STUDIES GENETIC BEHAVIOR FOR YIELD AND ITS COMPONENTS IN SOME BREAD WHEAT CROSSES

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ABSTRACT

Six – populations i.e., P_1, P_2, F_1, F_2, BC_1 and BC_2 were used in order to assess the nature of gene effects for six traits in three bread wheat crosses. Generation were grown in a field experiment at Sers- El-laian Agricultural Research station, A.R.C. during three successive seasons .

Significant useful heterosis in a positive direction was detected for number of kernels/spike and 100-kernel weight in the three crosses, spike weight in the first and second crosses. Highly significant negative inbreeding depression was obtained for number of spikes/plant in three crosses, spike length and number of kernels/spike in the third cross one and grain yield/plant in the first and second crosses.

Over - dominance towards the higher parent were detected for; number of spikes/plant, spike length and number of kernels/spike in the first and second crosses, 100-kernel weight in the three crosses and grain yield/plant in the second cross.

Significant E_1 and E_2 were detected for most studied traits. Additive gene effects were significantly exhibited in all studied traits except for; number of spikes/plant, spike length and grain yield/plant in the first cross one and 100-kernel weight in the first and second crosses.

Both dominance and epistasis were found to be significant for most of the attributes under investigations.

Heritability estimates in broad sense were high to moderate in magnitude with values between 93.98 for grain yield/plant to 44.99 for 100-kernel weight . High to moderate values of heritability estimates were found to be associated with high to moderate genetic advance as percentage of F_2 main in most cases.

INTRODUCTION

Wheat is one of the most strategic food crops in Egypt, in season 2005, the total caltivated area of wheat was about 3.01 million faddan, with an average yield of about 18.2 ardab/faddan* . Therefore, increasing wheat production is an important goal to reduce the gab between production and consumption. This can be achieved by developing high yielding varieties. The success of any breeding program in self and cross -pollinated species, depends on the present and amount of genetic variability and the involved types of gene effects in the inheritance of different characters in the used materials. To form a population with genetic variability for the characters in view, hybridization between genetically diverse parents must be done. Early generation testing is used to estimate genetic potential of individual lines on populations at early stage of inbreeding. The objective of the early generating testing is to eliminate lines or populations that do not merit consideration for further inbreeding and selection, (Fehr et al 1987) .

Grain yield in wheat is the product of tillers numbers, kernel weight and number of kernels/spike when each of these characters is measured without error; therefore, estimates of relative magnitudes

*Agric. Economic Res. Institute,2006

among components should be valid means for determining the cause of yield fluctuations as respected by Johanson et al (1966), Hsu and Walton (1971), and Knolt and Talukdar (1971).

Yield components breeding tend to increase grain yield and would be most effective, if the components involved were highly heritable, genetically independent or positively correlated, and physiologically unrelated or related in a positive manner. Heritability estimates are dependent on the method that used to calculate them, the populations from which the estimates are derived, the unit of measurement, and the environmental conditions encountered during the test. Because of these factors, a wide range of heritability estimates for the same trait have been reported in wheat by Sidwell et al (1976).

The present investigation was designated to estimate gene action, heritabillity values and expected genetic advance under selection for some agronomic characters in three wheat crosses .

MATERIALS AND METHODS

This investigation was carried out at Sers-El-laian Agricultural Research Station, A.R.C. during the three successive seasons,i.e., 2002/2003, 2003/2004 and 2004/2005. Six parental wheat genotypes representing as a wide divergent were selected for this study. The name, pedigrees are presented in Table (1). In the first season (2002/2003) the parental genotypes were evaluated in a randomized complete block design with three replications. Simultaneously pair crosses were performed to obtain F_1 grains. In the second season (2003/2004) the F_1 grains were sown to produce F_1 plants. Also, the F_1 plants of each cross were back crossed to their respective parents to produce the two back crosses (BC_1) and (BC_2).

