

GENE EFFECTS IN SOME BREAD WHEAT (*Triticum aestivum*, L.) CROSSES

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ABSTRACT: Six- populations i.e, Parents (P_1 & P_2), F_1 , F_2 Bc_1 and Bc_2 of three bread wheat (*Triticum aestivum*, L.) crosses PBW 343 x Gemmeiza 9, PBW 343 x WEEBILLI and WEEBILLI x FRET- 2 were grown during the three successive seasons, 2004/2005, 2005/2006 and 2006/2007 at the experimental farm of El-Gemmeiza Agric. Res. Station, ARC, Egypt. The non-allelic interaction, scaling tests (A,B,C and D) coupled with six types of gene actions were estimated in addition to determining the adequacy of genetic model controlling the genetic system of the inheritance of some economic traits. Heading date, maturity date, plant height, number of spikes/plant, number of kernels/spike, 100 kernel weight and grain yield/plant were studied. The obtained results can be summarized as follows:

Analysis of variance indicated significant differences among the generations studied for all traits studied. The results indicated the presence of non-allelic interaction in all studied traits in the three crosses except few casses which the values did not reach the significant levels. In the six parameters model, additive component (a) as well as dominance component (d) were significant in most casses. Additive x additive (aa) was significant in all casses except for number of spikes/plant in the first and third cross and 100-kernel weight in the third cross and grain yield/plant in the first cross. Additive x dominance (ad) component was significant in all casses except for maturity date and plant height in the second cross, 100-kernel weight in the first and third cross and number of spikes/plant in the three studied crosses. Also, dominance x dominance (dd) was significant for all traits in all crosses except number of kernel/spike in the third cross, 100-kernel weight in the second cross and grain yield/plant in the first cross.

Significant positive or negative heterosis values based on better parent values were obtained for all crosses and traits except in case of heading and maturity dates in the first cross, plant height in the second cross and number of kernels/spike in the third cross. Inbreeding depression values were found to be highly significant for mostly of all traits studied in the three crosses under investigation. The F_2 -deviation (E_1) was found to be significant for all traits studied in the three crosses except for, maturity date, plant height and 100-kernel weight in the first cross. Backcross deviation (E_2) was found to be significant for all traits study in the three crosses except for, maturity date in the third cross, plant height in the second and third cross and 100-kernel

weight in the first cross. Heritability estimates in both broad and narrow senses were found to be high in magnitudes for most traits studied in the three populations under investigation. High genetic advance under selection was found to be associated with high narrow sense heritability estimates for; number of spikes/plant, number of kernels/spike and 100- kernel weight in the three crosses and for plant height in the first cross and for grain yield/plant in the first and third crosses.

Key words: *Gene action- heterosis- wheat- heritability genetic advance under selection- six generation model*

INTRODUCTION

Wheat is the most important cereal crop in Egypt, increasing wheat production to narrowing the gap between production and consumption is considered the main goal in Egypt as well as in most countries all over the world (Shehab El-Din,1993).

Before the initiation of any breeding programme, the materials under investigation should be subjected to genetic analysis to find out the relative magnitude of various types of the genetic variances to formulate the most efficient breeding procedures to achieve quick and maximum improvement.

Improvement of yield in wheat through conventional breeding methods has reached a level at which phenomenal increase seem to be rather difficult. This warrant to think of some new breeding approach which might increase the yield considerably. The development of hybrid wheat is one way of increasing wheat production. Heterosis has long been observed in wheat, but to be of potential value, a hybrid should be more profitable than the best available commercial wheat varieties. The basic tools for hybrid wheat production, such as cytoplasmic male sterility, fertility- restoring system and cross-pollination under field condition are available (Wilson,1968).

The objectives of the present study are to investigate the genetical behaviour using six- populations model (Gamble, 1962), heritability and expected genetic advance under selection for grain yield and some of its components in three selected crosses.

