

DIALLEL CROSSES ANALYSIS FOR YIELD AND ITS COMPONENTS IN BREAD WHEAT

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ABSTRACT

A half diallel cross among seven bread wheat genotypes (Parents) namely R.C.B 143, R.C.B 70, R.C.B 122, Sakha 202, Sakha 206, Gemmeiza 7 and Sids1 were evaluated for yield and its components as well as some other agronomic characters in the F1 and F2 generations. Genotypes mean squares were significant for all studied characters. Mean squares for parents in crosses as an indication for heterosis were significant for all studied characters in the F1 and F2, except plant height and 1000-kernel weight in F1 and spike length, 1000-kernel and grain yield in F2. Both general and specific combining ability (GCA and SCA), were significant for all studied characters in the F1 and F2, except SCA for plant height in F1 and spike length in F1 and F2. These results indicate the importance of both additive and dominance genetic variance in the inheritance of most characters. Though most of estimates of not GCA/SCA exceeded unity, most of them was not significant to show the probability of equal importance of both addition and non-addition gene action. Moreover, the parents P4 (R.C.B 122) and P5 (R.C.B 70) were the best combiners for grain yield in F1 and F2 but P6 (Gemmeiza 7) in F1 only. Meanwhile, significant SCA effects for grain yield were found in the crosses between (P1xP3), (P1xP7), (P2xP4), (P2xP6), (P3xP4), (P4xP7), (P5xP6) and (P5xP7) in the F1 and (P1xP3), (P2xP3), (P3xP7), (P4xP5), (P4xP6), and (P5xP7), in the F2. The additive variance effects were significant for all studied characters except for 1000 kernel weight, grain yield and total plant weight in the F1, being significant for most characters in the F2. Over dominance effects of heterozygous loci were significant for most studied characters in the F1 and F2. Values of (H²/4H¹) analysis being less than 0.25 indicated asymmetric distribution of positive and negative alleles among parents for all characters in the F1 and F2. On the other hand, narrow sense heritability was low for some characters, indicating the importance non-additive genetic effects.

INTRODUCTION

Wheat is the major cereal crop in Egypt, which receives the most attention of specialists in plant breeding to increase grain yield by developing high yielding wheat cultivars. The assessment of the nature of genetic variation is crucial to any breeding program, since the choice of an appropriate breeding method depends on the relative importance of various genetic parameters. In wheat, plant height and spike characters are important attributes that determine the desirability of progeny of any crosses. The appropriate selection for these characters may greatly contribute towards enhancement in the yielding ability. Dominance gene action would tend to favor the production of hybrids, whereas additive gene action signifies that standard selection procedures would be more effective in breeding about advantageous changes in the characters (Edwards *et al.*, 1976).

Successful breeding programs need continuous information on the genetic variation and systems governing grain yield and its components.

However, contradictory results were obtained by several authors with respect to genetic systems governing wheat grain yield and its components. For instance Uddin and Joarder (1987), Hendawy (1990) and Ikram and Tanah (1991) indicated that additive and non-additive gene effects played equal roles in the inheritance of grain yield, number of spike/plant, number of kernels/spike and kernel weight. Moreover, El Hennawy (1992) revealed that additive and dominance gene effects were important for grain yield and number of kernels/spike. From eight wheat genotypes, Mahmoud (1999) revealed that additive and non-additive gene effects were controlling the genetic systems of grain yield and its components. In addition, El-Sayed *et al.* (2000), Mostafa (2002) and El-Sayed (2004) found that both additive and dominance variances were significant for number of spikes/plant, number of kernels/spike, kernel weight and grain yield/plant. Similarly, Hamada Tawfelis (2001) showed that additive and non-additive gene effects have important roles in controlling the genetic system for plant height, number of spikes/plant, number of kernels/spike, kernel weight and grain yield/plant.

On the other hand, Sharma and Smith (1986) as well as Salem and Hassan (1991) found that non-additive gene effects were more important in the inheritance of grain yield/plant and number of spikes/plant. Similarly, Dawam and Hendawi (1990) and Darwish (1992) found that dominance gene effects were significant for grain yield/plant, number of kernels/spike and kernel weight. Reversely to that, Mekhamer (1995) reported that additive gene effects were significant for number of kernels/spike and kernel weight. On the other side, El-Sayed *et al.* (2000), Ashoush *et al.* (2001), Abd El-Hameed (2002) and El-Sayed (2004), found that GCA and SCA were significant for days to heading and plant height.

Concerning the heritability values, Tamam and Abd El-Gawad (1999) found high heritability, in broad and narrow sense, for days to heading, number of spikes/plant, kernel weight and grain yield/plant, being low for number of kernel of kernel/spike. On the other hand, El-Sayed *et al.* (2000) found that these values were medium or low for spike length, number of spikes/plant, number of kernels/spike and grain yield/plant, while estimates for number of days to heading and 1000-kernel weight, fluctuated from medium to high.