Table (1): The name, pedigree and origin of the six bread wheat

Genotype	Pedigree	Origin
P_1	NS 732/HER//SH1#4414CROW"S" ICW91-0182-0BR-2AP-1AP-0AP.	Mexico
P_2	Desconocido # 6/4/B1-1133/3/cmh79A . 955*2/cno-79//79A.955/Bows . SD6120-14sd-2sd-1sd-0sd .	Egypt
P_3	KARAWAN-2 SWM6828-6AP-2AP-1AP-2AB-1AB-0AB .	Mexico
P_4	SAHA61/MILDRESSMO73/POL//I.aest-BON/CNO-7C. CGM4615-2GM-10GM-1GM-0GM .	Egypt
P_5	MIANYANG20	Mexico
P_6	SW89-2089/KAUZ CMSS93 B00870S-2Y-010-010Y-010M-7Y-0M .	Mexico

At the same time, pair crosses were made to produce new F_1 grains. At the same time, F_1 plants were self – pollinated to produce F_2 grains. In the third season (2004/2005) the obtained grains for the six populations i.e., P_1, P_2 , F_1 , F_2 , BC_1 and BC_2 of the three crosses were evaluated using a randomized complete block design with three replications . Each row consisted of 4 m long with 20 cm. apart, and 10 cm space between plants. .Each plot consisted of 18 rows: two rows for each parent and F1 totaling 80

plants and three rows for each back cross progenies totaling 120 plants and six rows for F_2 generation totaling 240 plants for each cross.

Data were recorded on individual guarded plants, for plant height, number of spikes/plant, spike length, number of spikelets / spike, number of kernels/ spike, , 100-Kernel weight as will as grain yield / plant .

Various biometrical parameters in this study, were calculated because F_2 genetic variance was found to be significant for all studied characters . Heterosis (%) was expressed as percentage increase of the F_1 value above the mid – parent one .

Inbreeding depression .(Id%) was also estimated as the average percentage decrease of the F_2 from the F_1 . In addition, F_2 deviation (E_1) backcross deviation (E_2) were measured as suggested by Mather and Jinks (1971) Likewise, potence ratio (p) was also calculated according to Peter and Frey (1966) . The gene actions, i.e. , additive (a) dominance (d), additive x additive (aa) additive x dominance (ad) and dominance x dominance (dd) were estimated using the method illustrated by Gamble (1962). Heritabillity was calculated as both of broad and narrow senses according to Mather,s procedure (1949) . Predicted genetic advance (Ag) was computed according to Johanson et al (1955) . Genetic gain represented as a percentage of the F_2 mean performance (Ag%) was obtained using the method of Miller et al (1958).

RESULTS AND DISCUSSION

In the recent year, plant breeding played an important role in improving yield of most crop plants. The essential informations for the breeder is to assess and quaintly the causes of variation. Estimates of genetic parameters have impact on choosing the appropriate method of breeding and/or selection program. One of the most important problems, which convert the breeder is the direct selection for yield because it is considered as a quantative character. Thus, it highly influenced by the environmental fluctuation. Therefore, the direct selection for yield is misleading. Consequently, the main task for the breeder is to determine the highly heritable characters which contribute significantly to yield (Hamada et al 1997). On the other hand, O'Brien et al (1978), Shebeski (1967) and Makenzei and Lambert (1961), suggested that, selection for yield should be commence in the earliest possible generations.

The genetic variance in F2 plants for all studied traits in all crosses were significant, consequently the other needed parameters were estimated . Table (2) show the means and variances of the parental varieties, F_1, F_2, Bc_1 and Bc_2 populations for six quantitative characters studied in the three crosses.

The results revealed significant differences among the parental genotypes involved in the present investigation, suggesting presence of considerable amount of genetic variation. Thus, parental genotypes were genetically different for loci controlling the studied characters. The presence of fair amount of genetic variation offer breeder broad genetic base for further improvement and valid to be used for further genetic assessment. The F_1

mean values exceeded the mid-parent values for all studied traits except for; number of spikes/plant and grain yield/plant in the first cross; number of spikes/plant in the second cross and also except of number of spikes/plant, spike length and grain yield/plant in the third cross. These results indicated the prence of heteroic effect for these characters and also indicating that increasing alleles were more frequent than decreasing ones. On the other hand, F_1 means were less than the mid-parent values for the traits that mentioned above indicating that the decreasing genes were more frequent than the increasing one.

