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ESTIMATION OF EPISTASIS, ADDITIVE AND DOMINANCE VARIATION IN CERTAIN BREAD WHEAT (*Triticum aestivum*, L) CROSSES

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ABSTRACT

This investigation was carried out at El-Gemmeiza Agric. Res. Station, ARC, Egypt, during the three successive seasons, 2006/2007, 2007/2008,and 2008/2009 to study heterosis, heritability in addition to determining the adequacy of genetic model controlling the genetic system for some economic traits.

Six population (P_1, P_2, F_1, F_2, Bc_1 and Bc_2) for three crosses were used in this study coming through four bread wheat genotypes. These crosses were PBW343 x Sakha94, Gemmeiza 9 x Sakha line and Sakha 94 x Gemmeiza 9. Analysis of variance showed a significant differences among the studied generations means for all studied traits. Scaling test showed that most studied characters were significant indicating the presence of non- allelic interactions. Dominance gene effects were generally higher in magnitude than additive ones in the three crosses, indicating that dominant genes playing important role in the inheritance of such traits beside the additive one. The hybrid (Gemmeiza 9 x Sakha line) gave a highly significant (aa), (ad) and (dd) with positive values for number of days to heading and number of kernels / spike indicating the importance of gene interactions in the genetic system. On the other hand, the (aa) negative values obtained for number of spikes / plant and grain yield / plant in the first cross indicate that the materials used in this study have a decreasing alleles expression which makes improving it through selection in the early generations could not be effective.

The second cross gave the highest negative heterotic effect towards earliness for number of days to heading and number of days to maturity with moderate heritability in narrow sense and with a genetic advance being 5.05 and 5.39 day for both characters, respectively. Significant positive heterotic effects relative to better parent were obtained for number of kernels/spike and 100- kernel weight in the first and second cross and number of spikes/ plant, 100- kernel weight and grain yield / plant in the third one.

INTRODUCTION

Wheat is the most important cereal crop in Egypt and world wide. In Egypt, increasing grain yield of cereal crops is considered one of the important national goals in order to face the growing populations needs therefore, it has become necessary to develop genotypes which characterized by showing superior performance (Shehab El-Din , 1993).

The plant breeder is interested in estimating gene effects in order to formulate the most advantageous breeding procedures for improving his breeding program. Therefore, breeders needs information about the nature of gene action, heterosis, inbreeding depression, heritability and predicted genetic gain from selection for characters, related to yield and yield components. Since, decision about effective breeding system to be used is mainly dictated by type of gene action controlling the genetic variation, such informations help the breeders to predict the effective breeding program which can be used in the early generations . Thus, the obtained, genetic informations from multi populations (P_1, P_2, F_1, F_2, Bc_1 and Bc_2) are considered the one which may give detailed early genetic informations of the employed genotypes.

Many investigators studied the type of gene effect in wheat and reported that dominance was relatively more important than additive for grain yield, while additive genetic effect was predominated in the expression of plant height and heading date Amaya *et al.*(1972). Meanwhile, Khalifa *et al.* (1997) and El-Sayed *et al.* (2000), found that additive-dominance model was adequate for revealing the inheritance of grain yield and its components. On the other hand, Amawate and Behl (1995) reported that dominance gene effect was more important than additive one in most traits which indicate the presence of both types of gene effects. The results of Sharma *et al.* (1998) and Yadav and Nersinghani (1999) came to a conclusion that, additive gene effects were predominant for yield and yield components, though non-additive gene effects were also important. Hamada (2003), Tammam (2005) and Abd El-Majeed (2005) revealed that, additive and dominance components of gene actions were detected for most traits studied.

The present work was undertaken to study the behavior of gene action and other genetic parameters for seven traits in three bread wheat crosses by using their six populations i. e., P_1, P_2, F_1, F_2, Bc_1 and Bc_2.

