

A DIALLEL CROSS ANALYSIS FOR SOME QUANTITATIVE CHARACTERS IN BREAD WHEAT (*Triticum aestivum* L.)

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Abstract

A diallel cross among seven bread wheat genotypes (parents) namely; Shakha 8, Sakha 69, Sids 1, Attila, Opata, Line 88 and Giza 168 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 vs crosses as an indication for heterosis were significant for all studied characters in the F₁ and F₂ except for number of spikelets/spike in the F₁ and F₂ and for maturity date in the F₂ only. Both general and specific combining ability (GCA and SCA, respectively), were significant for all studied characters in the F₁ and F₂, except for number of spikelets/spike, number of kernels/spike in the F₁ and for maturity date in the F₂. These results indicate the importance of both additive and dominance genetic variance in the inheritance of most characters. However, the additive gene action (GCA) was of great importance in the performance of most studied characters. Moreover, the parents P₆ (Line 88) and P₃ (sids 1) were the best combiners for grain yield. Meanwhile, significant SCA effects for grain yield were found in the crosses between P₁ × P₃, P₂ × P₆ and P₄ × P₆ in the F₁ and P₁ × P₃, P₁ × P₄ and P₄ × P₆ in the F₂. The additive variance effects were significant for all studied characters except for 100 kernel weight in the F₁ and was 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; except for maturity date in the F₂. On the other hand, narrow sense heritability was low for some characters, indicating the importance non-additive genetic effects.

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 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 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 these character would prove useful in the development of better cultivars. 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. 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 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 Mahmoud (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) and Mostafa (2002) 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 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.

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-Sayesd *et al.* (2000), Ashoush *et al.* (2001) and Abd El-Hameed (2002), found that GCA and SCA were significant for days to heading, maturity, plant height, number of spikletes/spike and flag leaf area.

Concerning the heritability values, Tamam and Abd El-Gawad (1999) found that heritability in broad and narrow sense values for days to heading, number of spikes / plant, kernel weight and grain yield / plant were high, while, the narrow sense heritability 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 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 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 2000/2001, to 2002/2003. Six bread wheat cultivars and one promising line representing a wide range of genetic variability were selected for this study, (Table 1).

Table 1. Names and Pedigrees of Seven Parents of Bread Wheat .

No.	Name and Pedigree	Origin
P ₁	Sakha 8. Indus 66/ Norteno"s".	Egypt
P ₂	Sakha 69. Inia/RL 4220//7c/yr"s".	Egypt
P ₃	Sids 1. HD 2172/Pavon"s"/1158.571 Maya 74 "s"	Egypt
P ₄	Attila ND/VG 9144//Kal/Bb/3/ yaco/4/ve"s".	Mexico
P ₅	Opata Biy/Jyb.	Mexico
P ₆	Line 88 Bow "s"/Crow "s".	Mexico
P ₇	Giza 168 MRL/BUC//Seri.	Egypt

In 2000/2001 season , all possible crosses (without reciprocals) among the seven parents were made . In the second season, (2001/2002) 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 (2002/2003) 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 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 heading date (HD), maturity date (MD), flag leaf area (F.L.Area), measured in cm^2 , plant height (PL.H), measured in cm, number of spikelets/spike (No. spt/sp), number of spikes/plant, (No. sp/pl), number of kernels/spike (No. kls), 100-kernel weight (100-k.wt), and grain yield/plant (Gy/pl).

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

RESULTS AND DISCUSSION

Analysis of variance for all studied characters (heading date, maturity date, flag leaf area, plant height, number of spikelets/spike, number of spike/plant, number of kernels/spike, 100 kernel weight and grain yield/plant), for F_1 and F_2 are in Table (2). Analysis indicated that the significant mean squares of genotypes for all studied characters in the F_1 and F_2 , suggesting the presence of true differences among genotypes. Mean squares due to parents vs. crosses were significant for all studied characters indicating heterosis of F_1 and F_2 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 F_1 and F_2 generation. The same level of significance was found in most cases for SCA ability for all studied characters except for number of spikelets/spike, number of kernels/spike in the F_1 and for maturity date in the F_2 . 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 characters studied except the number of spikelets/spike, 100 kernel weight in the F_1 and F_2 and plant height in the F_2 only. The ratio of GCA/SCA suggested a predominant role for additive type of gene action for these characters and that selection could be successful.