The present study was initiated to estimate heritability and nature of gene action for grain yield and its components as well as some other agronomic characters in seven parental dial crosses of bread wheat.

MATERIALS AND METHODS

The field work of this investigation was conducted at Etay El-Baroud Agricultural Research Station, Behera Governorate, Egypt, during the three successive growing seasons 2001/2002, to 2003/2004. Seven bread wheat cultivars representing a wide range of genetic variability were selected for this investigation, (Table 1).

Table (1): Names and Pedigrees of Seven Parents of Bread Wheat.

No.	Variety or Line	Name and Pedigree	Origin
1	R.C.B 143	Sx/Cardinal.	Syria
2	Sakha 202	BL 1133/3/CMH79A.955*2/CNO79// CMH79 A.955/Bow"s"CM.106804-1S-1S-2S.	Egypt
3	Sakha 206	BL 1133/3/CMH79A.955*2/CNO79// CMH79 A.955/Bow"s"CM.106804-1S-4S-3S.	Egypt
4	R.C.B 122	Star"s"SWM7215-2Y-iY-0Y-2Y-0Y-41m-0Y.	Mexico
5	R.C.B 70	Shi H4414/Crow"s"Swm 11508-4AP-2AP-1AP- 2AP-0AP.	Mexico
6	Gemmiza 7	CMH74A.630/SX//SER182/AGEWT CGM4611-2GM-3GM-1GM-0GM.	Egypt
7	Sids 1	HD21/PAVON"S"//1158.57/MAYA74"S".	Egypt

In 2001/2002 season, all possible crosses (without reciprocals) among the seven parents were done. In the second season (2002/2003) the 28 entries (21 F₁^s and 7 parents) were planted in the field using the randomized complete block design (RCBD) with three replications according to Steel and Torri (1980). In (2003/2004) F₂ and parents were planted in the field using RCBD with three replications. Each entry was planted in a plot of two rows; for parents and F₁ and six rows for F₂. Every row was 3.0 m long and 30 cm. apart, and contained 15 seeds, spaced 20 cm. Apart. Data were recorded on a random sample of 10 guarded plants from each row. The studied characters were days to heading, plant height, (cm.), spike length (cm.), number of spikes/plant, number of kernels/spike, 1000-kernel weight (gm.), grain yield/plant (gm.), and Total plant weight (gm.).

The analysis of variance for general and specific combining ability estimates were obtained by employing Griffing's (1956) diallel crosses analysis designated as method 2, model 1 and further genetic analysis was carried out as described by hayman (1954).

RESULTS AND DISCUSSION

Analysis of variance for all studied characters (days to heading, plant height, spike length, number of spike/plant, number of kernel/spike, 1000 kernel weight, grain yield/plant and total weight/plant), for F₁ and F₂ are in table (2). Analysis indicated that the significant mean squares of genotypes for all studied characters in the F₁ and F₂., suggesting the presence of ture differences among genotypes. Mean squares due to parents vs. crosses were significant for all studied characters of the F₁ and F₂ except plant height, and 1000 kernel weight in the F₁ and spike length, 1000 kernel weight and grain yield in the F₂, this indicating hetrosis of the most F₁ and F₂ crosses.

Table (2) shows the results of the analysis for GCA, SCA and the GCA/SCA ratio. The variance associated with GCA was significant in all studied characters in the F₁ and F₂ generation.

Table (2): Observed mean squares from ordinary analysis and combining ability analysis in the F1 and F2 generation of wheat crosses.