MATERIALS AND METHODS

The present study was carried out at El-Gemmeiza Agric. Res. Station A.R.C., Egypt, during three successive seasons of 2006/2007, 2007/2008 and 2008/2009. Four bread wheat genotypes (*Triticum aestivum* L.) were chosen for this study on the basis of their genetic diversity and origin, Table (1). These genotypes were PBW343, Sakha94, Gemmeiza 9and Sakha line. In 2006/2007 season, three crosses were made involving the aforementioned genotypes, P_1 x P_2, P_3 x P_4 and P_2 x P_3 to produce F_1 hybrid. In 2007/2008 growing season some of F_1 plants for each cross were backcrossed to both its two parents to produce the backcrosses (Bc_1 and Bc_2). The rest of F_1 plants were selfed to produce F_2 seeds. In 2008/2009 season, the six population seeds i. e., P_1, P_2, F_1, F_2, Bc_1 and Bc_2 of the three crosses were sown in a randomized complete block design with four replications. Each plot consists of 20 rows, eight rows for F_2 generation, two rows for P_1, P_2, as well as F_1 and three rows for Bc_1 and Bc_2. The rows were 3.0m long spaced 30cm apart and seeds were spaced 10 cm within row.

Data were recorded on 25 individual guarded plants for P_1, P_2 and F_1 and 60 plants for Bc_1 and Bc_2 and 75 plants for the F_2 in each replicate for the studied characters, number of days to heading, number of days to maturity, plant height (cm.), number of spikes/plant, number of kernels/spike, 100-kernel weight (gm.) and grain yield/plant (gm.). All recommended field practices for wheat production in the area were adopted in all growing seasons.

Table (1): 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	INDIA
P_2	SAKHA 94	OPATA/RAYON//KAUZCMBW90Y3180- OTOPM- 3Y-O1OM- O1OM- O1OY- 1OM-O15Y- OY-OAP- OS.	Egypt
P_3	Gemmeiza9	ALD"s"/SHUAC//CMH74A. 630/SX GM 4583- 5GM-1GM - OGM	Egypt
P_4	Sakha line	D6301/HEINEV11/ERA/3/BUC/4/LIRA/5/SPB/61GIZA 144//PIN$^{\text{"s"}}$/BOW$^{\text{"s"}}$ S.13582- 8S- 1S- OS- YR- 1S- OS	Egypt

Statistical and genetic analysis:-

To determines the presence or absence of non-allalic interactions, scaling test as outlined by Mather (1949) was used. The quantities A, B, C and D and their variances were calculated to test the adequacy of the additive-dominance model in each case where:-

A = $2\,\overline{Bc}_1 - \overline{P_1} - \overline{F_1}$

B = $2\,\overline{Bc}_2 - \overline{P_2} - \overline{F_1}$

C = $4\,\overline{F_2} - \overline{2F_1} - \overline{P_1} - \overline{P_2}$

D = $2\,\overline{F_2} - \overline{Bc_1} - \overline{Bc_2}$

The variance of these estimates were calculated as follows:-

V(A) = 4V($\overline{Bc_1}$) + V($\overline{P_1}$) + V($\overline{F_1}$)

V(B) = 4V($\overline{Bc_2}$) + V($\overline{P_2}$) + V($\overline{F_1}$)

V(C) = 16V($\overline{F_2}$) + 4V($\overline{F_1}$) + V($\overline{P_1}$) + V($\overline{P_2}$)

V(D) = 4V($\overline{F_2}$) + V($\overline{Bc_1}$) + V($\overline{Bc_2}$)

The standard error of A, B, C and D was obtained by taking the square root of their respective variances. T-test was calculated by dividing the effects of A, B, C and D on their respective standard error.

Type of gene effects estimated according to Gamble (1962) as follows:-

m = $\overline{F_2}$

a = $\overline{Bc_1}$ - $\overline{Bc_2}$

d = $\overline{F_1}$ - 4$\overline{F_2}$ - ½($\overline{P_1}$)+ ½ ($\overline{P_2}$) +2($\overline{Bc_1}$) +2($\overline{Bc_2}$)

aa = 2($\overline{Bc_1}$) + 2($\overline{Bc_2}$) – 4($\overline{F_2}$)

ad = 2($\overline{Bc_1}$) - ($\overline{P_1}$) - 2($\overline{Bc_2}$) + ($\overline{P_2}$)

dd = ($\overline{P_1}$) + ($\overline{P_2}$) +2($\overline{F_1}$) + 4($\overline{F_2}$) – 4($\overline{Bc_1}$) – 4($\overline{Bc_2}$)

