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GENETIC STUDIES ON GRAIN YIELD AND ITS COMPONENTS IN TWO BREAD WHEAT CROSSES

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ABSTRACT

This research was carried out at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, during the three growing seasons of 2013/14, 2014/15 and 2015/16 to estimate genetic variance components and type of gene action controlling the inheritance of yield and its component characters, using six-population model. Genetic materials used in this study included six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the two bread wheat crosses (Sakha 95 X Giza171) and (Sakha 95 X Line 1). Results revealed that, the mean effects (m) were highly significant for all characters in both crosses, indicating that these characters are quantitatively inherited. Also, the relative importance of additive and dominance effects varied with characters and crosses. The most predominant type of epistasis was additive X dominance (ad) and dominance X dominance (dd) in most characters, proving that these characters were greatly affected by these types of gene action. Broad-sense heritability values were high for all studied characters in both crosses, while narrow sense heritability, their values were ranged from low to moderate for the two crosses. Based on the obtained results, both crosses could be useful in the breeding program to develop promising lines. However, heritability and expected genetic advance from selection were higher in magnitude in the first cross (Shaka 95 X Giza 171), indicating that this cross could be more useful in isolating new promising lines and hence development of new cultivar(s) having high yielding ability.

Key words: ***Triticum aestivum*, Six Populations, Gene Action, Heritability, Grain Yield, Yield components.**

INTRODUCTION

Wheat is the leading cereal crop all over the world. In Egypt, there is a wide gap between wheat production and consumption. Thus, the main objective of the local breeding program is to increase yield production *via* developing new cultivars having high-yield potentiality and through using developed cultural practices.

Wheat breeders are always looking for new sources of promising genotypes to improve grain yield, its components and other agronomic characters. Therefore, the genetic diversity is very essential for breeders to create new developed promising genotypes.

A better understanding of the inheritance and type of gene action for grain yield characters would help wheat breeders to increase and stabilize grain yield.

Wheat grain yield is determined by cultivar ability through several yield components such as, number of spikes per unit area, number of grains per spike and grain weight (Ahmedi and Bajelan 2008, Mohsin *et al* 2009, Al-Naggar and Shehab-Eldeen 2012, Sial *et al* 2013 and Sharshar and Esmail 2019.)

Good information and understanding of the genetics and gene effects of breeding materials will lead to good selection and better genetic improvements. The maximum progress through selection program could be activated when additive gene action plays the main role of the genetic variance. Mainwhile, the non-additive gene action would be useful in the hybridization program for improving these characters. In the context, many genetic models to study the genetics and gene action were introduced by Mather (1949), Hayman and Mather (1955), Gamble (1962), and Mather and Jinkes (1971).

The present investigation aimed to recognize the type of gene action and to estimate some genetic parameters in two spring bread wheat crosses using the six population model and hence, to use these materials in the national wheat breeding program, to develop new promising cultivars.

MATERIALS AND METHODS

This investigation was carried out through the three wheat successive growing seasons from 2013/2014 to 2015/2016, at Sakha Agricultural Research Station, Agricultural Research Center (ARC), Egypt, to study the genetic behavior of grain yield and its components in two bread wheat crosses. The names, pedigree and selection history of the three studied parental genotypes are presented in Table (1).

Table 1. Name, pedigree and selection history of the three parental bread wheat genotypes.

Parent	Parent name	Pedigree and selection history
1	Sakha 95	PASTOR//SITE/MO /3/ CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/4/WBLL1. CMA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.
2	Giza 171	SAKHA 93/GEMMEIZA 9 S.6-1GZ-4GZ-1GZ-2GZ-0S.
3	Line 1	SAKHA8/YECORA ROJO

At the first season (2013/14), the new wheat cultivar Sakha 95 was crossed to both Giza 171 and Line 1.

In the next season (2014/15), the obtained F_1 hybrid seeds of each cross were separately sown to produce F_1 plants. Part of these plants were back crossed to each of their respective parents. Seeds of the two backcrosses (BC_1 and BC_2) were obtained. The rest of F_1 plants were left for self pollination to produce F_2 seeds.

In the third season (2015/2016), the obtained seeds of the six populations, i.e. P_1, P_2, F_1, F_2, BC_1 and BC_2 each cross were sown in a randomized complete blocks design with three replicates. Each replicate consisted of 20 rows (one row for each of $P_{1,}$ P_2 and F_1, four rows for each of $BC_1$and BC_2 and nine rows for each F_2). Each row was 4 m in length and 30 cm apart while grains were 20 cm apart. To avoid the border effects, two additional border rows were planted.