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 number of spikelets/spike in the F_1 and F_2 and maturity date in the F_2 only.

Table 2. Mean squares from ANOVA and combining ability analysis in the F_1 and F_2 generation of wheat crosses.

Source	d.f	HD	MD	F.L Area	PLH.	No.Spt /SP	No.SP. /PL	No. K/S	100 K.wt	G.Y /Pl.
F_1: Hybrids										
Genotypes	27	34.39*	6.95*	321.82*	61.42*	1.24*	31.55*	88.06*	0.34*	34.67*
Parents	6	71.42*	9.05*	66.15*	97.64*	1.75*	11.50*	172.14*	0.59*	80.15*
F_1 Hybrids P vs. F_1	20	24.54*	5.17*	248.54*	38.42*	1.12*	35.58*	57.47*	0.37*	22.01*
GCA	1	9.14*	30.04*	396.88*	304.48*	0.76	71.25*	195.34*	1.23*	15.00*
SCA	6	105.54*	16.28*	1084.14*	142.41*	3.46*	22.24*	218.11*	0.30*	115.49*
GCA/SCA	20	14.06*	4.28*	104.01*	18.32*	0.61	34.32*	50.90	0.35*	11.58*
		7.50	3.80*	10.42	7.77*	5.67	0.65	4.29*	0.84	9.97*
F_2: Crosses										
Genotypes	27	27.76*	3.19*	333.34*	129.94*	1.01*	29.48*	350.46*	1.69*	122.88*
Parents	6	6.83*	3.60*	608.71*	126.01*	1.50*	12.14*	10.23*	0.16*	108.12*
F_2 : Crosses	20	16.20*	3.15*	250.13*	108.81*	0.88*	33.66*	377.88*	0.49*	114.98*
P.Nvs. F_2	1	15.75*	1.43	345.20*	335.16*	0.61	49.80*	1243.42*	32.30*	369.53*
GCA	6	95.06*	6.75*	1094.91*	89.38*	1.96*	19.00*	337.49*	0.59*	121.31*
SCA	20	8.54*	2.17	115.74*	141.53*	0.74*	32.90*	354.16*	1.89*	123.33*
GCA/SCA		11.13	3.11	9.46	0.63	2.65	0.58	0.95	0.31	0.98

- Significant at 5% level of probability

Estimates of GCA effects for parents in F_1 and F_2 are presented in Table 3. Significant positive values would be interest except for heading and maturity dates where significant negative effects would be useful. For heading date P_2 (Sakha 69) and P_7 (Giza 168) were the best combiners but the P_1 (Sakha 8) for maturity date was the best combiner for both traits in the F_1 and F_2 . For flag leaf area, plant height, number of spikelets/spike, number of spikes/plant, number of kernels/spike and grain yield/plant P_3 (sids 1) the best combiner for this characters. Giza 168 (P_7) had the desirable (gi) for 100 kernel weight. The parental line P_6 (line 88) was good combiner for increasing grain yield/plant. Sakha 8 (P_1) expressed significant positive (gi) for number spikes/plant.

Specific combining ability effects of the parental combinations for the studied characters are presented for the F_1 and the F_2 generations in Tables 4 and 5, respectively. For heading date the crosses ($P_1 \times P_3$), ($P_1 \times P_4$), ($P_2 \times P_6$) and ($P_3 \times P_6$) gave significant negative effects, in the F_1 and F_2 generations, for maturity date cross ($P_1 \times P_4$) and cross ($P_5 \times P_6$) had negative significant effects in the F_1 and F_2 . Cross ($P_1 \times P_4$) exhibited negative and significant SCA effect for both heading and maturity (earlines). For flag leaf area 4 crosses in the F_1 and 5 crosses in the F_2 showed

