

ESTIMATION OF GENETIC PARAMETERS USING FIVE POPULATIONS OF SOME BREAD WHEAT CROSSES

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ABSTRACT

Two experiments were carried out using two crosses namely Giza 168 x Gemmeiza 7 and Irina x Sids 1. Five populations (P1, P2, F1, F2 and F3) for each cross were used in this investigation.

Significant positive heterotic effects were obtained for number of spikes/plant and grain yield/plant in the first cross. On the other hand, significant negative heterotic effects were found for number of kernels/spike, number of spikes per plant and grain yield per plant in the second cross. Over dominance towards the higher parent for number, of kernels/spike and grain yield per plant observed in the first cross. Inbreeding depression estimates were found to be significant for all studied attributes except for number of spikes/plant and grain yield/plant in the first cross. On the other side inbreeding depression were significant negative for kernel weight in the second cross. F2 deviation (E1) were significant for all studied characters for two crosses except for number of spikes/plant and grain yield/plant in the first cross. Moreover, F3 deviation (E2) were significant for all studied characters in two crosses except for grain yield/plant in the first cross.

The (additive – additive x dominance) gene effect was significant for all studied characters in two crosses. These results suggest the potential for obtaining further improvement in most studied characters. In addition, dominance and epistasis were found to be significant for most of the studied attributes.

High to medium values of heritability estimates were found to be associated with high and moderate expected and actual grain in most characters. This obtained results indicated that selection for the studied characters could be used in the early generations but may more effective if postponed to late one.

These study concluded that it may be take in consideration the first cross (Giza 168 x Gm. 9) to improve the breeding program in the national wheat research program.

INTRODUCTION

It is well known that the development of a wheat varietal improvement strategy should be based upon the genetic information of heritability and types of gene action controlling yield and other agronomic traits. It is also known that the diallel analysis is an attempt to partition phenotypic variation into genotypic and environmental components and to subdivide genotypic variation into additive and non-additive components. These estimates can be used to draw inferences about the genetic systems involved yield and its components and the best breeding strategy to be used to improve them. Furthermore, maximum progress in improving a character would be expected with a carefully designed pedigree selection program when the additive gene action is the main component, whereas the presence of high non-additive gene action would suggest the use of a hybrid program. In addition, the effectiveness of selection will be determined by calculating heritability value as a narrow sense. In this respect, the majority of reports on genetic behavior of yield and its components in wheat indicated that, the

additive components of genetic variance are being more important than those attributed to non-additive components (Abull-Naas *et al* 1991).

This study was conducted to be study the gene effect, heritability and comparison between actual and expected genetic gain of two bread wheat crosses derived from five parental bread wheat genotypes using five populations of each cross.

MATERIALS AND METHODS

Two crosses were used in the present study derived from four wide diversified parental bread wheat cultivars. The names, pedigree and origin of the parental genotypes are given in Table (1). These genotypes were used to obtain the following two crosses, Giza 168 x Gemmeiza 7 and IrinexSids 1.

The present study were carried out at El-Giza Agricultural Research Station during four successive seasons from 2001/2002 to 2004/2005. In the first season (2001/2002), the parental genotypes were crossed to obtain F1 seeds. In the second season (2002/2003), the hybrid seed of the two crosses were sown to give F1 plants. These plants were selfed to produce F2 seeds. Moreover, the same crosses were made to ensure fresh hybrid seeds. The new hybrid seed and part of obtained seeds from F1 plants (F2 seeds) were kept in refrigerator the final experiment. In the third season (2003/2004), two F1 seeds were sown to produce F1 plants, each of F1 plants were selfed to produce F2 seeds. In addition, F1 and F2 plants were selfed to produce F2 and F3 seeds respectively. In the fourth season (2004/2005) the obtained seeds for the five Populations P1, P2, F1, F2 and F3 of the two crosses were evaluated using a randomized complete block design with three replications. The experimental unit was two rows for each of parents and F1 progenies totaling 20 plants from each of them, 20 rows for F2 generation totaling 200 plants and five rows for F3 families totaling 50 plants. Each row was 2 m. long and 20 cm. apart between rows. The plants within row were 10 cm. space. The data were recorded on individual guarded plants for, number of spikes/plant, number of kernels/spike, 100-kernel weight (g) and grain yield/plant (g). Various biometrical parameters in this study may only be calculated if the F2 genetic variance was found to be significant. In this concern, F2 genetic variance was significant. Heterosis % was expressed as percentage increase in F1 performance above the better parent value. Potance ratio (P) was also calculated according to Peter and Frey (1966). Inbreeding depression % was estimated as the average percentage decrease of the F2 from F1. In addition, F2 deviation (E1) and F3 (E2) were measured as suggested by Mather and Jinks (1971).

