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Genetic Analysis of Two Bread Wheat Crosses (*Triticum Aestivum* L.) Using Six Populations Techniques

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ABSTRACT

Non-allelic interaction scaling test (A, B, and C) coupled with joint scaling test x_2 and six parameters model were applied to test the adequacy of genetic model and estimates the genetic components for days to heading, flag leaf area, number of spikes / plant, number of grains/spike, 1000-grain weight and grain yield/plant using six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of two wheat crosses; Gemmeiza11 × Misr1 and Gemmeiza 12 × Misr2, A randomized complete block design with three replications was used. The obtained results indicated the importance of additive genetic variance (D) in the genetic control of days to heading and flag leaf area for Gimmeiza 12 × Misr 2 and amount of spikes/plant in two crosses. Heritability in narrow sense was more than 0.50. While the dominance genetic variance (H) was found to be the prevalent type controlling for the remaining characters in two crosses, the value of $(H/0)^{05}$ was more than one for these characters and heritability in narrow sense as less than 0.50. The non-allelic interaction (A, B and C) coupled with joint scaling test (X_2) revealed that simple genetic model was adequate for explaining the inheritance of amount of spikes/plant for Gemmeiza 12 X Misr1, epistasis played a great role of controlling remaining characters in two crosses. Additive (d) and additive X dominance (J) were significant for days to heading and number of grains /spike (in two crosses), 1000 grain weight and grain yield / plant in two crosses cross (Gemmeiza × Misr 2).

Keywords: Genetic Analysis; Bread Wheat Crosses; Six Populations techniques.
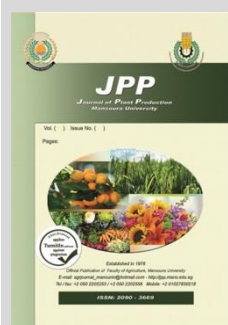
INTRODUCTION

Decision making about effective breeding method to be used is mainly dictated by the type of gene action controlling the genetic variation, such information is helpful for the breeders to predict in early generation of breeding. Programme, the potential of recombinant lines that could be derive following a series of selfing generations in this respect, additive and dominance gene effects, with great importance of dominance were found to be controlled heading date, number of grains/spike, and grain yield/plant by Pawar *et al.* (1988) and Alkadoussi and Eissa (1990); flag leaf area, number of spikes /plant and 1000-grain weight by Shehab El-Din (1997) and Salama (2002). The inheritance and genetic model for grain weight/spike were investigated by Alkaddoussi and Eissa (1989).They indicated that digenic model was appropriated to ascertain the genetic model for grain yield/plant. Non - allelic interaction parameters genetic model to test for epistasis were studied by Salama (2002). Mitkess and Dawla (1983), Chatrath *et al.* (1986), Awaad (1996) and Salama (2007) indicated that additive gene action was the predominant type controlling heading data, number of grains/spike and grain yield/plant. Limited studies were carried out to study the genetic control of yield and yield attributes characters in wheat, Sharma *et al.* (1996) Esmail (2002) and Sultan, *et al.* (2005).Therefore, the objective of this work was studying the genetic control of yield and yield attributes characters by using the six population biometrical approach of wheat varieties to be used in breeding program. It was performed to outline how to increase grain yield of wheat.

MATERIALS AND METHODS

1- Description of the parental genotypes and experimental procedures:

The present study was carried out at Tag EI-Ezz Research Station, Dakhlia Governorate Agriculture Research Center, during three winter successive growing seasons i.e. 2016/2017, 2017/2018 and 2018/2019. In. 2016/2017 season the parental wheat genotypes of local origin were grown and two crosses were made by hand; Gemmeiza11 X Misr1 and Gimmeiza12 X Misr2. The pedigree of the parental wheat genotypes are shown in Table 1.

Table 1. Names and pedigree of the used wheat genotypes.

