

تقدير المعايير الوراثية لبعض الصفات الكمية فى هجن قمح الخبز

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الملخص العربي

تهدف هذه الدراسة الى معرفة قوة الهجين والسلوك الوراثى ودرجة التوريث والتحصين الوراثى المتوقع وكذلك طبيعه الفعل الجينى لبعض الصفات الكمية فى هجينين من قمح الخبز هما (سحا ٩٣ × السلالة ١) و (جميزة ١٠ × السلالة ٢). اختير لهذه الدراسة أربعة تراكيب وراثية والتي بها مدى واسع من الاختلافات. هذه التراكيب هى : سحا ٩٣، جميزة ١٠، السلالة ١ او السلالة ٢. تم استخدام العشائر الستة فى هذه الدراسة وهى الاب الاول، الاب الثانى، الجيل الاول، الجيل الثانى وكلا من الجيل الرجعى الاول والثانى ويمكن إيجاز أهم النتائج المتحصل عليها فيما يلى :- (١) اظهرت النتائج وجود قوة هجين مقدارها ٤.٧، ٦.٥ % لمحصول الحبوب / نبات لكل من الهجين للاول والثانى على التوالى عند مقارنتها بالاب الافضل ولكنها لم تصل الى حد المعنوية وكذلك بالنسبة للصفات الاخرى المدروسة.

(٢) كان الفعل الجينى المضيف عالى المعنوية بالنسبة لصفات طرد السنابل، طول النبات ووزن المائه حبه فى كلا الهجينين تحت الدراسة . وكانت تاثيرات الفعل الجينى التفوقى المضيف × المضيف معنويه لكل من صفة عدد السنابل / النبات ومحصول الحبوب / النبات . بينما كان الفعل الجينى التفوقى المضيف × السيادةى معنويا فقط فى الهجين الاول بالنسبة لصفة طرد السنابل.

(٣) كانت قيم درجه التوريث بمعناها العام عالية بالنسبة لمعظم الصفات المدروسة . وكذلك اظهرت الكفاءة الوراثية بمعناها الضيق قيمة عالية لكل من صفات طرد السنابل ، عدد السنابل / النبات ومحصول الحبوب / النبات فى الهجينين.

(٤) كانت قيم التحسين الوراثى المتوقع عالية و كانت مرتبطة بقيم كفاءة التوريث بمعناها الضيق لكلا من صفة عدد السنابل / النبات ومحصول الحبوب / النبات فى كلا الهجينين وصفة طول النبات وعدد الحبوب / السنبل فى الهجين الاول.

ESTIMATION OF GENETIC PARAMETERS FOR SOME QUANTITATIVE TRAITS IN TWO BREAD WHEAT CROSSES (*Triticum aestivum*, L.)

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ABSTRACT: *This investigation aimed to study the potentiality of heterosis expression, heritability, expected genetic advance, nature of gene actions for some quantitative traits in two bread wheat crosses. Four parental genotypes (Sakha 93, Gemmeiza 10, Line 1 and Line 2) were chosen for a previous study on basis of presence of a wide range of variability.*

Six populations (P₁, P₂, F₁, F₂, BC₁ and BC₂) were used in this study to estimate some genetic parameters . The results showed that no useful heterotic effects were found for all traits studied relative to better parents.

Heterosis for grain yield did not reach the significant level being 4.7% and 6.5% in the first and second cross, respectively.

Inbreeding depression values were found to be significant for days to maturity in the two crosses. Additive gene effects (a) were found to be highly significant for days to heading, plant height and 100- kernel weight in both crosses. Additive x additive (aa) epistatic type of gene effects were found to be significant for number of spikes per plant and grain yield per plant. Additive x dominance (ad) type of digenic epistasis was found to be significant only for days to heading in the first cross. High heritability estimates in broad sense were detected for mostly all traits studied. Narrow sense heritability estimates were found to be high for days to heading, number of spikes per plant and grain yield per plant in both crosses. High genetic gain was found to be associated with high narrow sense heritability for number of spikes per plant and grain yield in both crosses and plant height and number of kernels per spike in the first cross.