The estimates of mean effect parameter (m), additive-additive x dominance (d*), dominance (h), dominance x dominance (e) and additive x additive (i) were obtained by five parameters model illustrated by Hayman model according to Singh and Chaudhary (1985).

Heritability was calculated in both broad and narrow sense according to Mather's procedure (1949) and parent off spring regression according to Sakai (1960). Furthermore, the expected and actual genetic advance (Δg) was computed according to Johansen *et al* (1955). Likewise, the genetic gain

represented as percentage of the F2 and F3 mean performance ($\Delta g\%$) was estimated using the method of Miller / (1958). On the other hand, Hendawy (1998) reported that, non-additive components of genetic variance seemed to be more important inheritance of certain characters in wheat. Heritability was estimated for most traits by many investigators (Abul-Naas *et al* 1991; and Mosaad *et al* 1990), but variant estimates have been reported.

Table (1): The name, pedigree and origin in for four parental bread wheat cultivars.

Genotype (Name)	Pedigree	Origin
Giza 168	MRL/BUC//SERI. CM93046-8M-0Y-0M-2Y-0B-0GZ.	EGYPT
Gemmeiza 7	CMH74A. G30/SX//SERI 82/AGENT. CGM4611-2GM-3GM-1GM-0GM.	EGYPT
Irina	BUC/FLK//MYNA/VUL. CM91575.	MEXICO
Sids 1	HD21/PAVON"S"//1158.57/MAYA74"S".	EGYPT

RESULTS AND DISCUSSION

Varietal differences in response to their genetic background were found to be significant in most characters under investigation. The genetic variances within F2 populations were also found to be significant for all studied characters in the two crosses. Therefore, different biometrical parameters used in this investigation were estimated. Means and variances of five populations i.e., P1, P2, F1, F2 and F3 for the studied characters in the two crosses are presented in Table (2). Heterosis percentage over better parent, potance ratio (P), inbreeding depression percentage, E1, E2 and different gene action for the four studied characters are given in Table (3).

Table 2: Means (\bar{x}) and variances (s^2) for the studied characters using the five populations (P1, P2, F1, F2 and bulk F3 families) for two bread wheat crosses.

Characters	Parameters	Giza 168 x Gemmeiza 7					Irina x Sids 1				
		P1	P2	F1	F2	F3 bulk	P1	P2	F1	F2	F3 bulk
No.of spikes/plant	X	21.54	19.75	22.95	21.32	18.95	25.15	18.3	20.8	19.85	16.5
	S ²	5.94	3.49	5.78	34.75	23.95	6.35	4.82	3.92	23.09	17.35
No. of kernels/spike	X	80	69.8	68.15	67.95	64.16	74.95	79.92	77.62	68.95	59.82
	S ²	20.10	16.85	18.5	251.2	170.9	20.85	14.11	27.62	112.64	75.88
100-kernels weight (g)	X	4.46	5.04	5.34	5.3	5.69	4.43	4.08	4.62	5.013	5.052
	S ²	0.036	0.03	0.032	0.239	0.141	0.02	0.023	0.025	0.221	0.139
Grain yield/plant (g)	X	55.35	52.9	59.95	58.5	55.25	63.93	53.42	57.3	51.85	50.9
	S ²	18.75	17.92	16.35	294.55	181.75	18.18	11.31	12.29	180.95	115.95

Exploitation of heterosis is considered to be one of the outstanding achievements of plant breeding. In self-pollinated crops like wheat, the scope for utilization of heterosis depends mainly upon the direction and magnitude of heterosis. The heterosis over better parent may be useful in identifying the best hybrid combinations but these hybrids can be immense practical value if they involve the best cultivars of the area (Prasad *et al* 1988).