Serial number	Genotypes	Pedigree
1	Gemmeiza11	Maya 74/ on // 1160 .147/3/Bb/Gall /4 /Cha „S,,
2	Misr1	T. aestivum / Bon // Cno 7/CCno /Mfd // Man „S,,
3	Gemmeiza 12	Vcm / Cmo 67 „S,, /7C/3/Kal / Bb
4	Misr2	Giza 155 //Pit62 //LR64/3/Tzpp/ Knott

In second season 2017/2018 seeds of two F_1 's crosses were sown to produce F_1 plants and crossed between P_1, P_2 and F_1 to obtain backcross 1 (BC_1) (F_1 X P_1), backcross 2 (BC_2) (F1 X P_2) and P1 X P_2 (F_1 seeds) and the F_1 plants were selfed to produce F2 seeds. In the third season 2016/2017 obtained seeds of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the two crosses were sown on 20th November 2018 and evaluated using a

randomized complete block design (RCBD) with three replications. Rows were 2 m length. Spacing between rows was 20 cm. While it was 10 cm between plants. Plot area was 6 m^2 (2 x 3 m). The experimental plot consists of two rows for each parent, F_1 and backcrosses and five rows for F_2 generation. The recommended agricultural practices of wheat production were applied.

2- Recorded data:

The studied characters were; days to heading (day), flag leaf area (cm^2), number of spikes /plant, number of grains/spike, 1000- grain weight (g) and grain yield / plant (g). Data were recorded on 10 individual plants for each of the parental genotypes as well as F1's, 20 in BC$_1$ and BC$_2$ and 50 in F$_2$ were labeled in each replicate.

3- Biometrical analysis:

The "t" statistical test was applied to test the differences between parental genotypes for the studied characters before considering the biometrical analysis.

a- Testing for the genetic model:

The scaling test A, B and C were applied according to Mather and Jinks (1982), formulae to test the presence of non-allelic interactions were as follows:

$$A = 2\overline{Bc_1} - \overline{P_1} - \overline{F_1}$$
$$B = 2\overline{Bc_2} - \overline{P_1} - \overline{F_1}$$
$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$$

Joint scaling test proposed by Cavalli (1952) as indicated X2 was applied to test the adequacy of the genetic model controlling the studied characters. Due to the unknown biased effect of non-allelic interaction the simple genetic model (m), (d) and (h) was applied when epistasis was absent, whereas, in the presence of nonallelic interaction the analysis was proceeded to estimate the interaction types involved using the six-parameters genetic model of Jinks and Jones (1958) as follows:

$$m = \text{Mean of } \overline{F_2}.$$
$$d = \text{Additive gene effects} = \overline{Bc_1} - \overline{Bc_2}$$

h= Dominance gene effect= $\overline{F_1} - 4\overline{F_2} - (1/2)\overline{P_1} - (1/2)\overline{P_2} + 2\overline{B_1} + 2\overline{B_2}$

i= Additive x Additive=$2\overline{Bc_1} + 2\overline{Bc_2} - 4\overline{F_2}$

j= Additive x Dominance= $\overline{Bc_1} - (1/2)\overline{P_1} - \overline{Bc_2} + (1/2)\overline{P_2}$

I= Dominance x Dominance= $\overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{Bc_1} - 4\overline{Bc_2}$

The significance of genetic components was tested using "t" test as follows:

$$\pm t = \frac{effect}{\sqrt{Variance\ of\ effect}}$$

The genetic components of variance for each character in the studied crosses were partitioned into additive (D), dominance (II) genetic variance and environmental variance (E) using Mather (1949) and Mather and Jinks (1971) formula as follows:

$$Ew = {}^1\!/_4 \cdot (VP1 + VP2 + 2VF1)$$
$$D = 4\,VF2 - 2\,(VBc\,1 + VBc2)$$
$$H = (VBc1 + VBc2 - VF2 - Ew)$$
$$F = VBc2 - VBc1,)$$

$(H/D)^{0.5}$ = Average degree of dominance F/ (DxH) 0 ·5 provides little evidence that the dominance at different loci are particularly consistent in sign or magnitude.

