

ESTIMATES OF GENETIC EFFECTS FOR YIELD AND ITS ATTRIBUTES IN CERTAIN BREAD WHEAT CROSSES.

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ABSTRACT

This investigation was carried out at Bahteem Agric. Res. Station through the three growing seasons of 2005/2006, 2006/2007 and 2007/2008 aiming to study gene effects for yield and its components in four bread wheat crosses namely; 1- (Gemmeiza 9 X Giza 168); 2- (Sids 1 X Giza168); 3- (Sids 1 X Sakha 8) and 4- (Sakha 8 X Gemmeiza 9).

The results showed that additive gene effects (d) was important in the inheritance of spike grain weight, number of grains/spike and kernel weight in the 1st cross. Meanwhile, dominance genetic variance was the main components controlling the inheritance of plant height, spike grain weight, number of grains/spike and kernel weight mainly in other crosses.

The results of the two digenic epistatic effects additive X additive (i) and dominance X dominance (L) confirm its importance role in the genetic system controlling most of the studied characters. Over-dominance cases were involved in the inheritance of plant height, spike grain weight, number of grains/spike and 100-kernel weight in the 1st cross, while partial dominance was present for both number of spikes/plant and total weight/plant in the same cross.

The 4th cross gave the highest heterotic value over its better parent for grain yield/plant followed by the 3rd cross and at the same time gave highly heterotic values for at least one of its yield components for number of grains/spike.

The highest estimates of narrow sense heritability were detected for plant height, grain yield/plant, kernel weight and number of grains/spike in the 1st cross. Moderate heritability estimates were also detected for total weight/plant in the 1st and 2nd crosses.

High expected genetic gain were found to be associated with high narrow sense heritability estimates which makes selection for such traits in the early generations possible

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the world's leading grain crop. Wheat breeders are always looking for means and sources of genetic improvements in grain yield, its components and other agronomic characters. Genetic diversity is the crucial background for the breeders to have better recombinants by creating heritable variability upon which selection can be practiced. Knowledge of genetic relationship among individuals or populations is essential for the breeders in planning their crosses to gain better selections for genotypes having high yield and to develop new promising lines or cultivars. Crumpacker and Allard (1962) reported that efficiency in breeding of self-pollinating crop plant depends first, on accurate identification of hybrid combinations that have the potentiality of producing maximum improvements and second, on identifying in the early segregating generations, superior lines among the progeny of the most promising hybrids.

Therefore, information on the genetics and gene effect of breeding materials could ensure long-term selection gains and better genetic improvements. However, this research was conducted to study the gene effects of four bread wheat crosses derived from four parental bread wheat genotypes using six populations of each cross.

MATERIALS AND METHODS

The present study was carried out at Bahteem Agric. Res. Station, El-Qualyobia Governorate A.R.C., Egypt, during three successive seasons from 2005/2006, to 2007/2008. Four bread wheat cultivars i.e., Gemmeiza 9(P1); Giza 168(P2); Sids 1(P3) and Sakha 8(P4) were chosen for this investigation on the basis of their wide diversity in pedigrees as shown in Table 1. In 2005/2006 season, the parent genotypes were sown at three planting dates to make four crosses among the parents to produce F₁ hybrids designated as follows, the first cross (P1 X P2); second cross (P3X P2); third cross (P3 X P4); and the fourth cross (P4 X P1). In 2006/2007 growing season, crosses were made among the F₁ hybrids of each cross and its two respective parents to produce the backcrosses (BC₁ and BC₂) populations. The rest of the F₁ hybrid plants were selfed to produce F₂ generation. In addition, to some parental spikes were also selfed to maintain the parental purity. In 2007/2008 season, the six populations including P₁, P₂, F₁, F₂, BC₁ and BC₂ of each cross were sown in a randomized complete block design with three replications. Each replicate consisted of one row for each of the parent and F₁ hybrid, two rows for each backcrosses and four rows for the F₂ populations. Rows were 2 m. long and 30 cm. apart and 10 cm. between plants within rows. Recommended field practices for wheat production were adopted in all growing seasons.

Table 1: The name, pedigree and origin of the four parental bread wheat genotypes.