significantly positive SCA. The results indicated that the crosses ($P_1 \times P_3$) ($P_3 \times P_7$), ($P_4 \times P_6$) and ($P_5 \times P_7$) had the best desirable SCA effect for this trait. For plant height, one cross in the F_1 and 5 crosses in the F_2 gave significant positive SCA effects, also cross ($P_3 \times P_7$) was desirable (sij) in the F_1 and F_2 . For number of spikelets/spike the both crosses ($P_1 \times P_4$) and ($P_1 \times P_5$) for F_1 and ($P_1 \times P_4$), ($P_1 \times P_5$) and ($P_3 \times P_5$) showed the highest positive significant SCA values for this characters in the F_2 . For number of spikes/plant five and four crosses for F_1 and F_2 respectively, showed significant positive (sij). Also the cross ($P_1 \times P_3$) gave the highest positive SCA values for this traits in the F_1 and F_2 generations. Two and six crosses in the F_1 and F_2 respectively exhibited significant positive SCA effect for number of kernels/spike, also the best combination was ($P_1 \times P_3$) in the F_2 generation. Regarding 100 kernel weight nine crosses in the F_1 and the 15th crosses in the F_2 had significantly positive SCA effect. The cross ($P_1 \times P_3$) and ($P_5 \times P_7$) in the F_1 and cross ($P_3 \times P_7$) and ($P_4 \times P_5$) in the F_2 have the highest desirable SCA effect for this characters. For grain yield/plant in the F_1 crosses ($P_1 \times P_3$), ($P_2 \times P_6$), ($P_4 \times P_6$) and ($P_5 \times P_7$) but in the F_2 crosses ($P_1 \times P_3$), ($P_1 \times P_4$) and ($P_4 \times P_6$) showed significantly positive SCA effects.

Table 3 . Estimates of general combining ability (GCA), effects of Wheat Parents from F₁ and F₂ diallel crosses.

S. of .v	HD	MD	F.L. Area	No. Spt/SP	No. Spt /sp	No. SP./Pl.	No. K /SP	100 K.wt	G.Y /Pl.
F₁ Hybrid									
P ₁	-0.249	-1.545*	-1.606*	-0.234	-0.203	1.118*	2.634*	0.129*	-2.816*
P ₂	-2.063*	0.011	-4.460*	0.707	-0.047	-0.841	-2.472*	-0.138*	1.303
P ₃	0.085	0.751*	12.922*	3.490*	0.612*	1.104*	2.329*	0.065	2.601*
P ₄	2.307*	0.233	-1.904*	-0.586	-0.532*	-0.238	-3.002*	-0.061	-0.680
P ₅	0.307	0.360	2.504*	1.211	-0.040	-0.392	-0.658	-0.025	-1.325
P ₆	2.418*	0.270	-6.353*	-0.480	0.253*	-0.338	-2.567*	-0.090*	2.716*
P ₇	-2.804*	0.640*	-1.103	-4.108*	-0.043	-0.513	3.736*	0.120*	-1.799*
L.S.D 5%									
Gi	0.527	0.458	1.383	1.537	0.234	0.936	2.263	0.080	1.691
Gi-Gj	0.805	0.699	2.112	2.348	0.357	0.975	3.456	0.120	2.584
F₂ Crosses									
P ₁	-0.048	-0.836*	-1.843*	-2.630*	-0.095	1.343*	-3.581*	-0.199*	-2.681*
P ₂	-1.492*	-0.132	-4.158*	0.328	0.054	-0.793*	-4.336*	0.051	1.049
P ₃	0.175	0.794*	12.295*	2.375*	0.428*	1.028*	5.968*	-0.108*	2.856*
P ₄	0.286	0.164	-2.295*	-0.292	-0.478*	-0.217	2.252*	-0.054	-0.941
P ₅	0.138	-0.280	2.660*	-0.913	0.054	-0.663	-1.252	0.100*	-1.125
P ₆	2.026*	0.201	-6.473*	-1.111	0.079	-0.346	1.049	-0.042	2.422*
P ₇	-3.085*	0.090	-0.840	2.244*	-0.042	-0.353	-0.101	0.251*	-1.581
L.S.D 5%									
Gi	0.549	0.433	1.273	1.931	0.193	0.703	1.677	0.085	2.021
Gi-Gj	0.838	0.662	1.944	2.295	0.295	1.075	2.562	0.130	3.087

* Significant at 5% level of probability.

