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ESTIMATION OF GENETIC PARAMETERS IN THREE BREAD WHEAT CROSSES

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ABSTRACT: *Four genotypes of bread wheat (Triticum aestivum L.) , i. e. Sakha 93, Giza 163, Gemmeiza 9 and Line1 were crossed to produce three crosses, Sakha 93 x Line1, Line1x Giza 163 and Giza 163 x Gemmeiza 9 to determine some genetic parameters in the five populations P_1, P_2, F_1, F_2 and F_3 model the genetic parameters were determined for number of days to heading and maturity, plant height, number of spikes per plant, number of kernels per spike, 100-kernel weight and grain yield per plant. The experiments were carried out at Sakha Agricultural Research Station in four seasons during 2007/2008 to 2010/2011. Data revealed the presence of highly significant differences among crosses, among populations, and among populations within each cross for all studied characters. The calculated values of C and D scaling tests for all studied characters in the three crosses were significant, except for grain yield per plant in the second cross. The additive and non- additive gene effects were found important in controlling the inheritance of most studied characters. High heritability values in broad- sense were detected for all studied characters in the three crosses. However, high values of narrow- sense heritability were detected for days to heading and maturity in the three crosses. The expected genetic advance estimates, in the F_2 generation were low for 100-kernel weight in three crosses, while, showed high values for number of kernels per spike in the second and third crosses, and grain yield per plant in the first and second crosses. Significant negative heterosis to earlier parent was detected for days to heading and maturity in the third cross. Significant positive heterosis was detected for grain yield per plant in the three crosses.*

Key words: *Wheat, genetic parameters, yield and yield components, heritability, heterosis*

INTRODUCTION

The success in breeding program depends on the magnitude of variability in available germplasm characters along with efficient management and utilization. Progress in crops varietal improvement has been slow due to lack of imagination ,vision and efficiency in assessing the components of genetic variation for various quantitative traits (Amawate and Behl 1995). The importance of wheat is increasing day by day due to increased human need pressure in the Egypt. An understanding of genetic factors controlling characters of yield and its components is a primary step for successful breeding studies. The mode of inheritance and the type of gene action for traits related to grain yield would direct wheat breeders for increasing and stabilizing this character. Additive x additive gene effects were significant for days to heading and grain yield/plant (Abd El-Kreem (2012) and Hamam (2013)). The additive, dominance and epistatic gene effects were important in controlling the inheritance of number of kernels per spike and grain yield (Abd El-Rahman and Hammad 2009). Traits that has high heritability and show high expected genetic advance might be substantially considered in selection programs, since, those traits are mainly influenced by the major effects of additive gene. The main objective of the recent study was to elucidate the breeding value of three crosses that could be utilized in breeding program for wheat yield improvement. This objective includes the study of the genetic variance, type of gene action, heritability, heterosis and expected genetic advance for some yield and agronomic characters.

MATERIALS AND METHODS

The present study was carried out at the experimental farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, through the period from 2007/2008 to

2010/2011. Four diverse bread wheat cultivars and Lines were selected and used for this study, names and pedigrees are presented in Table (1).

In 2007/08 season, the parental genotypes were crossed to obtain F_1 hybrid seeds of three crosses. viz. Sakha 93/ Line 1, Line 1/ Giza 163 and Giza 163/ Gemmeiza 9. In 2008/09 season, F_1 hybrid seeds were sown to produce the F_2 seeds of the three crosses. In 2009/10 season F_1 and F_2 for each cross were grown in order to obtain F_2 and F_3 seeds. Moreover, the four parents were planted and the same crosses were repeated to obtain additional and fresh F_1 seeds. An evaluation experiment was carried out in 2010/11 season. The experiment included the five populations (P_1, P_2, F_1, F_2, and F_3) of each cross planted in the third week of November a using randomized complete block design with three replications. The plots were rows of 3. 0 m long spaced 30cm apart and seeds were spaced 20 cm within the row for each cross, one row was planted for each of parent and F_1, while 6 and 20 rows were devoted for each of F_2 generation and F_3 families, respectively. Data were recorded on individual guarded plants for days to heading and maturity, plant height, number (No.) of kernels/spike, number (No.) of spikes/plant, 100-grain weight (g) and grain yield/plant (g). Simple scaling tests (C and D) were applied according to Mather and Jinks (1982) formula to test the presence of non- allelic interactions. According to the methodology of Gamble (1962), the following notation for gene effects have been used: additive (a), dominance (d), additive × additive (aa), dominance × dominance (dd) effect.

