Estimate of Genetic Parameters Using Six Populations in Bread Wheat

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Abstract:

Six genotypes including first and second parents, first and second retrograde crosses with first and second generations of two wheat crosses, namely Sids 12 x Sakha 93 (cross 1) and Sids 1 x Sids 14 (cross 2) were established during three successive seasons of 2016/2017, 2017/2018 and 2018/2019 at the Experimental Farm of Faculty of Agriculture, Al-Azhar University, Assiut. obtained results showed that there were significant differences among the six populations mean of the current crosses for most studied traits, which provides the existence of genetic variation for these traits. The additive gene effects were significant for all studied traits, except for days to 50% heading and of 100-grains weight in cross 2 and number of spikes /plant in cross 1. The dominance gene effects were found to be significant and highly significant for most studied traits, except for days to 50% heading and number of kernels /spike in cross 2. The additive x additive type of gene effects was positive and highly significant for plant height and grain yield/plant in the two crosses and number of spikes/plant and weight of 100 grains in cross 2. High expected genetic advance was recorded in the second generation (F_2) for grain yield per plant in the two hybrids, indicated a continuous increase in variance. Through these studies, it can be recommended that early selection of these genotypes can be carried out to obtain a high yield.

Keywords: *Wheat, Six populations, Gene action, Heritability, Genetic advance.*

Introduction:

The first and main source of cereals in Egypt is the wheat crop *(Triticum aestivum* L.), which represents most of the nutritional value in the world at the general level and in Egypt on the private level. Wheat crop one of the most important food crops in the world and in Egypt. The production rate was about 701 to 741 million tons of wheat from 223 million hectares in 2011 and 2017 (FAO, 2019). One of the most important features of wheat grain for humans is that it provides half of the caloric needs, as well as gives a reasonable amount of protein, which is not insignificant. Therefore, it is described as the most important crop in the world, which is almost grown worldwide.

It was noted that the most important and best method that was feasible and most effective in the programs of wheat crop breeding is indirect selection, i.e. selection for traits that are associated with the crop, such as the number of spikes or the average weight of the grain. Increasing the yield and obtaining genotypes with distinct yields in yield per acre (Chandara *et al*., 2004). Results showed a high interactions effects between the different genetic components for studied traits. (Fathi and Mohamed, 2010). In this research, light was shed on the type of genetic action that controls on grain yield /plant and other traits, and the knowledge of the extent of genetic progression of the genotypes under study in bread wheat.

Materials and Methods:

This research was carried out during 2016/2017, 2017/2018 and 2018/2019 seasons in the experimental farm of the Faculty of Agriculture, Al-Azhar University, Assiut branch. Bread wheat (*Triticum aestivum* L.) were used for the following cultivars in the following table. The name, pedigree and origin of the parents are presented in (Table 1).

In the first season, grains of crosses was obtained by hybridization between two parents of each cross.

Table 1. The name, pedigree and origin of genotypes used in the two bread wheat crosses.

Cross		Parent	Pedigree	Origin
Cross 1	P1	Sids- 12	BUC//7C/ALD/5/MAYA74/0N//1160 Egypt/47/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL -//CMH74A.63014*SX.SD7096-4SD-1SD-1SD-0SD	Egypt
	P2	Sakha 93	SAKHA 92/ TR 810328:	Egypt
Cross 2	P1	Sids- 1	MRL/BUC/SER1	Egypt
	P2	Sids- 14	BOW"S"/Vee"S"//Bow"S"/TSI/3/Beni Sewef 1 SD293-1SD-2SD-4SD -Osd	Egypt

In the second season, some F_1 plants were crossed to their parents to produce BC_1 (F_1 X P_1) and BC_2 (F_1 X P_2) generations. It was also possible again to make more hybridization between the parents to increase the seeds of F_1. Also, some plants of the first generation were isolated to obtain the seeds of F_2 that are used to evaluate of all generations.

In the third season, the six clusters, i.e., F_1, F_2, P_1, P_2, BC_2 and BC_1 of the two hybrids were grown in a randomized complete block design with three replicates. Each replication consisted of 36 rows (12 rows for F_2, 6 rows for each BC_1 and BC_2 3 rows for each of rows P_1, P_2, and F_1). The row was 5.0 m long, the interval between them of 60 cm, and the plants were 20 cm apart. The recommended agricultural methods for wheat production were followed in all growing seasons.