MATERIALS AND METHODS

The present study was carried out at El-Gemmeiza Agric. Res. Station A.R.C., Egypt, during three successive seasons 2004/2005, 2005/2006 and 2006/5007. This study aimed to estimate; heterosis, heritability and types of gene action of some quantitative characters in three bread wheat crosses. Four bread wheat (*Triticum aestivum* L.) genotypes i.e, PBW 343, GEMMEIZA 9, WEEBILLI and FRET- 2, which will be designated in the text as P₁, P₂, P₃ and P₄, respectively were chosen for this study on the basis of their wide of genetic diversity. The name, pedigree and origin for the parental genotypes are presented in Table (1). In 2004/2005 season, three crosses were made, P₁ x P₂, P₁ x P₃ and P₃ x P₄ to produce F₁ hybrids. In 2005/2006 season some of

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F₁ plants of each cross were backcrossed to their respective two parents to produce the backcrosses (Bc₁ and Bc₂). The rest of the F₁ plants were selfed to produce F₂ seeds. In 2006/2007 season, the six populations i.e, P₁, P₂, F₁, F₂, Bc₁ and Bc₂ for the three crosses were sown in a randomized complete block design with four replications. Each replicate for every cross was planted with 40 grains in two rows for each of the two parents and their F₁'s, 100 grains in five rows of each of the two backcrosses and 200 grains in ten rows for the F₂ population. Plants were sown in rows, 2.0 m long and 30 cm apart and 10 cm within rows. Recommended field practices for wheat production were adopted in all growing seasons.

Data were recorded on 36, 36, 180 and 90 guarded plants for; both parents, F₁, F₂ and backcrosses of each cross, respectively for every replicate. Data were recorded on an individual guarded plants for; heading date, maturity date, plant height, number of spikes/plant, number of kernels/spike, 100 kernel weight and grain yield/plant.

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

Parents	Name	Pedigree	Origin
P ₁	PBW 343	ND/VG9144//KAL/BB/3/YACO/4/VEE#5 CM 5836-4Y-OM-OY-8MOY-01ND	Mexico
P ₂	Gemmeiza 9	ALD"s"/SHUAC//CMH74A.630/SX GM4583-5GM-1GM-OGM	Egypt
P ₃	WEEBILLI	WEEBILLI CGSS95B000146T-099Y-099B-099Y-099B-35Y-0B	Mexico
P ₄	FRET- 2	FRET- 2 CGSS96Y000146T-099B-099Y-099B-12Y-0B	Mexico

Statistical and genetic analysis:-

To determines the presence or absence of non-allalic interactions, scaling test as outlined by Mather (1949) was used. The t-test was used to examine the existence of genetic variance between parental means. Statistical procedures used herein would only be computed if the F₂ genetic variance was found to be significant. A one tail (F) ratio was used to examine the existence of genetic variance within the F₂ population. The degrees of freedom for this test were considered as infinity. If calculated (F) ratio was equal to or larger than the tabulated ones, various biometrical parameters needed in this investigation would be computed. Heterosis (H), was expressed as percent increase of the F₁ mean performance above the respective better parent, i.e ($\frac{F_1 - BP}{BP} \times 100$).

Inbreeding depression (I.d) was measured as the average percent decrease of the F₂ from the F₁. F₂ deviation (E₁), was calculated as the deviation of the F₂ mean performance from the average of F₁ and mid-parent value. Backcrosses deviation (E₂), was computed as the deviation of the two

backcrosses performance from their F_1 and mid-parent performances. The validity of some estimates were examined by t-test. Nature of gene action was studied according to the relationships illustrated by Gamble (1962). In this procedure the means of the six populations of each cross were used to estimate six parameters of gene action. A test of significance of these parameters was conducted by the t-test. Heritability was estimated in both broad and narrow senses for F_2 generation, according to Mather's procedure (1949). The predicted genetic advance under selection (ΔG) was computed according to Johnson *et al.* (1955). This genetic gain represented as percentage of the F_2 mean performance was also obtained following (Miller *et al.*, 1958).

RESULTS AND DISCUSSION

Varietal differences in response to their genetic background were found to be highly significant in most characters under investigation in each of the three crosses studied. The genetic variances within F_2 populations were also found to be highly significant for all traits studied in all the three crosses under investigation. Consequently, the various genetical parameters used in this investigation were estimated for all traits studied. The existence of the significant genetic variability in F_2 populations in spite of the insignificant differences between the parental cultivars for some characters in the three crosses, may suggest that the genes of like effects were not completely associated in the parental cultivars i.e.; these genes are dispersed (Mather and Jinks, 1982).

Means and variances of the six- populations i.e., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 for all traits studied in the three crosses are given in Table (2).