The main objective of plant breeding program is to produce plants that perform certain functions better than the existing types. For this, the plant breeder must have sufficient information on the inheritance of economic traits if he is intending for efficient planning of the breeding program.

The diallel analysis as outlined by Hayman (1954) is an attempt to partition phenotypic variation into genotypic and environmental components and to subdivide genotypic variation into its additive and dominance components. Which can be used to draw inferences about the genetic system.

The estimates of the genetic components of variation D, F, H_1, H_2 and h^2 obtained by Hayman's analysis for F_1 and F_2 are presented in Table 6. The additive components of genetic variance effect (D) were significant for all traits in the F_1 except 100 kernel weight. On the other hand the additive variance was significant with heading date, maturity date, flag leaf area, number of spikelets/spike in the F_2 generation. The dominant component (H_1) was significant for all studied characters at the F_1 and F_2 except number of spikes/plant in the F_1 and maturity date in F_2 . Values of (H_1) for heading date, flag, leaf area, number of spikes/plant and number of kernels/spike in the F_1 and the all studied characters in the F_2 were smaller than the respective (D), indicating the importance of the additive gene action in the inheritance of these characters. However the values of (H_1) were larger in magnitude than the respective (D) for maturity date, plant height, number of spikelets/spike, 100 kernel weight and grain yield/plant in the F_1 only. The components of variation due to the dominance effect associated with gene distribution (H_2) was significant for all studied characters in the F_1 and F_2 except number of spikes/plant. The values of H_2 were consistently lower than those of H_1 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 F_1 and F_2 indicated that the effects of dominance is due to heterozygosity. The covariance of additive and dominance (F) was not significant for all studied characters except heading date, maturity date and number

Table 4 . Estimates of specific combining ability (SCA), effects for all the studied characters in the hybrids.

Genotypes	HD	MT	F.L.	Pl.H.	No.		No.	100	G.Y
					Are a	Spt /SP			
P ₁ × P ₂	0.407	-0.120	2.468	0.143	0.309	-1.627*	-4.970	0.252*	-1.627
P ₁ × P ₃	-3.073*	0.806	12.559*	-1.707	0.217	5.760*	-2.147	0.486*	15.335*
P ₁ × P ₄	-2.963*	-1.343*	2.605	2.902	0.928*	3.190*	2.811	-0.041	2.878
P ₁ × P ₅	2.370*	1.583*	1.488	3.206	0.635*	-0.799	1.114	0.459*	-1.142
P ₁ × P ₆	2.259*	1.287*	0.911	0.230	-0.524	-3.340*	4.735	-0.330*	-8.375*
P ₁ × P ₇	1.148	0.917	-1.632	1.991	-0.428	-3.463*	-0.371	-0.263*	-1.577
P ₂ × P ₃	-0.259	-0.750	-1.867	-0.214	0.428	2.984*	3.509	0.229*	-3.964
P ₂ × P ₄	-0.481	0.435	-3.404	1.328	-0.128	-2.471*	-4.740	-0.178	-1.861
P ₂ × P ₅	-0.815	-0.639	0.045	1.865	-0.387	1.385	3.123	-0.341*	-0.543
P ₂ × P ₆	-2.259*	-0.602	1.545	-1.710	-0.413	1.179	3.642	0.274	4.218*
P ₂ × P ₇	2.296*	1.028	2.275	2.050	-0.250	-0.666	-0.538	-0.373*	-3.671
P ₃ × P ₄	0.370	1.028	2.711	0.912	-0.254	-3.079*	5.666*	0.053	-5.003*
P ₃ × P ₅	-0.296	-0.046	-9.527*	2.949	0.454	-1.991*	1.183	-0.323*	-3.460
P ₃ × P ₆	-4.741*	1.324*	-3.423*	0.953	0.128	1.358*	2.914	0.241*	2.799
P ₃ × P ₇	0.148	-0.046	4.856*	-4.966*	0.424	-4.389*	-2.575	0.011	-2.026
P ₄ × P ₅	-0.852	1.139*	2.093	-0.309	-0.269	-1.888*	3.214	-0.040	-3.450
P ₄ × P ₆	3.037*	0.843	10.976*	3.082	0.206	0.164*	1.459	-0.039	9.071*
P ₄ × P ₇	1.259	0.139	1.985	-2.290	-0.131	-1.154*	0.142	0.348*	-5.530
P ₅ × P ₆	-0.630	-1.565*	-1.965	2.653	-0.087	-2.636	-3.095	0.215*	-6.596*
P ₅ × P ₇	-0.741	1.398*	6.942*	5.113*	0.309	3.267*	-3.498	0.402	3.635
P ₆ × P ₇	-0.185	0.435	-5.288*	0.904	-0.046	-1.637	6.911*	0.122	-6.204*
L.S.D 5%									
S II	1.298	1.128	3.405	3.729	0.567	1.556	5.488	0.193	4.122
Sij - SIk	2.265	1.968	5.945	6.509	0.990	2.717	9.580	0.337	7.197
Sij - SKl	2.119	1.841	5.561	6.089	0.926	2.542	8.962	0.315	6.733