Key words: *Six populations, Heterosis, Inbreeding depression, Heritability, Genetic advance*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important and strategic cereal crop all over the world. It provides over 20% of calories and protein for human nutrition and considered as a staple food for over 35% of the world's population in more than 40 countries. In Egypt, wheat is the main winter cereal crop used as a staple food for urban and rural societies and the major source of straw for animal feeding. However, total wheat consumption has

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increased drastically due to over population growth which reached about 2.5% per year. Egypt imports about 45% of its wheat requirements. This reflects the size of the problem and the efforts needed to increase wheat production. Thus, increasing production per unit area appears to be one of the important factors for narrowing the wheat production gap. This can be achieved by breeding for high yielding cultivars which is considered as ongoing process of the national wheat research program.

Developing early maturing and high grain yield cultivars requires definite selection of parental genotypes with wide genetic base and making crosses to help breeders in identifying genotypes with desired characteristics.

The plant breeder is interested in identifying gene effects in order to formulate the most advantageous breeding procedures for improvement of the attribute in question. Therefore, breeders need information about nature of gene action, heterosis, inbreeding depression, heritability and predicted genetic gain from selection for earliness, yield and yield components.

Six generation analysis provides information on the relative importance of average effects of the genes (additive effects), dominance deviations, and effects due to non allelic genetic interactions in determining genotypic values of the individuals and, consequently, means genotypic values of families and generations (Viana 2000). Generation mean analysis is a simple but useful technique for estimating gene effects for a polygenic trait, its greatest merit lying on the ability of estimating epistatic gene effects such as additive x additive (aa), dominance x dominance (dd) and additive x dominance (ad) (Singh and Singh, 1992).

The research reported herein was carried out to provide information about gene effects and available genetic variability for the most important quantitative traits of wheat (*Triticum aestivum* L.).

MATERIALS AND METHODS

This experiment was carried out at the Experimental Farm of El Gemmeiza, Agricultural Research Station, Egypt through the three successive seasons of 2007/2008, 2008/2009 and 2009/2010. Four bread wheat genotypes were chosen on basis of previous informations regarding their agronomic performance, representing a fairly wide range of variability. The name, pedigree and origin of these genotypes are presented in Table (1).

Table (1). Name, origin and pedigree of the parental wheat genotypes used in the study.

Name	Origin	Pedigree
Line 1	Egypt	GEM Line# 27/PL//CMH79 A.955*2/CNO79//CMH 79A.955/BOW"s"//GEM#9
Line 2	Egypt	WW33/Vee"s"/AU/UP301/Bow"s"/4/Jup/Bjy"s"//URES/3/ Vee"s"//Top-Sannine/Ald"s"
Sakha 93	Egypt	Sakha92/ TR81032

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		S8871-1S-2S-1S-0S
Gemmeiza 10	Egypt	Maya 74"s"/ON//1160-1473/BB/GII/4/CHAT"s"/5/Crow"s"

In 2007/ 2008 growing season, two initial crosses were made (Sakha 93 x Line 1 and Gemmeiza 10 x Line 2) and designated in the text as first and second cross; respectively. F₁ plants were self pollinated and backcrossed to both their respective parents to obtain F₂ and backcross seeds in 2008 / 2009 growing season. The six populations P₁, P₂, F₁, F₂, BC1 and BC2 of each cross were sown in 2009/ 2010 growing season using a randomized complete block design with three replicates. Each plot consists of 6 rows of F₂ generation, 3 rows of Bc1 and Bc2 and 2 rows of the other three non segregated populations i.e. p₁, p₂ and F₁. The rows were 3.0 meters long with 30cm apart and seeds were spaced 10 cm within each row. Normal agricultural practices were applied as usual for the ordinary wheat fields in the area. Data were recorded on 30 randomly selected competitive plants in each entry for p₁,p₂ and F₁ and 90 plants for Bc1 and Bc2 and 300 plants for the F₂ for the studied characters i.e days to heading, days to maturity, plant height, number of spikes per plant, number of kernels per spike, 100 kernel weight and grain yield per plant.