Scaling test A, B, C and D in Table (3) showed that, all the characters studied in the three crosses were significant except, eleven out of eighty four estimates. These results, in general, indicated the presence of non-allelic interaction. On the other hand, if scaling test A, B, C and D were significant this may indicate the inadequacy of the simple model in computing the differences between population means. Also, the insignificant scaling test estimates would indicate the absence of non-allelic interactions and the additive-dominance model is adequate. These results were in agreement with those obtained by Hamada *et al.* (2002), Hamada (2003), Tammam (2005), Abd El-Majeed (2005), El-Sayed and El-Shaarawy (2006) and Moshref (2006).

Genetic analysis of generation means to give estimates of additive (a), dominance (d) and the three epistatic (aa), (ad) and (dd) were obtained according to relationships illustrated by Gamble (1962) and presented in Table (3). The estimated mean effects parameter (m), which reflect the contribution due to the over-all mean plus the locus effects and interaction of the fixed loci, were found to be highly significant for all traits in the three crosses. The additive gene effects (a) were found to be highly significant for all traits in the three crosses studied except; number of spikes/plant and 100-

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kernel weight in the first cross. Also, the additive genetic effects did not reach the significant level in the second cross for number of spikes/plant. However, in the third cross, the estimates of the additive gene effects were found to be insignificant for maturity dates and 100-kernel weight. It is of interest to mention that, the presence of the additive genetic effect in the inheritance of these traits would be suggested the potential for obtaining further improvement of the characters which exhibited highly significant estimates of additive effects (a). Dominance gene effects (d) were found to be highly significant for heading dates, plant height, number of grains/spike and grain yield/plant in the three crosses under examination. Dominance gene effects were also found to be highly significant in the first and second cross for number of spikes/plant and 100-kernel weight.

Highly significant additive x additive (aa) epistatic type of gene action to be highly significant of gene action was found for; heading dates, plant height and number of grains/spike in the three crosses studied. The estimated values of additive x additive epistatic type were detected to be significant for 100-kernel weight in the first and second cross and for grain yield/plant in the second and third cross and for number of spikes/plant in the second cross only. Additive x dominance (ad) epistatic effect of gene action was found to be significant for heading dates, number of kernels/spike and grain yield/plant in the three crosses under examination. Also, the estimated values of additive x dominance (ad) types of digenic epistasis were found to be significant for maturity dates and plant height in the first and third crosses and for 100 –kernel weight in the second cross.

Dominance x dominance (dd) epistatic gene effect was found to be significant for; heading and maturity dates, plant height and number of spikes/plant in the three crosses and for number of kernels/spike and 100-kernel weight in the first cross and for number of kernels/spike and grain yield/plant in the second cross and for 100-kernel weight and grain yield/plant in the third cross. It is worth to mention that the three epistatic types aa, ad and dd were found to be accompanied by significant estimates of both E_1 and E_2 epistatic scales in most traits studied and it would ascertain the presence of epistasis in such large magnitude as to warrant great deal of attention in wheat breeding programs. Also, concerning the relative importance of both additive and dominance gene action, it was found that, the later one was greater in magnitude in all traits studied in the three crosses under investigation (Table 3 and 4). Consequently, it could be concluded that, the presence of both additive and non-additive gene action in most traits studied would be indicated that, the selection procedures based on the accumulation of additive gene effects should be successful in improving all traits under investigation. However, to maximize selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variances are involved would be preferred. Similar results were previously reported by

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Hewezi (1996), Hendawy (1998), Hamada (2003) Moussa (2005), El-Sayed and Moshref (2005), and Hendawy *et al.* (2007).

In self pollinated crops such as wheat, plant breeders have been investigated the possibility of developing hybrid cultivars. Thus, the utilization of heterosis in various crops through the world has tremendously increased the production either for human food or livestock feed. Heterosis is a complex phenomenon which depends on the balance of different combinations of genotypic effect as well as the distribution of plus and minus alleles in the parents. Heterosis is expressed as the percentage deviation of F_1 mean performance from the better parent or mid parents of the traits. As it will be expected, better- parent for plant height was the short one and heterosis relative to the mid-parent value may be also effective. On the other hand, a few days for both heading and maturity dates may be the best. In this concern, percentage of heterosis over better parent values are presented in Table (4). Negative significant heterotic values were obtained for; heading and maturity date in the second and third crosses. Thus, this crosses can be utilized in breeding for early heading and or maturity. The third cross had a positive and significant heterotic values for; plant height, number of spikes/plant, 100-kernel weight and grain yield/plant. Positive and significant heterosis was obtained for plant height, number of kernels/spike and 100 kernel weight in the first cross, and 100kernel weight in the second cross. These results were in agreement with those obtained by El-Sayed *et al.* (2000), Hamada *et al.* (2002), Moustafa (2002), Hamada (2003), Hendawy (2003) and El-sayed and El-Shaarawy (2006). Significant and positive better parent heterotic effects for grain yield/plant was detected for cross $P_3 \times P_4$ (41.49%), therefore, it could be concluded that, the single cross ($P_3 \times P_4$) exhibited a great potential for commercial hybrid wheat production.