Characters were evaluated using individual plants from the six groups (30 plants of P_1, P_2 and F_1; 60 plants for BC_1 and BC_2; and 120 plants of F_2). The following traits were recorded, Number of days to 50% heading, Plant height (cm), Number of spikes/plant, Number of grains/spike, Weight of 100 grains, g, and grain yield/plant, g.

Statistical and genetic analysis:

Genetic analysis was done using generation means. Scaling tests (A, B and C) were applied according Mather and Jinks (1982) to test the presence of non-allelic interaction as following:

$$A = 2 B_1 - P_1 - F_1$$
$$B = 2 B_2 - P_2 - F_1$$
$$C = 4 F_2 - 2 F_1 - P_1 - P_2$$

Those parameters of genetic model (m, a, h, aa, ad and dd) were estimated according to Jinks and Jones (1958) and Hayman (1958),

m= mean

a = additive effect = $B_1 - B_2$.

h =dominance effect = $4 F_2 -1/2 F_1 +1/2 P_2 -2 P_1 +2Bc_2 + 2Bc_1$.

aa= additive x additive gene interaction =$2Bc_1 + 2Bc_2 - 4F_2$.

ad = additive x dominance = $Bc_1 - 1/2 P_1 - Bc_2 + 1/2 P_2$.

dd = dominance x dominance = $P_1 + P_2 + 2F_1 + 4 F_2 - 4 Bc_1 - 4Bc_2$.

The genetic components of variance were calculated by the for-

mulas of F_2 variance obtained according to Mather and Jinks (1982) as:

E (environmental variance) = 1/3 (VP1 + VP2 + VF1)

D (additive variance) = 4 VF2 – 2 (VBC1 + VBC2)

H (dominance variance) = 4 (VF2 – 1/2VD - VE)

The significant of the genetic components were tested using the *t* test, where t = effect / (variance effect)$^{1/2}$

Heterosis:

Estimates of heterosis (%) were calculated as the percent deviation of F_1 mean performance from the mid-parent or better parent as follows:

Heterosis from the mid-parent % (M.P) = (F_1-MP) / MP × 100

Heterosis from the better-parent % (BP) = (F_1 – BP) / BP × 100

Inbreeding Depression (I. D %): its values measured from the following eqyation:

(I.D %) = (F_1-F_2 / F_1) × 100

Variances of I.D deviation = VF_1 + VF_2

T: I.D =F_1 + F_2 / (V.I.D)$^{0.5}$

Phenotypic and genotypic coefficients of variability were calculated as outlined by Burton (1952) as:

$$PCV = (\sqrt{VP} / \overline{X})100$$

$$GCV = (\sqrt{VG} / \overline{X})100$$

The average degree of dominance (ā): Was calculated by the formula presented by Mather and Jinks (1982):

$$\bar{a} = (H/D)^{1/2}$$

Complete dominance is considered when ā = + 1.0, partial dominance is indicated when is between $\pm$ 1.0, while, over-dominance is considered if lies the ratio exceeded $\pm$ 1.0. If degree of dominance value is equal to zero, it indicates the absence of dominance. The positive and negative signs indicate the direction of dominance.

Heritability:

Two estimates of heritability were presented:

Heritability in broad-sense (h^2b): was estimated according to the following formula presented by Mather and Jinks (1982):

% $h^2{}_b$ = (VG/VP) x100

Heritability in narrow-sense ($h^2{}_n$): it was estimated according to the following formula presented by Mather and Jinks (1982):

% $h^2{}_n$ = (1/2D /VP) x 100

Expected gain from selection (G.S):

The expected gain from selecting (G.S) was calculated according to Allard (1960):

G.S% = [(K x σ ph x $h^2{}_n$) / F_2] x 100.