At the same time, the F_2 mean value were less than F_1 one for; plant height, spike length, number of kernels/spike, 100-kernel weight and grain yield/plant in the first cross; spike length, number of kernels/spike, 100-kernel weight and grain yield/plant in the second cross and plant height, spike length, 100-kernel weight in the third cross indicating the role of dominance gene action in the inheritance of these characters and exhibited desirable recombinations in segregating generations as well as the occurrence of trasgressive segregation.

Heterosis, inbreeding depression percentages and different gene action parameters in the three crosses for the six traits studied are given in Table (3)

In self-pollinated crops such as wheat, plant breeder have been investigated the possibility of developing hybrid cultivars. The feasibility of growing hybrid cultivars depends on the economic production of large quantities of hybrid seeds and significant superiority in yield as well as best performance of hybrids compared to the current commercial cultivars.

The significant level of heterosis however, is still an open question since both positive and negative heterosis have been reported. Investigators evaluated their different cultural practices. Thus, it is difficult to draw a general conclusion since heterosis found in hybrid derived from one group of parents in a particular location is not necessarily found under other circumstances (Mahrous 1998).

Significant positive useful heterotic effects towards the mid parent values were found for spike length in the first and second crosses, number of kernels/ spike, plant hight and 100- kernel weight in all studied crosses . In contrast, significant negative heterotic effects were found for, number of spikes / plant in all studied crosses , spike length in the third cross and grain yield / plant in the first and third crosses. These results were in harmony with those obtained by Rady et al (1981), El-Hosary et al (2000) Moustafa (2002) and Moshref (2006).

The potence ratio as an indicated to the average dominance of the whole gene set of one parent or the other and can not indicate of the actual dominance of individual genes of a certain characters. Thus, it was showed indicator to the existence of over –dominance towards the higher parent for number of spikes /plant ,spike length and number of kernels per spike in the first and second crosses , as will as 100- kernel weight and grain yield/ plant in the second one. On contrast, there was over- dominance towards the lower parent for number of spikes/ plant and spike length in the third cross, plant height in the second cross and grain yield/plant in first and third crosses .

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Similar results were reported by Mosaad et al (1990), Abul- Naas et al (1991), Al-Kaddoussi et al (1994), Khalifa et al (1997) and Abd El- Aty et al (2005) .

Partial dominance towards the higher parent was found for plant height and number of kernels /spike in the third cross. On the other hand, partial dominance was detected toward the lower parent for grain yield/ plant in the first cross   . Similar result were reported by Moustafa (2002) and Moshref (2006) Inbreeding depression measured the reduction in performance of F_2 generations due to inbreeding. Highly significant positive inbreeding depression values were detected for 100- kernel weight in the three studied crosses as will as spike length and number of kernels / spike in the first and second crosses, grain yield/ plant in the second cross and plant height in the first and third cross. Meanwhile, highly significant negative inbreeding depression values were obtained for plant height in the second cross, number of spikes/ plant in all studied crosses, spike length and number of kernels / spike in the third cross and grain yield/ plant in the first and third crosses. Since, both heterosis and inbreeding depression are two coincides to same phenomena, therefore, it is logically to expect that the expression for heterosis in the F_1 population will be followed by appreciable depression in the F_2 performance .

Insignificant heterosis effect and significant inbreeding depression was obtained for grain yield/plant in the second cross (Table, 3). The contradiction between signs for dominance and epistatic effects of most parameters may lead to the observed absence of heterotic effects (El-Hosary (1983)). Also, they reported that the reduction in values of non-additive genetic components is logically caused by means of inbreeding depression. These result are in agreement with those of Hamada et al (2002) and Esmail and Kattab (2002) .