Cross No.	Name	Pedigree	Origin
1	Gemmeiza 9 (P1)	Ald "S"/Huace "S" //CMH74.630/SX CGM 4583 – 5GM – 1GM -0GM.	Egypt
2	Giza168 (P2)	MRL/BUC//Seri CM 93046 -8M – 0Y – 0M – 2Y – 0B – 0GZ.	Egypt
3	Sids 1 (P3)	HD 2172/Pavon "S"//1158.57/Maya74S" SD46 – 4SD – 2SD – 1SD- 0SD.	Egypt
4	Sakha 8 (P4)	Indus/Norteno "S"	Egypt

Data were recorded on 20 individual guarded plants for P₁, P₂, F₁ and 30 plants for BC₁ and BC₂ and 40 plants for F₂ in each replicate for plant height, number of spikes/plant, total weight/plant, grain yield/plant, spike grain weight, number of kernels/spike and 100-kernel weight.

Statistical and genetic analysis:-

Nature of gene action was studied according to the relationships illustrated by Hayman, (1958). In this procedure the means of the six populations of each cross were used to estimate the six parameters of the gene action. Moreover, heterosis (H) was expressed as percent increase of the F₁ mean performance above its respective better parent,

$$H\% = [(F_1 - B.P)/B.P] \times 100$$

Inbreeding depression (I.D), was also measured as the average percent decrease of the F₂ from the F₁

$$I.D\% = [(F_1 - \bar{F}_2)/\bar{F}_1] \times 100$$

Heritability in broad and narrow senses was estimated according to the formula presented by Mather (1949) and predicted genetic gain from selection was calculated using Johanson *et al.* (1955) method.

RESULTS AND DISCUSSION

Varietal differences in response to their genetic background were significant in most characters under investigation. The genetic variance within F₂ population was also significant for all studied characters in the four crosses; therefore, the different biometrical parameters used in this investigation were estimated. Means and variances of the six populations P₁, P₂, F₁, F₂, BC₁ and BC₂ for the studied characters of the four crosses are presented in Table 2. Heterosis, inbreeding depression percentage and different gene action parameters in four crosses for the studied characters are given in Table 3.

The choice of the most efficient breeding procedures depends on a large extent on the knowledge of the genetic system contributing the characters because it is helpful in deciding the breeding procedures to be followed for improvement these characters. Therefore, the nature of gene action was computed according to Hayman, (1958). The estimates of various types of gene effects presented in Table 3 showed that the mean parameter (m) for all studied attributes which reflected the contribution due to the overall mean plus the locus effects and interactions of the fixed loci were highly significant.

The additive gene effects (d) were significant with positive values for total weight/plant in the 3rd and 4th crosses, spike grain weight in the 1st cross, number of grains/spike in the 1st and 4th crosses and grain weight in the 2nd one.

These results indicated that selection using the pedigree method may be more effective in improving such characters. Amaya *et al.* (1972), Hendawy (1998) and El-Hosary *et al.* (2000) reported that additive gene effects was significant and involved in the inheritance of yield and its attributes. Meanwhile, a significant negative additive gene effects was only shown in the 1st cross for grain yield while, the other crosses were fluctuated from either positive or negative but didn't reach the significant level.

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Dominance gene effects (h) were significant with positive values for plant height, spike grain weight and number of grains/spike in three crosses, total weight/plant in the 4th cross and in all studied crosses for grain weight.

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Dominance gene effects seemed to form a major part in the inheritance of plant height, spike weight, number of grains/spike and kernel weight. The importance of dominance gene effects was indicated by its relative magnitude and sign. The positive effect of dominance genes for plant height as shown in the 2nd, 3rd and 4th crosses indicated that dominance was in the direction of tallness. Significant negative values of dominance gene effects were detected for number of spikes/plant in all crosses, biological yield/plant in three crosses and grain yield/plant in the 3rd cross. Similar results were previously reported by Mohamed (2001) and El-Shaarawy (2008).

Additive X additive (i) types of epistasis were significant with positive values for plant height, spike grain weight and number of grains/spike in all studied crosses except the 1st one, total weight/plant in the 4th cross and grain weight in all crosses. Significant negative values were obtained for plant height in the 1st cross, number of spikes/plant in all crosses, total weight/plant in the 1st and 2nd crosses, grain yield/plant in both 3rd and 4th crosses and number of grains/spike in the 1st cross. These results indicate that the materials used in this study have a decreasing alleles expression for these characters which makes selection to improve them could not be effective in the early generations with the exception of plant height in the 1st cross for which selecting short stemmed lines could be possible.