Inbreeding depression is measured as the percent deviation of F_2 from F_1 mean performance. The estimates of inbreeding depression values are present in Table (4). Inbreeding depression values were found to be highly significant for almost all studied traits in the three crosses under investigation. It is of interest to note that heterosis in F_1 generation should be followed by appreciable reduction in F_2 generation, since the two parameters are in two sides of the same phenomena. The present results were found to agree with this expectation in most cases and that was previously obtained by El-Hosary *et al.* (2000) Esmail and Kattab (2002), Hendawy (2003), and Hendawy *et al.* (2007).

On the contrary, this expectation was not fulfilled in some cases, where significant heterosis and insignificant inbreeding depression were obtained. 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).

Heritability in both broad and narrow sense and genetic advance under selection were computed and the obtained results are presented in Table (4). High estimates of broad sense heritability were found for; heading date in the three crosses under examination; maturity date, plant height and 100-kernel weight in the first, third cross and; number of spikes/plant and grain yield/plant in the first cross. Moderate broad sense heritability estimates were found for the rest traits studied except for; maturity date, plant height and grain yield/plant in the second cross and for; number of spikes/plant in the third cross where low estimates of broad sense heritability were detected. High estimates of narrow sense heritability were found for; heading date, maturity date and plant height in the first and third crosses under examination. Moderate narrow sense heritability estimates were found for the rest of the traits studied except for; number of spikes/plant, number of kernels/spike and grain yield/plant in the three crosses and heading date, maturity date, plant height and 100-kernel weight in the second cross where low estimates of narrow sense heritability were detected (Table 4). The differences in magnitudes of both broad and narrow sense heritability estimates were found for most traits under investigation would be ascertained the presence of both additive and non-additive genetic variance in the inheritance of most traits in the three crosses under investigation as previously obtained from gene action parameters study. The same conclusion was previously reached by Seleem (1993), Hendawy (1994), El-Hennawy (1995), Hewezi (1996), El-Hosary *et al.* (2000), Moussa (2005), Shahid *et al.* (2005), and Hendawy *et al.* (2007).

Genetic advance under selection which are given in Table (4) show the possible gain from selection as percent increasing in the F_3 over the F_2 mean when the most desirable 5% of the F_2 plants are selected. Genetic advance under selection (Δg %) was found to be moderate to high for; number of spikes/plant, number of kernels/spike, 100-kernel weight and grain yield/plant in all the three crosses studied and ; plant height for the first and third crosses . Relatively low genetic advance were obtained for the rest of the traits studied (Table 4). Johnson *et al.* (1955) reported that, heritability estimates along with genetic gain upon selection were more valuable than the former alone in predicting the effect of selection. On the other hand, Dixit *et al.* (1970) pointed out that high heritability is not always associated with high genetic advance, but in order to make effective selection, high heritability values should be associated with high genetic gain. In the present investigation, high genetic gain was found to be associated with high narrow sense heritability estimates for; number of spikes/plant, number of kernels/spike and 100-kernel weight in the three crosses and for plant height in the first cross and for grain yield/plant in the first and third crosses. Therefore, selection for these traits in these three populations should be effective and satisfactory for successful breeding purposes however, selection for the rest characters studied could be of less effectiveness.