Source	d.f	Days of heading	Plant height (Cm.)	Spike length (Cm.)	Number of spikes per plant	Number of kernel per spike	1000-kernel weight (gm.)	Grain yield (gm.)	Total plant weight (gm.)
F1:Hybrides									
Replication	2	4.41	228.31	2.87	3.30	4.78	251.17*	12.02	4464.50
Genotypes	27	192.15**	5513.71*	16.11**	81.32**	309.28**	217.59**	929.00**	58968.77**
Parents	6	293.22**	728.05**	23.54**	75.28**	446.55**	241.93**	522.97**	34369.10**
Crosses	20	148.89**	469.99*	13.68**	63.03**	280.66**	210.86**	973.36**	50996.18**
Pvs.C	1	450.85**	104.17	20.00**	483.36**	58.14**	206.23	2477.83**	366018.90**
GCA	6	106.61**	437.78**	3.45**	49.21**	185.50**	146.48**	100.82**	19274.30**
SCA	21	51.89**	95.08	5.92	20.79**	79.55**	51.40**	369.34**	19765.38**
Error		9.15	218.67	2.09	4.90	13.56	53.93	11.94	3188.01
GCA/SCA		2.06	4.60	0.58	2.37	2.33	2.50	0.27	0.98
F2:Croses									
Replication	2	0.44	109.00	4.44	0.84	2.94	45.51	521.47	6.18
Genotypes	27	134.97**	692.18**	5.59*	51.50**	279.88**	180.90**	1709.06**	26845.52**
Parents	6	305.39**	547.11**	9.20**	73.75**	290.50**	293.49**	1926.60**	64275.83**
Crosses	20	70.28**	749.98**	4.51	29.31**	289.44**	153.89**	1728.71**	15256.47**
Pvs.C	1	406.30**	406.51*	5.44	361.94**	24.81*	45.44	10.74	34044.20**
GCA	6	52.52**	623.39**	3.47**	38.24**	202.53**	513.78**	825.41**	10813.56**
SCA	21	42.84**	118.54**	1.41	11.15**	62.08**	1114.32**	496.62**	8415.64**
Error		9.63	61.58	2.59	3.76	6.08	16.99	279.51	604.49
GCA/SCA		1.23	5.26	2.47	3.43	3.26	0.46	1.66	1.29

The same level of significance was found in most cases for SCA for all studied characters except for plant height and spike length in the F1 and for spike in the F2. Thus both GCA and SCA revealed the presence of both additive GCA and dominance SCA types of gene effects were indicated for most characters. From Table (2) it could be noticed that GCA was relatively larger than SCA for the studied characters, except the spike length, grain yield and total plant weight in the F1, and 1000 kernel weight in the F2 only. However, significant ratios of GCA/SCA suggested a predominant role for additive type of gene action for plant height, consistently over the two generation, being for ns/pl & nk/s in F2 only.

Parents vs. the hybrids mean squares (Table 2), as an indication to average heterosis overall crosses were found to be significant for all studied characters except plant height and 1000 kernel weight in the F1 and spike length, 1000 kernel and grain yield/plant in the F2 only.

The mean performance of the seven parental genotypes of wheat are presented in Table (3). The Cultivar R.C.B 143 (P1) ranked the top for the lowest days to heading.

Table (3.a): The genotypes mean performance for all the studied traits in the F1 generation.

Geno- types	Days to heading	Plant height (Cm.)	Spike length (Cm.)	Number of spikes per plant	Number of kernel per spike	1000-kernel weight (gm.)	Grain yield (gm.)	Total plant weight (gm.)
P1	93	145.33	15.0	15.0	75.0	46.33	47.67	417.67
P2	95.33	112.33	19.0	6.33	100.0	62.67	31.33	61.67
P3	102	129.33	19.33	10.0	101.0	59.33	48.67	189.67
P4	103.33	103.33	13.0	20.0	71.33	42.67	61.67	233.33
P5	122.67	102.33	12.0	18.33	77.33	57.0	70.0	165.0
P6	102.33	111.33	15.67	17.33	83.67	59.33	46.73	205.0
P7	95.33	124.67	17.0	18.0	76.0	41.0	37.8	185.0
P1xP2	93.33	124.00	15.0	11.0	84.67	59.07	55.67	173.33
XP3	95.67	137.33	20.67	14.67	97.67	62.83	80.0	443.33
XP4	108.33	129.33	16.67	18.67	79.0	49.63	47.33	326.67
XP5	112.00	114.00	15.33	23.0	75.33	44.33	42.0	336.67
XP6	118.33	87.67	20.33	24.33	97.0	47.77	46.33	393.33
XP7	114.33	144.00	19.33	26.0	81.33	46.37	75.0	300.0
P2xp3	105.00	117.67	16.33	14.33	101.67	59.27	54.67	546.67
XP4	98.33	125.00	15.0	21.67	78.0	52.17	77.33	326.67
XP5	88.67	110.00	15.0	28.0	72.33	51.53	59.67	215.0
XP6	109.00	115.00	20.33	16.0	102.67	59.9	102.7	333.33
XP7	104.33	120.00	16.67	17.0	89.0	50.67	38.0	186.67
P3xP4	108.67	114.00	16.33	27.67	91.0	46.67	74.33	513.33
XP5	108.67	114.33	16.67	20.33	73.67	57.4	43.0	326.67
XP6	108.33	104.00	13.0	18.0	72.67	37.8	53.0	563.33
XP7	103.33	127.33	15.67	17.67	82.67	51.1	40.0	303.33
P4xP5	114.67	107.33	20.33	25.0	75.0	48.67	54.0	558.33
XP6	107.33	110.00	15.33	18.33	80.67	50.73	53.67	226.67
XP7	104.33	107.67	17.33	24.0	84.33	43.07	62.33	260.0
P5xP6	113.33	105.00	16.33	20.33	93.67	32.17	82.0	550.0
XP7	105.00	105.00	16.63	22.0	86.33	31.57	93.0	470.0
P6xP7	105.67	113.33	18.33	23.33	94.67	46.33	61.0	220.0
L.S.D 5%	4.99	24.39	2.39	3.65	6.07	12.11	5.7	93.13
1%	6.57	32.12	3.14	4.81	8.0	15.95	7.51	122.63