The type of epistasis was determined only when dominance (d) and dominance × dominance (dd) effects were significant. The heritability in broad- sense (h^2_b) and narrow- sense (h^2_n), and the value of heterosis (expressed as the performance of F_1's over better parent) values were estimated according to Mather and Jinks (1982). The expected genetic gain resulting from selection in a character (GS %) was computed by the formula reported by Allard (1960).

RESULTS AND DISCUSSION

The observed values of all population means with their variance in the three crosses for the studied traits are given in Table (2). Parental differences, in response to their genetic background, were significant in most characters under investigation.

Table 1. Name and pedigree of the four parental wheat genotypes

Genotype	Pedigree
Sakha 93	Sakha 92/ TR 810328 S 8871-1S-2S-1S-0S
Gemmeiza 9	Ald "S" / Huac // Cmh 74A. 30 / Sx CGM 4583-5GM-1GM-0GM
Giza 163	T.aestivum/Bon//Cno/7c.
Line 1	SAKHA 93 /3/ VEE / PJN // 2*KAUZ S.14954-4S-1S-1S-1S-0S

Table 2. Values of all generation means with their variance on the three crosses for the studied traits.

Characters /Crosses		Statistical Paramete				
		P_1	P_2	F_1	F_2	F_3
Days to heading						
	$\bar{X}$	93.20	79.57	88.63	82.34	85.71
1	S^2	1.13	0.60	0.72	31.81	27.11
	$\bar{X}$	79.57	117.00	97.87	95.45	97.13
2	S^2	0.60	0.68	0.53	78.20	56.50
	$\bar{X}$	117.00	107.15	109.80	109.74	113.40
3	S^2	0.68	2.03	0.98	42.62	52.07
Days to maturity						
	$\bar{X}$	147.27	146.20	146.73	147.48	146.83
1	S^2	1.10	0.58	0.62	8.44	7.29
	$\bar{X}$	146.20	157.73	149.73	150.29	152.36
2	S^2	0.58	0.68	0.48	20.81	16.47
	$\bar{X}$	157.73	154.80	155.85	156.95	165.82
3	S^2	0.68	0.59	0.56	46.71	37.34
plant height						
	$\bar{X}$	93.50	103.17	96.00	103.95	105.40
1	S^2	5.43	6.01	4.14	51.40	43.06
	$\bar{X}$	103.17	117.83	117.00	111.27	107.62
2	S^2	6.01	11.52	6.21	116.16	95.88
	$\bar{X}$	117.83	112.00	123.00	122.25	126.13
3	S^2	11.52	8.95	6.32	135.62	165.69
No. of spikes/ plant						
	$\bar{X}$	22.77	17.63	15.27	17.32	17.29
1	S2	3.98	7.14	3.79	24.67	16.15
	$\bar{X}$	17.63	21.93	19.70	17.12	18.88
2	S2	7.14	9.10	9.67	54.56	38.95
	$\bar{X}$	21.93	19.15	20.10	16.76	19.36
3	S2	9.10	7.50	8.41	46.00	38.21
No. of kernels/ spike						
	$\bar{X}$	55.07	55.10	66.23	57.44	58.33
1	S2	17.79	11.61	16.87	127.87	112.82
	X	55.10	59.67	60.33	50.50	49.57
2	S2	11.61	33.95	23.33	241.44	197.52
	$\bar{X}$	59.67	68.50	64.20	56.89	50.48
3	S2	33.95	13.95	47.85	281.18	341.22
100-kernel weight						
	$\bar{X}$	4.74	5.55	5.55	5.39	5.49
1	S2	0.07	0.12	0.12	0.61	0.47
	$\bar{X}$	5.55	3.80	5.80	4.98	4.90
2	S2	0.12	0.07	0.06	1.19	0.83
	$\bar{X}$	3.80	4.77	5.22	4.75	4.76
3	S2	0.07	0.09	0.06	0.90	0.74
grain yield per plant						
	$\bar{X}$	45.31	39.77	51.21	39.31	39.39
1	S2	11.27	10.32	9.08	227.74	175.68
	$\bar{X}$	39.77	33.07	45.07	42.08	40.75
2	S2	10.32	32.00	17.53	375.08	240.76
	$\bar{X}$	33.07	47.86	50.82	35.76	34.81
3	S2	32.00	19.85	25.45	209.70	138.77