Statistical procedures:

The t-test was used to examine the existence of genetic variance between parental means. Statistical procedures used herein would only be computed if the F₂ genetic variance was found to be significant. A one tail "F" ratio was used to examine the existence of the genetic variance within the F₂ population .The degrees of freedom for these tests were considered as infinity. If calculated "F" ratio was equal to or larger than the tabulated ones, various biometrical parameters needed in this investigation would be computed .Heterosis (H), was expressed as percent increase of the F1 mean performance above the respective better parent, i.e (F1-B.p)/B.P x 100 .

Inbreeding depression (I.d.) was measured as the average percent decrease of the F₂ from the F₁ .Inbreeding depression .

$$I.d.\% = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_2}} \times 100$$

F₂ - deviation (E₁) was calculated as the deviation of the F₂ mean performance from the average of F₁ and mid parent value (Marani, 1968) . Back cross deviation (E₂), was computed as the deviation of the two backcrosses performance from the F₁ and mid parent performances (Marani, 1968).Hertability was calculated in both broad and narrow sense according to (Mather,1949). The validity of the previous estimates were examined by t-test. Nature of gene action was studied according to the relationships illustrated

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by (Gamble, 1962). The predicted genetic advance under selection (ΔG) was computed according to Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Means and variance of the studied traits for P1, P2, F1, F2, BCI and BC2 of the two crosses are shown in Table (2). Generally, the differences between each two parents were found to be significant. The genetic variances within F2 populations were also found to be significant for all traits studied in both crosses. Consequently, the various genetical parameters were computed.

Heterosis:

Heterosis was estimated as the percent increase of the F1 mean performance above its respective better parent value. No useful heterotic effects relative to better parents were found for all traits studied in both crosses under study (Table 3). Meanwhile, heterosis for grain yield did not reach the significant level being 4.7 and 6.5 % in the first and second crosses, respectively. Similar results were previously obtained by El-Massry, (2009).

Inbreeding depression:-

Inbreeding depression values were found to be significant for days to maturity in both crosses, days to heading, number of kernels per spike and grain yield per plant in the first cross and number of spikes per plant and plant height in the second one (Table 3). Heterosis in F1 generation should be followed by appreciable reduction in F2 generation, since the two parameters are the two sides of the same phenomena. The present results agreed with this expectation in most cases studied. However, these expectations are not fulfilled in some other cases, for instance 100- kernel weight in the two crosses, showed highly significant heterosis in the negative direction and positive insignificant inbreeding depression. Also, plant height and days to maturity in the first cross. The contradiction between heterosis and inbreeding depression estimates could be due to the presence of linkage between genes in these materials (Van der Veen, 1959). Also, as for grain yield per plant in the first cross and number of spikes per plant in the second cross. There were significant inbreeding depression and insignificant heterosis. The present results were in accordance with those previously obtained by Esmail and Kattab (2002) and El-Nahas (2005).

F2 performance:

F2 mean performance was found to deviate significantly from the average of the F1 and mid-parent value E1 for days to maturity, number of spikes per plant and grain yield per plant in the two crosses, days to heading and plant

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height in the second cross indicating that epistasis was present in the inheritance of these traits. These results was also found by Esmail and Kattab (2002) and El-Massry (2009).

Table 2

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Table 3

Backcross-performance:

Backcross deviation (E2) was found to be significant for days to maturity in both crosses, grain yield per plant in the first cross and number of spikes per plant, plant height and 100- kernel weight in the second one. Also, the F2 deviation was accompanied by backcross deviation in most cases under study, indicating the presence of epistasis in such large magnitude as to warrant great deal of attention in the breeding program for improving these traits.