Results and Dissection:

The mean values and standard error for the six generations were calculated for the two crosses for six traits and presented in Table 2. The results showed that there are significant differences among the mean of six populations in the two wheat crosses for all studied traits, which indicates the presence of the genes were well enough variation for all studied traits. Results showed that the average values of all parents were lower than for first generation, BC_1 and BC_2 for plant height, number of spike / plant, number of kernels / spike, weight of 100 grains and grain yield / plant in the two crosses, excluding 50% flowering of heading in both hybrids. The first backcrossed mean values were higher than the both parents in the two hybrids for number of spike / plant, weight of 100 grains and grain yield / plant ex-

cluding days to 50% heading, plant height and number of kernels / spike. The second backcrossed mean values were higher than the both parents in the two hybrids for number of spike / plant, number of kernels / spike and grain yield / plant, excluding days to 50% heading, plant height and weight of 100 grains. It became clear through the analysis that there is a high degree of genetic variation between the different hybrids. With excluding, plant height in the two crosses whereas the F_1 value was lower than in both parents. Similar results were obtained by Awaad (1996), Abd El-Rahman and Hammad, (2009), Zaazaa *et al,* (2012), Amin (2013) and El massry and El-Nahas (2018).

Table 2. Mean performance of parents, F_1, F_2, BC_1 and BC_2 generations in two bread wheat crosses for all studied traits.

Characters generation	Days to 50 heading	Plant height	No. spike/plant	No. kernels/spike	Wighet 100 - grains	Grain yield/plant
Cross 1(Sids 12 x Sakha 93)						
p_1	94.56±0.102	86.44±0.621	6.05±0.050	71.11±1.22	5.45±0.007	19.49±0644
p_2	99.85±0.302	96.14±0.444	6.89±0.017	68.33±0.432	6.11±0.010	17.55±0.506
F_1	85.12±0.353	98.56±0.412	8.52±0.056	77.87±1.77	5.16±0.156	27.75±0.819
F_2	98.95±0. 798	94.76±0.624	6.96±0.75	74.42±1.29	5.27±0.06	15.79±0.589
BC_1	88.55±0.678	85.75±0.675	7.77±0.055	68.26±1.83	6.22±0.008	20.29±0.429
BC_2	86.44±0.733	85.25±0.456	6.95±0.025	74.95±1.83	5.34±0.004	25.11±0.911
L. S.D.$_{0.05}$	1.89	1.72	0.937	2.542	0.496	1.787
Cross 2(Sids 1 x Sids 14)						
p_1	96.93±0.509	112.22±0.675	8.08±0.050	64.98±1.11	5.02±0.007	19.55±0431
p_2	94.76±0.342	109.34±0.54	7.13±0.313	68.45±1.27	5.19±0.13	26.75±0.439
F_1	90.55±0.413	119.88±0.545	11.17±0.898	77.89±0.545	5.98±0.123	32.77±1.44
F_2	90.76±0.989	111.88±0.121	8.56 ±0.343	76.99 ±1.98	5.64 ±0.085	27.49 ±0.729
BC_1	90.08±0.998	108.76± 0.434	9.43±0.452	64.58±1.62	5.28±0.089	28.71±0.459
BC_2	89.18±0.377	100.85±0.544	9.95±0.199	68.93±1.55	5.26±0.078	26.87±0.755
L. S.D.$_{0.05}$	1.93	1.87	1.22	2.98	0.829	1.79

Results of scaling test (A, B and C) together with the six parameters model and type of epistasis are calculated and given in Table (3) and revealed the presence of non-allelic interaction for all traits studied in both crosses. It is worthy to mention that at least one of the A, B and C tests were significant for all studied traits except, days to 50% heading and number of spike / plant in both crosses. It became clear through the results obtained from the analysis that the model of the six parameters is the best to clarify the gene action of the traits that were studied in this research. Also, when measuring factor, A, B and C, the value was weak, which makes it unimportant, which shows that the interactive model did not provide an explanation of the gene action. The results are in general agreement with those by Shafey *et al.* (1993), Tammam (2005), Kattab *et al.* (2010) and El-Aref *et al.* (2011) for number of spike / plant, number of kernels / spike and grain yield / plant and Moussa (2010) for days to 50% heading and plant height. On the other hand, Abd El-Rady (2018) obtained that the scaling test indicated the presence of non-allelic interaction for all studied traits except number of spike per plant in one cross, and grain yield / plant (g) in other crosses under normal conditions.