Significant with positive values for additive X dominance (j) types of epistasis were found for total weight/plant in all studied crosses except for the second one, spike grain weight in the 1st and 2nd crosses, number of grains/spike in the 1st and 4th crosses and grain weight in the 2nd cross. Negative additive X dominance type of epistasis was detected only for grain yield/plant in the 2nd cross.

Data concerning the digenic epistatic gene effects, dominance X dominance (l) revealed different positive and significant estimates for both number of spikes/plant and biological yield/plant in all studied crosses except the 4th one, grain yield/plant in all crosses and both spike grain weight and number of grains/spike in the 1st cross only. Meanwhile, significant with negative values (l) were found for plant height in all crosses except the 1st one, spike grain weight in the 3rd and 4th crosses, number of grains/spike in two crosses and kernel weight in all crosses with one exception. The absolute relative magnitudes of epistatic gene effects to the mean effects were somewhat variable depending on the cross and the studied character. The obtained results are in agreement with the findings of El-Shaarawy (2008).

Heterosis is a complex phenomenon which mainly depends on the balance of different combinations of genotypic effect as well as the distribution of plus or minus alleles in parents. The expression of heterosis as percentage deviation of F₁ mean performance from the better parent for all studied characters are presented in Table 3. Significant positive heterotic effects were obtained for plant height (6.22%), total weight/plant (22.33%), grain yield/plant (35.21%) and kernel weight (8.03%) in the 4th cross, and both of spike grain weight and number of grains/spike in all studied crosses with one exception. However, significant negative heterotic effects were found for plant height in the 3rd cross, total weight/plant in all studied crosses

except for the 4th one and grain weight in the second cross. Similar results were reported by Gautam and Jain (1985), Moshref (1996), Hendawy (1998) and El- Hosary *et al.* (2000).

The 4th cross (Sakha 8 X Gemmiza 9) gave the highest heterotic value over its better parent for grain yield/plant being (35.21%) followed by the 3rd cross (14.78%) and at the same time gave highly heterotic values for at least one of its yield components being (20.27% and 18.84%) for number of grains/spike. The 4th cross would be of great interest in wheat breeding program for selecting the best recombinants in the segregating population and accurate identify the promising lines characterized by its high yielding ability.

Significant inbreeding depression with positive values for were found for plant height in the 3rd and 4th crosses, total weight/plant in three crosses and grain yield/plant, spike grain weight, number of grains/spike and kernel weight in all studied crosses. Meanwhile, negative inbreeding depression values were detected for plant height in the 1st and 2nd crosses, number of spikes/plant in all crosses and for total weight/plant only in the 3rd cross. Heterosis in F₁ generation should be followed by appreciable reduction in F₂ generation, since the two parameters are two sides of the same phenomena as for plant height in the 1st and the 2nd crosses, number of spikes/plant in all crosses and total weight/plant in the 3rd cross. However, this expectation was not valid in some other cases. The obtained results were partially in harmony with those obtained by Gautam and Jain (1985) and Khalifa *et al.* (1997). The contradiction between heterosis and inbreeding depression estimates could be due to the presence of linkage between genes in these materials (Van der Veen, 1959).

The potence ratio values showed the average degree of dominance of the whole gene set of one parent or the other and cannot indicate the actual dominance of individual genes of a certain character. The dominance values were more than +1.0 for plant height in the 1st and 4th crosses indicating cases of over-dominance towards the taller parent. Meanwhile, over-dominance towards the higher parent were detected for number of spikes/plant in the 2nd and 3rd crosses, biological yield/plant in the 3rd cross, spike grain weight in three crosses, number of grains/spike in the 1st and 2nd crosses as well as for higher grain weight in the 1st and 3rd crosses. However, negative over-dominance towards the lower parent were reported for number of spikes/plant, biological yield/plant and kernel weight in the 4th cross, grain yield/plant in all studied crosses with one exception, spike weight in the 3rd cross and number of grains/spike in the 3rd and 4th crosses. The existence of over-dominance in wheat was previously reported by Ketata *et al.* (1976), Jastasra and Paroda (1980), Rady *et al.* (1981) Mosaad *et al.* (1990), Abul-Nass *et al.* (1991), Al-Kaddoussi *et al.* (1994), and Eissa *et al.* (1994).

