47.97±1.60	62.00±0.68	39.32±0.97	NS	**
		S^2	14.41	14.87	213.12	229.76	13.93	282.22		

** = significant at 0.01 level of probability.
Cross 1= Giza 168× Sids 13 Cross 2 = Gemmeiza 9 × Misr 2 Cross 3 = Sids 12 × Misr 2

Table 3: Scaling test of the studied characters in the three wheat crosses.

Character	Cross	A	B	C
DH	C1	1.71*±0.67	1.74*±0.83	5.59**±1.32
	C2	2.66**±0.71	1.69**±0.65	1.62±0.92
	C3	0.70*±0.34	-0.64±0.63	-0.85±1.06
DM	C1	-1.43±0.80	-2.52**±0.65	-9.29**±1.06
	C2	0.77±0.48	0.49±0.48	-2.26**±0.77
	C3	1.02±0.60	-2.64**±0.87	-11.32**±1.15
PH	C1	-2.50±3.79	8.11**±3.07	8.83*±4.26
	C2	-8.78**±1.59	-2.17±1.77	3.83±2.58
	C3	-26.11**±2.61	0.22±3.15	22.39**±4.67
SP^{-1}	C1	-4.99**±0.94	-1.58±1.01	-11.58**±1.41
	C2	-5.62**±1.01	-3.28**±1.04	-6.65**±1.46
	C3	-4.73**±0.97	-6.99**±1.12	-10.77**±1.59
KS^{-1}	C1	-3.60±2.85	0.93±2.60	-22.45**±3.20
	C2	-20.81**±3.57	-1.17±2.97	-17.67**±4.78
	C3	14.88**±4.00	-9.40**±3.49	-42.21**±5.15
KW	C1	-0.71**±0.14	0.04±0.13	-0.82**±0.16
	C2	-0.28±0.17	-0.31±0.17	-0.47±0.26
	C3	1.46**±0.24	-0.32*±0.16	-0.50±0.30
GYP^{-1}	C1	-16.34**±3.35	-8.48**±3.23	-35.63**±4.04
	C2	-24.61**±3.23	-4.03±3.63	-17.71**±4.86
	C3	-17.80**±3.23	-12.33**±3.34	-59.70**±4.23

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

Cross 1= Giza 168× Sids 13 Cross 2 = Gemmeiza 9 × Misr 2 Cross 3 = Sids 12 × Misr 2

Also, days to physiological maturity, kernel weight and grain yield per plant in the three crosses. These results indicated the presence of dominance gene effect in the inheritance of these characters. Meanwhile, the negative value of (h) observed in plant height and number of spikes per plant in the first two crosses and number of kernels per spike and grain yield per plant in the second cross. These results indicated that the alleles responsible for less value of the trait were dominant over the alleles controlling high value. These results are in harmony with those obtained by Khattab *et al* (2010) for plant height, number of spikes per plant, number of kernels per spike, kernel weight and grain yield per plant.

With respect to additive × additive type of gene effects (i), positive and significant to highly significant effects were detected for number of spikes per plant in the first cross, days to heading in the second cross, kernel weight in the third cross and number of kernels per spike in the first and the third cross. All crosses had also highly significant and positive effects for days to physiological maturity. So, early generation selection for these characters might be effective for wheat breeding program.

Similar results were reported by Koumber and El-Gammaal (2012) for plant height, number of kernels per spike and kernel weight and Zaazaa *et al* (2012) for number of spikes per plant and grain yield per plant.

Additive × dominance type of gene effects (j) was found to be positively significant for days to physiological maturity and kernel weight in the third cross. However, the negative sign of interaction in some cases also suggested dispersion of genes in the parents. Similar results have been reported by Novoselovic *et al* (2004) for grain yield per plant and Abd El-Rahman and Hammad (2009) for number of kernels per spike and kernel weight.

