

GENETIC STUDIES IN SOME BREAD WHEAT CROSSES

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(Manuscript received 30 July 2006)

Abstract

A diallel cross among seven bread wheat (*Triticum aestivum* L.) genotypes (parents) namely, Giza 164, Line 1, IRENA, Line 2, Sids 1, Sakha 8 and Gemmiza 7 were evaluated for yield and its components as well as some other agronomic characters in the F_1 and F_2 generations. Genotypes mean squares were significant for all studied characters. Mean squares for parents vs crosses as, an indication for heterosis, were significant for all characters in F_2 , and for heading date, number of kernels/spike, 100 kernel weight and grain yield/plant in F_1 . Both general and specific combining ability (GCA and SCA, respectively), were significant for all studied characters in the F_1 and F_2 except for grain yield/plant in the F_2 which was significant for SCA only. These results reflect the importance of both additive and dominance genetic variances in the inheritance of these characters. However, the additive gene action (GCA) was of great importance in the performance for all studied characters except for number of kernels/spike in the F_1 and grain yield/plant in the F_2 where dominance was more pronounced. Moreover, the parents P_2 (Line 1), P_3 (IRENA), P_6 (Sakha 8) and P_7 (Gemmiza 7) were the best combiners for grain yield/plant. Meanwhile, significant SCA effects for grain yield were found in the crosses between $P_1 \times P_3$, $P_2 \times P_5$, $P_2 \times P_6$, $P_3 \times P_6$, $P_4 \times P_7$, $P_5 \times P_6$ and $P_5 \times P_7$ in the F_1 and $P_3 \times P_5$ and $P_4 \times P_5$ in the F_2 . The additive variance effects were significant for all characters except for number of kernels/spike in the F_1 and grain yield/plant in F_1 and F_2 . Over dominance effects of heterozygous loci (h_2) were significant for number of kernels/spike, kernel weight and grain yield/plant in the F_2 and heading date and number of spikes/plant, in the F_2 . Value of $H_2/4H_1$ analysis being less 0.25 indicated asymmetric distribution of positive and negative alleles among parents for 5 and 3 characters in the F_1 and F_2 , respectively.

On the other hand, narrow sense heritability was low for some characters, indicating the importance non-additive genetic effect.

INTRODUCTION

Wheat, the major cereal crop in Egypt, receives the most attention from wheat breeders, to increase grain yield by developing high yielding wheat cultivars. The main objective of plant breeding program is to produce plants that perform certain functions than the existing types. For this, the plant breeder must have sufficient information on the inheritance of the economic characters if he is intending for efficient planning of the breeding program. 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. The diallel analysis as outlined by Hayman (1954) is an attempt partition phenotypic variation into genotypic and environmental components and to subdivide genotypic variation into used to draw inferences about the genetic system. In wheat, plant height and spike characters are, important attributes that determine the desirability of the progeny of any cross. The appropriate selection for these characters may greatly contribute towards enhancement in the yielding ability. Thus, information on the nature of gene action with respect to this character would be useful in the development of better Cultivars. Edwards et. al., 1976 stated that dominance 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 .

Successful breeding programs need continuous information about the genetic variation and systems governing grain yield and its components. Contradictory results were obtained by several authors with respect to genetic systems governing wheat grain yield and its components. For instance, Ikram and Tanah (1991) and El-Sayed - (2004), indicated that additive and non-additive gene effects played equal roles in the inheritance of grain yield, number of spikes/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. Furthermore, results obtained by Mohamed (1999) from eight wheat genotypes 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) Similarly, Hamada and 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, and El-Sayed and Moshref (2005), found that both additive and dominance variances were significant, for number of spikes/plant, number of Kernels/spike, kernel weight and grain, yield/plant.

On the other hand, Salem and Hassan (1991) as well as Moshref (2006) found that non-additive gene effects were more important in the inheritance of grain yield/plant and number of spikes/plant Similarly, 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-Sayesd et. al., (2000) and Ashoush et. al., (2001) found that GCA and SCA

were significant for days to heading and maturity, plant height, number of spikelets/spike and flag leaf area.

Concerning the heritability values, Tamam and Abd EI-Gawad (1999) and El-Sayed (2004), found that values of heritability in broad and narrow senses for days to heading, number of spikes/plant, kernel weight and grain yield / plant were high. Meanwhile, the narrow sense heritability value for number, of kernels/spike was low. 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. They also, reported that these estimates for number of days to heading and 1000-kernel weight, fluctuated varied from medium to high.

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

MATERIALS AND METHODS

This study was conducted at EL-Giza Agricultural Research, Station, Agricultural Research Center (ARC), during the three successive growing seasons 2003/2004 to 2005/2006. Five bread wheat cultivars and two promising lines, Line 1 and Line 2 representing a wide range of genetic variability were selected for this study, (Table I).

Table 1. The name, pedigree and origin of seven parental wheat genotypes.