The variance values needed in this concern were obtained as follows:-

Vm = V($\overline{F_2}$)

$$Va = V(\overline{Bc_1}) + V(\overline{Bc_2})$$

$$Vd = V(\overline{F_1}) + 16V(\overline{F_2}) + \tfrac{1}{4}V(\overline{P_2}) + \tfrac{1}{4}V(\overline{P_1}) + 4V(\overline{Bc_1}) + 4V(\overline{Bc_2})$$

$$Vaa = 4V(\overline{Bc_1}) + V(\overline{Bc_2}) + 16V(\overline{F_2})$$

$$Vad = 4V(\overline{Bc_1}) + V(\overline{P_1}) + V(\overline{Bc_2}) + V(\overline{P_2})$$

$$Vdd = V(\overline{P_1}) + V(\overline{P_2}) + 4V(\overline{F_1}) + 16V(\overline{F_2}) + 16V(\overline{Bc_1}) + 16V(\overline{Bc_2})$$

The standard error of a, d, aa, ad and dd was obtained by taking the square root of their respective variances. T-test values were calculated by dividing the effects of a, d, aa, ad and dd on their respective standard errors.

The amount of heterosis was expressed as the percentage deviation of F_1 mean performance from the better-parent values. Inbreeding depression was calculated as the difference between the F_1 and F_2 means expressed as a percentage of the F_1 mean Wynn *et al* (1970). T-test was used to determine the significance of these deviation where the standard error (S-E) was calculated as follows:

S-E for patter-parent heterosis calculated as follows:

$$(\overline{F_1} - \overline{BP}) = (V\overline{F_1} + V\overline{BP})^{½}$$

And S-E for inbreeding depression were estimated as follows:

$$(\overline{F_1} - \overline{F_2}) = (V\overline{F_1} + V\overline{F_2})^{½}$$

Heritability in both broad and narrow sense were estimated according to Mather (1949), predicted genetic gain from selection (Δg) was calculated according to Johanson *et al.* (1955).

RESULTS AND DISCUSSION

Mean performance :-

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

In general , the mean performance of P_2 in the three crosses and BC_2 and F_2 in the second cross were the earliest in their days to heading . BC_2 in the second cross was the best for early maturing. The mean performance of F_2 population in the first cross and Bc_1 in the second cross have the highest values for number of spikes / plant. On the other hand , P_2,F_1, were the best in their performance having the highest number of kernels/spike in the second cross which also characterized by having the heaviest kernel weight especially in the F_1, F_2 , $Bc_1$and Bc_2. Meanwhile , P_2 and F_2 in the first cross and P_2 in the second cross recorded the highest grain yield/plant .

2

Gene effects :-

The choice of the most efficient breeding procedures depends largely on the knowledge of the genetic system contributing the characters to be selected because it is helpful in deciding the nature of gene action which computed according to Gamble,(1962) .

Scaling test A,B,C and D presented in Table (3) showed that all the studied characters in the three crosses were significant except few cases which indicate presence of non-allelic interactions and the inadequacy of the simple model in interpreting the differences between population means. Also , the scaling test estimates for insignificant ones indicate the absence of non-allelic interactions and the additive-dominance model is adequate in this case . These results were in agreement with those of Serivastava *et al* .(1992) , Hamada *et al* (2002) , Tammam (2005) , Abd EL-Majeed (2005) , EL-Sayed and El-Shaarawy (2006), Hendawy *et. al* (2009) and Gad (2010)

The mean parameter (m) for all studied attributes which reflect the contribution due to the overall mean plus the locus effects and interactions of the fixed loci were highly significant.

Additive gene effect (a) was positive and significant for days to heading, days to maturity, plant height and number of kernels / spike in the second and third cross and grain yield /plant and number of spikes /plant in the three crosses.

Meanwhile, the first cross showed a negative and significant (a) effect for days to heading, days to maturity(towards earliness) and plant height, and positive and insignificant values for 100-kernel weight. . These results indicate that improving the performance of these traits may be more effective by using the pedigree selection program, Abul-Nass *et al* .(1993) .