Recorded data

Data were recorded on 30 individual guarded plants for F_1, 45 plants for P_1 and P_2, 75 plants for BC_1 and BC_2 and 300 plants for the F_2 collected from all of the three replications for each cross.

The following characters were recorded:

1- Spikes/plant (S/P): Number of spikes per plant.
2- Kernels/spike (K/S): Number of grains per spike.
3- Kernel weight (KW) in g: recorded as a weight of 100 grains randomly taken from each plant.
4- Grain yield/plant (GY/P) in g: recorded by weighing the grains of each individual plant.

Heterosis was estimated as the percent of the deviation of F_1 hybrid over its mid-parent (MP) and better parent (BP) value. Inbreeding depression was also estimated as the average percentage decrease of the F_2 from the F_1. Moreover, potence ratio (P) was calculated using the formula proposed by Peter and Frey (1966).

The population means and the variances were used to compute the scaling tests A, B and C and to determine the type of gene effects according to Mather (1949) and Hayman and Mather (1955).

The six parameter model introduced by Gamble (1962) was used to estimate different gene effects. Furthermore, heritability in broad and narrow senses were calculated according to Mather (1949) and the predicted genetic advance under selection was calculated according to Johnson *et al* (1955).

RESULTS AND DISCUSSION

Means and variances of P_1, P_2, F_1, F_2, BC_1 and BC_2 populations of the two wheat crosses for all studied characters (yield and yield components) are presented in Table (2).

Data presented in Table (2) showed that the F_1 generation mean values lied between P_1 and P_2 mean values in the two crosses, indicating partial dominance for grain yield and yield components characters in the two crosses, except for grain yield in the first cross (Sakha 95 X Giza 171)

Mean of F_2 generation for all characters was intermited between the two parents in both crosses except for spikes/ plant in the second cross and 100-kernel weight in the first cross indicating that these traits are quantitatively inherited. Similar results were obtained by Sharshar and Esmail (2019) and Shehab-Eldeen and Abou-Zeid (2020).

In general, means of BC_1 plants were close to those of their respective female parents and means of BC_2 plants were close to their respective male parents for all traits in the two studied crosses, except for spikes/plant and kernels/spike in cross II (Sakha 95 X Line 1). These results are in harmony with the results obtained by Gad (2010), Al-Naggar *et al* (2012), Sharshar and Esmail (2019) and Shehab-Eldeen and Abou-Zeid (2020).

The highest magnitude of variance was reported by the F_2 generation for all studied characters followed by those of backcross generations.

On the other hand, the lowest variance magnitude was manifested by parents and F_1 populations which is also expected from the breeder point of view due to the homogeneity of such populations. So, variances observed in these populations (P_1, P_2 and F_1) are due to the environmental factors. These results are matching with those of Al-Naggar and Shehab-Eldeen (2012), Sharshar and Esmail (2019) and Shehab-Eldeen and Abou-Zeid (2020).

Table 2. Means ($\bar{X}$) and variances (S_2) of P1, P2, F_1, F_2, BC_1 and BC_2 populations of the two wheat crosses for studied characters.