No.	Parent	Origin
P ₁	Gizal64 = KvZ Buho "S" x Kal-B.B.,	Egypt
P ₂	Mildeess Mo 73/pol//T. aest.-Bon/con (Line 1)	Mexico
P ₃	IRENA	Mexico
P ₄	Tsi/vee "s" //Giza 165 t (Line 2)	ICARDA
P ₅	Sids 1 = Hd 2172/Pavon "s" x 1158.57 Maya 74 "s"	Egypt
P ₆	Sakha 8 = Indus 66 x Norteno "s"	Egypt
P ₇	Gemmeiza7=CMH74A.630./SX//Seri 82/Gent. CGM 4611-2GM-3GM-GM-OGM	Egypt

In 2003/2004 season, all possible crosses (without reciprocals) among the seven parents were made. In the second season (2004/2005), the 28 entries (21 F₁'s and 7 parents) were planted in the field using the randomized complete block design (RCBD) with four replications according to Steel and Torri (1980). In (2005 / 2006) F₂ and parents were planted in the field using RCBD with four replications. Each entry

was planted in a plot of three rows, for parents and F_1 and six rows for F_2 . 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/row from each row. The studied characters were number of days to heading (DH) and number of days to maturity date (DM), spike length (Sp. L.) measured in cm, plant height (PI. H) measured in cm., number of spikes/plant, (No. S/P), number of kernels/spike (No. K/S), 100-kernel weight (K. Wt), and grain yield/plant (Gy/P.).

The analysis of variance for combining ability effects was calculated according to Griffing (1956), and further genetic analysis was carried out as described by Hayam (1954).

RESULTS AND DISCUSSION

1) Analyses of variance

The mean performance of the seven parental cultivars for F_1 hybrids and F_2 crosses is presented in Table 2 and Table 3, respectively. The results showed that there were significant differences among parents and in the F_1 , F_2 generations of the crosses for all studied characters.

The analysis of variance for all the studied characters is presented in Table 4. Significant genotypes, mean squares were detected for all studied characters indicating the wide diversity among the parental materials used in the study. Results also showed that mean squares due to parents were significant for all studied characters except for grain yield/plant in the F_2 . The hybrids in the F_1 and crosses in the F_2 were significant for all the studied characters except for number of spikes/plant in the F_2 crosses revealing overall differences between hybrids and crosses. Mean squares due to parents vs. crosses were significant for most characters in the F_1 and all characters in the F_2 indicating heterosis of F_1 and F_1 populations.

Moreover, the variance associated with GCA and SCA was significant in all studied characters in the F_1 and F_2 generation except for GCA for grain yield/plant in the F_2 , Table 4. Thus, both GCA and SCA revealed the presence of both additive and dominance types of gene effects for the studied characters. From Table 4, it could be noticed that GCA was relatively larger than SCA for all studied characters except for number of kernels/spike in the F_1 and grain yield/plant in the F_2 . The ratio of GCA/SCA suggested the predominant role for additive type of gene action for these characters and that selection could be successful.

Table 2. Means of characters studied for seven parents and their 21 F₁ hybrids.

<i>Genotypes</i>	<i>DH</i>	<i>DM</i>	<i>Pl. H.</i>	<i>S. L.</i>	<i>No. SP./P.</i>	<i>No. K/SP</i>	<i>100 K. Wt</i>	<i>G.Y/P.</i>
P ₁	86.0	141.7	88.2	11.7	13.0	50.5	44.07	26.05
P ₂	99.0	139.3	103.6	10.5	13.4	40.6	45.50	24.09
P ₃	95.3	137.3	88.4	12.0	14.4	51.1	33.68	22.31
P ₄	85.3	139.0	108.8	12.3	9.4	35.1	55.78	19.81
P ₅	81.0	139.7	84.0	10.5	10.0	32.9	74.46	27.57
P ₆	87.7	146.0	85.3	10.6	18.4	46.4	34.35	24.70
P ₇	87.7	144.7	90.3	12.0	12.8	31.1	37.79	22.54
P ₁ × P ₂	96.0	143.3	91.6	13.1	10.4	64.6	44.29	30.75
P ₁ × P ₃	94.0	135.7	95.8	12.2	11.2	56.5	44.39	28.44
P ₁ × P ₄	92.0	134.3	88.9	12.2	10.2	42.8	42.8	20.39
P ₁ × P ₅	85.7	136.0	89.5	10.3	10.2	48.7	52.52	24.86
P ₁ × P ₆	90.7	145.3	87.3	10.9	14.6	40.9	41.69	25.15
P ₁ × P ₇	94.0	138.3	83.0	11.6	12.2	47.2	41.69	22.42
P ₂ × P ₃	94.3	136.3	91.1	13.0	10.4	51.5	44.02	27.25
P ₂ × P ₄	91.3	136.0	106.8	12.8	12.0	28.1	49.54	29.52
P ₂ × P ₅	81.7	133.3	103.1	12.5	15.8	51.5	45.96	42.05
P ₂ × P ₆	89.0	139.7	97.3	12.6	14.2	32.7	49.10	39.07
P ₂ × P ₇	93.3	137.7	88.2	11.9	15.6	52.5	43.43	33.95
P ₃ × P ₄	94.0	138.3	97.5	12.1	12.2	44.0	39.62	19.69
P ₃ × P ₅	94.7	138.3	99.2	10.3	9.6	57.5	41.17	23.98
P ₃ × P ₆	96.7	145.0	88.4	12.5	19.4	47.9	36.07	35.64
P ₃ × P ₇	95.0	144.7	92.5	11.3	16.2	39.2	34.85	24.74
P ₄ × P ₅	97.0	146.7	99.7	12.3	6.2	51.3	49.27	15.84
P ₄ × P ₆	92.3	146.3	103.3	11.4	7.6	56.5	44.65	18.73
P ₄ × P ₇	92.7	146.3	104.1	12.5	9.8	59.2	41.89	27.71
P ₅ × P ₆	96.0	146.7	93.7	31.8	10.8	56.3	42.94	29.43
P ₅ × P ₇	95.7	146.3	94.4	11.5	15.2	60.3	37.64	38.29
P ₆ × P ₇	92.7	144.0	83.7	11.5	13.0	55.9	38.92	30.47
L.S.D 5 %	2.50	2.7	0.81	9.5	1.5	2.3	3.00	3.19