Concerning the type of dominance × dominance (l), positively significant and highly significant effects were detected for plant height and number of spikes per plant in the height in the second two crosses and number of kernels per spike and grain yield per plant in the second cross. Positive and significant results confirm the importance role of dominance x dominance gene interactions in the genetic system which controls these characters. Negative and significant values were detected for number of kernels per spike in the first cross, days to heading and days to physiological maturity in the second cross and days to physiological maturity and kernel weight in the third cross. These results suggest the scope of heterosis breeding for the development of superior populations. The above results are in conformity with the findings of Tonk *et al* (2011) for plant height and number of spikes per plant and Zaazaa (2012) for number of kernels per spike.

Table 4: Gene action parameters for studied characters of the three wheat crosses.

Character	Cross	m	d	h	i	j	l
DH	C1	106.12** ±1.62	-2.75**±0.12	-2.24±3.97	-2.14±1.62	-0.03±1.04	-1.32±2.42
	C2	106.86**±1.26	0.72**±0.08	8.41**±3.27	2.72*±1.25	0.97±0.94	-7.07**±2.07
	C3	102.71**±1.21	-3.32**±0.09	1.18±2.86	0.90±1.21	1.34±0.69	-0.96±1.71
DM	C1	153.26**±1.36	0.77**±0.14	6.32±3.48	5.34**±1.36	1.09±1.00	-1.38±2.19
	C2	155.33**±0.90	-0.15±0.12	7.77**±2.24	3.52**±0.89	0.28±0.64	-4.77**±1.40
	C3	147.27**±1.50	-1.67**±0.09	16.37**±3.77	9.70**±1.49	3.67**±1.04	-8.08**±2.34
PH	C1	101.14**±6.35	1.58**±0.25	3.25±16.67	-3.22±6.35	-10.61*±4.84	-2.39±10.53
	C2	131.19**±3.26	-0.08±0.30	-40.58**±8.25	-14.78**±3.25	-6.61**±2.30	25.72**±5.14
	C3	152.44**±6.05	-2.33**±0.31	-114.11**±15.06	-48.28**±6.04	-26.33**±4.04	74.16**±9.25
SP^{-1}	C1	17.54**±1.73	-1.75**±0.21	3.94±4.50	5.01**±1.72	-3.41**±1.32	1.55±2.88
	C2	21.07**±1.78	-1.75**±0.21	-10.89*±4.63	-2.25±1.77	-2.34±1.36	11.15**±2.98
	C3	16.44**±1.78	-6.95**±0.25	-10.72*±4.62	-0.96±1.76	2.26±1.37	12.68**±3.01
KS^{-1}	C1	52.45**±4.85	0.63**±0.32	38.21**±12.86	19.79**±4.84	-4.53±3.82	-17.12*±8.18
	C2	78.88**±6.54	4.83**±0.29	-40.80*±16.61	-4.31±6.53	-19.64**±4.60	26.29*±10.31
	C3	68.22**±7.30	11.88**±0.26	3.96±18.74	17.93*±7.29	-5.48±5.27	6.35±11.69
KW	C1	4.18**±0.20	0.18**±0.05	-0.50±0.54	0.15±0.20	-0.75**±0.18	0.52±0.35
	C2	4.87**±0.25	0.30**±0.06	-0.50±0.65	-	-	-
	C3	3.54**±0.39	0.25**±0.05	4.63**±0.98	1.63**±0.38	1.78**±0.28	-2.77**±0.61
G.Y	C1	40.43**±5.84	-1.86**±0.48	-2.64±15.40	10.81*±5.82	-7.86±4.56	14.00±9.80
	C2	55.55**±6.59	8.03**±0.48	-43.12*±16.88	-10.92±6.57	-20.58**±4.78	39.55**±10.55
	C3	16.93**±5.91	0.23±0.49	44.52**±15.49	29.57**±5.89	-5.47±4.55	0.55±9.83

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

Cross 1= Giza 168× Sids 13 Cross 2 = Gemmeiza 9 × Misr 2 Cross 3 = Sids 12 × Misr

Heterosis estimates:

Heterosis effect focused on breeding self-pollinated plants. Data presented in Table 5 showed heterotic effect calculated as percentage over mid and better parents and inbreeding depression for the studied traits in the three crosses. The results represent significant positive heterosis relative to mid-parents in the third cross for plant height, number of spikes per plant, kernel weight and grain yield per plant. The same indication was observed for plant height, number of spikes per plant and number of kernels per spike in the first cross. In addition, significant positive heterosis over the mid-parents was proved for number of spikes per plant, kernel weight and grain yield per plant in the second cross. On the other hand, desired (negatively significant) heterotic effects were found in the three crosses for days to heading and in the third cross for days to physiological maturity. Therefore, these crosses can be used in breeding for early heading and or physiological maturity.

Negative percentage over the mid parent was obtained for number of kernels per spike in the second and third cross and for kernel weight in the first one. Absence of significant heterosis in other cases could be due to the internal cancellation of heterosis components. Similar results were already reported by Khan and Ali (2011) for number of kernels per spike and plant height, Bilgin *et al* (2011) for plant height, number of kernels per spike, kernels weight and grain yield per plant and Beche *et al* (2013) for number of spikes per plant, number of kernels per spike, kernel weight and grain yield per plant.

Concerning heterosis over the better parent, desired significant heterotic effects were obtained for days to heading, number of spikes per plant and kernel weight in the second cross, grain yield per plant in the third cross. Also, the results denoted highly significant positive heterosis for plant height in the first and third crosses and for grain yield per plant in the third cross. These results indicated that dominance direction was toward the best respective parent. The significant heterotic effect might be due to the dominance and/or dominance × dominance effects. These results are in accordance with those obtained by Khan and Ali (2011) for plant height, Koumber and El-Gammaal (2012) for plant height, number of kernels per spike, 1000-kernel weight and grain yield per plant, Zaazaa *et al* (2012) for number of spikes per plant, number of kernels per spike, kernel weight and grain yield per plant and Khattab *et al* (2010) for plant height, number of spikes per plant, number of kernesl per spike and grain yield per plant.

Table 5: Estimates of Heterosis over mid parent (MP%) and better parent (BP%), Inbreeding depression (ID%), Heritability in broad sense (h_{bs}) and narrow sense(h_{ns}) and expected genetic advance (GS%) for the studied traits in the three wheat crosses.

Character	Cross	Heterosis %		Inbreeding depression (ID%)	Heritability percentage		Expected genetic advance (GS %)
		M.P	B.P		$h_{b.s}$ %	$h_{n.s}$ %	
DH	C1	-1.36**	1.32**	-2.05**	97.12	97.12	13.20
	C2	-1.26**	-0.61**	-1.01**	96.02	56.45	3.90
	C3	-0.66**	2.63**	-0.13	97.22	97.22	12.81
DM	C1	-0.25	0.23	1.34**	93.78	81.38	4.47
	C2	-0.33	-0.23	0.19	90.02	90.02	4.10
	C3	-0.89**	0.17	1.37**	97.50	95.24	6.05
PH	C1	4.17**	2.51**	-0.16	98.59	37.46	13.53
	C2	-0.07	-0.14	-0.86	95.08	94.04	16.94
	C3	8.00**	5.63**	-1.27	98.45	98.45	37.90
SP^{-1}	C1	2.14**	-5.21**	13.62**	89.05	60.89	31.91
	C2	13.37**	3.73**	13.69**	88.53	58.62	33.99
	C3	18.84**	-17.98**	22.55**	83.25	65.29	49.32
KS^{-1}	C1	1.80**	0.91	8.52**	96.81	16.42	6.62
	C2	-13.68**	-18.93**	-1.06	98.72	85.29	54.63
	C3	-8.84**	-19.89**	8.59**	99.11	71.02	44.66
KW	C1	-3.02**	-6.80**	3.31**	67.58	13.59	3.70
	C2	6.94**	0.66**	5.55**	62.66	62.66	23.66
	C3	4.56**	-0.25**	4.47**	92.79	87.41	41.60
GYP^{-1}	C1	1.07	-2.48**	17.73**	95.02	28.21	22.03
	C2	16.47**	-1.29	15.59**	96.79	76.24	71.46
	C3	33.33**	32.68**	36.57**	94.90	43.07	37.90