Characters	Crosses	Statistical parameters	P_1	P_2	F_1	F_2	BC_1	BC_2	LSD 0.05
Spikes/ plant	**Sakha 95 x Giza 171**	$\bar{X}$	**27.89**	**20.04**	**24.40**	**22.52**	**23.76**	**18.49**	**3.8**
		S^2	**5.56**	**3.12**	**7.73**	**63.60**	**56.13**	**46.55**	
	Sakha 95 x Line 1	$\bar{X}$	**27.89**	**21.28**	**22.36**	**28.08**	**24.93**	**25.97**	**3.4**
		S^2	**5.56**	**12.92**	**9.57**	**88.53**	**74.44**	**73.20**	
Kernels/ Spikes	**Sakha 95 x Giza 171**	$\bar{X}$	**54.89**	**44.00**	**50.95**	**49.40**	**47.83**	**48.00**	**6.4**
		S^2	**29.54**	**10.38**	**28.27**	**209.20**	**161.28**	**173.36**	
	Sakha 95 x Line 1	$\bar{X}$	**54.89**	**35.91**	**46.40**	**41.75**	**37.29**	**41.24**	**5.5**
		S^2	**29.54**	**24.85**	**36.09**	**203.71**	**181.48**	**175.91**	
100-kernel weight (g)	**Sakha 95 x Giza 171**	$\bar{X}$	**4.01**	**3.57**	**3.91**	**4.05**	**4.02**	**4.40**	**0.38**
		S^2	**0.12**	**0.03**	**0.07**	**1.52**	**1.07**	**1.49**	
	Sakha 95 x Line 1	$\bar{X}$	**4.01**	**2.82**	**3.06**	**3.34**	**3.48**	**3.04**	**0.27**
		S^2	**0.12**	**0.04**	**0.10**	**1.12**	**0.83**	**1.06**	
Grain yield plants	**Sakha 95 x Giza 171**	$\bar{X}$	**40.10**	**36.65**	**40.85**	**38.5**	**39.85**	**32.94**	**3.1**
		S^2	**23.50**	**14.96**	**15.12**	**254.16**	**220.20**	**194.33**	
	Sakha 95 x Line 1	$\bar{X}$	**40.10**	**20.00**	**33.30**	**27.40**	**33.95**	**25.33**	**3.0**
		S^2	**23.50**	**27.30**	**29.10**	**182.67**	**161.26**	**152.04**	

Gene effects

The application of the scaling test (Table 3) showed that at least one of the scales A, B and C tests was significant (except for 100-kernel weight in the second cross), proving the presence of epistasis and indicating that using the six parameter model to detect different genetic components is valid for the two wheat crosses and studied characters.

Estimates of gene effects calculated from the generation mean analysis of the two wheat crosses for the studied characters are presented in Table (3).

Both studied crosses exhibited highly significant mean effects (m) for all studied characters indicating that these characters were quantitatively inherited. These results are in harmony with those reported by Hendawy (1998), Afiah (1999) and Sharshar (2015), El-Seidy *et al.* (2017), Sharshar and Esmail (2019), Shehab-Eldeen *et al.* (2020) and Shehab-Eldeen and Abou-Zied (2020).

Table 3. Estimates of scaling test and gene effects for all the studied traits in the two wheat crosses.

Characters	Crosses	Scaling test			Gene effects					
		A	B	C	(m)	(a)	(d)	(aa)	(ad)	(dd)
Spikes/ plant	Sakha 95 x Giza 171	-4.77*	-7.46**	-6.65**	22.52**	5.27**	-5.15*	-5.58	1.35	17.81**
	Sakha 95 x Line 1	-0.39	8.30**	18.43**	28.08**	-1.04	-12.75**	-10.52**	-4.35**	2.61
Kernels/ Spikes	Sakha 95 x Giza 171	-10.09**	1.05	-3.10	49.40**	-0.17	-4.39	-5.94	-5.57**	14.98
	Sakha 95 x Line 1	-26.77**	0.17	-16.51**	41.75**	-3.95	-8.94	-9.94	-13.40**	36.39**
100-kernel weight (g)	Sakha 95 x Giza 171	0.12	1.32**	0.79*	4.05**	-0.38*	0.76	0.64	-0.6**	-2.08**
	Sakha 95 x Line 1	-0.11	0.2	0.41	3.34**	0.44**	-0.68	-	-	-
Grain yield/ plant	Sakha 95 x Giza 171	-1.25	-11.62**	-4.45	38.50**	6.91**	-5.95	-8.42**	5.19*	21.29*
	Sakha 95 x Line 1	-5.50	-2.64	-17.10**	27.40**	8.62**	12.21*	-8.96	-1.43	-0.82

a = additive, d =dominance and m = mean effects, *and ** = significant at 0.05 and 0.01 probability levels, respectively

Additive (a) gene effects were highly significant and positive for spikes/plant in the first cross, 100-kernel weight in the second cross and for grain yield in both crosses. This indicates an enhancing effect due to this type of gene action (additive) in the inheritance of such characters and hence suggesting the possibility of obtaining further improvements of this characters using pedigree selection program. Similar findings are reported by Al-Naggar and Shehab-Eldeen (2012), Hammam (2013), Abd El-Aty *et al* (2014) and Patel *et al* (2018) and Sharshar and Esmail (2019).