Table 3. Means of characters studied for seven parents and their 21 F2 crosses.

<i>Genotypes</i>	<i>DH</i>	<i>DM</i>	<i>Pl. H.</i>	<i>S. L.</i>	<i>No. SP./P.</i>	<i>No. K/SP</i>	<i>100 K. Wt</i>	<i>G.Y/P.</i>
P ₁	82.66	125.67	112.88	11.73	9.00	46.57	6.197	18.60
P ₂	99.00	141.00	128.25	12.63	11.50	45.00	6.742	22.33
P ₃	89.33	132.67	105.00	12.93	9.33	64.53	4.657	22.03
P ₄	83.00	127.00	125.75	14.83	11.67	60.23	5.273	23.27
P ₅	75.00	114.67	103.75	16.75	4.87	88.97	5.623	18.00
P ₆	92.00	133.33	107.75	11.40	11.17	59.33	3.623	16.67
P ₇	83.76	128.67	110.00	12.80	12.10	61.93	5.200	22.80
P ₁ × P ₂	78.33	124.67	111.75	12.85	8.93	60.30	5.697	21.30
P ₁ × P ₃	76.33	123.00	113.78	12.63	8.53	55.47	4.840	22.30
P ₁ × P ₄	78.67	126.00	116.15	15.83	7.93	55.60	4.550	15.10
P ₁ × P ₅	73.67	110.00	106.83	12.13	8.63	61.17	5.073	18.47
P ₁ × P ₆	79.67	128.33	107.00	11.38	9.20	49.20	4.613	16.83
P ₁ × P ₇	81.67	130.67	103.63	12.25	8.60	66.53	5.180	22.73
P ₂ × P ₃	88.00	129.67	109.75	12.35	8.53	60.40	4.713	18.17
P ₂ × P ₄	79.67	126.67	131.13	13.68	7.57	76.03	4.547	14.30
P ₂ × P ₅	81.67	132.33	113.50	14.28	6.80	66.63	5.150	13.33
P ₂ × P ₆	92.33	135.33	114.25	12.83	9.23	64.20	4.660	16.37
P ₂ × P ₇	91.67	131.33	106.00	11.75	7.13	64.53	5.117	16.87
P ₃ × P ₄	84.33	126.33	110.88	11.48	6.93	58.07	4.963	15.40
P ₃ × P ₅	79.33	124.33	98.85	15.85	10.43	72.53	5.420	25.77
P ₃ × P ₆	86.67	131.67	111.00	12.18	8.73	54.27	5.787	21.43
P ₃ × P ₇	90.00	133.33	109.38	11.20	7.47	54.50	4.603	11.53
P ₄ × P ₅	73.67	109.67	114.38	14.58	8.60	61.37	5.720	21.77
P ₄ × P ₆	88.00	133.33	95.75	12.00	9.50	63.53	4.497	16.20
P ₄ × P ₇	77.67	121.67	115.18	12.10	8.87	62.63	4.373	21.13
P ₅ × P ₆	83.67	128.00	103.75	12.73	8.50	58.30	3.990	12.97
P ₅ × P ₇	89.67	134.67	108.25	11.70	8.57	54.87	3.900	13.53
P ₆ × P ₇	86.67	128.67	108.43	12.25	9.77	54.57	4.93	19.47
L.S.D 5 %	2.98	2.73	8.72	1.58	2.34	10.11	0.796	6.80

Table 4. Observed mean squares from ordinary and combining ability analysis in the dial lei.