Gene effects:

The effect of genetic parameters for genes, which includes mean, additional influence, dominance, additional x dominant, and x dominant, was shown in Table 5. It was found through the results that the average in all the traits studied in the first and second crosses was significant, and considering the additional effect was significant, positive or negative, for all studied traits, except 50% of flowering to title, weight of 100 grains in hybrid 2, and the number of spikes/plant in hybrid 1 were not significant. It was found that the obtained results were in harmony with the publication of Abdul Rahman (2013). on the other hand to those results, it was found that the effect of host genes is not significant as found by Zaazaa *et al.* (2012). Days to 50%, the title and the number of grains / spike in cross 2, while it was positive and highly significant for the weight of 100 seeds and the yield of grains / plant in both crosses. By comparing between the additional effect and the dominance effect, it was found that the dominance effect is higher than the additional effect. This was in most of the traits, which showed that the best method of breeding is the pedigree method. These results are consistent with that of Khattab *et al.* (2010), Zaazaa *et al.* (2012) and Khaled (2013) on spike/plant count, kernel/spike count, weight 100 grains and grain yield/plant.

The values additive x additive (aa) type of gene effects were positive and highly significant for plant height, weight of 100 grains and grain yield / plant in both crosses. While it was negative and highly significant for number of kernels / for number of kernels / spike in the two crosses So, from the observations of the results, it can be conclude that there is possibility to select this traits i.e. weight of 1000 grains and the yield in the early generation. These results are in accordance with those El-Aref *et al.* (2011) and Amin (2013). On the other hand, Akhtar and Chowedry (2006) revealed that the negative additive x additive (aa) type of gene effects ‹were recorder for plant height and grain yield per plant. The parameters additive x dominance (ad) was significant and positive highly significant for days to 50% heading, plant height and weight of 100 grains in cross 1, while it was negative and highly significant were by obtained for grain yield / plant in the two crosses and days to plant height and number of kernels / spike in cross 2. The additive x dominance gene effects were not significant for days to 50% heading in cross 2 and number of spike / plant in the two crosses. Similar results have been reported by Abd El- Rahaman and Hammad (2009) for number of kerlines and kernel weight. The interaction between the dominant alleles was between them was significant or highly significant and positive in cross 1. for number of kernels / spike in cross 1 and number of number of spike / plant in two crosses. Similarly, Fethi and Mohamed (2010) found that the parameters dominance effects and third types epistatic dominance x dominance epistasis were more important than additive effects and other epistasis components for grains / spike. A significant or highly significant and negative dominance x dominance (dd) gene interactions

were obtained for plant height and 100- grain weight and days to 50% heading in the two hybrids and number of kernels / spike in cross 2. Also, the dominance x dominance (dd) gene effects were not significant for grain yield / plant in the two crosses. It can be said that it is possible to improve the superior population groups and these results came in agreement with those reported by El-Aref *et al.* (2011), and Amin (2013).

The type of epistasis was determined as complementary when dominance (d) and third type of epistatic effect dominance x dominance (dd) gene effects have same sign and duplicate epistasis when the sign was different. Thus, selection in the early generations is effective when the additive effects is greater than the non-additive effect, also, the non-additive portion are greater than additive, the improvement of the characters needs intensive selection through later generations. These results are in harmony with those reported by Kattab *et al.* (2010), Amin (2013) and Abd El- Rady (2018).

Heterosis, inbreeding depression (%) and phenotypic (PCV) and genotypic (GCV) coefficient of variation:

Heterosis, depression of inbreeding (%) and coefficient of phenotypic and genetic variance were shown in hexagonal wheat crosses, and this was calculated for all the traits under study in Table 4 by calculating the Heterosis that was calculated from the mean of the two parents and also calculated from the best parent. The Heterosis of the hybrid was positive and highly significant for the number of spikes per plant and grain yield per plant in both crosses, and in days up to 50% in the hybrid 1. On the other hand, it was significant and negative in the weight of 100 grains in the cross 1 and the height of the plant in the cross 2. The results obtained are in harmony with Kattab *et al.* (2010), Zaazaa *et al.* (2012), Abd Alla and Hassan (2012), Elmassry and El-Nahas (2018) and Kumar *et al.* (2018).