Nature of gene action:-

Genetic analysis of generation which were calculated according to relationships illustrated by Gamble (1962) which gives estimates of the six parameters model i.e. mean effect (m), additive (a), dominance (d) and the three epistatic types additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd). The estimates of the mean effects (m) which due to the over all mean plus the locus effects and the interaction of the fixed loci, were found to be highly significant indicating that all studied characters were quantitatively inherited (Table 3)

Additive gene effects (a) were found to be highly significant for days to heading, plant height and 100- kernel weight in both crosses under investigation. The additive gene effects were found to be highly significant for number of spikes per plant and number of kernels per spike in the first cross. Meanwhile, in the second cross, the additive gene action was found to be significant only for days to maturity. These results would suggest the potential for obtaining further improvements for these traits.

The dominance gene effects (d) were found to be significant for number of kernels per spike and grain yield per plant in the first cross, and for days to heading and 100- kernel weight in the second cross suggesting that the dominant factors playing a great role in the inheritance of these traits.

Additive x additive (aa) epistatic type of gene effects were found to be significant for number of spikes per plant and grain yield per plant in the first cross and for days to heading and 100- kernel weight in the second one.

Additive x dominance type of digenic epistasis was found to be significant only for days to heading in the first cross. While, in the second one, the epistatic type dominance x dominance was detected to be significant for days to maturity, plant height and 100- kernel weight.

It is worth to mention that the three epistatic types aa , ad and dd were accompanied by significant estimates of both E1 and E2 epistatic scales in most traits studied and that would ascertained presence of epistasis in such

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large magnitude as to warrant great deal of attention in a wheat breeding programs. The presence of both additive and non additive gene actions in most traits studied would indicate that selection procedures based on the accumulation of additive effect would be successful in improving all traits under investigation. However, to maximize selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variances are involved would be preferred.

A great deal of attention of epistasis was reported in wheat by Darwish and Ashoush (2003), Bayoumi, (2004), Heidari *et al.* (2006), Dawwam *et al.* (2007), Hendawy and seleem (2007) El-Shaarawy (2008) , El-Massry (2009) Hendawy *et al.* (2009) and Dawwam *et al.* (2010).

Heritability and genetic advance:

Heritability is one of the most important parameter for determination the genetic behavior of a metric character. It is expressed as the proportion of the variance attributed to the average effect of genes. However, the most important function of the heritability in the genetic study of quantitative characters as its predictive role. It expresses the reliability of the phenotypic value as a guide to the breeding value. The possible advance through selection based on phenotypic value can therefore, be predicted only from knowledge of the degree of correspondence between phenotypic value and breeding value. The degree of correspondence is measured by heritability estimates. The heritability estimates enter into almost every formula connected with breeding methods and many practical decisions about the techniques followed depends on its magnitude.

Heritability in both broad and narrow sense and genetic advance under selection were calculated and the obtained results are presented in Table (4). High heritability estimates in broad sense were observed for mostly all traits studied. Narrow sense heritability estimates were found to be high for days to heading, number of spikes per plant and grain yield per plant in both crosses. Meanwhile, high narrow sense heritability values were detected for days to maturity, plant height and number of kernels per spike in the first cross. Moderate narrow sense heritability values were obtained for plant height in the second cross. Low narrow sense heritability estimates were found for 100-kernel weight in the two crosses and for days to maturity and number of kernels per spike in the second cross.

Genetic advance under selection which are given in Table (4) showed the possible gain from selection as percent increase in the F3 over the F2 mean when the most desirable 5% of the F2 plants are selected. Genetic advance under selection (ΔG %) was found to be high in magnitudes for all characters studied.

Johnson *et al.* (1955) reported that heritability estimates along with genetic gain upon selection were more valuable in predicting the effect of

selection than the former alone. Also, Dixit *et al.* (1970) pointed out that high heritability is not always associated with high genetic advance, but in order to make your selection more effective, high heritability should be associated with high genetic gain. In the present study, high genetic gain was found to be associated with high narrow sense heritability for number of spikes per plant and grain yield per plant in both crosses and plant height and number of kernels per spike in the first cross. Therefore, selection for these characters should be effective and satisfactory for successful breeding purposes. While, the remaining characters, selection for it would be effective, but probably of less success.

Table (4): Heritability (Bs & Ns) ,Genetic advance upon selection and Genetic advance as percentage for some quantitative characters in two bread wheat crosses.