S. of V.	d.f.	D.H.	D. M.	PLH.	S. L.	No. SP./P.	No.K/SP	100K. Wt	g./p.
<i>F₁ Hybrid</i>									
Genotypes "G"	27	65.29*	56.74*	165.23*	3.51*	4.16*	280.18*	195.01*	18.18*
Parents "P"	6	115.43*	30.41*	273.10*	4.15*	7.67*	210.13*	631.27*	11.17*
Hybrids "F ₁ "	20	41.02*	67.44*	138.18*	3.49*	3.32*	255.99*	64.10*	533.11*
P. Vs. F ₁	1	250.00*	0.67	39.84	0.04*	0.05	1184.30*	195.52*	85.90*
GCA	6	73.14*	122.97*	475.16*	10.70*	10.01*	114.47*	555.13*	25.39*
SCA	21	63.05*	37.97*	76.68*	1.45*	2.49*	327.52*	92.12*	16.05*
Error	54	2.34	2.70	33.66	0.24	0.09	8.18	3.38*	0.43
GCA/SCA		1.16	3.24	6.20	7.38	4.02	0.35	6.02*	1.58
<i>F₂ Crosses</i>									
Genotypes "G"	27	120.94*	152.83*	247.00*	8.69*	7.08*	211.16*	1.21*	40.62*
Parents "P"	6	180.86*	198.44*	290.23*	14.11*	19.29*	631.58*	2.42*	21.60*
Crosses "F ₂ "	20	98.61*	475.76*	154.13*	143.98*	2.62	95.24*	0.70*	42.33*
P. Vs. F ₂	1	190.58*	65.03*	177.76*	5.95*	31.37*	7.00*	2.811*	120.71*
GCA	6	115.12*	126.33*	154.40*	5.01*	2.91*	132.33*	0.58*	5.20*
SCA	21	18.64*	29.15*	35.14*	1.36*	2.37*	52.69*	0.36*	15.93*
Error	54	3.34*	2.83	26.83*	0.95*	2.08	38.73*	0.24	17.54
GCA/SCA		6.18	4.33	4.41	3.68	1.24	2.51	1.61	0.33

Significant at 5% level of probability.

2) General Combining ability (GCA)

Estimates of GCA effects for parents in the F₁ and F₂ are presented in Table 5. Significant positive values for the studied characters would be of interest except for heading and maturity dates where significant negative effects would be useful. For heading and maturity dates P₁ (Giza 168) was the best combiner for both traits in the F₁ and F₂. Also, P₅ (Sids 1) seems to be good combiner for heading date in the F₁ and F₂. P₂ (line 1) and P₃ (IRENA) in the F₃ and P₄ (Line 2) and P₅ (Sids 7) in the F₂ were good combiner for maturity date. These results suggest that these parents (Giza 168, Line 1, IRENA, Line 2 and Sids 1) were considered good general combinersto decrease

number of days to heading or maturity. With respect to plant height, P₂ (Line I) and P₄ (Line 2) in the F₁ and F₂ had the positive and significant GCA effects while P₆ (Sakha 8) and P₇ (Gemmeiza 7) were negative and significant in the F₁ and F₂, suggesting that these parents were considered as good general combiners to increase or decrease plant height. For spike length, P₂ (I in 1) and P₅ (Sids 1) in the F₁ and P₄ (Line 2) and P₅ (Sids 1) in the F₂ were good combiner to increase spike length. For number of spikes/plant P₂ (Line 1), P₃ (IRENA) P₆ (Sakha 8) and P₇ (Gemmeiza 7) in the F₁ and P₆ (Sakha 8) in the F₂ the best combiner for this characters. Parents No. 5 (Sids1) in the F₁ and F₂ and P₃ (IRENA) in the F₁ had the desirable (gi) for number of kernels/spike. With respect to 100 kernel weight P₂ (Line1), P₄ (Line2) and P₅ (Sids1) in the F₁ and P₁ (Giza 168) and P₂ (Line1) in the F₂ had positive and significant

Table 5. General combining ability effects for the studied characters in the diallel.

Parents	DH	DM	Pl. H.	S. L.	No. SP/P.	No. K/SP	100 K. Wt	G.Y/P.
F ₁ Hybrid								
P ₁	-1.116*	-1.243*	-4.259*	-0.224*	-0.099	2.315*	0.107	-0.222
P ₂	1.032*	-2.503*	3.844*	0.869*	0.286*	-2.070*	1.815*	1.506*
P ₃	2.772*	-1.614*	-1.052	-0.009	0.382*	2.004*	-4.837*	-0.216
P ₄	-0.487	-0.169	7.452*	-0.131	-0.766*	-3.174*	3.148*	-1.432*
P ₅	-2.413*	-0.095	-0.348	0.810*	-0.877*	1.182*	7.490*	-0.760*
P ₆	0.190	3.497*	-2.923*	-0.790*	0.701*	0.241	-3.219*	0.659*
P ₇	0.402	2.127*	-2.711*	-0.524*	0.375*	-0.499	-4.504*	0.465
C.D. 5%								
gi	0.545	0.585	2.067	0.175	0.108	1.019	0.655	0.232
Gi-gi	0.833	0.895	3.158	0.268	0.164	1.556	1.000	0.355
F ₂ Hybrid								
P ₁	-4.058*	-2.868*	-0.187	-0.294	-0.031	-4.678*	0.291*	0.479
P ₂	4.386*	4.688*	0.258*	-0.019	0.010	-1.156	0.272*	-0.291
P ₃	1.460*	1.540*	-2.548*	-0.181	-0.202	0.088	-0.010	1.505*
P ₄	-2.466*	-2.460*	5.377*	0.683*	0.158	0.577	-0.059	0.313
P ₅	-4.317*	-5.720*	-3.723*	1.289*	-1.094*	7.699*	0.086	-0.643
P ₆	3.423*	3.206*	-3.431*	-0.778	0.684*	-2.308*	-0.445*	1.224*
P ₇	1.671*	1.614*	-1.745*	-0.700*	0.476	-0.223	-0.136	0.361
C.D. 5%								
gi	0.647	0.597	1.570	0.299	0.511	2.207	0.173	1.085
Gi-gi	1.883	0.911	2.430	0.456	0.780	03.371	0.253	1.140