The cultivar Sakha 202 (P2) ranked the first for 1000 kernel weight and the second for number of kernel per spike. Sakha 206 (P3) ranked the first for number of kernel per spike and the second for 1000 kernel weight. The cultivar R.C.B 122 (P4) ranked the first for number of spike per plant and the second for grain yield per plant. The cultivar R.C.B. 70 (P5) ranked the first for the grain yield per plant and the second for number of spike per plant. The mean performance of the tested 21 crosses are presented in table (3). The earliest crosses to heading were (P1xP2) and (P1xP3). The eight crosses (P1xP5), (P1xP6), (P1xP7), (P2xP5), (P3xP4), (P4xP5), (P4xP7) and (P6xP7) possessed the highest number of spikes/plant, while the five crosses (P1xP3), (P1xP6), (P2xP3), and (P2xP6) and (P6xP7) possessed the highest number of kernel/spike. The heaviest 1000 kernel weight crosses were (P1xP2), (P1xP3), (P2xP3), (P2xP6). The four crosses (P1xP3), (P2xP6), (P5xP6) and (P5xP7) possessed the highest grain yield/plant.

Table (3.b): The genotypes mean performance for all the studied traits in the F2 generation.

Genotypes	Days to heading	Plant height (Cm.)	Spike length (Cm.)	Number of spikes per plant	Number of kernel per spike	1000-kernel weight (gm.)	Grain yield (gm.)	Total plant weight (gm.)
P1	94.33	142.0	14.0	14.0	61.33	44.33	74.0	156.0
P2	98.33	112.33	19.0	7.0	87.67	64.67	23.33	50.33
P3	97.0	121.33	17.0	10.33	91.67	57.67	29.33	62.33
P4	101.0	102.67	14.33	20.0	79.0	52.33	75.67	135.0
P5	123.0	105.0	14.67	20.0	77.67	45.67	74.67	117.67
P6	102.0	113.0	15.67	18.0	85.67	48.67	87.67	385.0
P7	93.33	125.0	16.0	16.33	79.67	34.0	74.0	403.0
P1xP2	101.67	149.0	15.67	14.67	92.67	43.33	64.67	210.0
XP3	94.0	144.0	16.0	20.33	77.33	53.0	71.0	296.0
xP4	91.67	119.33	15.33	23.0	58.33	46.67	64.33	164.33
xP5	98.67	138.0	15.0	24.67	75.33	46.67	86.67	265.33
xP6	96.67	131.67	15.67	20.67	80.0	38.33	34.0	227.0
xP7	102.67	144.67	15.0	22.67	62.67	40.67	44.33	179.0
P2xp3	95.67	146.0	16.33	13.33	92.67	45.67	66.0	235.67
XP4	93.33	120.33	16.0	14.67	77.67	46.33	65.67	164.67
xP5	94.0	111.0	16.33	17.0	80.33	54.67	39.67	204.0
xP6	102.0	106.67	16.33	18.33	83.0	58.0	52.33	206.67
xP7	91.33	112.33	15.33	19.33	82.33	47.67	43.33	199.0
P3xP4	93.67	87.67	14.67	21.33	90.67	54.0	35.0	167.0
XP5	82.67	117.33	17.0	19.0	89.0	46.33	55.33	199.67
xP6	95.67	125.0	12.67	24.67	68.33	36.67	51.0	261.67
xP7	94.67	127.67	14.0	21.0	88.0	65.67	78.33	230.67
P4xP5	95.0	118.33	15.0	21.67	87.0	49.67	104.0	441.67
XP6	97.33	110.33	15.33	23.33	66.33	47.33	92.0	330.0
xP7	95.67	102.0	12.0	20.0	72.67	43.0	71.0	310.0
P5xP6	101.0	122.33	16.0	18.33	77.0	50.33	59.0	298.33
XP7	98.33	124.67	14.0	19.0	87.67	55.0	124.67	163.67
P6xP7	104.67	112.33	16.0	20.67	72.67	37.33	31.0	150.0
L.S.D 5%	5.12	12.94	2.65	3.2	4.07	6.8	27.57	40.55
1%	6.74	17.04	3.49	4.21	5.35	8.95	36.31	53.4

P1, P2, P3 and P7 may be good combiners for early heading since they showed negative general effects, being significant in one generation. P2 & P3 are the best combiners for k/s & kwt as P4 & P5 were for s/pl and gy/pl,

all being consistently are the two generation P4, P5 & P6 are valuable for short stems.