The choice of the most efficient breeding procedures depends to a large extent on the knowledge of the genetic system contributing the characters to be selected. Therefore, the nature of gene action was also computed according to Gamble (1962). The estimates of various types of gene effects contributing to the genetic variability are presented in Table (3).

F_2 mean deviation (E1) was found to be significant positive for number of spikes / plant in the three crosses; plant height, spike length and number of kernels / spike in the third cross as will as plant height in the second cross and grain yield / plant in the first cross. On the other hand, significant negative F_2 deviations were detected for spike length, number of kernels/ spike, 100 - Kernel weight and grain yield / plant in the second cross, plant height and number of kernels / spike in the first cross . These results clearly show the contribution of epistatic gene effects in the performance of inheritance these of these traits. Table (3) .

Significant back cross deviation (E2) was found to be significant for all traits in the three crosses except 100- kernel weight and grain yield / plant in the second cross and spike length and 100- kernel weight in the first cross one and that would ascertained the presence of epistasis in such large magnitude as to warrant great deal of attention in wheat breed programs .
Nature of gene action was also computed according to Gamble (1962). The mean effect parameters (m) reflect the contribution due to the over all mean

plus the locus effects and interaction of the fixed loci. For all studied traits, the mean parameters (m) effect was significant in all crosses for all studied traits, indicating the potentiality of improving performance of these traits by using pedigree selection program.

The additive gene effects (a) were found to be highly significant for plant height in the first and third crosses, number of spikes / plant in the second and third crosses, number of kernels/spike in the first cross, 100 - kernel weight in the third cross and grain yield / plant in the second and third crosses, suggesting the potential for obtaining further improvement of these traits by using pedigree selection program . These results are in agreement with those of similar approaches that reported by Amaya et al (1972) Bakheit et al (1989) Mosaad et al (1990) Gouda et al (1993) Hendawy (1994) and Hendawy (2003) .

On the other hand, highly significant negative additive gene effects were obtained for; number of spikes / plant, spike length and number of kernels / spike in the second and third crosses and plant height only in the second one, indicating that the additive gene effects were less important in the inheritance of these traits .

In autogonous crops i.e., wheat and barly, the breeder is normally aiming at isolating parental combinations that are likely to produce desirable homozygous segregants. The utility of attempts at identifying such pure lines is facilitated by the preponderance of additive genetic effects in self pollinating crops (Josh and Dhawam 1966).

The estimates of dominance gene effects were highly significant for all the studied traits except for; 100 - kernel weight in the first cross and spike length in the second one. Moreover, the dominance gene effects were more important and greater than the additive gene effects in the inheritance of most studied traits (Table 3) .

Significant of additive (a) and dominance (d) components indicated that, both additive and dominance gene effects were important in the inheritance of these studied traits. Therefore, selecting desired characters could be practiced in the early generations but may be more effective in the later one. On the other hand, the dominance value did not reach to the significant level for spike length in the second cross and 100-kernel weight in the first one, however, it was greater than its standard error.

Dominance gene action would tend to favor the production of hybrids, while, for additive gene action, the significant stander selection procedures would be effective in brining about advantageous changes in the characters. These results were coincident with those reported by Hassan (1993) Al-Kaddoussi et al (1994) and Abd El- Nour (2006) .

Significant positive additive x additive (aa) type of epistasis was found for; number of kernels / spike in the three studied crosses, plant height in the first and third crosses, number of spikes/plant in the first and second crosses, 100 - kernel weight in the second and third crosses and grain yield / plant in the second cross. Meanwhile, significant negative additive x additive type of gene action was found for plant height in the second cross, number of spikes/plant and spike length in the third cross and grain yield/plant in the first and third crosses.

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Significant positive additive x dominance (ad) type of epistasis was found for plant height, number of kernels / spike, spike length and grain yield / plant in the first cross .On the other hand, significant negative additive x dominance type of gene action was found for; plant height, spike length in the second and third crosses and 100- kernel weight in the first and second ones. Similar conclusion was reached by Hendawy (1998), Hamada et al (2002), Esmail and Kattab (2002) and Abd El- Mojeed (2005) .