* Significant at 5% level of probability.

GCA effects. These results indicated that each Sids 7, Giza 164, line 1 and Line 2 had additive gene effects in the inheritance of 100 kernel weight. For grain yield/plant P2 (Line 1) and P6 (Sakha 8) and P7 (Gernmeiza7) in the F₁ and P3 (IRENA) and P6 (Sakha 8) in the F₂ had positive and significant GCA effects for this trait. These results suggested that Line 1, Sakha 8, Gemmeiza 7 and IRENA had additive gene action and were considered as good combineif for increasing grain yield/plant. This may be due to the high linkage between yield and number of spikes/plant.

3) Specific combining ability (SCA)

Specific combining ability of the parental combinations for the studied characters are presented for the F₁ and F₂ generation in Tables 6 and 7, respectively. For heading date, P₂×P₃, P₂×P₄, P₂×P₅ and P₂×P₆ in the F₁ and P₁×P₂, P₁×P₅, P₂×P₃, P₂×P₄, P₂×P₇, P₄×P₅, P₄×P₇ and P₆×P₇ in the F₂ showed negative and significant SCA effects for heading date indicating the presence of considerable non-allelic gene effects in these combinations. For maturity dates, six crosses in the F₁, i.e. P₁×P₃, P₁×P₄, P₁×P₅, P₁×P₇, P₂×P₅, and P₂×P₆ and eleven crosses in the F₂ P₁×P₂, P₁×P₃, P₁×P₅, P₁×P₆, P₂×P₃, P₂×P₄, P₂×P₅, P₃×P₆, P₄×P₅, P₄×P₇ and P₆×P₇ showed negative significant SCA effects. So, segregating lines may have earliness for maturity. Crosses P₁×P₅, P₂×P₃, P₂×P₄, P₄×P₅, and P₆×P₇ exhibited negative and significant SCA effect for both heading and maturity in the F₂. Thus it is earliness crosses?

Crosses P₁×P₃ and P₃×P₅ in the F₁ and crosses P₁×P₃, P₂×P₄ and P₃×P₆ in the F₂ were positive and significant SCA effects for plant height, also cross P₁×P₃ was desirable sij in the F₁ and F₂. For spike length, three crosses, P₁×P₅, P₂×P₅, and P₃×P₆ in the F₁ and other three crosses in the F₂, P₁×P₄, P₃×P₅ and P₆×P₇ has positive and significant SCA effects For number of spikes/plant, seven crosses in the F₁, P₂×P₄, P₂×P₅, P₂×P₇, P₃×P₄, P₃×P₆, P₃×P₇, and P₅×P₇ and as well as cross P₃×P₅ in the F₂ showed positive and significant SCA effects indicating that.

They had considerable non-allelic gene effects in these combinations. For number of kernels/spike twelve crosses in the F₁ P₁×P₂, P₁×P₃, P₂×P₃, P₂×P₅, P₂×P₇, P₃×P₅, P₄×P₅, P₄×P₆, P₄×P₇, P₅×P₆, P₅×P₇ and P₆×P₇ and five crosses in the F₂ P₁×P₂, P₁×P₇, P₂×P₄, P₂×P₆, and P₂×P₇ showed positive and significant SCA, also P₁×P₂ and P₂×P₇ showed positive and significant SCA in the F₁ and F₂, so segregating lines may have high number of kernels/spike. The crosses P₁×P₃, P₂×P₃, P₂×P₆, and P₂×P₇ in the F₁ and crosses P₃×P₆, and P₄×P₅ also P₆×P₇ in the F₁ and F₂ showed positive and significant SCA in kernel weight, these results indicating these crosses contained an epistatic effect in the inheritance of this trait. Meanwhile for grain yield/plant the crosses P₁×P₃, P₂×P₄, P₂×P₅, P₂×P₆, P₃×P₆, P₄×P₇ and P₅×P₇ in the F₁ and crosses P₃×P₅ and P₄×P₅ in the

F₂ showed positive and significant SCA effects, these results suggesting that these crosses had non-allelic gene action for increasing grain yield/plant and could be used in the segregating generations to produce lines that have high grain yield/plant. Similar results were obtained by El-Sayed (2004), El-Sayed and Moshref (2005) and Moshref (2006).