Characters	Cross	Hertitability %		Genetic advance	
		Broad (Bs)	Narrow (Ns)	Δg	Δg %
Days to heading(days)	I	81.946	59.110	5.149	5.370
	□	84.282	65.808	6.079	6.331
Days to maturity(days)	I	89.107	63.621	4.560	3.067
	□	33.160	28.777	1.332	0.909
Plant height(cm)	I	93.697	57.726	22.916	20.349
	□	82.180	39.056	7.240	6.350
Number of spikes per plant	I	72.233	64.003	7.771	60.701
	□	63.275	53.601	5.926	44.805
Number of kernels per spike	I	65.465	53.665	23.087	32.282
	□	39.391	25.720	6.781	10.604
100- kernel weight(g)	I	81.283	24.848	6.269	10.828
	□	42.475	17.188	2.399	4.566
Grain yield per plant(g)	I	75.449	55.258	25.453	65.257
	□	79.370	63.089	29.392	87.487

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الملخص العربي

تهدف هذه الدراسة الى معرفة قوة الهجين والسلوك الوراثى ودرجة التوريث والتحسين الوراثى المتوقع وكذلك طبيعه الفعل الجينى لبعض الصفات الكمية فى هجينين من قمح الخبز هما (سحا ٩٣ × السلالة ١) و (جميزة ١٠ × السلالة ٢). اختير لهذه الدراسة أربعة تراكيب وراثية والتي بها مدى واسع من الاختلافات. هذه التراكيب هى : سحا ٩٣، جميزة ١٠، السلالة ١ او السلالة ٢. تم استخدام العشائر الستة فى هذه الدراسة وهى الاب الاول، الاب الثانى، الجيل الاول، الجيل الثانى وكلا من الجيل الرجعى الاول والثانى ويمكن إيجاز أهم النتائج المتحصل عليها فيما يلى :- (٥) اظهرت النتائج وجود قوة هجين مقدارها ٤.٧، ٦.٥ % لمحصول الحبوب / نبات لكل من الهجين للاول والثانى على التوالى عند مقارنتها بالاب الافضل ولكنها لم تصل الى حد المعنوية وكذلك بالنسبة للصفات الاخرى المدروسة.

(٦) كان الفعل الجينى المضيف على المعنوية بالنسبة لصفات طرد السنابل، طول النبات ووزن المائه حبه فى كلا الهجينين تحت الدراسة . وكانت تأثيرات الفعل الجينى التفوقى المضيف × المضيف معنويه لكل من صفة عدد السنابل / النبات ومحصول الحبوب / النبات . بينما كان الفعل الجينى التفوقى المضيف × السىادى معنويا فقط فى الهجين الاول بالنسبة لصفة طرد السنابل.

(٧) كانت قيم درجة التوريث بمعناها العام عالية بالنسبة لمعظم الصفات المدروسة . وكذلك اظهرت الكفاءة الوراثية بمعناها الضيق قيما عالية لكل من صفات طرد السنابل، عدد السنابل / النبات ومحصول الحبوب / النبات فى الهجينين.

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(٨) كانت قيم التحسين الوراثى المتوقع عالية و كانت مرتبطة بقيم كفاءة التوريث بمعناها الضيق لكلا من صفة عدد السنابل / النبات ومحصول الحبوب / النبات فى كلا الهجينين و صفة طول النبات وعدد الحبوب / السنبل فى الهجين الاول.

Table (2) : Means (\bar{X}) and variances (S^2) of P1 , P2, F1 , F2, Bc1 and Bc2 populations for some quantitative characters in two bread wheat crosses .