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التأثير الجيني في بعض هجن قمح الخبز

جمال عبدالرازق الشعراوي

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

الملخص العربي

أجريت هذه الدراسة بالمزرعة البحثية لمحطة البحوث الزراعية بالجميزة - مركز البحوث الزراعية خلال ثلاثة مواسم زراعية ٢٠٠٤/٢٠٠٥ ، ٢٠٠٥/٢٠٠٦ و ٢٠٠٦/٢٠٠٧ بغرض دراسة كل من قوة الهجين والسلوك الوراثي ودرجة التوريث والتحسين الوراثي المتوقع بالانتخاب وذلك لسبعة صفات هي تاريخ التزهير، تاريخ النضج، طول النبات، عدد السنابل في النبات، عدد حبوب السنبل، وزن الـ ١٠٠ حبة ومحصول الحبوب في النبات وذلك في ثلاثة هجن من قمح الخبز هي الأول PBW 343 X Gemmeiza 9 والثاني WEEBILL و PBW 343 X الثالث WEEBILLI X FRET-2 ويمكن تلخيص النتائج المتحصل عليها كما يلي:

- أوضحت النتائج المتحصل عليها من تحليل التباين وجود اختلافات معنوية بين العشائر الوراثية تحت الدراسة لجميع الصفات في جميع الهجن الثلاثة كما لوحظ وجود تباين غير أليفي لمعظم الحالات حيث كانت قيم الفعل الجيني المضيف وكذلك السيادة معنوية لمعظم القيم ماعدا بعض الحالات القليلة.

- كان التفاعل الجيني من نوع المضيف x المضيف معنويا لجميع القيم ماعدا صفة عدد السنابل في النبات للهجينين الأول والثالث و صفة وزن الـ ١٠٠ حبة في الهجين الثالث و صفة محصول الحبوب في النبات في الهجين الأول. كما لوحظ أن التفاعل الجيني من نوع المضيف x السيادة كان معنويا لكل الصفات المدروسة في هجن الدراسة ماعدا صفتي النضج وطول النبات في الهجين الثاني و صفة وزن الـ ١٠٠ حبة في الهجينين الأول والثالث و صفة عدد السنابل في النبات في الهجن الثلاثة. وأظهرت النتائج أن التفاعل الجيني التفوق من النوع السيادة x السيادة كان معنويا لجميع القيم ماعدا صفة عدد حبوب السنبل في الهجين

الثالث وصفة وزن الـ ١٠٠ حبة في الهجين الثاني وصفة محصول الحبوب في النبات في الهجين الأول.

- أوضحت النتائج وجود قوة هجين معنوية منسوبة للأب الأحسن في الهجن الثلاثة لكل الصفات ماعدا صفة تاريخ التزهير و النضج في الهجين الأول وصفة طول النبات في الهجين الثاني وصفة عدد حبوب السنبل في الهجين الثالث.

- كان تأثير التربية الداخلية معنويا لمعظم الصفات تحت الدراسة.

- كانت انحرافات الجيل الثاني معنوية لجميع الصفات في الهجن الثلاثة تحت الدراسة ما عدا صفات ميعاد النضج وطول النبات ووزن الـ ١٠٠ حبة في الهجين الأول وكانت انحرافات الهجن الرجعية معنوية لجميع الصفات ما عدا صفة النضج في الهجين الثالث وصفة طول النبات في الهجين الثاني وصفة وزن الـ ١٠٠ حبة في الهجين الأول.

- كانت قيم الكفاءة الوراثية بمعناها العام والدقيق عالية المعنوية لمعظم الصفات المدروسة في العشائر الثلاثة تحت الدراسة وكانت القيم العالية للتحسين الوراثي المتوقع بالانتخاب مرتبطة مع التقديرات العالية لدرجة التوريث بمعناها الدقيق وذلك في صفات عدد السنابل في النبات وعدد حبوب السنبل ووزن الـ ١٠٠ حبة في الهجن الثلاثة المستخدمة وكذلك لصفة طول النبات في الهجين الأول وصفة محصول النبات في الهجينين الأول والثالث.

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Table (2) :- Means (\bar{x}) and variances (S^2) of P_1 , P_2 , F_1 , F_2 , Bc_1 and Bc_2 populations of the three wheat crosses for the all traits studied.