The type of epistaeis type dominance x dominance (dd) was found to be significant for all traits under study except; spike length in the first and second crosses, 100 - kernel weight in the first one .

The presence of both additive and non - additive gen actions in all studied attributes may be indicated that, selection procedures based on the accumulation of additive gene effect may be successful in improving all trait under investigation. However, for maximizing selection advance procedures which are known to be effective in shifting gene frequency when both additive and non - additive gene effects are important in the inheritance of these characters . Therefore , selection of desired character could be practiced in the early generations but it would be more effective in later ones (Sehab El-Din 1993) .

Heritability estimates are important to the breeder since it quantifies the expected improvement upon selection. To achieve genetic improvement through selection, heritability must be reasonably high . In the present investigation, heritability estimates as a bread sense were high to moderate in magnitude with values between 93.98 for grain yield/plant to 44.99 for l00 – kernel weight, Table(4)

High estimates of narrow sense heritahility were found for plant height in the three studied crosses suggesting the importance of straight forward phenotypic selection method to improve this character. Moderate narrow sense heritaility estimates were found for; spike length in the second cross, number of kernels/spike in the second cross, number of kernels/spike in the first cross except number of spikes /plant,100-kernel weight and grain yield / plant in the three crosses , number of kernels /spike in the second cross and so spike length in the first cross one ,where low narrow sense heritability estimates were   observed for these traits indicating that the improvement of these characters could be achieved through pedigree method or population improvement. Similar results were previously reported by Jatasra and Paroda (1980), Hassan (1993), Moustafa (2002) and Abdel-Aty et al (2005) Genetic advance under selection (Δg%) was found to be high to moderate in magnitude for all trails under investigation in the three studied crosses except for; plant height in the three crosses, number of spikes/plant and spike length in the first cross and number of kernels /spike in the second cross, where (Δg%) was found to be relatively low 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 should be associated with high genetic gain .

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In the present study ,high to moderate genetic advance (Δg%) was found to be associated with moderate narrow sense heritability estimates for; spike length in the second and third crosses. Consequently, selection for these traits should be effective and satisfactory. Concerning the rest of the traits studied i.e., number of spikes /plant and 100 – kernel in the second and third crosses, and grain yield /plant in the second cross, high to moderate genetic advance were found to be associated with relatively low narrow sense heritability estimates, hence selection for these traits would be less effectiveness .

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دراسة السلوك الوراثي للمحصول ومكوناته في بعض هجن قمح الخبز

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- تم إجراء هذا البحث فى محطة البحوث الزراعية بسرس الليان فى مواسم ٢٠٠٢/ ٢٠٠٣ و ٢٠٠٣ /٢٠٠٤ و٢٠٠٥/٢٠٠٤ على ثلاثة هجن من قمح الخبز بهدف تقدير طبيعة التأثير الجيني باستخدام متوسطات الأجيال لصفة المحصول ومكوناته لإيجاد تراكيب وراثية جديدة يمكن الانتخاب من خلالها فى الأجيال الانعزالية للحصول على سلالات جديدة تتفوق فى صفاتها المحصولية وقد استخدم لذلك ستة من التراكيب المتباعدة وراثيا وكل من الجيل الأول والثاني والجيلين الرجعيين.

1- كانت قوة الهجين على أساس متوسط الأبوين معنوية وموجبه لصفه عدد الحبوب فى السنبلة ووزن ١٠٠ حبه فى الثلاثة هجن.

٢-لوحظ وجود سيادة فائقة فى صفات عدد السنابل فى النبات وطول السنبلة فى الهجين الأول والثاني بينما صفة ١٠٠ حبه فى الهجن الثلاثة وصفه محصول النبات فى الهجين الثاني فقط.

٣- كانت التربية الداخلية معنوية وسالبة فى نقص متوسط الجيل الثاني عن الجيل الأول فى صفة عدد السنابل فى الهجن الثلاثة وصفة طول السنبلة وعدد الحبوب فى الهجين الثالث ومحصول النبات الفردي فى الهجين الأول والثالث .