In autogamous crops, i.e, wheat and barley, the breeder is usually aiming to isolate parental combinations that are likely to produce desirable homozygous segregation. The utility of attempts in identifying such pure lines is facilitated by the preponderance of additive genetic effects Joshi *and* Dhawan (1966).

The estimates of dominance (d) effects were significant for all studied traits except days to heading in the first cross. The estimates of dominance were positive and significant for days to heading and grain yield / plant in the second and third cross , days to maturity and 100- kernel weight in the first and third cross, number of spikes/ plant in the second one and plant height and number of kernels / spike in the three crosses. Meanwhile, negative and significant dominance effects were recorded for days to maturity and 100-kernel weight in the second cross, number of spikes / plant in the first and third cross and grain yield / plant in the first cross. These results indicating the importance role of dominance gene effects in the inheritance of these traits. On the other hand, significant of additive (a) and dominance (d) components indicated that both additive and dominance gene effects were important in the inheritance of these traits. Also, selecting desirable characters may be practiced in the early generations but it would be effective in the late ones. Similar results were obtained by El- Hosary *et al*. (2000) and Hendawy (2003).

3

Estimates of epistatic gene effects ; additive x additive (aa), additive x dominance (ad), and dominance x dominance (dd) are presented in Table (3). Significant estimates of (aa) epistatic gene effects were positive and significant for days to maturity in the first cross, number of spikes / plant and grain yield / plant in the second cross, 100- kernel weight in the third one and days to heading, plant height and number of kernels / spike in the three crosses. Meanwhile, (aa) was negative and significant in case of days to maturity and 100- kernel weight in the second cross, and number of spikes / plant in the first and third cross and grain yield / plant for the first one.

Data concerning epistatic gene effects , additive x dominance (ad) showed different positive and significant estimates for plant height, number of spikes / plant and grain yield / plant in the first cross, days to heading , days to maturity , plant height, number of spikes / plant and number of kernels / spike in the second cross, days to maturity, plant height, number of spikes /plant , number of kernels /spike and grain yield / plant in the third cross. While (ad) epistatic effects were negative and significant for days to heading and 100- kernel weight in the first cross , 100- kernel weight and grain yield /plant in the second cross and 100- kernel weight in the third one. These results indicate that the inheritance of these traits were affected by the duplication effect of epistatic genes.

The dominance x dominance (dd) gene effect differed according to crosses and characters, being positive and significant for days to heading, days to maturity and number of kernels / spike in the second cross while these characters showed negative and significant values in the first and third cross. Positive and significant (dd) effects were detected for plant height in the first cross and was negative and significant in the second and third cross, while number of spikes / plant , and grain yield / plant were positive and significant in the first and third crosses and negative and significant in the second one. (dd) effects for 100- kernel weight were positive and significant in the first and second cross and negative and significant in the third one. Positive and significant results confirm the importance role of dominance x dominance gene interactions in the genetic system which control these characters. Similar results were reported by Singh *et al*. (1985), Serivastava *et al*. (1992), Tammam (2005) , El- Sayed *et al*. (2000) and Hendawy *et al* (2009).

The absolute relative magnitude of the epistatic gene effects to the mean effects were somewhat variable depending on the cross and the studied traits. Generally, the absolute magnitude of the epistatic effects were larger than additive or dominance effects. Therefore, it could be concluded that homozygous x homozygous and heterozygous x homozygous non – allelic interactions were more important than that the heterozygous x heterozygous interaction in the inheritance of most studied traits. The study further revealed that epistatic gene effects were as important as additive and dominance gene effects for most of the traits. The failure in detecting epistatic gene effects based on the generation mean analysis does not necessarily indicate that non – allelic interactions not play role in the determination of phenotypic value. Nighawan *et al*. (1969) had also reported the importance of all the three types of gene actions. On the other hand, Ketata *et al.* (1976)

postulated non – additive gene action of sizable amount for grain yield in wheat. Thus, the system of inbreeding employed in exploiting any character depends on the gene action involved in its expression for predicted gain in selection progress Abul- Naas *et al.* (1993).