** = significant at 0.01 level of probability.

Sharma and Sain (2004) mentioned that significant positive heterosis over the better parent was observed in wheat. They added that significant heterobeltiosis in wheat is attributed to the major combined effects of additive × dominance and dominance × dominance gene effects. Absence of significant heterosis in other cases could be due to the internal cancellation of heterosis components. The results of heterosis suggested that hybrid vigour is available for the commercial production of wheat and selection of desirable hybrids among the crosses having heterotic and heterobeltiotic effects in other characters is the best way to improve the grain yield of bread wheat (Memon, 2010).

Inbreeding depression:

With respect to the inbreeding depression relative, measured as reduction in performance of F_2 generation compared to F_1 generation (Table 5), the results revealed that highly significant positive inbreeding values were obtained for most studied characters in the three crosses except for days to heading in the first and second cross where highly significance negative values were evident (Table 5). However, these results are logic and expected since the expression of heterosis in F_1 will be followed by a considerable reduction in F_2 due to homozygosity. The obtained results are in accordance with those obtained by Zaazaa *et al* (2012) for number of spikes per plant, number of kernels per spike and grain yield per plant and Moussa (2010) for days to heading and days to physiological maturity.

Heritability estimates:

Knowledge of heritability of a trait guides a plant breeder to predict behavior of succeeding generations and helps to predict the response to selection. Estimation of broad-sense heritability estimates (Table 5) indicated higher importance of genetic effects in control of traits. Comparison between broad and narrow-sense heritability estimates revealed equal importance of additive and non-additive effects in genetic control of traits. Broad-sense heritability estimates the genetic proportion (additive + dominant + interaction) of the total phenotypic variation, while narrow-sense heritability estimates only the additive portion. Almost crosses had larger or equal broad-sense heritability and smaller narrow-sense heritability. Considerable differences were observed between broad-sense and narrow-sense heritabilities in all crosses. These results suggest that dominance gene action was primarily responsible for the inheritance of most traits in these crosses. Heritability in narrow sense as estimated using F_2 and backcross data were high for most traits in these crosses. These results indicate that selection may be more effective for improving traits of genotypes in early generations. On contrary, low narrow sense heritability were estimated for number of kernels per spike and kernel weight in the first cross. These results indicate that environmental effects have a larger contribution than genetic effects for these traits. Moreover, heritability estimates showed a moderate narrow sense heritability for plant height in the first cross and grain yield per plant in the first and third cross.

Similar approaches of broad-sense heritability estimates were coincident with those reported by Hammad *et al* (2012) for days to heading, days to physiological maturity, plant height, number of spikes per plant, number of kernels per spike, kernel weight and grain yield per plant. On the other hand, the results of heritability in narrow sense were similar to these obtained by Farshadfar *et al* (2013) for plant height and Khattab *et al* (2010) for number of spikes per plant, number of kernels per spike and grain yield per plant.

Expected genetic advance estimates:

Percentage of expected genetic advance from selection is more useful parameter as a selection tool when considered jointly with heritability estimates (Johnson *et al*., 1955). The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan 1993). Thus the heritability estimates will be reliable if accompanied by high genetic advance. The expected genetic advance values for the seven characters of the three crosses evaluated are presented in Table 5. These values are also expressed as percentage of the crosses mean for each character so that comparison could be made among various characters, which had different units of measurement. The expected genetic advance as percent of F_2 ranged from (3.70 %) for kernel weight in cross I to (71.46 %) grain yield per plant in cross II. It was low for number of kernels per spike and kernel weight in the first cross, days to heading in the second cross and days to physiological maturity in the three crosses. The expected genetic advances calculated for the remaining characters were high, and hence, it could be concluded that selection for these characters would be effective in early generations.