Significant positive heterotic effects were found for all studied characters except for, number of spikes/plant in the first cross and for number of kernels/spike and grain yield/plant which showed significant negative one the second one. Similar results were reported El-Hosary *et al* (2000), Moustafa (2002), Hendawy (2003), El-Sayed (2004) Abdel-Nour, Nadya *et al* (2005), Abdel-Nour, Nadya (2006), Abdel-Nour, Nadya and Moshref (2006). Number of spikes/ plant, number of kernels/spike and kernel weight are the main components of grain yield/plant, Hence, if it is found in increasing heterosis one or more of these attributes with others being constant would lead to favorable yield increase in hybrid. The lack of significance in heterosis of number of spikes/plant in the first cross could be due to the lower magnitude of the non-additive gene action. These results are in agreement with these of El-Rassas and Mitkees (1985). The pronounced heterotic effect for kernel weight in the first cross (giza 168 x Gemza 7) and second cross (Irina x Sids 1) would be of interest in a breeding program for high yielding ability by selecting this character.

The Potence ratio (P) showed over-dominance towards the higher parent for all studied characters except for, number of spikes/plant, and grain yield/plant which showed complete dominance towards the lower parent while number of kernels/spike showed complete dominance towards the higher parent. These results are in harmony with those obtained by Mosaad *et al* (1990), Abul-Naas *et al* (1991), Al-Kaddoussi *et al* (1994); Moustafa (2002), Hendawy (2003), Abdel-Nour, Nadya (2006) and Abdel-Nour, Nadya and Moshref (2006).

Significant values of inbreeding depression were detected for all studied characters except for; number of kernels/spike in first cross and for grain yield/plant in the second one. However, significant negative inbreeding depression values was detected for 100-kernel weight in the second cross.

This is a valid results, since the expression of heterosis in the F1 will be followed by considerable reduction in F2 performance. The obtained results for most cases were in harmony with that obtained by Khalifa *et al* (1997).

Significant heterosis and insignificant inbreeding depression were obtained for grain yield/plant in the first cross. Moreover, significant positive heterosis and significant negative inbreeding depression for kernel weight in the second cross was detected. 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).

Significant positive F2 deviation (E1) were indicated for kernel weight for two crosses. Meanwhile, significant negative values were obtained for number of spikes/plant, number of kernels/spike and grain yield/plant in the second cross, and for number of kernels/spike in the first one. These results may refer to the contribution of epistatic gene effects in the performance of these characters. On the other hand, insignificant F2 deviation (E1) was detected for number of spikes/plant and grain yield/plant in the first cross. This may indicate that the epistatic gene effects have minor contribution in the inheritance of these characters.

Significant positive F3 deviation (E2) was revealed for kernel weight in the two crosses. Moreover, significant negative values were detected for the rest studied the characters of the two crosses except for grain yield/plant in the first cross. These results would ascertain the presence of epistasis in such large magnitude as to warrant great deal of attention in breeding programs.

Nature of gene action was determined by using the five parameters analysis (Hayman's model) according to Singh and Chaudhary (1985) are presented in Table 3. The estimated mean effect parameter (m), which reflects the contribution due to over all mean plus the locus effect and interactions of the fixed loci, was found to be highly significant for all the studied characters. The additive gene effect (d*) was significantly positive for; number of spikes/plant and grain yield/plant in the two crosses, for the kernels/spike in the first cross; and for kernel weight in the second one. Meanwhile, the additive gene effect (d*) was significantly negative for the rest studied characters in two crosses. These results suggest the potential for obtaining further improvement for these characters by using pedigree selection program. Similar results were obtained by El-Hosary *et al* (2000), Moustafa (2002), Hendawy (2003), El-Sayed (2004), Abdel-Nour *et al* (2005) Abdel-Nour, Nadya (2006) and Abdel-Nour, Nadya and Moshref (2006).