Estimates of GCA effect for parents in F1 and F2 are presented in table (4). Significant positive values would be interest except for days to heading and plant height. For days to heading P1, P2 and P7 were the best combiners for ear lines in the F1, but P3 and P4 were the best combiners in the F2. For number of spike per plant and grain yield per plant P4 and P5 were the best combiners both F1 and F2, P6 was good combiner for increasing grain yield per plant and number of kernel per spike in the F1.

Specific combining ability effects for the studied characters are presented for the F1 and the F2 generation in Tables 5.a and 5.b, respectively. Four, two five, seven nine, one, eight crosses showed significant specific combining ability effects for days to heading, plant height, spike length, number of spike per plant, number of kernel per plant, 1000 kernel weight, grain yield per plant and total plant weight in the F1, this crosses (P1xP3), (P1xP7), (P2xP4), (P2xP6), (P3xP4), (P4xP7), (P5xP6) and (P5xP7) are considered to be promising hybrids for grain yield improvement purpose, as they showed high specific combining ability effects and involved one of the parents as good combiner. It is worthy to note that the first this hybrids were a result of crossing poor x good and good x good general combiners.

In F2, Six, five, one, nine, six, four, six, eight crosses showed significant specific combining ability effects for days to heading, plant height, spike length, number of spike per plant, number of kernel per spike, 1000 kernel weight, grain yield per plant total plant weight respectively.

The crosses (P1xP3), (P3xP7), (P4xP5) and (P5xP7) are considered to be promising hybrids for grain yield improvement purpose. The most promising crosses are both generation may be P1xP3 & P5xP7. In such hybrids, desirable transgressive segregates would be expected in the subsequent generations, if the additive genetic system present in the good combiner and the complementary epistatic effects.

The diallel analysis as obtained by Hayman (1954) is an attempt to partition phenotypic variation in to genotypic and environmental component and to further subdivision of genotypic variation in to its components, which can be used to draw inferences about the genetic system.

The estimates of genetic components of variation, i.e. D,F,H.,H2, and h^2 obtained by Hayman's analysis for F1 and F2 are presented in table (6). The additive compents of genetic variance effect (D) were significant for all traits in both generation, except 1000 kernel weight, grain yield per plant and total plant weight, in F1. The dominant component (H1) was significant for all studied characters at both generation except plant height in the F1. In the two generation values of (H1) were larger in magnitude than the additive component (D) indicating predomination of dominance gene action in all traits. The components of variation due to the dominance effect associated with gene distribution (H2) was significant for all trais except plant height and 1000 kwt in F1 and spike length in F2.

Table (4): Estimates of general combining ability (GCA), effects of parents from F1 and F2 generation.

Source	Days to heading	Plant height (Cm.)	Spike length (Cm.)	Number of spikes per plant	Number of kernel per spike	1000-kernel weight (gm.)	Grain yield (gm.)	Total plant weight (gm.)
F1 Hybrid								
P1	-1.39*	10.6**	0.41	-0.62	-1.6*	0.38	-2.95**	25.39*
P2	-5.46**	0.52	0.3	-3.62**	5.44**	6.52**	-1.95**	-75.02**
P3	-0.76	4.64	0.41	-2.29**	4.67**	3.83**	-2.88**	55.09**
P4	0.87	-3.51	-0.74**	2.46**	-5.41**	-2.55	2.67**	10.91
P5	5.24**	-7.92**	-1.03**	2.46**	-5.37**	-2.18	5.15**	22.94
P6	2.91**	-8.22**	0.15	0.2	3.26**	-0.65	2.65	12.94
P7	-1.42*	3.89	0.49	1.42**	-1.00	-5.35**	-2.59**	-52.24**
L.S.D								
5% gi	1.09	5.32	0.52	0.8	1.33	2.64	1.24	20.32
1% gi	1.43	7.01	0.69	1.05	1.75	3.48	1.64	26.76
5% gi-gj	1.66	8.13	0.8	1.23	2.02	4.04	1.9	31.04
1% gi-gj	2.19	10.71	1.05	1.60	2.67	5.32	2.5	40.88
F2 Crosses								
P1	-0.65	15.73**	-0.25	0.5	-7.39**	-3.27**	0.75	-13.52**
P2	-0.57	0.1	1.23**	-4.24**	5.39**	4.25**	-14.22**	-50.52**
P3	-3.28**	2.35	0.19	-1.02**	5.98**	3.32**	-10.11**	-28.89**
P4	-1.24*	-11.76**	-0.66*	1.61**	-2.76**	0.55	8.56**	8.04
P5	3.98**	-3.05*	-0.03	1.13**	1.79**	0.8	12.49**	3.63
P6	2.39**	-3.87**	0.04	1.39**	-1.87**	-2.38**	-1.29	52.04**
P7	-0.65	0.5	-0.51	0.65	-1.13*	-3.27**	3.82	29.22**
L.S.D								
5% gi	1.12	2.82	0.58	0.7	0.89	1.48	6.02	8.85
1% gi	1.47	3.72	0.76	0.92	1.17	1.95	7.92	11.65
5% gi-gj	1.71	4.32	0.89	1.07	1.36	2.27	9.19	13.52
1% gi-gj	2.25	5.68	1.17	1.4	1.79	2.99	12.10	17.8

Table (5.a): Estimates of specific combining ability (SCA), effects for all the studied characters in the hybrids.