*, Significant at 5% level of probability.

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

Genotypes	HD	MT	F.L.	Pl.H.	No.	No.	No.	100	G.Y
			Are a		Spt /SP	SP/Pl.	K /SP	K.wt	/Pl.
P ₁ × P ₂	-0.139	0.361	2.665	-1.586	0.244	-2.271*	1.963	0.582*	-3.236
P ₁ × P ₃	-1.806*	0.102	14.711*	-3.133	-0.144	6.157*	22.232*	0.045	15.503*
P ₁ × P ₄	-2.250*	-1.602*	3.428*	-4.033	1.209*	4.353*	11.855*	-0.399*	6.126*
P ₁ × P ₅	1.898*	0.509	1.886	1.322	0.510*	-0.974	-8.914*	0.313*	-1.300
P ₁ × P ₆	1.009	1.028	1.522	3.187	-0.505*	-3.808*	-8.613*	0.378*	-9.157*
P ₁ × P ₇	0.454	0.139	-1.644	18.164*	-0.170	-4.222*	0.917	0.475*	-2.337
P ₂ × P ₃	-0.361	-0.269	-2.364	-1.455	-0.282	3.214*	11.144*	-0.165	-3.750
P ₂ × P ₄	0.528	0.694	-3.096	1.076	0.348	-3.114*	-6.510*	0.424*	-3.867
P ₂ × P ₅	-1.324	-0.528	-0.558	3.364	-0.461	1.689	1.635	0.623*	-0.236
P ₂ × P ₆	-2.213*	-1.009	1.581	6.895*	-0.210	1.575	2.076	0.628*	4.000
P ₂ × P ₇	1.565	0.102	1.712	-3.127	0.138	-0.385	-3.947	0.362*	-3.133
P ₃ × P ₄	0.528	0.435	-0.174	2.028	0.086	-2.678*	-1.131	0.444*	-4.477
P ₃ × P ₅	-1.324	-0.454	-9.826*	-7.017*	0.717*	-1.989*	-4.437*	0.359*	-4.603
P ₃ × P ₆	-3.880*	0.398	-4.826*	-2.686	0.195	0.640	13.348*	0.154	1.117
P ₃ × P ₇	0.898	0.176	4.955*	8.159*	0.097	-5.203*	-1.835	0.808*	-3.290
P ₄ × P ₅	-0.435	0.509	2.875	0.650	-0.256	-1.470	-2.367	0.778*	-3.880
P ₄ × P ₆	0.009	1.028	10.308*	-2.405	0.405	0.666	18.051*	0.440*	5.623*
P ₄ × P ₇	0.787	0.139	1.879	5.826*	-0.837	-0.944	-2.135	0.427*	-5.477*
P ₅ × P ₆	0.824	-1.194*	-2.091	3.136	-0.414	-2.931*	-1.084	0.529*	-7.070*
P ₅ × P ₇	-0.398	1.917*	6.804*	4.981*	0.348	4.579*	15.106*	0.291*	4.620
P ₆ × P ₇	0.380	-0.380	-5.167*	-1.688	0.016	-2.219*	-10.706*	0.601*	-6.607*
L.S.D 5%									
S II	1.351	1.066	3.130	4.755	0.474	1.723	4.130	0.210	4.977
Sij - Sik	2.359	1.871	5.471	8.301	0.828	3.024	7.209	0.307	8.689
Sij - Skl	2.206	1.751	5.118	7.765	0.775	2.828	6.744	0.342	8.128