Dominance gene effect (h) was significant positive for all studied characters of two crosses except for kernel weight which showed significant negative. Significance of these components indicated that, both additive and dominance gene effects are important in the inheritance of these characters. Therefore, selecting desired characters may be practiced in the early generations but may be more effective in late ones (Shehab El-Din 1993).

Dominance x dominance (e) type of gene action was significant for kernel weight and number of kernels per spike in the first one. On the other hand, additive x additive type of epistasis (i) was detected to be significant positive for all studied characters except for kernel weight which seemed negative significant in the first cross. The importance roles of both additive and non-additive gene action in most studied characters indicated that selection procedures based on the accumulation of additive gene effects may be very successful in improving these characters. Similar results were reported by Gouda *et al* (1993); Al-Kaddoussi *et al* (1994), Hosary *et al* (2000), Moustafa (2002). Hendawy (2003), Abdel-Nour, Nadya (2006) and Abdel-Nour, Nadya and Moshref (2006).

Heritability in both broad and narrow senses, between generations (parent off- spring regression) are presented in Table (4). High heritability values in broad sense were detected for all studied characters.

High to moderate estimates of narrow sense heritability and parent off-spring regression was found for all studied characters in the two crosses. The differences in magnitude of both and narrow sense and parent off- spring regression, heritability estimates for all studied characters would be ascertained the presence of both additive and non-additive gene effects in the inheritance of these characters. This conclusion was also confirmed by estimates of gene action parameters.

Table 3: Heterosis, potence ratio, inbreeding depression and gene action parameters for the two bread wheat crosses.

Characters	cross	Heterosis % over B.P Ratio (P)	Inbreeding depression %	Gene action parameters							
				Potence Ratio (P)	m	d*	h	e	i	E1	E2
No. of spikes/plant	I	6.55	7.1*	2.575	21.32**	0.895*	7.407**	-8.293*	6.892**	-0.478	-5.695**
	II	-17.3**	4.57*	-0.27	19.85**	3.425**	9.567**	-15.333**	17.342**	-1.413**	-9.525**
No. of kernels/spike	I	14.01**	0.293	1.323	67.95**	5.1**	10.24**	19.68*	27.19**	-3.575**	-14.73**
	II	-2.88*	11.17**	0.074	68.8**	-2.485**	30.127**	-25.573**	24.972**	-9.028**	-35.415**
100-kernels weight (g)	I	5.95**	0.749*	2.034	5.3**	-0.29**	-1.013**	2.187**	-2.184**	0.255**	1.229**
	II	4.29**	-8.51**	2.086	5.013**	0.175*	-0.366**	-0.84*	-0.381	0.576**	1.229**
Grain yield/plant (g)	I	8.31**	2.42	4.755	58.5**	1.225**	9.633*	-13.467	6.259*	1.463	-3.575
	II	-10.37**	9.51**	-0.262	51.85**	5.255**	6.167*	9.467	18.052**	-6.138**	-14.175**

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

Table 4: Heritability and expected versus actual gain for all studied characters in two crosses of bread wheat.

Characters	Cross	Heritability --		Expected gain		Actual gain	
		broad sense	narrow sense	Δg	% of F2	Δg	% of F3
No. of spikes/plant	I	83.37	64.2	7.796	36.57	7.54	39.8
	II	83.02	44.91	4.446	22.4	5.28	32
No. of kernels/spike	I	92.64	63.94	20.876	30.72	21.083	32.86
	II	81.71	71.27	15.58	22.6	13.7	22.91
100-kernels weight (g)	I	86.61	81.59	0.822	15.5	0.649	11.4
	II	88.69	75.11	0.727	14.51	0.632	12.52
Grain yield/plant (g)	I	94.5	76.14	26.92	46.02	23.63	42.76
	II	92.31	71.84	19.91	38.39	18.2	35.76

Similar results were obtained by Gouda *et al* (1993), El-Sayed (2004) and Abdel-Nour-Nadia *et al* (2005). Also, Table (4) showed that the expected versus actual genetic gain for all studied characters. The expected genetic advance ($\Delta g\%$ of F2) and actual genetic advance ($\Delta g\%$ of F3) ranged from moderate to high for all studied characters in the two crosses except for kernel weight in two crosses. These results indicate that the possibility of practicing selection in early generation to enhance these characters and hence selecting high yielding genotypes. Dixit *et al* (1960) pointed out high genetic advance, but in order to make effective selection, high heritability should be associated with high genetic gain.