F_1 values were between the vales of its two parents for some characters ,while were higher than its better parent for cross three for plant height, cross one and two for No. of kernels/spike, Crosse two and three for 100-grain weight and the three crosses for grain yield/plant, these results indicated the presence of partial and over dominance effects, respectively. The variance of the F_2 populations was higher than that of F_3, F_1 and parents for most of the studied traits. Transgressive segregation in F_2 generation has been recorded for most of the traits as the mean values of F_2 progenies was found higher than parental means (maturity, plant height, No. of kernels/spike and grain yield/plant) or lower than the parental means (plant height, No. of spikes/plant and No. of kernels/spike).. Similar trend was previously reported by Mahgoub and Hammad(2006) and Abdel-Aal (2011).

Scaling test

One or both C and D scaling tests were found significant for all the three crosses providing non allelic interaction for inheritance of all the studied traits (Table 3). The simple scaling test (C and D) was used to detect the presence of non-allelic interaction. Significance of any component of the epistatic scales indicates the presence of non-allelic interactions amongest the genes controlling traits. The C and D scaling test for most of the crosses and traits showed that at least one or both were found significant indicating the presence of non allelic interaction in the inheritance of the traits under study. However, non significant values for both C and D scales in cross 2 for grain yield per plant indicate non interacting mode of inheritance. In the mane time the parameters C and D showed significance for the different traits, indicating the adequacy of the five parameters as a model to explain the type of gene action controlling the traits of these crosses. These results are in agreement with those obtained by Abd El-Aty and Katta (2007) and Saint Pierre *et al.* (2010).

Types of gene action:

Types of gene action for the studied characters in the three crosses are presented in Table (3). For all studied traits, the mean parameters (m) effect was significant in the three crosses, for all studied traits, indicating the potentiality of improving prformace of these traites by using pedigree selection program.

The additive gene effect (a) was highly significantly for all characters in the three crosses, except cross one for number of kernels/spike. The additive gene effect (a) was highly significantly and positive for days to heading and maturity, number of spikes/plant in the first and third cross. Also, plant height in the third cross, 100-kernel weight in the second cross and grain yield/plant in the first and second crosses. While, it was significant and negative for days to heading and maturity, number of spikes/plant in the second cross, plant height in the first and second crosses, number of kernels/spike in the three crosses, 100- kernel weight in the first and third crosses and grain yield/plant in the third cross. These results suggested the potential for obtaining further improvement for the former traits by using selection in early generations but would more affection if selection was postponed to late one.These results are in agreement with those obtained by Abdel Nour and Zakaria (2010). and Yadav and Singh (2011).

The dominance gene effect (d) was highly significant for all characters in the three crosses except, number of spikes/plant, number of kernels/spike and 100-grain weight in the first cross . Dominance gene effect (d) was positively significant for all traits, except for days to heading in the first and second crosses, days to maturity and number of spikes/plant in the second and third crosses and plant height in the first and third crosses. The significant in these components indicated that both additive and dominance gene effects are important in the inheritance of these traits. Therefore, selection of desired traits could be practiced in early generations but would be more effective in the late ones. These results are in agreement with those obtained by Saint Pierre *et al.* (2010), Yadav and Singh (2011) and Koumber and El Gammaal (2012).

Estimates for epistatic gene effects, i.e., additive X additive and dominance X dominance, are presented in Table (3). Additive x additive gene effects were significant for all characters in the three crosses ,except for, number of spikes /plant in the third cross, number of kernels/spike in the second cross and grain yield/plant in the first cross. Similarly, dominance X dominance gene effects were significant for all studied traits, exceptfor, plant height in the second cross and number of kernels/spike, 100-grain weight and grain yield/plant in the third cross. The important roles of both additive and non-additive gene action in certain studied traits indicated that selection procedures based on the accumulation of additive effects would be very successful in improving these traits. Similar approaches were reported by Aykuttonk *et. al.* (2011) and Hamam (2013).