* Significant at 5% level of probability.

of kernels/spike in the F_1 and heading date and number of spikelets/spike in the F_2 indicating an excess of recessive overdominance alleles, (Table 6). The degree of dominance $(H_1/D)^{1/2}$ was higher than unity for maturity date, plant height, number of spikelets/spike, 100 kernel weight, and grain yield/plant in the F_1 and F_2 , number of spikes/plant and number of kernels/ spike in the F_2 only, indicating an overdominance effect. For heading date and flag leaf area in the F_1 and F_2 and number of spikes/plant and number of kernels/spike in the F_1 the value of $(H_1/D)^{1/2}$ was less than unity indicating partial dominance effect. Values of $H_2/4H_1$ were less than 0.25 for all studied traits in the F_1 and F_2 (except maturity date in the F_2 was 0.268), revealing asymmetric distributions of positive and negative alleles among parents. On the other hand the maturity date showed 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 number of spikelets/spike and number of kernels/spike show that the proportion of dominant alleles is greater than recessive alleles in the parents. This conclusion is also supported by the fact that the value of $(H_2/4H_1)$ was less than 0.25.

Narrow sense heritability estimates ranged from 19.80 for number of kernels/spike to 70.90 in the maturity date in the F_1 and ranged from 12.06 for 100 kernel weight to 69.00 for flag leaf area in the F_2 . On the other hand broad sense heritability was lowest in the F_1 and F_2 for number of spikelets / spike 23.80 and 18.92, respectively and highest (94.60 and 95.60) for flag leaf area in the F_1 and F_2 , respectively. These results agree with those obtained by El-Sayed (2000), Hamada and Tawfelis (2001) and Mostafa (2002).

Table 6 . Estimates of genetic components and ratios from Hayman's analysis F₁
and F₂ diallel crosses of bread wheat .