Heterosis :

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 or mid parent 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, early heading and maturity may be preferable for developing genotypes characterized by early maturing and high grain yield. In this concern, percentage of heterosis over better parent values are presented in Table (4). Negative significant heterosis was obtained for days to heading in the first and second cross and days to maturity in the second one. Therefore, this crosses can be utilized in breeding for early heading and or maturity . Plant height heterosis values were also negative and significant in the first cross, so it can be utilized for developing wheat cultivars with suitable plant height and hence can response to N- fertilizers without having lodging problems . The third cross had positive and significant heterosis values for number of spikes / plant , 100- kernel weight and grain yield /plant being 4.13%, 6.28% and 7.79%, respectively . Positive and significant heterosis was obtained for number of kernels / spike and 100- kernel weight in the first and second cross and 100- kernel weight in the third one. These results are in agreement with those obtained by El-Sayed *et al*. (2000), Hamada *et al*.(2002), Hamada (2003), Hendawy (2003) , El- Sayed and El-Shaarawy (2006)and Gad. (2010). Significant and positive better parent heterosis values for grain yield / plant which was obtained in the third cross, could be considerd as a promising one in our wheat breeding program when planning for producing a hybrid wheat.

Inbreeding depression:-

Inbreeding depression measured the reduction in performance of the F_2 generation due to inbreeding. Significant positive values were obtained for 100-kernel weight in the first and third cross , grain yield /plant in the second and third cross. Number of days to heading in the second and third cross showed significant positive results, and number of days to maturity in the first cross. Also, significant positive values were detected for number of kernels / spike in the first and second cross and for plant height in the first and third cross. On the other hand, significant negative inbreeding depression values were obtained for number of spikes / plant in the three crosses . Significant effects for both heterosis and inbreeding depression seems logic since the expression of heterosis in F_1's were followed by considerable reduction in the F_2 performance. Also, reduction in values of non- additive genetic components is logically caused by means of inbreeding depression . These results were in agreement with those obtained by Abul- Naas *et al* (1993), Hendawy (2003) , El- Sayed and El-Shaarawy (2006) and Gad (2010).

Heritability estimates:-

Assessment of heritability of various traits is of considerable importance in crop improvement program, for example, to predict the response to selection, Nyguist (1991) and to identify optimum environments for selection, Allen *et al*. (1978). Heritability has been estimated in several experimental situations in literature.

Heritability estimates depending on magnitudes of its genetic variance components of additive and dominance. The highest broad sense heritability was obtained for number of days to heading in the first cross being (90.60) and days to maturity in the second cross being (90.98%), Table (4). Meanwhile, the lowest estimates were resultant for; number of days to heading, 100- kernel weight and grain yield /plant in the third cross with values 58.58 %, 59.83 % and 54.46 % ,respectively. Heritability in narrow sense as estimated by using F_2 and backcross data, were low for plant height and days to heading in the third cross being 19.85% and 15.45% , respectively, and high for both days to heading and maturity (50.24 % and 59.05%) , plant height (70.84%), number of spikes /plant (53.3%), 100 kernel weight (52.5%) and grain yield/ plant (46.4%) in the first cross.

The results revealed also that, the genetic variance was mostly attributed to the additive effects of genes for the other studied traits. This confirm the previous results that found by means of gene action estimates of additive genetic portion, which was mostly predominant. These results were in harmony with those obtained by El- Sayed *et al*. (2000), El- Hosary *et al.* (2000), Hamada *et al*. (2002), Hendawy (2003) and El- Sayed, and El-Shaarawy (2006)

Genetic advance:-

The genetic advance upon selection as well as its percentage of the F_2 mean for the studied characters are presented in Table (4). The highest genetic advance (Δg) were detected for days to heading, days to maturity, plant height, and 100 kernel weight in the first cross being 6.3 day, 6.4 day, 10.9 cm and 5.7 gm, respectively. Meanwhile, (Δg) values in the second cross were 6.2, 8.6,and 7.35 for number of spikes/ plant , number of kernels/ spike and grain yield/ plant, respectively. Low genetic advance values were obtained for days to heading , plant height and 100- kernel weight in the third cross being 1.63, 2.9 and 2.06, respectively. In the present work, high genetic advance was found to be associated with high heritability estimates for number of spikes / plant , 100- kernel weight and grain yield/ plant in the three crosses. Therefore, selection in these particular populations should be effective and satisfactory in the early generations for successful breeding purposes. Also, moderate and low genetic advance was found to be associated with moderate or low heritability estimates.