Broad (T_n) and narrow (T_b) sense were computed from the genetic variance using six populations according to Mather and Jinks (1982) formulae.

RESULTS AND DISCUSSION

1- Mean performance:

Before considering the biometrical analysis for the studied characters, the "t" statistical test was applied for testing parental genotypes involved. The "t" value was significant; suggesting that employed displayed enough amount of genetic variability. Thus, genetic differences for the genes controlling the studied characters were detected Table 2.

Mean and Standard error of the six populations ($\overline{P}_1$, $\overline{P}_2$, $\overline{F}_1$, $\overline{F}_2$, $\overline{Bc}_1$ and $\overline{Bc}_2$) of two wheat crosses for studied characters are given in Table 2. According to the mean of $\overline{F}_1$ as compared with its standard error (S.E.).

Table 2 . Mean performance ± standard error of the six populations of the two wheat crosses for studied characters.

Characters Crosses	Days to heading (days)		Flag leaf area(cm^2)		Number of spikes/plant		Number of grains /spike		1000 - grain weight (g.)		Grain yield / plant (g.)	
	1	2	1	2	1	2	1	2	1	2	1	2
$\overline{P}_1$	99.5 ±0.23	100.10 ±0.19	42.97 ±0.29	43.80 ±0.34	7.66 ±0.11	6.45 ±0.09	65.82 ±0.36	69.11 ±0.31	59.33 ±0.29	62.17 ±0.38	19.70 ±0.10	21. 12 ±0.08
$\overline{P}_2$	93.0 ±0.20	92.5 ±0. 13	45.0 ±0.18	40.23 ±0.20	6.33 ±0. 13	5.83 ±0.15	62.14 ±0. 29	58.32 ±0.28	65.46 ±0.24	57.35 ±0.31	18.51 ±0.14	26.49 ±0.07
$\overline{F}_1$	96.32 ±0. 31	91.85 ±0.26	47.24 ±0.33	45.81 ±0.37	8.13 ±0. 17	6.92 ±0.19	69.18 ±0.39	73. 81 ±0.41	67.28 ±0.35	66. 53 ±0.34	25. 93 ±0.16	24.54 ±0. 11
$\overline{F}_2$	102.01 ±0.71	99.53 ±0.93	46.16 ±0.84	44.82 ±0.92	7.73 ±0. 28	6.52 ±0.37	68.88 ±0.91	72.53 ±0.82	66. 21 ±0.84	65.42 ±0.79	24.17 ±0.28	23.34 ±0.23
$\overline{BC}_1$	103. 36 ±0.54	100.52 ±0.48	46.02 ±0.94	44.51 ±0.91	6.82 ±0.19	6.14 ±0.38	69.88 ±0.67	71.93 ±0.65	61.72 ±0.51	64.81 ±0.58	23.09 ±0.23	22.08 ±0.26
$\overline{BC}_2$	92.01 ±0.75	90. 10 ±0.92	47.93 ±0.65	42.13 ±0.61	6.98 ±0.27	6.73 ±0.20	65.16 ±0.93	59.99 ±0 88	68.16 ±0.95	58.35 ±0.87	24. 73 ±0.26	20.49 ±0.16
"t" test	**	**	**	**	**	**	**	**	**	**	**	**
h=Fl — (P1+P2)+ S.E	0.07 ±0.33	-4.45** ±0.28	3.26** ±0.37	3.79** ±0.41	1.13** ±0.18	0.78 ** ±0. 20	5.20** ±0.44	10 09** ±0.45	4.88** ±0.39	6.77** ±0.42	6.82** ±0.18	3.73** ±0.12