The highest estimates of narrow sense heritability associated with highest genetic advance for most of the studied traits in most of crosses indicated sufficient improvement of their variability traits. These results indicated the possibility of practicing selection in early generations for these traits. These results are in general agreement with those obtained by Sultan *et al* (2011) for plant height, number of spikes per plant, number of kernels per spike, kernel weight and grain yield per plant.

Estimates of variance components and average degree of dominance ratio:

The estimates of different variance components as well as the average degree of dominance $(H_1/D)^{1/2}$ are provided in Table (6). Estimates of variance components revealed that the additive variance (σ^2 D) was larger than dominance variance (σ^2 H) for all traits in most crosses. The obtained results indicated that additive variance played the greatest role for inheritance of these traits. Similar results were already reported by Sultan *et al* (2011) for plant height, number of kernels per spike, number of spike per plant, kernel weight and grain yield per plant. Overall studied characters, the phenotypic variance was greater than genotypic variance in the first and third crosses. These results indicated that, the environment had an important role in the expression of these characters. There is enough scope for selection based on these characters and the diverse genotypes can provide materials for a sound breeding program.

The average degree of dominance $(H_1/D)^{1/2}$ (Table 6) is more than unity for plant height, number of kernels per spike, kernel weight and grain yield per plant in the first cross as well as grain yield per plant in the third cross. These results back up indicate the presence of over-dominance suggesting early selection might improve these traits. On the contrary, the same parameter is less than unity for days to heading, plant height and grain yield per plant in the second cross as well as for kernel weight in the third cross. Also, days to physiological maturity in the first and third crosses, number of kernels per spike in the last two crosses and number of spikes per plant in the three crosses. These results confirm the role of partial dominance gene effects in controlling in these characters. Non-additive component was negative (an estimate to zero) the remaining characters. Hence, the average degree of dominance was not calculated. These results are in agreement with those obtained by Farooq *et al* (2010) for plant height, number of spikes per plant, number of kernels per spike, kernel weight and grain yield per plant. Moreover, similar results were reported by Abd El Rahman and Hammad (2008) for days to heading and days to physiological maturity and Sultan *et al* (2011) for plant height, number of spikes per plant, number of kernels per spike, kernel weight and grain yield per plant.

Table 6: Estimates of variance components and average degree of dominance for studied characters in three crosses.

Character	Cross	σ^2 ph	σ^2 E	σ^2 g	σ^2 D	σ^2 H	$(H/D)^{1/2}$
DH	C1	29.82	0.86	28.96	36.64	-7.68	-
	C2	0.54	12.90	7.59	5.32	1.92	0.84
	C3	19.01	0.53	18.48	27.95	-9.47	-
DM	C1	17.36	1.08	16.28	14.12	2.15	0.39
	C2	0.84	7.56	9.12	-1.56	0.17	-
	C3	22.35	0.56	21.79	21.29	0.51	0.15
PH	C1	320.88	4.53	316.34	120.20	196.15	1.28
	C2	5.18	100.06	98.97	1.09	12.98	0.11
	C3	385.11	5.97	379.14	411.34	-32.20	-
SP^{-1}	C1	25.62	2.81	22.81	15.60	7.21	0.68
	C2	3.08	23.77	15.74	8.03	-0.41	0.71
	C3	27.31	4.58	22.74	17.83	4.91	0.52
KS^{-1}	C1	173.50	5.54	167.96	28.48	139.48	2.21
	C2	5.22	403.94	348.96	54.98	-89.62	0.40
	C3	480.31	4.28	476.03	341.10	134.93	0.63
KW	C1	0.29	0.09	0.19	0.04	0.15	1.99
	C2	0.20	0.34	0.40	-0.07	-0.02	-
	C3	1.40	0.10	1.32	1.24	0.08	0.25
GYP^{-1}	C1	260.80	12.99	247.81	73.58	174.22	1.54
	C2	12.79	385.79	303.87	81.92	65.56	0.52
	C3	282.22	14.40	267.82	121.55	146.26	1.10