As it is well known, expected improvement via selection is directly proportional to heritability. Also, the expected response to selection varied with the phenotypic standard deviation of population means. This figure is a measure of low total variability in these traits and therefore reflects the total response that could be realized by breeding techniques. It is possible to visualize a situation where the heritability is high by little response can be expected, El- Hosary *et al*. (1997) and El- Sayed, and El-Shaarawy (2006)

Table (4) : Heterosis (BP), inbreeding depression , heritability (Bs&Ns), genetic advance upon selection and genetic advance as percentage for the studied traits in three wheat crosses.

Traits	Crosses	Heterosis $\overline{BP}$ %	Inbreeding depression %	Heritability %		Δg	Δg %
				Broad	Narrow		
Days to heading	I	-3.38**	-1.62*	90.60	50.24	6.33	6.23
	II	-6.23**	9.50**	71.04	44.53	5.05	5.56
	III	4.11**	7.92**	58.58	15.45	1.63	1.68
Days to maturity	I	1.82	1.08*	89.91	59.05	6.42	4.23
	II	-3.80**	0.13	90.98	43.35	5.39	3.55
	III	1.28	0.82	87.56	59.05	6.42	4.10
Plant height	I	-3.61**	4.99**	82.77	70.84	10.89	9.69
	II	9.19**	-0.61	80.57	36.62	5.10	4.17
	III	2.90	3.36**	64.12	19.85	2.90	2.61
No. of spikes/ plant	I	-14.51**	-26.86**	86.55	53.26	4.61	30.69
	II	-23.90**	-15.75**	82.49	46.59	6.16	53.08
	III	4.13**	-29.42**	74.02	41.45	4.70	30.00
No. of kernels /spike	I	4.47**	6.25**	77.78	49.78	6.12	8.86
	II	13.60**	26.96**	81.58	66.43	8.62	14.06
	III	-3.60**	-0.76	75.99	50.71	6.90	9.58
100 – kernel weight	I	17.30**	3.88**	93.31	52.46	5.76	11.02
	II	13.76**	-4.26**	94.78	46.43	5.77	9.79
	III	6.28**	6.90**	59.83	53.76	2.06	4.46
Grain yield/ plant	I	-4.11**	-27.61**	73.63	46.41	5.34	15.10
	II	-10.43**	25.41**	80.03	47.51	7.35	30.40
	III	7.79**	13.97**	54.46	49.48	5.63	20.94

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تقدير التباين التفوقى والتجميعي والسيادي في بعض هجن قمح الخبز

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أجرى هذا البحث فى محطة البحوث الزراعية بالجميزة فى ثلاثة مواسم زراعية هى ٢٠٠٧/٢٠٠٦و ٢٠٠٨/٢٠٠٧ و ٢٠٠٩/٢٠٠٨ بغرض دراسة قوة الهجين والكفاءة التوريثية بمعناها الواسع والضيق بالاضافة الى دراسة طبيعة ونوع الفعل الجينى المتحكم فى وراثة بعض الصفات الكمية فى بعض هجن القمح .

استخدمت في هذه الدراسة أربعة تراكيب وراثية من قمح الخبز ذات قاعدة وراثية عريضة وتم التهجين بينها لانتاج ثلاثة هجن هي (PBW 343 × سخا ٩٤ ، جميزة ٩ × سلالة سخا ، سخا ٩٤ × جميزة ٩) .

وجد أن التأثيرات الوراثية السيادية أعلى في قيمتها من التأثيرات الوراثية المضيفة فى الثلاث هجن موضحا أن تأثير الفعل السيادي كان يلعب الدور المهم فى وراثة الصفات تحت الدراسة بالإضافة إلى النوع المضيف .