Table 6. Specific combining ability effects for the studied characters in the F₁ diallel.

Genotypes	DH	DM	Pl. H.	S. L.	No. SP/P.	No. K/SP	100 K. Wt	G.Y/P.
P ₁ × P ₂	4.267*	6.139*	-1.835	0.099	-0.781*	16.751*	-1.507	0.212
P ₁ × P ₃	0.546	-2.417*	7.261*	0.077	-0.611*	4.544*	5.245*	1.163*
P ₁ × P ₄	1.806*	-5.194*	-8.176*	0.166	0.204	-3.946*	-4.329*	-0.305
P ₁ × P ₅	-2.602*	-3.602*	0.224	0.692*	0.315	-2.368	1.049	0.514
P ₁ × P ₆	0.176	2.139*	0.669	-0.442	0.204	-9.227*	0.922	-0.807*
P ₁ × P ₇	2.917*	-3.491*	-3.880	-0.042	-0.270	-2.219	-1.340	-1.525*
P ₂ × P ₃	-1.269*	-0.491	-5.509	-0.249	-1.263*	3.995*	3.166*	-0.963*
P ₂ × P ₄	-1.009*	-1.009	1.654	-0.327	0.419*	-14.227*	0.705	1.011*
P ₂ × P ₅	-8.750*	-8.750*	2.787	1.732	1.796*	4.818*	-7.218*	4.516*
P ₂ × P ₆	-3.639*	-3.639*	2.565	0.132	-0.315	-13.042*	6.613*	2.105*
P ₂ × P ₇	-0.102	-0.102	-6.783*	-0.868*	0.478*	7.432*	2.249*	0.592
P ₃ × P ₄	-0.083	-0.083	-2.783	-0.116	0.389*	-2.434	-2.569*	-0.594
P ₃ × P ₅	2.609*	2.509*	6.750*	0.477	-3.670*	6.744*	-5.355*	0.213
P ₃ × P ₆	2.287*	2.267*	-1.472	0.944*	1.322*	-1.982	0.246	2.681*
P ₃ × P ₇	0.028	0.028	2.446	-0.523	0.581*	-9.908*	0.320	-0.756*
P ₄ × P ₅	8.102*	8.102*	-1.220	-0.801*	-0.352*	5.721*	-5.247*	-1.282*
P ₄ × P ₆	1.213*	1.213	4.957	-0.068	-1.463*	11.862*	0.848	-1.739*
P ₄ × P ₇	0.954*	0.954	5.476	0.732*	-0.404*	15.269*	0.626	1.450*
P ₅ × P ₆	6.806*	6.806*	3.157	-0.608*	-0.285	7.240*	-5.211*	1.168*
P ₅ × P ₇	5.880*	5.880*	3.609	-1.208*	1.507*	11.981*	-9.220*	4.304*
P ₆ × P ₇	5.667*	5.667*	-4.546	0.458	-0.804*	8.521*	2.927*	0.278
C.D 5%								
Sij	0.833	1.899	6.699	0.570	0.349	3.302	2.122	0.753
Sij - Sik	2.355	2.532	8.932	0.750	0.465	4.402	2.829	1.004
Sij - Skl	2.203	2.368	8.355	0.710	0.434	2.059	2.647	0.470

Table 7. Specific combining ability effects for the studied characters in the F₂ diallel .