σ^2 ph = Phenotypic variance, σ^2 E = Environmental variance, σ^2 g = Genotypic variance
σ^2 D = Additive variance, σ^2 H = Dominance variance, $(H/D)^{1/2}$ = Average degree of dominance

REFERENCES

Abd El-Rahman, Magda E. and S.M. Hammad (**2009**). Estimation of some genetic parameters for some agronomic characteristics in three crosses of bread wheat. J. Agric. Sci., Mansoura Univ., **34(2)**: 1091-1100.

Afiah, S.A. N., N.A. Mohammad and M.M. Saleem **(2000)**. Statistical genetic parameters, heritability and graphical analysis in 8x8 wheat diallel cross under saline conditions. Annals Agric. Sci. **45**:257-280.

Allard, A.M. (**1999**). Principles of Plant Breeding. 2nd ed. Joh Wiley and Sons. N.Y., USA.

Ansari, B.A., A. Rajper and S.M. Mari (**2005**). Heterotic performance in F_1 hybrids derived from diallel crosses for tillers per plant in wheat under fertility regimes. *Indus. J. Agri. Eng. Vet. Sci.*, **19**: 28-31.

Beche, E., C. Lemes da Silva, E.S. Pagliosa, M.A. Capelin, J. Franke, G. Matei and G. Benin (**2013**). Hybrid performance and heterosis in early segregant populations of Brazilian spring wheat. AJCS **7(1)**:51-57.

Bilgin, O., A. Balkan, K.Z. Korkut and I. Başer (**2011**). Heterotic and heterobelthiotic potentials of bread wheat (*Triticum aestivum* L.) hybrids for yield and yield components. Journal of Tekirdag Agricultural Faculty, **8(2)**: 133-142.

El-Shaarawy, G.A. (**2012**). Gene effects for yield and yield components in some bread wheat crosses. Egypt. J. Plant Breed. **16 (4)**: 75-87.

Erkul, A., A. Unay and C. Konak (**2010**). Inheritance of yield and yield components in a bread wheat (*Triticum aestivum* L.) cross. Turkish Journal of Field Crops, **15(2)**: 137-140.

Farooq, J., I. Khaliq, A.S. Khan and M.A. Pervez (**2010**). Studying the genetic mechanism of some yield contributing traits in wheat (*Triticum aestivum* L.). Int. J. Agric. Biol., **12**: 241–246.

Farshadfar, E., F. Rafiee and H. Hasheminasab (2013). Evaluation of genetic parameters of agronomic and morpho-physiological indicators of drought tolerance in bread wheat (*Triticum aestivum* L.) using diallel mating design. AJCS **7(2)**:268-275.

Fethi, B. and E.G. Mohamed (**2010**). Epistasis and genotype by environment interaction of grain yield related traits in durum wheat. Plant Breeding and Crop Sci. **2 (2)**: 24-29.

Hammad, S.M., E.H. El-Seidy and M. A. H. Darwesh (**2012**). Inheritance of yield and its components in some spring wheat crosses. Proc. 13th International Conf. Agron.,Fac.of Agic., Benha Univ., Egypt, **9-10** September **2012**. *206 - 221.*

Johanson, H.W, F. Robinson and R.E. Comstock (**1955**). Estimation of genetic and environmental variability in soybeans. Agron. J., 47 : 314.

Khan, K. and S. Ali (**2011**). Heterosis study of certain important yield contributing parameters in wheat (*Triticum aestivum* L.). Agro Crop Sci., **2(2)**: 23-26.

Khattab, S.A.M., R.M. Esmail and A.M.F. AL-Ansary (**2010**). Genetical analysis of some quantitative traits in bread wheat (*Triticum aestivum* L.). New York Science Journal, **3(11)** 152-157.