The estimates of dominance (d) effects were negatively significant and negatively highly significant for spikes/plants in cross I and in cross II respectively. On the other hand, positive significant estimates of dominance appears in Cross II for grain yield, indicating the importance of dominance gene effects in the inheritance of these characters for these crosses.

Highly significant and negative additive X additive (aa) gene effects were detected in the second cross (Sakha 95 X Line 1) for spikes/plant and in the first cross (Sakha 95 X Giza 171) for grain yield. On the other hand, there were highly significant and negative additive X dominance (ad) gene effects for spikes/ plant in cross II, for kernels/spikes in both crosses and for 100-kernel weight in cross I. Meanwhile, significant and positive (ad) effects appeared in first cross for grain yield, indicating enhancing effects due to (ad) in the inheritance of grain yield of the first cross.

In addition, highly significant and negative dominance X dominance (dd) appeared in cross I for 100-kernel weight. On the other side, highly significant and positive gene effects (dominance X dominance) appeared in the first cross for spikes/plant and in the second cross for kernels/spikes. The significance and positive (dd) effects appeared in the first cross for grain yield, reflecting enhancing effects due to dd type of epistasis in the inheritance of these characters.

Results also showed that epistasis played an important role in most of the inheritance of these characters.

These results are in general agreement with those obtained by Al-Naggar and Shehab-Eldeen (2012), El-Seidy *et al* (2017), Khilwat *et al* (2019), Yassin and Gareeb (2019), Sharshar and Esmail (2019) and Shehab-Eldeen *et al* (2020).

Heterosis, inbreeding depression and potence ratio

Table (4) shows highly significant and heterosis positive values relative to mid parents in both crosses for all characters, except for spikes/plant in cross II (Sakha 95 X Line 1).

Table 4 Heterosis (%) relative to mid-parent (MP) and better parent (BP), inbreeding depression (ID %) and potence ratio (PR) for studied traits of the two wheat crosses.

Trait	Crosses	Heterosis MP	Heterosis BP	Inbreeding depression ID%	Potence ratio (PR)
Spikes/ plant	Sakha 95 x Giza 171	1.82**	-12.51**	7.69**	0.11
	Sakha 95 x Line 1	-9.05**	-19.82**	-25.6**	-0.67
Kernels/ Spikes	Sakha 95 x Giza 171	3.03**	-7.19**	3.05*	0.28
	Sakha 95 x Line 1	2.20*	-15.47**	10.02**	0.11
100-kernel weight (g)	Sakha 95 x Giza 171	3.21**	-2.43**	-3.46**	0.56
	Sakha 95 x Line 1	2.71**	-12.5**	12.82**	0.16
Grain yield	Sakha 95 x Giza 171	6.45**	1.87**	5.75**	1.43
	Sakha 95 x Line 1	10.82**	-16.96**	17.72**	0.32

***and **= significant at 0.05 and 0.01 probability levels, respectively**

For better parent heterosis, highly significant and negative values were found in all crosses for all traits, except for grain yield/plant, in first cross (Sakha 95 X Giza 171) where its better parent heterosis value was highly significant and positive. These results are similar to the earlier results reported by Zaazaa *et al* (2012), Hammam (2013), Abd El-Aty *et al* (2014), Sharshar and Esmail (2019) and Shehab-Eldeen *et al* (2020).

Inbreeding depression (ID) values were highly significant and positive in both crosses for all characters, except for spikes/plant in the second cross and for 100-kernel weight in the first cross, where their ID values was negative and significant. Negative inbreeding depression indicates the existence of transgressive segregants in the F_2 and segregating generations.

Potence ratio values were less than unity and positive in both crosses for all characters, except for spikes/plant in the second cross which was less than unity and negative, indicating the presence of partial dominance in the inheritance of these characters. On the other side, inbreeding depression in cross I (Sakha 95 X Giza 171) for grain yield was positive and more than unity, indicating the presence of overdominance controlling the inheritance of this character. The obtained results are matching with those of Al-Naggar *et al* (2012), Abd El-Aty *et al* (2014), Mansour (2016), El-Seidy *et al* (2017) and Sharshar and Esmail (2019).

Heritability and percentage of genetic advance:

Estimates of heritability in the broad sense as shown in (Table 5) were high in magnitude for all characters in both crosses. These results were in agreement with those of Mansour (2016), Reena *et* a*l* (2018), Sharshar and Esmail (2019), Shehab-Eldeen *et al* (2020) and Shehab-Eldeen and Abou-Zied (2020).