٤- اتضح من الدراسية مساهمة كل من الفعل الجيني المضيف والسيادي والتفوقى فى وراثة معظم الصفات المدروسة .

٥- كانت انحرافات الجيل الثاني E_1 وانحرافات الأجيال الرجعية E_2 معنوية فى معظم الصفات فى الهجن الثلاثة مما يوضح أهمية الفعل الجيني التفوقى في وراثة الصفات.

٦- أظهرت كفاءة التوريث بمعناها الواسع قيما عاليه الى متوسطه لمعظم الصفات اما الكفاءة الوراثية بمعناها الضيق فقد أظهرت قيما متوسطة ومنخفضة للصفات تحت الدراسة ارتبطت بنسب التحسين الوراثي .

Table (2) Means (x⁻) and variances (S²) of P₁,P₂,F₁,F₂,BC₁ and BC₂ populations of the three wheat crosses for the studied characters .

		Cross 1						Cross 2						Cross 3					
		P1	P2	F1	F2	BC1	BC2	P1	P2	F1	F2	BC1	BC2	P1	P2	F1	F2	BC1	BC2
Plant	**x⁻**	135.5	101.6	134.1	125.2	138.3	117.05	115.9	115.5	117.8	133.47	121.73	130.35	109.6	84.15	103.95	101.47	106.1	102.98
Height	**S²**	2.666	2.393	2.553	16.898	4.509	7.726	4.919	3.456	1.963	12.105	6.046	10.582	2.909	3.281	2.564	9.738	3.272	8.693
No. of spikes	**x⁻**	11.8	12.25	10.25	11.9	19.3	20.2	15.55	9.65	9.25	11.567	18.425	15.125	11.7	8.7	7.5	13.317	11.18	8.85
Plant	**S²**	2.745	2.314	2.531	6.194	6.973	5.893	1.572	1.565	1.713	4.232	7.974	5.658	2.364	1.949	2.09	4.597	4.069	3.389
Spike	**x⁻**	11.85	11.45	13.66	12.3	12.88	12.69	11.08	14.2	15.55	13.225	11.488	14.063	11.85	11.45	10.35	10.275	10.863	12.6
Length	**S²**	1.348	1.025	1.081	2.529	3.204	1.73	0.712	0.768	0.887	2.674	1.685	2.152	0.841	0.908	0.745	2.647	1.396	1.401
No of kernel	**x⁻**	74.05	77.9	79.4	70.8	78.25	66.675	73.6	83.2	98.15	71.983	75.025	81.775	55.05	67.5	63.9	64.517	67.0	87.025
Spike	**S²**	5.661	5.036	6.142	19.814	17.357	11.03	8.835	6.382	6.505	13.973	17.234	21.03	4.774	7.352	4.962	17.433	12.239	11.905
100-kernel	**x⁻**	5.22	4.365	5.395	5.197	4.993	5.238	5.07	4.77	6.58	5.358	5.733	6.063	5.08	4.755	5.495	4.387	5.813	5.505
Weight	**S²**	0.338	0.482	0.328	0.788	0.685	0.735	0.306	0.344	0.335	0.807	0.545	0.623	0.255	0.303	0.314	0.829	0.489	0.414
Grain yield	**x⁻**	26.623	37.468	29.86	27.495	54.563	55.556	41.66	25.42	41.895	30.692	42.678	54.383	28.425	23.775	21.6	36.24	33.068	30.31
Plant	**S²**	2.997	5.279	4.63	12.519	25.655	28.878	5.197	3.391	4.745	16.6	21.443	22.778	4.925	3.662	3.385	14.191	12.537	11.335

Table (3): Heterosis, potence ratio, inbreeding depression percentages and gene action parameters in the three wheat crosses .