Koumber, R.M. and A.A. El-Gammaal (**2012**). Inheritance and gene action for yield and its attributes in three bread wheat crosses (*Triticum aestivum* L.). World Journal of Agricultural Sciences, **8 (2)**: 156-162.

Mather, K. and J.L. Jinks (**1982**). Biometrical Genetics. 3 ed. Chapman and Hall, London: 396.

Memon, J. (**2010**). Genetic Basis of Heat Tolerance in Bread Wheat (*Triticum aestivum* L.). Ph.D. Thesis, University of Agriculture, Faisalabad.

Memon, S.M, B.A. Ansari and M.Z. Balouch (**2005**). Estimation of genetic variation for agroeconomic traits in spring wheat (*Triticum aestivum* L.). Ind. J.Pl. Sci. **4**:171-175.

Memon, S.M., M.U. Qureshi, B.A. Ansari and M.A. Sial (**2007**). Genetic heritability for grain yield and its related characters in spring wheat. Pak. J. Bot, **39(5)**: 1503-1509.

Misra S.C., V.S. Rao; R.N. Dixit, V.D. Surve and V.P. Patil (**1994**). Genetic control of yield and its components in bread wheat. Indian J. of Genetics **54**:77-82.

Moussa, A.M. (**2010**). Estimation of epistasis, additive and dominance variation in certain bread wheat (*Triticum aestivum*, L.) crosses. J. Plant Prod., Mansoura Univ., Vol. **1 (12)**: 1707 – 1719.

Novoselovic, D., M. Baric, G. Drezner, J. Gunjaca and A. Lalic (**2004**). Quantitative inheritance of some wheat plant traits. Genetics and Molecular Biology **27(1)**: 92–98.

Sharma, S.N. and R.S. Sain (2004). Genetics of awn length of durum wheat under normal- and late-sown environments. Sabrao J. Breeding and Genetics, **36(1)**: 23-34.

Singh, K.N. and R. Chatrath (**1992**). Genetic variability in grain yield and its component characters and their associations under salt stress conditions in tissue culture lines of bread wheat (*Triticum aestivum* L. em Thell.) Wheat information Service **75**:46-53.

Singh, P. and S.S. Narayanan (**1993**). Biometrical Techniques in Plant Breading. Kalyani Publishers.

Singh, R.P. and S. Singh (**1992**). Estimation of genetic parameters through generation mean analysis in bread wheat. Indian J. Genet., **52(4)**: 369-375.

Sultan, M.S., A.H. Abd Elatife, M.A. Abdel-Moneam and M.N.A. El-Hawary (**2011**). Genetic parameters for some yield and yield components characters in four crosses of bread wheat under two water regime treatments. J. plant Prod., Mansoura Univ., Vol. **2(2)**: 351-366.

Tonk, F.A., E. Ilker and M. Tosun (**2011**). Quantitative inheritance of some wheat agronomic traits. Bulgarian J. of Agric. Sci., **17 (6)**: 783-788.

Zaazaa, E.I., M.A. Hager and E.F. El-Hashash (**2012**). Genetical analysis of some quantitative traits in wheat using six parameters genetic model. American-Eurasian J. Agric. & Environ. Sci., **12 (4):** 456-462.

الملخص العربى

تقدير بعض الثوابت الوراثية بواسطة تحليل متوسط الجيل لثلاثة هجن من قمح الخبز

ماجدة السيد عبد الرحمن

قسم بحوث القمح- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية - مصر

أجريت هذه الدراسة في ثلاثة مواسم زراعية وهي ٢٠١٠/٢٠٠٩، ٢٠١١/٢٠١٠، ٢٠١٢/٢٠١١ م بمحطة البحوث الزراعية بسخا- مصر. تم تحليل التأثير الجيني باستخدام متوسطات ست عشائر من قمح الخبز لثلاثة هجن ناتجة من خمسة آباء لتقدير الثوابت الوراثية. وكانت الهجن المستخدمة هي جيزة ١٦٨ × سدس ١٣، جميزة ٩ × مصر ٢، سدس ١٢ × مصر ٢. وقد تم تسجيل المتوسطات لسبع صفات وهي عدد الأيام حتى طرد السنابل، عدد الأيام حتى النضج الفسيولوجي، ارتفاع النبات، عدد السنابل لكل نبات، عدد حبوب السنبلة، وزن المائة حبة، محصول الحبوب للنبات.