Table 3. The scaling test and estimates of the additive, dominance and interaction parameters in two bread wheat hybrids for all studied traits.

Character	Cross	Genetic parameter								
		A	B	C	M	a	H	Aa	Ad	dd
Days to 50 %heading	1	12.13** ±0.512	6.98** ±0.347	-5.43 ±0.234	**98.95**** **±0. 798**	8.76** ±0.121	24.76** ±1.59	21.88** ±1.17	9.99** ±0.54	-17.22** ±2.12
	2	2 ±0.123	-2.12 ±0.561	4.76 ±0.227	**90.55**** **±0.413**	2.44 ±0.822	7.81 ±0.114	4.21 ±0.532	3.78 ±0.421	-12.65** ±0.176
Plant height	1	8.99** ±0.990	3.66 ±0.129	-35.49** ±4.65	**94.76**** **±0.624**	5.99** ±0.188	19.65** ±3.11	31.88** ±3.15	9.99** ±0.54	-17.22** ±1.22
	2	-3.46 ±0.123	13.92** ±1.12	-4.64 ±2.134	**109.88**** **±0.545**	-9.16** ±0.909	12.56* ±3.43	14.53** ±2.01	-8.61** ±0.878	-25.26** ±3.88
Number of spikes/plant	1	-1.84 ±1.17	-12.25** ±1.02	2.05 ±1.09	**6.96**** **±0.75**	2.06 ±0.988	-4.56** ±0.323	-3.82** ±0.212	1.27 ±0.657	4.97** ±0.213
	2	2.43 ±1.05	4.54** ±0.321	-1.09 ±0.675	**11.17**** **±0.898**	-12.33** ±0.867	13.85** ±1.33	9.63** ±1.13	-2.12 ±0.962	14.55** ±1.65
Number of ker-nels/spike	1	7.29** ±0.00	22.19** ±0.00	45.62** ±0.00	**74.42**** **±1.29**	-7.03** ±0.00	-15.62** ±2.35	-18.46** ±0.00	8.51** ±0.00	-11.19** ±1.76
	2	15.21** ±2.36	-19.27** ±1.878	-11.96** ±1.12	**77.89**** **±0.545**	12.64** ±1.05	-6.75 ±3.77	-15.09** ±3.13	-17.19** ±1.231	19.36** ±1.48
Wighet of 100 -grains	1	2.024** ±0.765	-1.79 ±0.767	-3.41** ±0.123	**5.27**** **±0.06**	2.171** ±0.124	4.44** ±0.453	3.811** ±0.123	11.86** ±1.15	-4.52** ±0.989
	2	2.59** ±0.435	2.14 ±0.467	-2.21** ±0.102	**5.98**** **±0.123**	1.85 ±0.656	3.89** ±0.106	3.03** ±0.103	1.46* ±0.101	-5.75** ±0.294
Grain yield/plant	1	-6.76** ±0.344	3.67 ±0.677	-12.62* ±3.56	**15.79**** **±0.589**	-4.68** ±0.463	18.51** ±3.12	9.43** ±1.012	-5.17** ±0.565	-6.56 ±3.94
	2	4.82** ±0.348	-2.63 ±0.812	8.26** ±0.998	**32.77**** **±1.44**	-8.93** ±1.98	12.92** ±2.09	3.78** ±0.325	-5.46** ±0.128	-6.33 ±2.98

Concerning inbreeding depres-sion, the values were positive and highly significant for most traits in two hybrids, but, it was highly sig-nificant and negative for plant height in cross 1. However, these results the expected as the it was obtained that the heterogeneity in F_1 is followed by a significant decrease in F_2 due to homozygosity. The results are in harmony with those obtained by Zaazaa *et al.* (2012) and El massry and El- Nahas (2018) for number of spike / plant, number of kernels / spike and grain yield / plant and Moussa (2010) for days to heading. Kumar *et al.* (2018) found that significant inbreeding depression was

recorded frequently for yield and yield contributing traits.