Genotypes	Days to heading	Plant height (Cm.)	Spike length (Cm.)	Number of spikes per plant	Number of kernel per spike	1000-kernel weight (gm.)	Grain yield (gm.)	Total plant weight (gm.)
P1xP2	-4.88**	-3.57	-2.42**	-3.92**	-4.1*	2.26	2.04	-99.56**
P1xP3	-7.25**	5.47	3.14	-1.58	9.68**	8.72**	27.3**	40.33
P1xP4	3.79**	5.8	0.29	-2.32*	1.08	1.9	-10.92**	-32.15
P1xP5	3.08*	-5.13	-0.75	2.01*	-2.62	-3.8	-18.62**	-34.19
P1xP6	11.75**	-31.17**	3.07**	5.6**	10.42**	-1.86	-11.89**	32.48
P1xP7	12.08**	13.06	1.73**	6.05**	-0.99	1.43	22.01**	4.33
P2xp3	6.16**	-3.94	-1.08	1.08	6.64**	-0.99	0.97	244.07**
P2xP4	-2.14	11.54	-1.27	3.68**	-6.95**	-1.71	18.08**	68.26**
P2xP5	-16.18**	0.94	-0.97	10.01**	-12.66**	-2.72	-1.96	-55.44*
P2xP6	6.49**	6.24	3.18**	0.27	9.05**	4.13	43.44**	72.99**
P2xP7	6.16**	-0.87	-0.82	0.05	-0.36	-0.41	-15.99**	-8.59
P3xP4	3.49*	-3.57	-0.05	8.34**	6.82**	-4.52	16.01**	124.82**
P3xP5	-0.88	1.17	0.58	1.01	-10.55**	5.84	-17.7**	-13.89**
P3xP6	1.12	-8.87	-4.27**	0.94	-20.18**	-15.29**	-5.31**	172.78**
P3xP7	0.45	2.35	-1.94**	-0.62	-6.92**	2.71	-13.06**	-22.04
P4xP5	3.49*	2.32	5.4**	0.94	0.86	3.49	-12.25**	201.96**
P4xP6	-1.51	5.28	-0.79	-3.47**	-2.1	4.03	-10.19**	-119.7**
P4xP7	-0.18	-9.17	0.88	0.97	5.8**	1.06	3.72*	-21.19
P5xP6	0.12	4.69	0.51	-1.47	10.86**	-14.91**	15.77**	191.59**
P5xP7	-3.88**	-7.43	0.51	-1.03	7.79**	-10.81	32.01**	176.78**
P6xP7	-0.88	1.2	0.99	2.57*	7.49**	2.43	2.41	-63.22
L.S.D								
Sij 5%	2.69	13.17	1.29	1.97	3.28	6.54	3.08	50.29
1%	3.55	17.35	1.7	2.6	4.32	8.61	4.05	66.23
Sij-Sik 5%	4.7	22.99	2.25	3.44	5.73	11.42	5.37	87.8
1%	6.19	30.28	2.96	4.53	7.54	15.04	7.08	115.62
Sij-Skl 5%	4.4	21.51	2.10	3.0	5.36	10.68	5.03	82.13
1%	5.79	28.32	2.77	4.24	7.05	14.07	6.62	108.15

Table (5.b): Estimates of specific combining ability (SCA), effects for all the studied characters in the F2 Crosses.