Partial dominance was found for plant height in the 3rd cross and both number of spikes/plant and total weight/plant in the 1st cross. Partial dominance in the negative direction was detected for plant height, grain yield/plant and kernel weight in the 2nd cross. El-Menshawy(1996) in Egypt indicate that partial dominance was present for number of spikes/plant and

kernel weight which coincide with our findings. Meanwhile, the potence ratio was almost 0.00 being 0.06 for biological yield/plant indicating that dominance was absent in this case.

Heritability is one of the most important parameters for determining the genetic behavior of a metric character. It is expressed as the proportion of the variance attributed to the average effect of genes. Heritability in both broad and narrow sense was estimated in this study and the obtained results are illustrated in Table 4. Broad sense heritability estimates were found to be high for all studied characters ranging from 61.76% to 92.22% with the exception of number of spikes/plant in the 2nd cross which showed a moderate heritability estimates being 48.40%.

The highest estimates of narrow sense heritability were detected for plant height (74.78%), grain yield/plant (65.66%), kernel weight (65.45%) and number of grains/spike (65.24%) in the 1st cross as well as number of spikes/plant. The second cross gave also a high heritability estimates for plant height, number of grains/spike, number of spikes/plant and kernel weight. The high heritability estimates reported here ensured that most of genetic variation of these characters is mainly due to the additive effect. The same conclusion was previously reached by many researchers among whom were Mosaad *et al.* (1990) and Moshref (1996).

Moderate estimates of narrow sense heritability were detected for total weight/plant in the 1st and 2nd crosses being 44.98% and 53.30% respectively. Moreover, grain yield/plant showed also a moderate heritability estimates in the 2nd and 4th crosses.

Low values of narrow sense heritability were observed for plant height (28.34%) in the 3rd cross, number of spikes/plant (11.37%) in the 2nd cross, total weight/plant (34.31%) and number of grains/spike (34.38%) in the fourth cross.

The differences in magnitudes of both broad and narrow sense heritability estimates for most of the studied characters which recorded here may be due to that the materials used in this study would ascertained the presence of both additive and non-additive genetic variance in the inheritance of these characters as the results obtained from gene action parameters. The same conclusion was previously reached by many researchers among whom were Jastara and Paroda (1980), Mosaad *et al.* (1990), Gouda *et al.* (1993) and Moshref (1996).

Genetic advance under selection which are presented in Table 4 showed the possible gain from selection as a percent increase in the F₃ over the F₂ mean when the most desirable 5% of the F₂ plants were selected. The results of the present study showed that the expected genetic advance (Δg) was ranged from 3.93 to 19.15 cm. for plant height, 5.03 to 8.20 gm, for biological yield/plant, and from 6.39 to 9.10 gm. for grain yield/plant. Meanwhile, the expected genetic advance values were ranged from (0.48 to 0.77 gm.) for spike grain weight and from (0.68 to 1.05 gm.) for kernel weight.

The high expected genetic gain obtained in the present study was found to be associated with high narrow sense heritability estimates as

clearly shown in the 1st and 2nd cross for plant height, number of grains/spike and kernel weight. Therefore, selection for such characters in the early generations should be effective. This coincide with a conclusion of Johanson *et al.* (1955) who reported that heritability estimates along with genetic advance upon selection (Δg) were more valuable in predicting the effect of selection. Meanwhile, other investigators among whom was Dixit *et al.* (1970) who showed that high heritability is not always associated with high genetic advance, but in order to make your selection more effective, high heritability should be associated with high genetic advance.

Moderate estimates of narrow sense heritability and high or moderate genetic advance (Δg) probably makes selection in the early generations of less success than in the former state as shown in the 1st and 2nd cross for biological yield/plant, and kernel weight in the 4th cross. Meanwhile, low narrow sense heritability which associated with low estimates of genetic gain as obtained for plant height in the 3rd cross and number of spikes/plant in the 2nd cross which makes selection for these characters in those crosses would be of less effectiveness.

As it is well known, the expected improvement from selection is directly proportional to the heritability values. Also, the expected response to selection varies with the phenotypic standard deviation of population means. This figure is measure the total variability in the character and therefore, reflects the total response that could be realized by breeding techniques.