Traits		Cross I ($P_1 \times P_2$)						Cross II ($P_1 \times P_3$)						Cross III ($P_3 \times P_4$)					
		P_1	P_2	F_1	F_2	Bc_1	Bc_2	P_1	P_2	F_1	F_2	Bc_1	Bc_2	P_1	P_2	F_1	F_2	Bc_1	Bc_2
Heading date	\bar{x}	104.83	100.00	105.60	97.69	105.37	108.67	104.00	87.07	91.90	85.27	99.03	95.63	82.13	99.03	91.97	83.43	86.97	92.97
	S^2	2.49	1.87	4.86	15.80	9.58	10.77	2.31	1.27	2.56	6.10	4.49	4.98	3.15	2.69	2.21	22.60	16.54	14.23
Maturity date	\bar{x}	154.17	151.90	154.73	154.21	155.09	149.42	153.93	147.07	151.20	148.30	149.10	145.77	143.10	152.07	154.27	147.31	151.38	151.37
	S^2	1.18	2.46	3.40	15.24	9.48	9.68	1.78	1.63	1.95	3.15	2.65	2.88	2.12	1.86	2.69	17.54	13.25	10.26
Plant height	\bar{x}	106.40	115.00	116.50	113.97	115.78	115.22	105.33	108.73	108.50	111.70	106.83	109.33	110.50	108.80	110.93	112.65	110.00	111.33
	S^2	7.47	13.94	18.85	250.14	145.99	132.90	13.30	11.45	15.81	24.56	20.19	21.12	15.26	11.87	14.25	77.54	56.21	46.11
No. of spikes/plant	\bar{x}	11.87	14.43	11.37	13.03	13.66	12.43	12.43	11.03	10.93	12.67	14.00	13.43	12.27	13.70	13.57	12.10	11.20	13.23
	S^2	5.27	5.77	8.40	20.83	16.34	15.74	9.45	8.65	10.12	22.75	17.65	19.10	12.34	10.56	13.25	22.12	12.54	20.99
No. of kernels/spike	\bar{x}	57.50	73.93	75.20	69.09	65.17	67.58	62.37	69.87	48.47	65.53	50.07	70.80	66.73	72.40	72.97	67.49	67.30	72.37
	S^2	49.69	96.51	90.05	188.72	120.49	170.51	92.11	86.99	94.16	195.25	148.15	165.54	56.36	68.66	70.11	158.58	133.21	118.55
100- kernel weight	\bar{x}	50.77	56.17	57.90	54.61	53.88	56.86	49.61	49.02	55.41	47.76	51.69	48.90	50.45	49.54	48.58	46.58	46.80	47.13
	S^2	36.40	38.60	27.42	115.62	90.22	77.65	11.20	9.50	11.30	22.38	16.25	19.10	20.44	29.13	25.10	65.88	53.22	45.10
Grain yield/plant	\bar{x}	35.49	53.20	33.23	32.69	33.82	39.04	26.86	29.43	26.20	29.77	29.20	32.76	28.55	36.06	40.40	32.82	39.02	35.78
	S^2	92.46	97.19	96.52	243.28	202.04	176.35	91.95	85.15	77.58	121.54	113.56	110.24	30.33	41.21	55.26	100.06	70.26	85.45

Table (3) :- Scaling test and gene action parameters of the studied traits in the three wheat crosses.