** significant at 0.01 level of probability

Results indicated that the mean of $\overline{F}_1$ was earlier than the early heading for cross 2 (Gimmeiza12 × Misr2) whereas, the F_1 exceeded its high performing parent (HP) for remaining studied characters in two crosses. The results provide evidence for present of over dominance gene effects and increasing alleles were more frequent in the genetic constitution of wheat parental genotypes, and that dominant gene were dispersed. The F_2 mean of the two studied crosses

in each character indicated high value from high parent for all studied characters in two crosses except cross 2 for days to heading indicated appreciable amount of genetic variability for these characters in the corresponding crosses. The heterotic effect as indicated by (h value) which indicated dominance deviations was positive and significant for all studied characters in two crosses except days to heading in two crosses. Significant and positive (h) value indicating that,

presence heterotic effects and the increasing alleles were more frequent than the decreasing ones in the genetic constitution of the parental genotypes. However, the negative and significant (h) value was obtained for days to heading at cross 2 providing evidence for the predominant of decreasing alleles over the increasing ones and the important role of dominance and I or dominance x dominance gene effects in the genetic control of these characters.

2- Component of genetic variance:

The assessment of the genetic variance (Table, 3) revealed that, the dominance genetic variance (h) were higher in magnitude than the corresponding additive (D) ones for days to heading and flag leaf area of 1 and 2 cross, number of grains/spike, 1000-grain weight and grain yield/plant for 1st and 2nd crosses. This resulted in average degree of dominance (H1/D) was more than unit However, additive component (D) was found to be the prevailed type controlling for the remaining character in two crosses. Thus phenotypic selection

would be effective in early segregating generations. The negative value "F" together with the ratio F (H1/D)0 for flag leaf area (two crosses), number of spikes / plant and grain yield/plant (cross 2).Thus the decreasing alleles were more frequent But, for the remaining characters in two crosses the increasing alleles exceeded the decreasing ones. Heritability in narrow sense was high for days to heading and flag leaf area (cross 2) 0.65 and 0.58, respectively, number of spikes/plant (1st cross) (0.60) and (cross 2) (0.63). Suggesting the importance of straight forward phenotypic selection method to improve characters in this respect AI Kaddoussi and Eissa (1989), Hassan (1993) and Salama (2002). But for the remaining characters heritability values ranged from (0.12) for flag leaf area (1st cross) to 0.48 for grain yield/plant (cross 1). These results are in accordance with those at AI Kaddoussi (1996), Sultan, *et al.* (2005) and Salama (2007).

Table 3. Components of genetic variance, derived parameters and narrow sense heritability (Tn) for the studied characters of two wheat crosses

Characters Crosses	Days to heading (days)		Flag leaf area(cm^2)		Number of spikes/plant		Number of grains/spike		1000 grain weight (g.)		Grain yield / plant (g.)	
	1	2	1	2	1	2	1	2	1	2	1	2
						Genetic parameters						
[D]	0.28	1.28	0.18	0.99	0.096	0.172	0.72	0.66	0.46	0.29	0.074	0.022
[H]	1.16	0.68	2.12	0.96	0.048	0.084	1.44	1.28	1.52	1.44	0.08	0.108
[E]	0.07	0.05	0.08	0.11	0.02	0.03	0.13	0.12	0.09	0.12	0.02	0.015
						Derived parameters						
[F]	0.28	0.62	-0.47	-0.45	0.04	-0.11	0.44	0.37	0.65	0.43	0.02	-0.04
"I H/O	2.03	0.72	3.43	0.98	0.71	0.70	1.41	1.39	1.81	2.23	1.04	2.22
F l''/J/ DH	0.49	0.67	-1.15	-0.46	0.19	-0.91	0.43	0.40	0.77	0.66	0.26	-0.83
Tn	0.28	0.65	0.12	0.58	0.60	0.63	0.42	0.41	0.33	0.23	0.48	0.21

3- Adequacy of genetic model:

The non-allelic interaction tests (A, B and C) for studied characters, (Table 4) provide evidence for the importance of epistasis in the inheritance of studied characters in two crosses except number of spikes/plant

(cross 2). Significance x2 suggested that the additive dominance model is not sufficient to explain the inheritance of these characters. Thus results confirm the findings of AI Kaddoussi and Eissa (1990) and Salama (2002).