Genotypes	DH	DM	Pl. H.	S. L.	No. SP./P.	No. K/SP	100 K. Wt	G.Y/P.
P ₁ × P ₂	-5.768*	-4.630*	-5.140*	0.270	0.066	5.696*	0.168	2.659
P ₁ × P ₃	-4.843*	-3.148*	5.69*	0.206	-0.123	-0.381	-0.407	0.363
P ₁ × P ₄	1.417	3.852*	0.140	2.542*	-0.082	-0.737	-0.648*	-4.144
P ₁ × P ₅	-1.731*	-8.889*	-0.085	-1.763*	0.869	-2.294	-0.269*	0.178
P ₁ × P ₆	-3.472*	0.518	-0.201	-0.447	-0.342	-4.252	-0.199	-0.874
P ₁ × P ₇	0.380	4.444*	-5.262*	0.351	0.266	10.996*	0.059	0.344
P ₂ × P ₃	-1.620*	-4.037*	-4.779*	-0.344	-0.164	1.030	-0.515*	-1.000
P ₂ × P ₄	-6.028*	-3.037*	8.671*	0.117	-1.490	7.174*	-0.632*	-4.179
P ₂ × P ₅	-2.176*	5.889*	0.146	0.112	-1.005	-0.348	-0.174	-4.185*
P ₂ × P ₆	0.750	-0.037	0.604	0.728	-0.349	7.226*	-0.134	-0.570
P ₂ × P ₇	1.935*	-2.445*	-9.332	-0.424	-2.242	5.474*	0.014	-1.656
P ₃ × P ₄	1.565	-0.222	-2.774	-1.922*	-1.912	-3.037	0.066	4.370*
P ₃ × P ₅	-1.583	1.037	-5.699*	1.848*	2.840	4.307	0.378	6.852*
P ₃ × P ₆	-1.991*	-0.556	6.160*	0.240	-0.638	-3.952	1.275*	3.200
P ₃ × P ₇	3.194*	2.704*	2.849	-0.813	-1.697	-5.804*	-0.217	-8.785*
P ₄ × P ₅	-3.324*	-9.630*	1.901	-0.291	0.647	-7.348*	0.727*	3.694*
P ₄ × P ₆	3.269*	5.111*	-17.015*	-0.799*	-0.231	4.826	0.034	-1.341
P ₄ × P ₇	-5.213*	-4.963*	0.724	-0.777*	-0.856	1.841	-0.398	2.007
P ₅ × P ₆	0.787	3.037*	0.085	-0.680	0.021	-7.530*	-0.617*	-3.619
P ₅ × P ₇	8.306*	11.296*	2.899	-1.783*	0.295	-13.048*	-1.016*	-4.637*
P ₆ × P ₇	-2.102*	-6.963*	2.782	0.834*	-0.282	-3.341	0.548*	1.878
C.D 5%								
Sij	1.602	1.477	3.936	0.738	1.266	5.461	0.430	3.676
Sij - Sik	2.798	2.579	6.871	1.290	2.207	9.534	0.750	6.915
Sij - Skl	2.617	2.412	6.428	1.206	2.065	8.919	0.702	6.002

4) Genetic components

The estimates of the genetic components of variation, D, H₁, H₂, h² and F obtained by Hayman's analysis for F₁ and F₂ are presented in Table 8. The additive components of genetic variance effect (D) were significant for days to heading, plant height, spike length, number of spikes/plant and kernel weight in the F₁. Similarly the additive variances were significant for all characters in the F₂ except for grain yield/plant. On the other hand the dominant components (H₁) were significant for all studied characters at the F₁ and F₂ except for number of spikes/plant, kernel weight in the F₁. Values of (H₁) for all studied characters in the F₁ and F₂ except for number of spikes/plant, kernel weight and grain yield/plant were larger than the receptive (D), indicating the importance of the dominance gene action in the inheritance of these characters.

However, the value of (D) was larger in magnitude than the receptive (H₁) for number of spikes/plant, 100 kernel weight and grain yield/plant in F₁ only. The components of variation due to the dominance effects associated with gene distribution (H₂) was significant for all studied characters in the F₁ and F₂ except for

number of spikes/plant and kernel weight in the F_1 . All H_2 values were smaller than H_1 values for all characters except number of spikes/plant and 100 kernel weight in the F_1 , indicating unequal allelic frequency. The over all dominance effect of heterozygous loci (h^2) was significant for number of kernels/spike, kernel weight and grain yield/plant in the and, heading date and number of spikes/plant in the F_2 indicating that the effects of dominance is due to heterozygosity. The covariance of additive and dominance effect (F) was not significant for all studied characters in the F_1 and F_2 except for plant height in the F_1 and heading date, number of spikes/plant, number of kernels/spike and kernel weight in the F_2 indicating an excess of recessive overdominance alleles.

The degree of dominance (H_1 / D)^{1/2} was higher than unity for all studied characters in the F_1 and F_2 except kernel weight in the F_1 , indicating an overdominance effect. For kernel weight in the F_1 , the value of (H_1 / D)^{1/2} was less than unity indicating partial dominance effect. The value of ($H_2/4H_1$) were less than 0.25 for days to heading, days to maturity, plant height, spike length and number of spikes / plant in the F_1 and days to heading, days to maturity and number of kernels / spike in the F_2 revealing asymmetric distributions of positive and negative alleles among parents.

Table 8. Estimates of genetic components and ratios from Haymen's analysis diallel.