The phenotypic coefficient (PCV) of variability values were higher than (GCV) for all traits stud-ied in the two crosses (Table 4). Re-sults indicated that the PCV and GCV values were much close, these re-vealed the major proportion of the observed variation was contributed by the genetic factor in additive ge-netic variance in most values for phe-notypic coefficient and genotypic co-efficient of variability. Therefore, these traits were highly affected by environmental factors. These results agreed with those obtained by Zaazaa *et al.* (2012).

Table 4. Heterosis, inbreeding depression %, phenotypic (PCV) and genotypic (GCV) co-efficient of variation in two bread wheat hybrids for all characters studied traits.

Characters	Crosses	Heterosis %		Inbreeding depression %	P.C.V %	G.C.V.%
		MP	BP			
Days to 50 % heading	1	23.51**	15.29**	14.05**	10.14	10.50
	2	-5.53*	-6.58*	-0.23	13.33	13.86
Plant height	1	7.96*	2.52	3.86**	10.75	11.52
	2	-5.91*	-9.36*	-11.83**	13.92	14.53
Number of spikes/plant	1	28.51**	18.17**	18.31**	58.29	61.82
	2	46.88**	38.24**	23.37**	49.27	54.17
Number of kernels/spike	1	11.69**	9.51*	4.43**	29.49	30.68
	2	12.53*	4.62	1.16	30.44	32.28
Wighet of 100 – grains	1	-10.73**	-15.55**	-2.13*	38.46	45.30
	2	8.63**	11.53**	5.45**	41.27	46.43
Grain yield/plant	1	49.86**	42.38**	43.10**	46.29	54.57
	2	41.56**	22.51**	16.11**	43.85	45.96

* & ** Significant and high Significant at 0.05 & 0.01 level of probabilities.

Genetic variance and of three parameters model:

Through the studied traits, the effect of the added genes was calculated and estimated, and the dominance effects of the genes were also calculated, and this was shown in Table (5). It was shown that the dominance genetic variance was more than the additional genetic variance in the two crosses, while the additional genetic variance was greater than the dominance for 50% of flowering and grain yield / plant in cross 1, where the increase of additive variance over dominance variance indicates that the effects of additive genes play a major role in the heritability of these traits and the use of early selection can be effective in identifying the strains that are characterized by high grain yield for these crosses under study. These results are consistent with what was published by Amina (2013) and Abdel-Radi (2018).

Also the results showed that the mean dominance score (H/D) 0.5 listed in Table (5) showed that partial dominant genetic effects were pre-sented for days to 50% flowering and grain yield/plant in hybrid 1. Amin (2013) found the same results. On the other hand, Abdullah and Mustafa (2011) found that the complete dominance was for the number of spikes/plant and weight of 100 grains in the first hybrid.

Heritability in the wide (Hb) and narrow (Hn) senses and genetic progression:

Estimates of heritability in the broad and narrow sense indicate that progress in the selection of plant traits. Where the higher it is, the easier and faster the choice, especially the degree of inheritance in the narrow sense in the breeding program. The degree of broad and narrow sense heritability and genetic progression are presented in Table 5. The wide and narrow sense heritability values were high for all traits studied in the first and second crosses and ranged from 71.96% for days to 50% in cross 1 to 93.39% for grain yield/plant in cross 1. Robinson *et al.* (1949) classified heritability values as low (0-30%), medium (30-60%) and

high (60% and above). The values of heritability in the narrow sense ranged from moderate to high in most traits, except for the plant height in hybrid 1 and the number of grains in the spike in cross 2, which confirmed that these traits were significantly affected by additive and non-additive effects and that these variances are heritable. In contrast, in traits where the degree of heritability is low, selection is difficult because the environmental impact is high. Our result agrees with Al-Arif *et al.* (2011), Amin (2013), Abdel-Radi (2018), Al-Masry and Al-Nahhas (2018), and Rania (2018) where they found that heritability in the broad sense was high values detected for all studied traits, which indicates that these traits are more heritable, while heritability in the narrow sense was low versus no. of spikes/plant crop and grain/plant, so the role of the extra part is low from calculating the expected genetic progression as a percentage of F_2 that ranged from 4.07 for plant height in cross 1 to 25.18 for grain yield per plant in cross 1 and ranged from 4.60 to weight of 100 seeds in cross 2. These values show that these traits can be improved. These results show the possibility of practicing selection in early generations and obtaining high-yielding genotypes. Moreover, the remaining traits for which values were found low we expect small genetic progression, indicating the role of environmental factors and the predominance of genetic action in the system of inheritance of these traits. These results are in agreement with Abdel-Radi (2018 and Shafey *et al.* (1993) and found that the highest genetic progression was obtained with respect to plant height, 1000 grain weight and grain/plant yield. On the other hand, Kuobisy (2011) stated that genetic progression was generally low for all traits studied in two hybrids.