Table 4. Testing for non-allelic interaction (A, B and C), x2 and six parameters genetic model gene effect for the studied traits of the two wheat crosses.

Parameters Characters	Cross No.	Non-allelic interaction test			Joint scaling test	Six – parameter genetic model					
		A	B	C	X$^{•}$	[M]	[d]	[h]	[i]	[j]	[L]
Days to Heading (day)	1	10.92** ±0.47	-1.3 ±1.55	22.9 ±2.91	**	102.01** ±0.71	11.35** ±0.93	-17.23** ±3.96	-17.66** ±4.14	8.1** ±1.69	11.70** ±3.97
	2	9.9** ±1013	-4.15* ±1.86	21.82** ±3.75	**	99.53** ±0.93	10.42** ±0.13	21.33** ±4.92	-16.88 ±4.91	6.62** ±2.65	11.94** ±4.49
Flag leaf area (cm^2)	1	1.83 ±1.97	3.62 ** ±1.35	2.19 ±3.42	**	46.16** ±0.84	-1.91 ±0.14	6.51 ±3.93	3.26 ±4.95	-0.89 ±1.83	-8.71 ±6.71
	2	4.94** ± 1.83	0.23 ± 1.29	3.63 ±3.77	**	44.82** ± 0.92	2.38* ± 1.09	-2.20 ±4.06	-6.0 ±4.13	0.59 ±2.85	8.37 ± 6.01
Number of spikes/ plant	1	-2.15** ± 0.43	-0.50 ± 0.59	0.67 ± 1.19	**	7.73** ± 0.28	-0.16 ± 0.33	-2.18 ± 2.25	-3.28 ± 2.23	-0.82** ± 0.26	5.97** ± 1.95
	2	-1.09 ±0.78	0.71 ± 0.47	-0.04 ± 1.54	N.S	6.52** ± 0.37	-0.59 ± 0.43	0.44 ± 1.61	-	-	-
Number of grains spike	1	4.76** ±1.43	2.36 ±1.93	9.2** 3.75	**	68.88** ±0.91	4.72** ±1.15	-0.24 ±5.99	-5.44 ±4.96	2.88** ±0.81	1.68 ±4.89
	2	0.94 ±1.39	2.15 ± 1.84	15.07** ±3.63	**	72.53** ± 0.88	11.94** ± 1.10	-16.18** ±4.92	-26.28** ±3.89	6.54** ± 1.86	37.49** ±6.95
1000-grain weight (g)	1	-3.17** ±1.11	3.58 ±1.96	5.49 ±3.43	**	66.21** ±0.84	-6.44** ±1.08	-15.19** ±3.62	-5.08 ±3.60	-3.37** ±0.69	4.67 ±4.35
	2	3 01 * ±1.27	-7.18** ±1.80	9.1** ± 3.27	**	65.42** ±0.79	6.46** ±1.05	-8.59** ±3.48	-15.36** ±3.46	4.05* ±1.75	21.62** ±4.32
Grain yield/ plan (g)	1	0.55 ±0.49	5.02 * ±0.56	6.61* ± 1.17	**	24.17 ** ± 0.28	-1.64** ± 0.34	5.78** ±1.92	-1.04 ±1.61	-2.23** ±0.83	-4.53* ± 2.01
	2	-1.5** ±0.55	-4.05** ±0.34	2.67** ±0.95	**	23.34** ±0.23	1.59** ±0.31	-0.4.48 ±1.42	-8.22** ±1.43	1.27** ±0.31	13.77**± 2.27