Generally, the most biometrical parameters resulted from the two crosses were higher in magnitude. Consequently, it could be concluded that the crosses (Giza 168 x Gemmeiza 7) would be of interest in a breeding program for bringing out the maximum genetic improvement.

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تقدير الثوابت الوراثية باستخدام العشائر الخمسة في بعض هجن من قمح الخبز
صباح حمزه أبو العلا
البرنامج القومي لبحوث القمح-معهد بحوث المحاصيل الحقلية-مركز البحوث الزراعية

أجرى هذا البحث في محطة بحوث الجيزة أربعة مواسم متتالية من ٢٠٠١/٢٠٠٢ حتى ٢٠٠٤/٢٠٠٥م على هجينين من قمح الخبز ومما (جيزة ١٦٨ X جميزه ٧) و(ايرينا X سنس ١) واشتملت الدراسة على كل من الأبوين والأجيال الأولى والثانية والثالثة وكانت النتائج كما يلي:

- ١- كانت قوة الهجين موجبة وعالية المعنوية بالنسبة لصفى عدد الحبوب في السنبله ومحصول الحبوب للنبات الفردى فى الهجين الأول.
- ٢- أوضحت دراسة طبيعة التوارث أن درجة السيادة كانت فائقة تجاه الأب الأعلى فى جميع الصفات تحت الدراسة بالنسبة للهجين الأول وكذلك فى الهجين الثانى فى صفة وزن الحبة.
- ٣- أوضحت الدراسة أن تأثير الفعل الجينى المتخفيف كان معنوياً وموجباً بالنسبة لجميع الصفات تحت الدراسة فيما عدا صفة وزن الحبة فى الهجين الأول وصفة عدد الحبوب فى السنبله فى الهجين الثانى.
- ٤- كان التأثير السيادةى للجين موجب وعالى المعنوية فى جميع الصفات تحت الدراسة فيما عدا صفة وزن الحبة التى أظهرت معنوية سالبة.
- ٥- تأثير التربية الداخلية كان موجباً ومعنوياً فى كل الصفات المدروسة ما عدا عدد الحبوب/سنبله وصفة وزن الحبوب للنبات الفردى بالنسبة للهجين الأول، بينما أظهرت قيمة سالبة ومعنوية بالنسبة لصفة وزن الحبة فى الهجين الثانى.
- ٦- كانت اعترافات الجيل الثانى (E1) واعترافات الجيل الثالث (E2) معنوية لمعظم الصفات فى الهجن تحت الدراسة مما يوضح أهمية الفعل الجينى التفرقى فى وراثه هذه الصفات.
- ٧- أظهرت الكفاءة الوراثية بمعناها الواسع قيمة عالية لمعظم الصفات كما أظهرت الكفاءة الوراثية بمعناها الضيق وكذلك الكفاءة الوراثية بين الأجيال فيما عدا صفة عالية إلى متوسطه مرتبطة بنسبة تحسين وراثى مرتفع إلى متوسط فى معظم الصفات المدروسة.
- ٨- كانت قيم التحسين الوراثى الفعلى المستحصل عليها بصفة عامة متطابقة مع القيم المتنبأ بها لتحسين المحصول وبكوناته من خلال الانتخاب ومن ثم يمكن للعربى الاعتماد على أنتم المتنبأ بها فى الانتخاب لتحسين الصفات المحصولية.
- ٩- أظهرت التأثيرات الوراثية المتخفيفه وكذلك الفعل الجينى الغير مضيف دوراً هاماً فى وراثه معظم الصفات المدروسة.
- ١٠- توصى الدراسة بأخذ الهجين الأول (جيزة ١٦٨ X جميزه ٧) فى الاعتبار عند عمل برامج تربية فى برنامج بحوث القمح.