Genotypes	DH	DM	Pl. H.	S. L.	No. SP./P.	No. K/SP	100 K. Wt	G.Y/P.
F ₁ Hybrid								
D	37.309*	9.241	80.772*	1.299*	0.891*	67.545	668.649*	40.126
F	53.363	-5.221	34.868*	-0.208	-5.782	130.760	225.326	5.52
H ₁	88.700*	52.710*	86.930*	1.814*	-11.289	456.319*	-274.478	22.323*
H ₂	64.926*	45.189*	65.272*	1.640*	-7.893	375.30*	-204.414	15.835*
H ²	46.272	-0.314	1.883	-3.448	-3.831	214.27*	422.390*	16.268*
E	0.766	0.897	11.332	8.312	7.891*	2.148	323.045*	0.141
(H ₁ /D) ^{1/2}	1.534	2.388	1.037	1.182	-3.56	2.599	-0.641	2.326
H ₂ /4H ₁	0.183	0.214	0.188	0.226	-0.175	0.453	0.641	2.326
KD/KR	2.713	0.788	1.525	0.873	-21.613	2.187	0.584	1.816
h ² /H ₂	0.713	0.007	0.029	-2.102	0.485	0.571	-2.228	1.027
hert. n. s	19.280	47.408	54.990	63.01	11.216	84.592	38.197	38.123
hert b. s	96.362	96.133	81.553	93.767	00.000	97.627	27.737	97.867
F ₂ Crosses								
D	59.038*	65.231*	90.227*	3.288*	5.623*	198.010*	0.728*	1.545
F	27.072*	21.99	31.964	1.990	8.832*	262.162*	0.829*	3.500
H ₁	78.266*	119.506*	121.873*	5.141*	9.077*	237.292*	1.335*	48.84*
H ₂	57.126*	107.229*	119.581*	4.461*	5.434*	136.965*	1.049*	46.081*
h ²	34.905*	1.681	29.977	0.714	5.521*	-4.823	0.370	19.750
E	1.238*	0.920	6.516	0.240	0.676	12.514	7.902	5.626
(H ₁ /D) ^{1/2}	1.151	1.354	1.162	1.251	1.256	1.095	1.355	5.623
H ₂ /4H ₁	0.182	0.224	0.495	0.46	0.387	0.144	0.389	0.256
KD/KR	1.497	1.280	1.340	1.638	4.142	4.060	2.539	1.505
h ² /H ₂	0.611	0.109	0.251	0.160	1.016	0.035	0.035	0.429
hert. n. s	63.111	50.204	42.41	42.195	12.194	27.895	18.345	2.301
hert b. s	97.057	98.347	90.229	89.771	7.817	80.701	81.100	67.629

On the other hand, the value of $(H_2/4H_1)$ for number of kernels/spike, kernel weight and grain yield/plant in the F_1 and plant height, spike length, number of spikes/plant, kernel weight and grain yield/plant in the F_2 was larger than 0.25 days to heading symmetric distribution of alleles among parents. The proportion of dominant and recessive genes in parents KD/KR for all studied characters in the F_1 and F_2 except maturity date, spike length and kernel weight in the F_1 gives the proportion of dominant genes in the parents.

broad sense heritability was lowest for kernel weight was (27.7 in the F_1 and grain yield/plant was 67.629 in the F_2 And highest for grain yield/plant in the F_1 and days to maturity in the F_2 with value (97.867 and 98.347) respectively. On the other hand taking heritability into consideration the estimates broad sense ranged from 11.2 taking for number of spikes/plant to 84.6 % for number of kernels /spike in the F_1 and ranged from 2.3 for grain yield/plant to 63.1% for days to heading in the F_2 . These results agree with those obtained by El- Sayed et al (2000) and Moshref (2002).

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دراسات وراثية على بعض هجن قمح الخبز

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أجري تقييم الهجن الدائرية لسبعة تراكيب وراثية من قمح الخبز بمحطة البحوث الزراعية بالحيزة خلال ثلاثة مواسم زراعية ٢٠٠٣ / ٢٠٠٤ و ٢٠٠٤ / ٢٠٠٥ و ٢٠٠٥ / ٢٠٠٦ لتقدير القدرة العامة والخاصة على الانتلاف في الجيل الأول والثاني والتعرف على العوامل الوراثية التي تتحكم في صفة المحصول ومكوناته وبعض الصفات الأخرى مثل تاريخ طرد السنابل - تاريخ النضج الفسيولوجي وارتفاع النبات ويمكن تلخيص النتائج كما يلي :

كان التباين الراجع إلى القدرة العامة والخاصة على الانتلاف معنوياً لكل الصفات المدروسة ما عدا محصول الحبوب في الجيل الثاني كان معنوياً للقدرة الخاصة على الانتلاف فقط . وكان تباين القدرة العامة للانتلاف أكبر من تباين القدرة الخاصة على الانتلاف لكل الصفات المدروسة ما عدا محصول الحبوب نبات في الجيل الأول والثاني وعدد حبوب السنبل في الجيل الأول مما يدل على إن الفعل الجيني المضيف أكثر أهمية في وراثه معظم الصفات المدروسة .

كانت الأباء الثاني (Line 1) والثالث (IRENA) والسادس (سحا ٨) والسابع (جميزة ٧) ذات قدرة عامة على الانتلاف بالنسبة لمحصول الحبوب وكانت الهجن $P_2 \times P_6$, $P_2 \times P_5$, $P_1 \times P_3$, $P_5 \times P_7$, $P_5 \times P_6$, $P_4 \times P_7$, $P_3 \times P_6$ في الجيل الأول والهجن $P_4 \times P_5$, $P_5 \times P_3$ في الجيل الثاني ذات قدرة خاصة على الانتلاف بالنسبة للمحصول .

كان توزيع الجينات الموجبة والسالبة غير منتظم لأغلب الصفات محل الدراسة ولوحظ وجود سيادة فائقة لبعض الصفات وسيادة جزئية لصفات أخرى وكانت درجة التوريث بمعناها الضيق والواسع عالية أو منخفضة في الصفات المختلفة .