Separation out the interaction types using six parameter genetic model revealed significant (d) gene effects

for all studied characters in two crosses except number of spikes/plant in two crosses positive and significant

dominance (h) was shown for days to heading (cross 2) and grain yield/plant (cross1). Similar results were obtained Hassan (1993) and Salama (2002).The most important digenic interaction as computed by the six parameter genetic model were; additive x dominance (J) for days to heading and number of grains/spike (two crosses), 1000-grain weight and grain yield / plant (cross 2). Significant dominance x dominance (L) were the prevailed type that controlled days to heading (two crosses), number of spikes/plant (cross 1), number of grains/spike, 1000-grain weight and grain yield / plant (cross 2).

This information are of great interest for wheat genotypes to raise grain yield and early mature ones to overcome the gap between production and consumption in Egypt.

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التحليل الوراثي لهجينين من قمح الخبز بإستخدام طريقة العشائر الست
أحمد أبوالنجا قنديل، مأمون أحمد عبدالمنعم، سعاد حسن حافظ وحسناء سليمان محمد جمعه
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أجريت هذه الدراسة بالمزرعة البحثية لمحطة البحوث الزراعية بتاج العز – دقهلية التابعه لمركز البحوث الزراعيه في المواسم ٢٠١٧/٢٠١٩، ٢٠١٨/٢٠١٧، ٢٠١٩/٢٠١٨. واستخدم اختبار التفاعلات الغير آليلية (C,B,A) (X^2) والنموذج الثلاثي والسداسي الوراثي لدراسة النظام الوراثي المتحكم وكذلك دراسة الاختلافات الوراثية وطبيعة الفعل الجيني في دراسة صفات عدد الأيام حتى طرد السنابل ومساحة ورقة العلم وعدد السنابل وعدد حبوب السنبلة ووزن الألف حبة ومحصول الحبوب للنبات الفردي. وذلك باستخدام العشائر الستة (الآباء والجيل الأول والهجن الرجعيه لكلا الأبوين والجيل الثاني) في هجينين من قمح الخبز المصري وهما : (جميزه١١ × مصر ١) و(جميزة ١٢ × مصر ٢). ويمكن تلخيص أهم النتائج في الآتي : أوضحت النتائج أهمية التباين الراجع للفعل الجيني المضيف في وراثة عدد الأيام حتى طرد السنابل ومساحة ورقة العلم للهجين الثاني (جميزة ١٢ مصر ٢) وعدد السنابل للنبات في كلا الهجينين وكان معامل التوريث بالمعنى الضيق أعلى من ٠,٥ لهذه الصفات. كان التباين الراجع للفعل السيادي للجين معنوياً لباقي الصفات في الهجن المدروسة وكانت قيمة متوسط درجة السيادة أعلى من الوحدة لهذه الصفات ومعامل التوريث بالمعنى الضيق أقل من ٠,٥. وجد أن النموذج الوراثي البسيط كان ملائماً لدراسة السلوك الوراثي لصفة عدد السنابل للنبات في الهجين الثاني بينما كان النموذج الوراثي البسيط غير ملائماً لدراسة السلوك الوراثي لباقي الصفات المدروسة. كان الفعل الجيني المضيف والتفاعل (المضيف x السيادي) معنوياً لصفة عدد الأيام حتى طرد السنابل وعدد الحبوب للسنبلة في كلا الهجينين ووزن الألف حبة ومحصول الحبوب للنبات في الهجين الثاني. وكان التفاعل السيادي في السيادي معنوياً لصفة عدد الأيام حتى طرد السنابل لكلا الهجينين وعدد السنابل الهجين الأول وعدد حبوب السنبلة ووزن الألف حبة ومحصول الحبوب للنبات في الهجين الثاني. بصفه عامه معرفة النظام الوراثي المتحكم في المحصول ومكوناته من الأسس الهامة لتحديد طريقة التربية المناسبة . وهذه المعلومات مهمة لتربية أصناف عالية المحصول ومبكرة النضج .