Through these results, we will continue to improve the production capacity in some of these patterns by selecting for the traits of the wheat crop.

Table 5. Genetic variance, broad (H_b) and narrow (h_n) sense heritability and expected genetic advance (G. S%) for characters in two crosses.

Characters	crosses	Genetic variance			(H/D)1/2	Heritability		G.S%
		D	H	E		Hb	Hn	
Days to heading	1	93.76	6.99	7.13	0.27	93.39	43.46	8.18
	2	46.11	99.55	11.73	1.47	92.55	14.65	6.32
Plant height	1	10.82	92.98	15.42	2.93	87.07	4.54	4.07
	2	61.22	172.55	20.97	1.68	91.77	12.02	6.69
Number of spikes/plant	1	3.1	13.36	2.05	2.08	88.92	8.37	10.55
	2	5.24	25.05	6.32	2.19	82.74	7.16	14.05
Number of kernels/spike	1	158.77	322.77	39.72	1.43	92.38	15.23	11.31
	2	67.25	494.7	70.16	2.71	88.90	5.32	7.01
Wighet of 100 – grains	1	1.39	2.72	1.59	1.40	72.10	12.18	13.76
	2	2.24	3.85	1.618	1.31	79.01	14.53	4.6
Grain yield/plant	1	48.51	4.92	20.82	0.32	71.96	32.67	28.96
	2	61.8	144.72	20.33	1.53	91.04	13.62	25.18

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تقدير القياسات الوراثية باستخدام العشائر الستة في قمح الخبز

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الملخص

أجريت هذه الدراسة بالمزرعة التجريبية البحثية بكلية الزراعة جامعــة الأزهــر – فــرع أسيوط خلال ثلاثــة مواســم زراعيــة هــى 2016 /2017 و 2017/ 2018 و2018/ 2019 لدراسة قوة الهجين ونوع الفعل الجيني ودرجة السيادة ودرجة التوريـث والتحـسين الـوراثي المتوقع لعدد الايام حتى طرد 50% من السنابل – طول النبات – عدد السنابل علــى النبــات – عدد الحبوب على السنبلة – وزن 100 حبة – محصول الحبوب على النبات في هجينــين مــن قمح الخبز هما (سدس 12 x سخا93) و (سدس x1 سدس14).

1– أوضحت النتائج المتحصل عليها من تحليل التباين وجــود اختلافــات معنويــة بــين العشائر الوراثية تحت الدراسة لجميع الصفات في الهجينين كما لوحظ وجود تباين غيــر اليلــى لمعظم الحالات حيث كانت قيم الفعل الجينى المضيف وكذلك السيادي معنوية لمعظم القيم ما عدا بعض الحالات القليلة.

2– أظهر الفعل الجيني الإضافي معنوية لمعظم الصفات ماعدا صفة عدد الايام حتى طرد 50% من السنابل ووزن 100حبة في الهجين الثاني وصفة عدد السنابل على النبات في الهجـين الاول كما أظهر الفعل الجيني السيادي معنوية لمعظم الصفات ماعدا صفة عدد الايام حتى طرد 50% من السنابل وعدد الحبوب على السنبلة في الهجين الثانى.

3 – أظهر الفعل الجيني من (الإضافي x الإضافي) معنوية وموجب فــي طــول النبــات ومحصول الحبوب على النبات في الهجين الاول والثاني وكذلك عدد السنابل على النبــات ووزن 100 حبة في الهجين الثاني.

4– أعطت قيم التقدم الوراثي المتوقع قيم عالية كنسبة مئوية من الجيــل الثــاني لــصفة محصول الحبوب لكل نبات في كل من الهجينين وتشير هذه النتائج إلى إمكانية الحــصول علــى تراكيب وراثية عالية المحصول.