Table 5. Heritability% in the broad (h^2_b) and narrow (h^2_n) sense and expected genetic advance from selection for the studied traits in the two wheat crosses.

Traits	Crosses	Heritability		Genetic advance	
		h^2 (b)	h^2 (n)	Δg	Δg%
Spikes/ Plant	**Sakha 95 x Giza 171**	**90.51**	**38.55**	**6.33**	**28.12**
	Sakha 95 x Line 1	**89.37**	**33.23**	**6.44**	**22.93**
Kernels/ Spikes	**Sakha 95 x Giza 171**	**88.47**	**40.04**	**11.93**	**24.15**
	Sakha 95 x Line 1	**84.47**	**24.56**	**7.22**	**17.30**
100-kernel weight (g)	**Sakha 95 x Giza 171**	**95.14**	**32.09**	**0.82**	**20.14**
	Sakha 95 x Line 1	**92.00**	**30.60**	**0.67**	**19.95**
Grain yield/plant	**Sakha 95 x Giza 171**	**93.24**	**36.90**	**12.12**	**29.22**
	Sakha 95 x Line 1	**85.08**	**28.49**	**7.93**	**28.94**

Δg% = Genetic advance as a percent of the mean.

On the other side, heritability estimates in the narrow sense were low to moderate for all studied traits in both crosses, and ranged from 24.56% in the second cross for kernels/spikes to 40.04% in the first cross for the same trait, indicating that these characters greatly affected by non-additive gene action and environmental effects suggesting that the inheritance is complex. These results are in agreement with those obtained by Abd El-Aty (2002), Salama (2002), El-Seidy *et al* (2017), Sharshar and Esmail (2019), Shehab-Eldeen *et al* (2020) and Shehab-Eldeen and Abou-Zied (2020).

It is worthy to note that the expected genetic advance Δ g estimates for grain yield, in both crosses were moderate. Thus, selecting desirable genotypes in the early generations may be useful, but it will be effective in later ones.

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دراسات وراثية على محصول الحبوب ومكوناته في هجينين من قمح الخبز.

مصطفى تاج الدين شهاب الدين

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

أجريت هذه الدراسة بمزرعة محطة البحوث الزراعية بسخا- كفرالشيخ خلال المواسم الثلاثة ٢٠١٣/٢٠١٤، ٢٠١٤/٢٠١٥ و ٢٠١٥/٢٠١٦ لدراسة مكونات التباين الوراثى وتأثير الفعل الجينى المتحكم في توريث صفات محصول الحبوب ومكوناته لهجينين من قمح الخبز (سخا ٩٥ X جيزة ١٧١) و (سخا ٩٥ X سلالة ١) باستخدام نظام العشائر الست (الأب الأول, الأب الثانى, الجيل الأول, الجيل الثانى, الهجين الرجعى الأول و الهجين الرجعى الثانى). أظهرت النتائج أن الفروق بين متوسطات الأجيال كانت عالية المعنوية بالنسبة لكل الصفات فى كلا الهجينين. كما أوضحت النتائج أهمية تأثيرات كل من الفعل الوراثى المضيف والسيادى والتى اختلفت تبعا للصفات والهجن. وكان للفعل الجيني المضيف X السيادي و السيادي X السيادي تأثير واضح واكبر من الفعل الجيني المضيف X المضيف في أغلب الصفات المدروسة. كما كانت قيم كفاءة التوريث بالمعنى الواسع مرتفعة فى كل الصفات لكلا الهجينين أما كفاءة التوريث بالمعنى الضيق تراوحت القيم من منخفضة إلى متوسطة لكلا الهجينين في كل الصفات محل الدراسة. وكان كلا الهجينين مبشرا ويمكن الاستفادة منه ويمكن الحصول من أجيالهم الانعزالية على سلالات متميزة، كما كانت قيم كفاءة التوريث و التحسين الوراثي المتوقع من الانتخاب في الهجين سخا ٩٥ X جيزة ١٧١ اعلى من نظيرتها في الهجين الآخر واستنادا على هذا، يمكن الاستفادة من هذين الهجينين وخاصة الهجين الأول في برامج التربية للحصول على سلالات متفوقة ومن ثم الحصول على صنف او أصناف ذات قدرة انتاجية عالية في المحصول من الحبوب.

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