Table (4): Heritability (b.s&n.s), genetic advance upon selection (Δg) and genetic advance as percentage (Δg %) for the characters studied in four bread wheat crosses

Cross	Parameter	Plant height	No.of spikes/plant	Total weight/plant	Grain yield/plant	Spike grain weight	No.of grains/spike	100-kernel weight
1-	h. b.s	88.59	79.53	79.26	81.83	73.33	81.68	78.18
	h. n.s	74.78	60.19	44.98	65.66	55.56	65.24	65.45
	Δg	19.15	8.05	6.21	9.10	0.77	9.04	1.00
	Δg %	21.84	67.08	12.53	75.68	31.72	17.83	23.53
2-	h. b.s	71.46	48.40	82.07	71.38	69.05	91.63	80.98
	h. n.s	65.73	11.37	53.30	56.16	35.71	73.42	62.75
	Δg	14.82	0.92	8.20	6.39	0.48	15.30	0.92
	Δg %	17.05	8.72	16.39	53.34	18.62	29.90	22.24
3-	h. b.s	67.36	81.64	79.47	77.49	61.76	89.55	81.36
	h. n.s	28.34	44.71	40.13	68.47	41.18	45.90	66.10
	Δg	3.93	6.03	5.58	8.41	0.49	8.15	1.05
	Δg %	4.93	52.40	15.73	65.98	21.41	14.65	26.15
4-	h. b.s	84.06	81.88	82.75	83.94	74.00	92.22	77.78
	h. n.s	44.68	60.71	34.31	47.65	38.00	34.38	48.89
	Δg	6.67	8.09	5.03	6.64	0.55	7.10	0.68
	Δg %	8.37	77.04	17.43	57.75	23.26	14.64	15.01

Generally, the most biometrical parameters resulted from the fourth cross was found to be higher in magnitude than those obtained from the other crosses. Consequently, it could be concluded that the cross (Sakha 8 X

Gemmeiza 9) would be of interest in a breeding programme for bringing up the maximum genetic improvement in the attributes studied.

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تقدير التأثيرات الوراثية للمحصول ومكوناته في أربعة هجن قمح الخبز عزة محمد عبد العال

معهد بحوث المحاصيل الحقلية – قسم بحوث القمح – مركز البحوث الزراعية - جيزة - مصر.

أجري هذا البحث في محطة البحوث الزراعية ببهيتيم محافظة القليوبية – مصر خلال ثلاثة مواسم زراعية هي ٢٠٠٦/٢٠٠٥ و ٢٠٠٧/٢٠٠٦ و ٢٠٠٨/٢٠٠٧ بهدف دراسة التأثيرات الوراثية على المحصول ومكوناته في أربعة هجن من قمح الخبز هي: - (جميزة ٩ X جيزة ١٦٨) ، ٢- (سدس ١ X جيزة ١٦٨) ، ٣- (سدس ١ X سحا ٨) ، ٤- (سحا ٨ X جميزة ٩). وقد أوضحت النتائج الآتى :-
أظهرت التأثيرات الوراثية المضيفة دوراً مهماً في وراثته صفة كل من وزن حبوب السنبله ' عدد الحبوب/السنبله ' وزن الحبوب في الهجين الأول – بينما كان التأثير السيادة المكون الرئيسي في وراثته كل من طول النبات ' وزن حبوب السنبله ' عدد الحبوب/السنبله ووزن الحبوب في ثلاثة من الهجن .
كان للتأثير التفوقى بطرزه المضيف X المضيف والسيادة X السيادة أهمية خاصة في وراثته معظم الصفات تحت الدراسة. ظهرت حالات سيادة فانقه في وراثته كل من صفة طول النبات ' وزن حبوب السنبله' عدد الحبوب/سنبله ووزن الحبوب وحالات سيادة جزئية لصفة عدد السنابل/نبات ووزن النبات الكلى في الهجين الأول.
أعطى الهجين الرابع أعلى قوة هجين لصفة محصول الحبوب/نبات عند مقارنته بالأب الأفضل يليه الهجين الثالث وفي نفس الوقت أعطى قوة هجين عالية لصفة واحدة على الأقل من مكونات المحصول لصفة عدد الحبوب/سنبله في كلا الهجينين على التوالى .
أعطى الهجين الأول كفاءة توريث عالية بمعناها الدقيق لصفات طول النبات ، محصول حبوب النبات ، وزن الحبوب وعدد الحبوب في السنبله. بينما أعطى الهجين الأول والثاني قيمة متوسطة لكفاءة التوريث لصفة الوزن الكلى للنبات.
أظهرت النتائج أن التحسين الوراثى المتوقع كان مرتبطاً بكفاءة التوريث العالية والتي تجعل الإنتخاب لهذه الصفات ممكناً في الأجيال المبكرة .