أعطى الهجين جميزة ٩ × سلالة سخا معنوية عالية لكل من التأثير المضيف × المضيف ، المضيف × السيادي والسيادي × السيادي وبقيمة موجبة لصفات هي عدد الأيام حتى طرد السنابل وعدد السنابل / النبات مشيرا إلى أهمية التأثير التفوقى في وراثة هذه الصفات . من ناحية أخرى كانت القيم السالبة للتأثير المضيف × المضيف لصفتي عدد السنابل / النبات ومحصول الحبوب / النبات في الهجين الأول مما يشير إلى أن التراكيب المستعملة في هذه الدراسة بها اليلات ذات تأثيرات متناقصة مما يجعل تحسين هذه الصفات بالانتخاب في الأجيال المبكرة غير فعال .

أعطى الهجين الثاني أعلى قيمة سالبة لقوة الهجين لصفتي عدد الأيام حتى طرد السنابل والنضج (في اتجاه التبكير) بقيم متوسطة لكفاءة التوريث بمعناها الدقيق وبتحسين وراثي قدره ٥,٠٥ ، ٥,٣٩ يوم لكلا الصفتين على التوالي . أشارت أيضا النتائج إلى وجود قوة هجين معنوية وموجبة عند مقارنتها بالأب الأحسن لكل من صفات عدد الحبوب / السنبلة ووزن ١٠٠ حبة في الهجين الأول والثاني وعدد السنابل ووزن ١٠٠ حبة ومحصول الحبوب / النبات في الهجين الثالث .

قام بتحكيم البحث

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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 three wheat crosses for the studied traits.

Traits		**Cross I (P_1 x P_3)**						**Cross II (P_2 x P_4)**						**Cross III (P_3 x 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**
Days to heading	$\bar{x}$	103.50	97.46	100.00	101.62	101.00	102.62	107.00	94.50	100.33	90.80	99.67	87.33	101.50	96.00	105.67	97.30	102.67	99.67
	S^2	3.25	2.71	4.58	37.36	25.70	30.25	8.65	7.84	9.79	30.25	21.35	25.68	10.25	7.84	14.65	26.35	23.65	24.98
Days to maturity	$\bar{x}$	150.75	153.46	153.50	151.84	152.00	153.50	158.00	151.50	152.00	151.80	153.33	146.33	156.00	153.50	158.00	156.70	159.00	154.67
	S^2	1.57	2.34	4.53	27.89	18.95	20.36	3.54	2.34	3.98	36.45	28.94	28.16	3.54	2.34	4.53	27.89	18.95	20.36
Plant height	$\bar{x}$	113.55	122.66	118.23	112.33	113.71	115.18	114.27	111.18	121.40	122.14	124.93	121.66	108.72	111.51	114.74	110.89	114.09	110.77
	S^2	8.96	7.45	12.35	55.65	38.65	33.23	7.25	8.10	11.25	45.63	35.64	38.91	17.25	14.51	22.31	50.23	43.28	47.21
No. of spikes/ plant	$\bar{x}$	13.85	14.21	11.84	15.02	14.11	10.58	13.18	11.22	10.03	11.61	14.26	12.02	11.62	13.37	12.10	15.66	13.71	12.50
	S^2	2.35	1.53	3.24	17.65	13.54	12.36	5.23	6.20	10.23	41.23	33.61	29.64	7.25	7.41	8.94	30.28	21.54	26.47
No. of kernels/ spike	$\bar{x}$	67.00	70.50	73.65	69.05	71.21	72.73	74.36	83.88	83.93	61.30	72.67	65.53	78.47	74.17	71.50	72.04	77.10	71.07
	S^2	5.61	7.89	10.23	35.60	25.64	27.84	6.34	5.34	10.23	36.65	25.31	27.65	7.51	9.56	14.37	43.64	34.94	30.21
100– kernel weight	$\bar{x}$	5. 385	4. 636	5. 438	5. 227	5. 219	5. 192	4. 710	4. 970	5. 654	5. 895	5. 875	5. 895	4. 776	4. 665	4. 958	4. 616	4. 672	4. 927
	S^2	1.32	1.24	3.14	28.24	24.35	17.58	1.32	1.24	3.14	16.42	24.35	3.46	1.29	1.36	1.52	3.46	2.61	2.45
Grain yield/ plant	$\bar{x}$	28.93	36.45	27.74	35.40	30.50	25.16	36.16	25.06	32.39	24.16	30.84	27.84	29.02	25.36	31.28	26.91	31.23	22.73
	S^2	5.63	7.84	11.24	31.24	25.64	22.34	8.15	10.23	15.36	56.32	44.63	41.25	17.28	10.91	13.56	30.56	21.64	24.36