Genotypes	Days to heading	Plant height (Cm.)	Spike length (Cm.)	Number of spikes per plant	Number of kernel per spike	1000-kernel weight (gm.)	Grain yield (gm.)	Total plant weight (gm.)
P1xP2	5.41**	12.04**	-0.68	-0.28	15.23**	-5.99**	14.85	52.12**
P1xP3	0.44	4.78	0.69	2.17*	-0.69	4.6*	17.07*	116.49**
P1xP4	-3.93**	-5.78	0.88	2.2*	-10.95**	1.05	-8.26	-52.10**
P1xP5	-2.15	4.19	-0.08	4.35**	1.49	0.79	10.15	53.31**
P1xP6	-2.56	-1.33	0.51	0.09	9.82**	-4.36*	-28.74**	-33.44**
P1xP7	6.48**	7.3*	0.4	2.83**	-8.25**	-1.14	-23.52**	-58.62**
P2xp3	2.04	22.41**	-0.45	-0.09	1.86	-10.25**	27.04**	93.16**
P2xp4	-2.33	10.85**	0.07	-1.39	-4.4**	-6.81**	8.04	-14.77
P2xp5	-6.89**	-7.19*	-0.23	1.43	-6.29**	1.27	-21.89**	28.97**
P2xp6	2.7	-10.7**	-0.31	2.5**	0.05	7.79**	4.56	-16.77
P2xp7	-4.93**	-9.41**	-0.75	4.24**	-1.36	-1.66	-9.56	-1.62
P3xp4	0.7	-24.07**	-0.23	2.06*	8.01**	1.79	-26.74**	-34.07**
P3xp5	-15.52**	-3.11	1.47*	0.2	1.79	-6.14**	-10.33	3.01
P3xp6	-0.93	5.37	-2.94**	5.61**	-15.21**	-12.62**	-0.89	16.6
P3xp7	1.11	3.67	-1.05	2.69**	3.7**	17.27**	21.33**	8.42
P4xp5	-5.22**	12.0**	0.32	0.24	8.53**	-0.03	19.67**	208.08**
P4xp6	-1.3	4.82	0.58	1.65	-8.47**	0.82	21.44**	48.01**
P4xp7	0.07	-7.89*	-2.19**	0.94	-2.88	-2.62	-4.67	50.82**
P5xp6	-2.85	8.11*	0.62	-2.87**	-2.36*	3.57	-15.48*	20.75
P5xp7	-2.48	6.07	-0.82	-1.46	7.57**	9.12**	45.07**	-91.1**
P6xp7	5.49**	-5.44	1.1	-0.06	-3.77**	-5.36**	-34.82**	-153.18**
L.S.D								
Sij 5%	2.76	7.99	1.43	1.73	2.2	3.67	14.89	21.9
1%	3.64	9.2	1.89	2.27	2.89	4.84	19.61	28.84
Sij-Sik 5%	4.82	12.2	2.5	3.02	3.83	6.41	26.0	38.23
1%	6.35	16.07	3.3	3.97	5.05	8.44	34.23	50.35
Sij-Skl 5%	4.51	11.42	2.34	2.82	3.59	6.0	24.32	35.76
1%	6.94	15.03	3.08	3.72	4.72	7.9	32.02	47.09

Table (6): Estimates of genetic components and various ratios from Hayman's analysis analysis F1 and F2 diallel crosses.

Genetic parameters and ratios	Days to heading	Plant height (Cm.)	Spike length (Cm.)	Number of spikes per plant	Number of kernel per spike	1000-kernel weight (gm.)	Grain yield (gm.)	Total plant weight (gm.)
F1 Hybrid								
D	94.74**	169.68*	7.14**	23.5**	144.43**	60.32	170.34	10378.5
F	106.99	9.24	11.77**	4.01	126.16	39.04	269.18	14425.16
H1	226.2**	216.27	24.54**	67.17**	338.27**	179.17*	1476.51**	74925.63**
H2	168.54**	202.0	19.06**	65.55**	280.67**	131.85	1340.04**	59946.35**
h2	42.98	16.33	3.39	89.39	8.68	28.54	460.39**	67767.16**
(H1/D)1/2	1.55	1.13	1.85	1.69	1.53	1.72	2.94	2.69
(H2/4H1)	0.19	0.23	0.19	0.24	0.21	0.18	0.23	0.2
KD/KR	2.15	1.05	2.6	1.11	1.8	1.46	1.73	1.7
H2/H2	0.26	0.08	0.18	1.36	0.03	0.22	0.34	1.13
Heritability n.s	0.34	0.41	0.07	0.37	0.34	0.39	0.05	0.25
b.s	0.96	0.65	0.88	0.94	0.96	0.77	0.99	0.95
F2 Crosses								
D	98.7**	161.28*	2.18**	23.37**	94.84**	91.83**	546.13**	21223.61**
F	159.68**	-99.05	1.90	12.7**	42.7	106.19	505.55	31773.61**
H1	197.07**	443.61**	3.93*	34.8**	268.52**	221.8**	1931.74**	39827.49**
H2	117.97**	390.76**	3.01	29.65**	222.64**	177.34*	1629.08**	26222.02**
h2	74.30**	65.49	0.53	0.94**	3.65	5.54	-45.04	6253.43
(H1/D)1/2	1.41	1.66	1.34	1.22	1.68	1.55	1.88	1.37
(H2/4H1)	0.15	0.22	0.19	0.21	0.21	0.2	0.21	0.17
KD/KR	3.68	0.69	1.96	1.57	1.31	2.19	1.65	3.41
H2/H2	0.63	0.17	0.19	2.26	0.02	0.03	-0.03	0.24
Heritability n.s	0.22	0.57	0.27	0.48	0.46	0.23	0.25	0.18
b.s	0.93	0.92	0.6	0.93	0.98	0.91	0.86	0.98