Character	statistics	Cross 1						Cross 2					
		P1	P2	F1	F2	Bc1	Bc2	P1	P2	F1	F2	Bc1	Bc2
Days to heading (days)	\bar{X} S^2	93.940 3.170	98.240 2.962	95.140 3.551	95.872 17.878	93.958 13.000	97.117 12.188	102.320 2.344	92.880 3.944	96.480 3.193	96.031 20.110	99.433 18.416	94.633 8.570
Days to maturity (days)	\bar{X} S^2	149.020 1.571	151.000 1.451	149.620 0.934	148.678 12.108	148.783 7.146	149.192 9.366	149.920 2.880	145.120 4.660	147.440 2.578	146.461 5.046	147.958 4.010	145.025 4.630
Plant height (cm)	\bar{X} S^2	103.60 33.198	116.080 20.932	113.440 16.088	112.614 371.357	107.633 236.318	113.175 292.028	106.700 15.071	122.940 12.098	118.420 16.126	114.019 80.988	109.500 60.120	117.775 70.226
Number of spikes per plant	\bar{X} S^2	12.520 11.220	7.780 9.114	13.11 16.008	12.803 34.744	12.967 22.310	10.475 24.941	12.420 8.779	10.320 12.304	12.080 10.647	13.225 28.799	13.058 24.677	12.058 17.484
Number of kernels per spike	\bar{X} S^2	61.060 135.404	87.480 198.908	64.180 117.538	71.517 436.133	64.158 230.874	74.358 407.431	64.000 90.655	63.540 102.417	64.780 104.787	63.950 163.814	64.583 140.000	62.533 145.495
100- kernel weight (gm)	\bar{X} S^2	41.199 28.974	67.259 25.251	58.594 30.000	57.896 150.000	51.420 127.604	62.120 135.124	46.784 26.728	59.368 34.659	52.563 17.863	52.549 45.922	50.223 43.905	58.391 40.046
Grain yield per plant (gm)	\bar{X} S^2	22.684 109.506	30.927 137.681	32.381 121.075	39.005 500.000	33.603 327.978	33.107 395.733	26.130 101.546	28.502 110.000	30.346 105.000	33.595 511.462	31.264 300.000	31.487 400.250

Estimation of genetic parameters for some quantitative traits in.....

Table (3) : Heterosis , inbreeding depression and gene action for some quantitative characters in two bread wheat crosses.

Characters	Crosses	Heterosis BP%	Inbreeding depression %	E1	E2	Gene action parameters					
						m	a	d	aa	ad	dd
Days to heading	I	1.277**	-0.770*	0.257	-0.155	95.872**	-3.158**	-2.289	-1.339	-1.008*	1.649
	□	3.876**	0.466	-1.009**	-0.013	96.031**	4.800**	2.891*	4.011**	0.080	-3.984
Days to maturity	I	0.403**	0.630**	-1.137**	-1.655**	148.678**	-0.408	0.849	1.239	0.582	2.071
	□	1.599**	0.664**	-1.019**	-1.977**	146.461**	2.933**	0.042	0.122	0.533	3.831**
Plant height	I	9.965**	0.728	1.084	-2.252	112.614**	-5.542**	-5.019	-8.839	0.918	13.342
	□	10.984**	3.716**	-2.601**	-5.965**	114.019**	-8.275**	2.072	-1.528	-0.155	13.458**
Number of spikes per plant	I	4.712	2.343	1.173**	0.182	12.803**	2.492**	-1.368	-4.328*	0.122	3.964
	□	-2.738	-9.478*	1.500**	1.667*	13.225**	1.000	-1.957	-2.667	-0.050	-0.667
Number of kernels per spike	I	-26.635**	-11.431**	2.292	0.067	71.517**	-10.200**	-19.123**	-9.033	3.010	8.900**
	□	1.219	1.281	-0.325	-1.433	63.950**	2.050	-0.557	-1.567	1.820	4.433
100- kernel weight	I	-12.883**	1.192	1.484	0.717	57.896**	-10.700**	-0.138	-4.503	2.330	3.069
	□	-11.462**	0.026	-0.270	2.975*	52.549**	-8.169**	6.518**	7.031**	-1.877	-12.981**
Grain yield per plant	I	4.701	-20.457**	9.412**	7.525*	39.005**	0.496	-17.022*	-22.598**	4.618	7.549
	□	6.470	-10.708	4.764**	5.089	33.595**	-0.224	-5.851	-8.880	0.962	-1.297

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