Genetic Comp.	HD	MD	F.L. Area	PLH.	No. Spt./SP	No. SP./Pl.	No. K./S	100 K.wt	G.Y /Pl.
F ₁ Hybrid									
D	23.079*	2.313*	178.460*	24.123*	0.4253*	1.888*	37.973*	0.015	-15.686*
F	13.569*	0.381*	40.917	13.888	0.0653	1.629	16.833*	0.001	-5.914
H ₁	19.451*	3.519*	124.97*	27.93*	0.5040*	1.512	18.882*	0.423*	29.854*
H ₂	14.698*	3.162*	105.093*	19.553*	0.3600*	0.004	16.840*	0.381*	26.407*
h ²	1.348	5.390*	71.138*	52.686*	0.6706*	-1.363	27.042*	0.218*	49.968*
(H ₂ /D)1/2	0.918	1.233	0.837	1.076	1.0886	0.895	0.705	5.344	-1.380
H ₂ /4H ₁	0.189	0.225	0.210	0.175	0.1786	0.001	0.223	0.225	0.221
KD/KR	1.942	1.143	1.317	1.730	1.1518	2.861	1.917	1.017	1.316
h ² /H ₂	0.092	1.705	0.677	2.695	1.8628.	-34.750	1.606	0.572	1.892
hert.n.s	61.800	43.400	70.900	41.100	61.57	23.400	33.000	19.800	-----
hert. b.S	93.700	73.400	94.600	62.800	68.57	23.500	45.000	67.800	36.091
F ₂ Crosses									
D	21.914*	0.642*	197.871*	32.328	2.767	2.791	26.699	0.034	24.871
F	12.586*	-0.539	70.711	66.085	24.1526*	3.583	14.981	-0.010	25.931
H ₁	10.164*	1.468	149.551*	177.507*	-62.128*	39.335*	426.134*	1.617*	138.105*
H ₂	7.199*	1.572**	120.265*	129.220*	37.2216*	35.405*	361.163*	1.544*	120.813*
h ²	2.428	-0.085	61.949*	102.144*	5.448	8.020	280.438*	5.921*	63.476*
(H ₂ /D)1/2	0.681	1.513	0.869	2.343	4.4384	3.754	3.995	6.876	2.356
H ₂ /4H ₁	0.177	0.268	0.201	0.182	-0.1497	0.225	0.212	0.239	0.219
KD/KR	2.458	0.565	1.517	2.547	-0.7579	1.412	1.151	0.960	1.597
h ² /H ₂	0.337	-0.054	0.515	0.790	0.1464	0.226	0.776	3.835	0.525
hert.n.S	69.900	36.100	69.000	14.700	92.975	13.40	27.700	12.600	15.600
hert. b.S	90.300	62.500	95.600	80.300	91.956	18.920	92.800	96.100	77.200

* Significant at 5% level of probability.

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تحليل بعض الصفات الكمية لبعض هجن قمح الخبز

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أجرى تقييم الهجن الدائرية لسبعة تراكيب وراثية من قمح الخبز بمحطة البحوث الزراعية بالجيزة ٢٠٠١/٢٠٠٠ و ٢٠٠٢/٢٠٠١ و ٢٠٠٣/٢٠٠٢ لتقدير القدرة العامة والخاصة على الائتلاف في الجيل الأول والثاني والتعرف على العوامل الوراثية التي تتحكم في صفة المحصول ومكوناته ويمكن تلخيص النتائج كمايلي:-

كان التباين الراجع الى القدرة العامة على الائتلاف معنوياً في كل الصفات تحت الدراسة في الجيل الأول والثاني ، كما كانت القدرة الخاصة على الائتلاف معنوية لجميع للصفات المدروسة مساعدا صفة عدد السنبيلات في السنبلة في الجيل الأول وتاريخ النضج في الثاني. وكان تباين القدرة العامة للائتلاف أكبر من تباين القدرة الخاصة للائتلاف مما يدل على أن الفعل الجيني المضيف أكثر أهمية في وراثه معظم الصفات المدروسة.

كان توزيع الجينات الموجبة والسالبة غير منتظم بالنسبة لكل الصفات في الجيل الأول والثاني ما عدا تاريخ النضج في الجيل الثاني . ولوحظ وجود سيادة فائقة لبعض الصفات وسيادة جزئية لصفات أخرى. وكانت درجة التوريث بمعناها الضيق أو الواسع عالية ومنخفضة في الصفات المختلفة.

أختلفت تقديرات درجة التوريث بمعناها الواسع والضيق بين الصفات والأجيال وكانت أعلى قيم درجة التوريث الواسع ٩٣,٧ لصفة التزهير وأقلها ٢٣,٥ لصفة عدد السنايل في النبات وسجلت درجة التوريث بمعناها الضيق أعلى قيمة لها مع صفة تاريخ النضج وأقلها مع محصول الحبوب / النبات وذلك في الجيل الأول .

أما بالنسبة للجيل الثاني كانت أعلى قيم لدرجة التوريث الواسع لصفة وزن ١٠٠ حبة وأقلها لصفة عدد السنايل في النبات وبالنسبة لدرجة التوريث في معناها الضيق للجيل الثاني أعلى قيمة لصفة التزهير وأقلها لصفة وزن ١٠٠ حبة .