Characters	crosses	Heterosis Bp%	Inbreeding depression	Gene action parameters								Potence ratio (P)
				m	A	D	Aa	Ad	Dd	E1	E2	
Plant height	I	31.99**	6.637**	125.2*	21.25**	25.45**	9.9**	3.4**	--15.3**	-1.125**	2.7**	-0.917
	II	1.9991**	-13.302**	133.47**	-8.62**	-27.62**	-29.72**	-8.82**	-7.44**	16.72**	18.58**	-10.50
	III	23.529**	2.386**	101.47**	3.12**	19.355**	12.28**	-9.605**	-28.79**	1.058*	8.255**	0.556
No- of spikes / plant	I	-16.326**	-16.098**	11.9**	-0.9	29.625**	31.4**	-0.675	-65.85**	0.762*	17.225**	7.889
	II	-40.51**	-25.049**	11.567**	3.3**	17.482**	20.832**	0.35	-44.232**	0.642*	11.700**	1.136
	III	-13.79**	-77.56**	13.317**	2.33**	-15.908**	-13.208**	0.83	8.548**	4.467**	2.33**	-1.50
Spike length	I	15.274**	9.956**	12.3**	0.19	3.95**	1.94	-0.01	-2.46	0.26	-0.355	10.05
	II	9.507**	14.952**	13.225**	-2.575**	1.112	-1.798	-1.015**	7.076**	-0.87*	-2.639**	1.865
	III	-12.658**	-18.599**	12.275**	-1.737**	-3.474**	-2.174*	-1.937**	-0.752	1.275**	1.463**	-6.50
No - of kernel /spike	I	1.926*	10.831**	70.8**	11.575**	10.075**	6.65*	13.5**	14.25**	-6.887**	-10.378**	1.779
	II	17.969**	26.66**	71.983**	-6.75**	45.418**	25.668**	-1.95	13.832**	-16.292**	-19.75**	4.115
	III	5.333**	-0.966	64.517**	-20.025**	52.607**	49.982**	-13.8**	-107.682**	1.929**	28.85**	0.422
100 - kernel weight	I	3.352**	3.67**	5.197**	-0.245	0.276	-0.326	-0.672**	0.239	0.103	0.044	1.409
	II	29.783**	18.571**	5.358**	-0.33	3.82**	2.16**	-0.48*	-2.752**	-0.392**	0.296	11.067
	III	8.169**	20.164**	4.387**	0.308**	5.666**	5.088**	0.146	-6.899**	-0.819**	0.906**	3.554
Grain yield / plant	I	-20.305**	-25.569**	37.495**	-0.993	-11.928**	-9.742**	4.429**	-6.685**	6.542**	8.214**	-0.403
	II	0.564	26.741**	30.692**	8.295**	39.709**	31.354**	0.175	-34.606**	-7.026**	1.626	1.029
	III	-24.011**	-67.778**	36.24**	2.758**	-22.704**	-18.204**	0.433	-13.152**	12.39**	15.678**	-1.935

Significant at 0.05 and 0.01 probability levels , respectively

Table (4) Heritabilily in broad and narrow sense genetic advance upon selection and genetic advance as percentage for the studied characters ,

Cross number	parameter	Plant height	No.of spikes/ plant	Spike length	No. of kernels/ spike	100- kernel / weight	Grain yield /plant
1	*h b*	91.89	64.62	54.488	71.672	51.39	93.984
	h n	68.89	6.69	4.903	56.73	19.796	41.246
	Δ g	5.834	3.425	0.16	5.202	0.362	3.007
	Δ g %	4.659	0.288	1.301	7.347	6.963	8.019
2	*h b*	71.532	88.9	70.49	79.078	59.356	88.499
	h n	62.632	35.475	56.51	29.813	30.483	28.521
	Δ g	4.489	1.504	1.903	2.295	0.564	7.427
	Δ g %	3.364	13.006	14.391	3.189	10.527	24.198
3	*h b*	73.75	53.578	79.272	67.326	44.991	71.876
	h n	67.56	37.829	62.285	61.504	29.301	31.781
	Δ g	4.343	1.669	2.087	5.289	0.439	2.466
	Δ g %	4.28	12.536	17.005	8.199	10.007	6.805

hb and hn = heritability in broad and narrow senses ,respectively : Δ g = genetic advance, Δ g% = genetic advance as percentage ,