Traits	Crosses	Scaling test				Gene action parameter					
		A	B	C	D	m	a	d	aa	ad	dd
Heading date	I	0.30	11.73**	-25.27**	-18.66**	92.23**	2.63**	8.97**	17.82**	-6.29**	-24.46**
	II	2.16**	12.29**	-33.79**	-24.12**	85.27**	3.40**	44.61**	48.24**	-5.07**	-62.69**
	III	-0.17	-5.07**	-31.39**	-13.08**	83.43**	-6.00**	27.54**	26.16**	2.45**	-20.93**
Maturity date	I	1.28**	-7.79**	1.31**	3.91**	155.30**	-6.04**	-19.28**	-19.00**	-11.69**	18.56**
	II	-6.93**	-6.73**	-10.20**	1.73**	148.30**	3.33**	-2.77**	-3.47**	-0.10	17.13**
	III	5.39**	-3.60**	-14.47**	-8.13**	147.31**	0.01	22.95**	16.26**	4.49**	-18.05**
Plant height	I	8.66**	-1.06**	1.47**	-3.06**	116.20**	4.20**	-16.09**	-15.32**	2.97**	23.65**
	II	-0.17	1.43**	15.72**	7.24**	111.70**	-2.50**	-12.99**	-14.45**	-0.80	13.19**
	III	-1.43**	2.93**	9.45**	3.97**	112.65**	-1.33**	-6.66**	-7.95**	-2.18**	6.45*
No. of spikes/plant	I	4.08**	-0.93	3.10**	-0.03	12.80**	-0.03	4.29**	1.66	-0.53	7.55**
	II	4.64**	4.90**	5.34**	-2.09**	12.67**	0.57	3.40**	4.20**	-0.13	-13.74**
	III	-3.43**	-0.80	-4.70**	-0.23	12.10**	-2.03**	1.05	0.47	-1.32	3.77*
No. of kernels/spike	I	-2.37**	-13.98**	-5.47**	5.43**	88.28**	5.70**	-51.17**	-50.12**	1.58**	49.22**
	II	-10.70**	23.27**	32.95**	10.19**	65.53**	-20.73**	-38.04**	-20.39**	-16.98**	7.82*
	III	-5.10**	-0.63	-15.09**	-4.69**	67.49**	-5.07**	12.76**	9.36**	-2.23**	-3.63
100-kernel weight	I	-0.92	-0.34	-4.30**	-1.52**	54.03**	-0.25	-13.73**	-13.82**	0.05	15.06**
	II	-1.63**	-6.64**	-18.41**	-5.07**	47.76**	2.80**	16.24**	10.15**	2.50**	-1.88
	III	-5.44**	-3.85**	-10.83**	-0.77	46.58**	-0.34	0.12	1.54	-0.79	7.75**
Grain yield/plant	I	-1.09**	-8.35**	-24.38**	-7.48**	50.79**	-3.45**	8.21**	-1.02	-4.63**	-4.94
	II	5.34**	9.90**	10.39**	-2.42**	29.77**	-3.56**	2.90**	4.85**	-2.28**	-20.08**
	III	9.10**	-4.91**	-14.14**	-9.16**	32.82**	3.25**	26.42**	18.33**	7.00**	-22.52**

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

Table (4) :- Heterosis (BP), inbreeding depression (%), Heritability estimates, genetic advanced (Δg) and genetic advance expressed as a percent of F2 means (Δg %) for all characters studied in three crosses under investigation .

Traits	Crosses	Heterosis \overline{BP} %	Inbreeding depression %	F2 deviation E1	Backcross deviation E2	Heritability %		Genetic advance	
						Broad sense	Narrow sense	Δg	Δg %
Heading date	I	0.73	7.49**	-6.32**	6.02**	80.55	71.21	5.83	5.97
	II	-11.63**	7.21**	-8.45**	7.23**	88.45	44.75	2.28	2.67
	III	11.97**	9.29**	-7.85**	-2.62**	87.72	63.85	6.25	7.50
Maturity date	I	0.37	0.34	0.33	-3.26**	84.58	74.27	5.97	3.87
	II	-1.78*	1.92*	-2.55**	-6.83**	43.28	24.44	0.89	0.60
	III	7.80**	4.51**	-3.62**	0.89	87.33	65.96	5.69	3.86
Plant height	I	1.30**	2.17**	0.37	3.80**	94.64	88.51	28.84	25.30
	II	-0.21	-2.95**	3.93**	0.63	44.95	31.80	3.25	2.91
	III	1.96**	-1.55**	2.36**	0.75	82.21	68.04	12.34	10.96
No. of spikes/ plant	I	-4.21**	-14.66**	0.77	1.57*	68.89	45.97	4.32	33.16
	II	-12.09**	-15.89**	1.34**	4.77**	58.65	38.46	3.78	29.83
	III	10.60**	10.81**	-1.18**	-2.12**	45.53	30.36	2.94	24.31
No. of kernels /spike	I	1.71*	8.13**	-1.37*	-8.17**	58.27	45.80	12.96	18.76
	II	-30.63**	-35.11**	8.24**	6.28**	53.35	39.34	11.32	17.28
	III	0.78	7.50**	-3.77**	-2.87**	58.98	41.24	10.70	15.85
100 – kernel weight	I	3.07**	5.68**	-1.07*	-0.63	70.47	54.81	12.14	22.23
	II	13.03**	13.81**	-4.60**	-4.13**	52.34	42.05	4.10	8.58
	III	-1.94*	4.11**	-2.71**	-4.64**	62.22	50.76	8.49	18.22
Grain yield/ plant	I	-6.37**	1.62*	-6.09**	-4.72**	60.79	44.47	14.29	43.70
	II	-2.45*	-13.62**	2.60**	7.62**	30.15	15.86	3.60	12.10
	III	41.49**	18.77**	-3.53**	2.10**	57.76	44.38	9.15	27.87

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