قام بتحكيم البحث

كلية الزراعة – جامعة المنصورة
مركز البحوث الزراعيه

أ.د / أحمد نادر السيد عطية
أ.د / أنور عبد الخالق عجيز

Table (2): Means (\bar{X}) and variances (S^2) of P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 Populations for the studied characters in four bread wheat crosses.

Character	Statistic	Cross I						Cross II					
		P_1	P_2	F_1	F_2	BC_1	BC_2	P_1	P_2	F_1	F_2	BC_1	BC_2
1- Plant height	\bar{X}	71.80	78.67	81.33	87.67	82.37	84.95	83.67	78.67	83.00	86.92	91.17	91.50
	S^2	19.93	18.33	15.00	154.56	87.89	105.65	17.50	12.50	18.33	119.85	60.09	100.83
2- No.of spikes/plant	\bar{X}	7.43	11.00	9.73	12.00	8.50	9.00	9.35	8.11	8.85	10.50	7.98	8.76
	S^2	10.40	9.77	6.33	42.15	26.80	32.13	10.23	9.00	5.36	15.31	13.81	15.07
3- Total weight/plant	\bar{X}	47.17	71.95	61.70	49.60	45.34	42.66	58.40	50.61	54.28	50.02	39.32	38.98
	S^2	17.18	9.47	5.00	44.98	35.11	34.62	11.88	11.81	7.13	55.76	37.72	44.08
4- Grain yield/plant	\bar{X}	17.95	23.55	16.33	12.02	10.70	13.91	16.27	11.91	15.89	11.98	9.49	10.79
	S^2	9.07	10.26	5.97	45.23	27.50	33.26	10.74	10.67	5.81	30.50	22.59	21.28
5- Spike grain weight	\bar{X}	2.57	2.66	2.71	2.42	2.73	1.81	2.25	2.79	3.25	2.56	3.04	2.76
	S^2	0.12	0.15	0.09	0.45	0.32	0.33	0.18	0.19	0.07	0.42	0.37	0.32
6- No. of grains/spike	\bar{X}	46.60	57.20	58.50	50.67	57.43	39.20	50.17	53.29	71.59	51.18	59.90	62.10
	S^2	10.87	9.10	5.74	45.20	25.41	35.50	9.83	10.17	6.29	102.38	59.82	69.77
7- 100-kernel weight	\bar{X}	4.67	4.68	4.71	4.25	4.76	4.61	4.23	4.93	4.42	4.15	4.90	4.45
	S^2	0.12	0.12	0.09	0.55	0.47	0.27	0.15	0.12	0.05	0.51	0.36	0.34

Table (2): Cont.

Character	Statistic	Cross III						Cross VI					
		P_1	P_2	F_1	F_2	BC_1	BC_2	P_1	P_2	F_1	F_2	BC_1	BC_2
1- Plant height	\bar{X}	83.33	80.67	81.67	79.67	84.33	82.67	76.67	77.20	82.00	79.67	83.33	82.67
	S^2	17.50	15.83	11.67	45.31	35.19	42.59	10.00	8.77	6.67	52.46	43.89	37.59
2- No.of spikes/plant	\bar{X}	8.33	8.80	8.86	11.50	7.89	8.35	7.40	6.20	8.33	10.50	8.00	6.80
	S^2	10.07	8.50	5.67	42.81	31.98	34.50	8.73	8.63	5.77	41.84	25.60	32.68
3- Total weight/plant	\bar{X}	45.07	35.56	33.83	35.50	38.48	28.75	28.04	26.29	34.30	28.85	34.19	29.05
	S^2	12.00	9.89	6.92	45.60	40.50	32.40	9.52	11.08	6.30	50.60	42.06	41.78
4- Grain yield/plant	\bar{X}	11.23	8.95	12.89	12.75	8.65	9.77	8.69	5.44	11.72	11.50	8.97	6.76
	S^2	9.98	8.79	5.85	35.58	23.50	23.30	8.21	8.58	5.63	45.77	32.98	36.75
5- Spike grain weight	\bar{X}	2.46	2.06	3.00	2.31	2.79	2.66	2.02	2.21	2.62	2.38	2.76	2.66
	S^2	0.14	0.17	0.09	0.34	0.30	0.24	0.19	0.15	0.07	0.50	0.49	0.32
6- No. of grains/spike	\bar{X}	49.68	40.80	59.04	55.65	57.93	57.33	48.00	47.03	57.73	48.50	61.23	54.03
	S^2	9.47	10.19	4.86	74.35	51.30	63.27	10.48	9.12	5.00	100.50	79.95	86.50
7- 100-kernel weight	\bar{X}	4.74	4.94	4.96	4.00	4.73	4.62	4.73	4.68	5.11	4.50	4.80	4.85
	S^2	0.14	0.12	0.07	0.59	0.41	0.38	0.11	0.13	0.07	0.45	0.35	0.33

Table (3): Heterosis, potence ratio, inbreeding depression and gene action parameters for the studied characters in four bread wheat crosses .