Cross I = P1x P3 (PBW 343 x Gemmeiza9)
Cross II = P2 x P4 (SAKHA 94 x Sakha line)
Cross III = P3 x P4 (Gemmeiza9 x Sakha line)

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

Traits	**Crosses**	**Scaling test**				***Gene action parameter**					
		A	**B**	**C**	**D**	**m**	**a**	**d**	**aa**	**ad**	**dd**
Days to heading	I	-1.50**	8.04**	5.52**	-0.51	101.62**	-1.75**	0.54	1.02*	-4.77**	-7.56**
	II	-7.99**	-20.17**	-38.96**	-5.40**	90.80**	12.34**	10.38**	10.80**	6.09**	17.36**
	III	-1.83**	-2.33**	-19.64**	-7.74**	97.30**	3.00**	22.40**	15.48**	0.25	-11.32**
Days to maturity	I	-0.25	0.04	-3.85**	-1.82**	151.84**	-1.50*	5.03**	3.64**	-0.14	-3.43**
	II	-3.34**	-10.84**	-6.30**	3.94**	151.80**	7.00**	-10.63**	-7.88**	3.75**	22.06**
	III	4.00**	-2.16**	1.30**	-0.27	156.70**	4.33**	3.79**	0.54	3.08**	-2.38**
Plant height	I	-4.36**	-10.53**	-23.35**	-4.23**	112.33**	-1.47*	8.59**	8.46**	3.08**	6.43**
	II	14.19**	10.74**	20.31**	-2.31**	122.14**	3.27**	13.30**	4.62**	1.73*	-29.55**
	III	4.72**	-4.71**	-6.15**	-3.08**	110.89**	3.32**	10.79**	6.16**	4.72**	-6.17**
No. of spikes/plant	I	2.53**	-4.89**	8.34**	5.35**	15.02**	3.53**	-12.89**	-10.70**	3.71**	13.06**
	II	5.31**	2.79**	1.98**	-3.06**	11.61**	2.24**	3.95**	6.12**	1.26*	-14.22**
	III	3.70**	-0.47	13.45**	5.11**	15.66**	1.21*	-10.62**	-10.22**	2.09**	6.99**
No. of kernels/ spike	I	1.77**	1.31**	-8.60**	-5.84**	69.05**	-1.52*	16.58**	11.68**	0.23	-14.76**
	II	-12.95**	-26.75**	-70.90**	-15.60**	61.30**	7.14**	41.01**	31.20**	6.90**	8.50**
	III	4.23**	-3.53**	-7.48**	-4.09**	72.04**	6.03**	3.36**	8.18**	3.88**	-8.88**
100–kernel weight	I	-3.85**	3.10**	0.11	0.43	52.27**	0.27	3.41**	-0.86	-3.48**	1.61*
	II	-2.08**	11.66**	25.92**	8.17**	58.95**	-8.17**	-8.20**	-16.34**	-6.87**	6.76**
	III	-3.90**	2.31**	-8.93**	-3.67**	46.16**	-2.55**	9.72**	7.34**	-3.11**	-5.75**
Grain yield/ plant	I	4.33**	-13.87**	20.74**	15.14**	35.40**	5.34**	-35.23**	-30.28**	9.10**	39.82**
	II	-6.87**	-1.77**	-29.36**	-10.36**	24.16**	3.00**	22.50**	20.72**	-2.55**	-12.08**
	III	2.16**	-11.45**	-9.57**	-0.14	26.91**	8.50**	4.24**	0.28	6.81**	9.01**

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