وقد أوضحت النتائج وجود تباين وراثي بين الآباء المستخدمة لجميع الهجن وذلك لجميع الصفات ماعدا عدد الحبوب في السنبلة للهجين الأول، عدد الأيام حتى النضج الفسيولوجي، ارتفاع النبات في الهجين الثاني، محصول النبات في الهجين الثالث. كما وجدت تباينات وراثية بين نباتات الجيل الثاني لكل الصفات في الثلاثة هجن. وقد أوضح تحليل متوسط الجيل باستخدام scaling test وجود تفاعلات جينية لجميع الصفات في الهجن الثلاثة ما عدا صفة وزن الحبوب في الهجين الثاني.

كانت التأثيرات الجينية المضيفة والسيادية والتفوقية مهمة في توارث كل من صفات عدد حبوب السنبلة في الهجين الأول، عدد الأيام حتى الطرد في الهجين الثاني، ووزن حبوب السنبلة في الهجين الثالث. كما أوضحت النتائج وجود قوة هجين موجبة ومعنوية لكل من متوسط الأبوين والأب الأفضل فى كل من صفة ارتفاع النبات في الهجين الأول والثاني، عدد السنابل لكل نبات في الهجين الثاني ومحصول الحبوب للنبات في الهجين الثالث.

كان تأثير التربية الداخلية معنوياً لجميع الصفات في الهجن الثلاثة ماعدا صفة عدد الأيام حتى الطرد لكل من الهجين الأول والثاني. كما كانت تقديرات المكافئ الوراثي بالمعنى العام والدقيق بصفة عامة متوسطة إلى مرتفعة لمعظم الصفات تحت الدراسة في الهجن الثلاثة، بينما كانت تقديرات المكافىء الوراثي بالمعنى الضيق منخفضة لكل

من عدد حبوب السنبلة ووزن المائة حبة ومحصول الحبوب للنبات في الهجين جيزة ١٦٨ × سدس ١٣، وكانت تقديرات التقدم الوراثي المتوقع من الانتخاب في الجيل الثاني منخفضة لكل من صفتي عدد حبوب السنبلة ووزن المائة حبة في الهجين الأول و أيضاً عدد الأيام حتى الطرد في الهجين الثاني وعدد الأيام حتى النضج الفسيولوجي في الهجن الثلاثة.

وأشارت تقديرات مكونات التباين إلى أن التباين الوراثي المضيف كان أعلى من التباين الوراثي السيادي لجميع الصفات في أغلب الهجن. كما كانت درجة السيادة أقل من الواحد لكل من صفة عدد الأيام حتى الطرد وارتفاع النبات ومحصول النبات في الهجين الثاني وصفة وزن الحبوب في الهجين الثالث، وأشارت النتائج إلى وجود سيادة جزئية في كل من عدد الأيام حتى النضج في الهجين الأول والثالث وعدد حبوب السنبلة في الهجين الثاني و الثالث وعدد السنابل للنبات في الهجن الثلاثة. وعلى العكس من ذلك فقد أوضحت النتائج وجود سيادة فائقة في كل من صفات ارتفاع النبات، عدد حبوب السنبلة، وزن المائة حبة، محصول النبات في الهجين الأول وكذا محصول النبات في الهجين الثالث. وبناءاً على هذه النتائج يمكن الإستفادة من الهجين الثاني جميزة ٩ × مصر ٢ للحصول على نباتات عالية في محصول الحبوب وأيضاً الاستفادة من الهجين الأول جيزة ١٦٨ × سدس ١٣ للحصول على نباتات مبكرة في النضج.