Character	Crosses	Gene action parameter						Heterosis BP%	Inbreeding depression (I.D)%	P
		m	d	h	i	j	l			
1- Plant height	I	87.67**	-2.58	-9.95	-16.04*	0.86	-5.47	3.38*	-7.80**	1.77
	II	86.92**	-0.33	19.49**	17.66*	-2.83	-54.66**	-0.80	-4.72*	-0.73
	III	79.67**	1.66	13.99**	15.32**	-0.67	-19.98**	-4.29**	2.45	0.57
	VI	79.67**	0.67	18.39**	13.32**	0.93	-27.45**	6.22**	2.84*	19.11
2-No.of spikes/plant	I	12.00**	-0.50	-12.49**	-13.00**	1.29	15.89*	-11.55	-23.33*	0.29
	II	10.50**	-0.78	-8.40**	-8.52**	-1.40	10.20*	-5.35	-18.64*	0.19
	III	11.50**	-0.46	-13.23**	-13.52**	-0.23	15.89*	0.68	-29.80	1.26
	VI	10.50**	1.20	-10.87**	-12.40**	0.60	13.06	12.57	-26.05*	-2.55
3- Total weight/plant	I	49.60**	2.68	-20.26**	-22.40**	15.07**	88.92**	-14.25**	19.61**	0.17
	II	50.02**	0.34	-43.71**	-43.48**	-3.56	104.45**	-7.05*	7.85*	0.06
	III	35.50**	9.73**	-14.03**	-7.54	4.98**	21.37**	-24.94**	-4.94	1.36
	VI	28.85**	5.14**	18.22**	11.08*	4.27*	-14.63	22.33**	15.89**	-8.15
4- Grain yield/plant	I	12.02**	-3.21*	-3.28	1.14	-0.41	23.80**	-9.03	26.39**	-1.58
	II	11.98**	-1.30	-5.56	-7.36	-3.48*	26.76**	-2.34	24.61**	-0.83
	III	12.75**	-1.12	-11.36**	-14.16**	-2.26	23.28**	14.78	1.09	-2.46
	VI	11.50**	2.21	-9.86	-14.54**	0.59	20.71**	35.21*	2.13	-2.88
5- Spike grain weight	I	2.42**	0.92**	-0.51	-0.60	0.97**	2.17**	1.88	10.70*	2.11
	II	2.56**	0.28	2.09**	1.36**	0.55**	-1.42	16.49**	21.23**	2.70
	III	2.31**	0.13	2.40**	1.66**	-0.07	-2.04**	21.95**	23.00**	-3.70
	VI	2.38**	0.10	1.83**	1.32**	0.20	-2.69**	18.55*	9.16	5.32
6- No. of grains/spike	I	50.67**	18.23**	-2.82	-9.42*	23.53**	36.96**	2.27	13.38**	1.25
	II	51.18**	-2.20	59.14**	39.28**	-0.64	-36.64**	34.34**	28.51**	12.73
	III	55.65**	0.60	21.72**	7.92	-3.84	-29.88	18.84**	5.74	-3.11
	VI	48.50**	7.20**	46.74**	36.52**	6.72**	-56.55**	20.27**	15.99**	-21.06
7- 100- kernel weight	I	4.25**	0.15	1.78**	1.74**	0.16	-1.71*	0.64	9.77*	7.00
	II	4.15**	0.45**	1.94**	2.10**	0.80**	-2.80**	-10.34**	6.11	-0.46
	III	4.00**	0.11	2.82**	2.70**	0.21	-1.80*	0.40	19.35**	1.20
	VI	4.50**	-0.05	1.71**	1.30**	-0.08	-0.97	8.03*	11.94**	-16.20

*, ** Significant at 5% and 1% probability levels , respectively .