The results of heritability, expected genetic advance and heterosis were included in Table (4). Heritability estimates in both broad and narrow senses indicated the importance of the non additive component in the inheritance of these traits and the relative importance of selection for these traits based on phenotypic expression.. On the other hand, high values of narrow sense heritability were detected for days to heading and maturity in the three crosses indicating the importance of the additive genetic effects in controlling of those characters and the effectiveness of selection in early generations.

Table 3 : Scaling test and types of gene action for the studied traits in the three wheat crosses.

Character / Cross	Scaling test C	Scaling test D	(m)	(a)	(d)	(aa)	(dd)
Days to heading							
1	-20.7**	5.4**	82.34**	6.82**	-4.78**	6.61**	34.73**
2	-10.5**	1.0ns	95.45**	-18.72**	-2.86*	-39.88**	15.37**
3	-194.7*	10.0**	109.74**	4.93**	53.59**	-29.23**	272.85**
Days to maturity							
1	3.0**	-1.1ns	147.48**	0.53**	1.24*	2.31**	-5.44**
2	-2.3*	5.0**	150.29**	-5.77**	-5.91**	-15.21**	9.61**
3	3.6*	36.8**	156.95**	1.47**	-24.37**	-21.02**	44.35**
plant height							
1	27.1**	17.0**	103.95**	-4.83**	-9.17**	-16.50**	-13.47**
2	-9.9**	-13.0**	111.27**	-7.33**	13.54**	-7.63**	-4.15ns
3	13.2**	30.2**	122.25**	2.92**	-9.83**	-12.08**	22.67**
No. of spikes/ plant							
1	-1.7ns	-5.9**	17.32**	2.57**	-1.30ns	8.77**	-5.60**
2	-10.5**	1.7ns	17.12**	-2.15**	-2.98*	-7.20**	16.28**
3	-14.2**	2.8ns	16.76**	1.39**	-4.69**	-1.47ns	22.75**
No. of kernels/ spike							
1	-12.9**	8.3**	57.44**	-0.02ns	3.48ns	-7.70**	28.24**
2	-33.4**	-17.5**	50.50**	-2.28**	9.05**	1.53ns	21.23**
3	-29.0**	-40.0**	56.89**	-4.42**	21.97**	13.02**	-14.68ns
100-kernel weight							
1	0.2ns	0.9**	5.39**	-0.40**	-0.16ns	-1.36**	0.96*
2	-1.0**	0.3ns	4.98**	0.87**	0.75**	1.37**	1.77*
3	0.0ns	1.0**	4.75**	-0.48**	0.30**	-1.60**	1.25ns
grain yield per plant							
1	-30.3**	-6.1ns	126.80**	2.77**	7.72**	4.59ns	32.16**
2	5.4ns	6.0ns	127.10**	3.35**	5.55**	--	--
3	-39.5**	-13.2**	127.00**	-7.39**	12.59**	-12.55**	35.03ns

m = Mean effects, a = additive effects, a dnd = dominance effects
*, ** = significant at 0.05 and 0.01 levels of probability, respectively.

Table 4. Heritability, expected genetic advance and heterosis based on better parents for studied characters in the three wheat crosses.

Characters/ Cross	Heritability	Expected genetic (Δg)		Heterosis
	h^2(b)	h^2(n)	advance	BP
Days to heading				
1	97.43	74.31	8.63	11.40**
2	99.31	61.39	11.18	23.00**
3	97.64	70.27	10.45	-0.06**
Days to maturity.				
1	90.94	60.69	3.63	0.36ns
2	96.33	63.59	5.98	2.42**
3	98.70	70.21	9.88	- 0.68**
plant height				
1	89.90	54.78	8.09	-6.95**
2	93.19	60.83	13.51	-0.71ns
3	94.61	63.23	16.77	4.38**
No. of spikes/ plant				
1	79.86	33.80	3.46	-32.94**
2	81.73	43.59	6.63	-10.18**
3	81.88	35.11	4.91	-8.36**
No. of kernels/ spike				
1	87.94	56.16	13.08	20.21**
2	90.49	53.55	17.14	1.12ns
3	90.65	54.71	20.82	-6.28**
100-kernel weight				
1	83.03	29.51	0.48	-0.01ns
2	93.12	43.48	0.98	4.53**
3	92.08	57.73	1.13	9.42**
grain yield per plant				
1	95.51	59.04	18.36	13.01**
2	94.68	39.84	15.90	13.34**
3	87.71	26.23	7.83	6.19**