All H2 values were smaller than H1 values for all traits which complies with the theoretical assumption of Hayman (1954) and could be a further proof for the unequal proportions of positive and negative alleles in the parents at all loci for these characters. The overall dominance effects of heterozygous loci was significant for most studied characters in the F1 and F2 indicating that the effects of dominance are due to heterozygosity. The covariance of additive and dominance (F) was not significant for all studied characters, except spike length in the F1 and days heading, number of spike per plant and total plant weight in the F2, indicating an excess of recessive overdominance alleles. From the aforementioned result, it could be concluded that the dominance genetic components (H) appeared to be the major portion of the genetic variation. This was confirmed by the insignificant magnitude of GCA/ SCA ratios.

The proportion of the genetic components are presented also in Table (6). The mean degree of Dominance, $(H1/D)^{1/2}$ was higher than unity for all studied traits in the F1 and F2, indicating an over dominance effect. Values of $(H2/4H1)$ were less than 0.25 for all studied traits in the F1 and F2, revealing asymmetric distribution of positive and negative alleles among parents. The ratio KD/kr show the proportion of dominant and recessive genes. Dominant genes in the parents were found for all studied traits in the F1 and F2 except plant height in the F2. This conclusion is also supported by the fact the value of $(H2/4H1)$ was less than 0.25. Low values for heritability were detected for all studied traits, indicating that most of the genetic variance are due to non-additive genetic effects. Being in support of previous conclusion of predomination of dominance gene action. These results agree with those obtained by El-Sayed (2000), Hamada and Tawfelis (2001), Mostafa (2002) and El-Sayed (2004).

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تحليل صفات المحصول ومكوناته لبعض هجن قمح الخبز

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أجرى تقييم الهجن الدائرية لسبعة تراكيب وراثية من قمح الخبز بمحطة إيتاي البارود بمحافظة البحيرة ٢٠٠٢/٢٠٠١ و ٢٠٠٣/٢٠٠٢ و ٢٠٠٣/٢٠٠٤ لتقدير القدرة العامة والخاصة على الانتلاف فى الجيل الأول والثانى والتعرف على العوامل الوراثية التى تتحكم فى صفة المحصول ومكوناته ويمكن تلخيص النتائج كما يلى:

كان التباين الراجع إلى القدرة العامة على الانتلاف معنويات كل الصفات تحت الدراسة فى كل من الجيل الأول والثانى كما كانت القدرة الخاصة على الانتلاف معنوية لجميع الصفات المدروسة صفة طول النبات وطول السنبله فى الجيل الأول وصفة طول النبات فى الجيل الثانى. وبرغم أن تباين القدرة العامة على الانتلاف كانت أكبر من تباين القدرة الخاصة للانتلاف مما يدل على أن الفعل الجينى المضيف الا أنها لم تكن معنوية فى معظم الأحوال قد تكون متكافئة مع الفعل السائد باستثناء صفات طول النبات وربما عدد السنابل وعدد الحبوب.

كان توزيع الجينات الموجبة والسالبة غير منتظم بالنسبة لكل الصفات فى الجيل الأول والثانى. ولوحظ وجود سيادة فائقة لبعض الصفات وسيادة جزئية لصفات أخرى وكانت درجة التوريث بمعناها الضيق أو الواسع عالية ومنخفضة فى الصفات المختلفة مما يدل على سيادة الفعل الجينى الغير مضيف باستثناء صفات طول النبات ودرجة ما عدد السنابل/نبات وعدد الحبوب/سنبله.

أختلفت تقديرات درجة التوريث بمعناها الواسع والضيق بين الصفات والأجيال وكانت أعلى قيم درجة التوريث الواسع ٩٨,٩% لصفة المحصول وأقلها ٦٥,٣% لصفة طول النبات وسجلت صفة التوريث بمعناها الضيق أعلى ٤١,٤% لصفة طول النبات وأقلها ٥,٣% لصفة المحصول وذلك فى الجيل الأول.

أما بالنسبة للجيل الثانى كانت أعلى قيم لدرجة التوريث الواسع لصفة عدد الحبوب فى السنبله ٩٨,١% وأقلها لصفة طول السنبله ٦٠,٤% أما بالنسبة لدرجة التوريث بمعناها الضيق ٤٧,٨% لصفة عدد السنابل فى النبات وأقلها لوزن النبات بالكامل ١٨,٤% وذلك فى الجيل الثانى.