For remaining studied characters, moderate to low values of narrow sense heritability were detected indicating the importance of the non-additive variance component in the inheritance of those characters. Therefore, selection for such traits might be useful in later generations. These results are in general agreement with those obtained by Abd El-Kreem (2012), Kahrizi *et al.* (2010) and Talebi and Fayyaz (2012).

Expected genetic advance in F_2 generations was from 18.36% for grain yield per plant in the first cross and 20.82% for number of kernels/ spike in the third cross. It might be concluded that selection for these characters would be effective.

Heterosis percentages over better parents (BP) were presented in Table (4). Data availed highly significant heterotic values for all characters, except for, days to maturity and 100-kernel weight in the first cross, plant height and No. of kernels/ spike in the second cross. Negative heterotic effects for heading and maturity dates, would be very useful when, selection for earliness might practice. In this respect, the significant negative heterosis relative to the earlier parent was detected for days to heading and maturity in the third cross. While, values of heterosis for grain yield per plant were positive and highly significant for the three crosses. Similar trend was previously reported by Abd El-Rahman and Hammad (2009) and Yadav and Singh (2011).

From the results, it might be concluded that, the cross: Line 1/ Giza 163 is the best population for yield and most of improving its components.

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تقدير الثوابت الوراثية في ثلاث هجن من قمح الخبز

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الملخص العربى

تم إجراء تهجين بين اربعة تراكيب وراثية من قمح الخبز وهي سخا ٩٣، جيزة ١٦٣ ، وجميزة ٩ وسلالة ١ وذلك لتحديد الثوابت الوراثية لعدد الأيام من الزراعة حتى طرد السنابل وعدد الأيام حتى النضج ، وطول النبات وعدد السنابل في النبات وعدد حبوب السنبلة ووزن المائة حبة ومحصول الحبوب للنبات فى ثلاث هجن ١– سخا ٩٣ x سلالة ١ ٢– سلالة ١ x جيزة١٦٣ ٣– جيزة ١٦٣x جميزة ٩ . وقد أجري هذا البحث في محطة البحوث الزراعية بسخا خلال أربعة مواسم زراعية متتالية من 2007/2008 - 2010/2011 باستخدام نموذج العشائر الخمسة (الأبوين ، الجيل الأول، الجيل الثانى و الجيل الثالث) وذلك لتقدير الثوابت الو راثية للمحصول ومكوناته.

وقد أظهرت النتائج وجود اختلافات عالية المعنوية بين الهجن وبين العشائر داخل الهجن في معظم الصفات المدروسة، وأوضحت نتائج اختبارات الـ Scaling وجود معنوية لكل الصفات ماعدا محصول الحبوب في الهجين الثاني. وقد كان للتأثيرات الجينية المضيفة والغير مضيفة أهميتها في وراثة معظم الصفات تحت الدراسة و أشارت تقديرات المكافئ الوراثي بالمعنى الواسع إلى أهمية مكونات التباين الوراثي الغير مضيفة لكل الصفات المدروسة.بينما أشارت تقديرات المكافئ الوراثي بالمعنى الضيق إلى أهمية مكونات التباين الوراثي المضيفة لعدد الأيام حتى الطرد والنضج فى الهجن الثلاث . وكانت تقديرات العائد الوراثي المتوقع من الانتخاب في الجيل الثاني منخفضة لوزن المائة حبة فى الثلاث هجن بينما كانت مرتفعة لعدد حبوب السنبلة فى الهجين الثانى والثالث ومحصول الحبوب للنبات في الهجين الأول والثانى. كما اظهرت النتائج ان قيم قوة الهجين كانت معنوية جدا وسالبة لصفتى عدد الأيام حتى طرد السنابل والنضج فى الهجين الثالث , بينما كانت معنوية جدا وموجبة لمحصول الحبوب للنبات فى الهجن الثلاثة.