

## GENETICAL ANALYSIS OF GRAIN YIELD AND SOME RELATED TRAITS IN BREAD WHEAT

MENSHAWY A.M.M.

National Wheat Research Program, Field Crops Research Institute, ARC.

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### Abstract

Genetical analysis for grain yield and some related traits was carried out at Sakha Agric. Res. Sta. during 2000/2001 and 2001/2002 wheat-growing seasons. Seven diverse bread wheat cultivars namely; Sakha 61, Sakha 93, Giza 163, Giza 164, Giza 168, Gemmeiza 9 and Sids 1 were crossed in a half-diallel set to study the relative magnitude of genetic components of variation and their derived parameters. Parents and  $F_1$  generations resulting from a  $7 \times 7$  diallel mating scheme were grown in space – planted experiment in 2001/2002 season. Analyzed data revealed the significant genotypic variation and validity of the basic assumptions for diallel analysis. The additive and dominance gene effects were significant and involved in the inheritance of all studied characters. Additive component played the major role in the inheritance of days to heading, plant height and grain filling period. Thus, phenotypic selection would be an effective procedure for improving those characters. Whereas, the dominance genetic variance was main component controlling the inheritance of number of kernels / spike, number of spikes/ plant, 100-kernel weight and grain filling rate. The dominance gene action was larger in its magnitude than additive ones, resulting in  $(H_1/D)^{1/2}$  more than unity for all characters except for days to heading, plant height and grain filling period. The "F" values coupled with KD/KR ratio, indicated excess of dominant increasing alleles for all characters except for plant height and number of spikes / plant. Heritability estimates in narrow sense were relatively high for days to heading, plant height and grain filling period; moderate for number of kernels/ spike, number of spikes / plant, grain yield and grain filling rate, while it was low for 100-kernel weight.

### INTRODUCTION

Breeders of wheat (*Triticum aestivum* L) are principally interested in improving the genetic potential of their materials to maximize economic gain per input unit. Therefore, they require information to identify and to select desirable genotypes efficiently, and to concentrate their genes in a line and variety that is commercially acceptable.

Yield is a complex entity associated with a number of component characters. So, it is essential to understand their inter-relationships. Such information is of great importance to the breeder in adopting proper selection method. Grain yield of wheat is determined partly by kernel weight, which is a function of the rate and duration of grain filling (Mou and Kronstad 1994).

A better understanding of the inheritance and type of gene action for traits related to grain yield would help wheat breeders to increase and stabilize this character. In this respect, additive and dominance gene effects with great importance of additive were found to control; days to heading (Menshawy 2000 and Abd El-Aty 2002); grain filling period and rate (Mou and Kronstad 1994 and Menshawy 1996). However, additive and dominance gene effects were significant and involved in the inheritance of plant height, number of spikes / plant, number of kernels/ spike and grain yield / plant (Awaad 2002). On the other hand Salem *et al.* (2000), reported that additive and dominance gene effects with great importance to dominance were found to control the genetic system of grain yield and its components.

Heritability in narrow sense ( $h_n$ ) is the most important because it provides a measure of the breeding value of a population and measures the proportion of the variation which is due to the additive effects of genes. However, heritability in narrow sense values were more than 50% for days to heading, grain filling period and rate and plant height (Mou and Kronstad 1994, Salama, 2000 and Salem *et al.* 2000). Meanwhile, Awaad (2002) reported that these values were lower than 50% for yield and its components.

## MATERIALS AND METHODS

The present investigation was conducted at Sakha Agricultural Research Station, Agricultural Research Center, Egypt, during the two wheat-growing seasons 2000-2001 and 2001-2002. Seven diverse bread wheat cultivars were selected and crossed in all possible combinations excluding reciprocals, in 2000/2001 season to produce their  $F_1$  crosses. Name and pedigree of these cultivars are shown in Table 1.

Table 1. Name and pedigree of the studied parental bread wheat cultivars.

Parent #	Name	Cross Name & Pedigree
1	Sakha 61	Inia / RL 4220 // 7c / Yr "S" CM15430 -2S-5S-0S-0S
2	Sakha 93	Sakha 92/ TR 810328 S 8871-1S-2S-1S-0S
3	Giza 163	T. Aestivum/ Bon // Cno / 7c CM33009 -F-15M-4Y-2M-1M-1M-1Y-0M
4	Giza 164	KVZ / Buha "S" // Kal / Bb CM33027-F-15M-500Y-0M
5	Giza 168	Mrl / Buc // Seri CM 93046-8M-0Y-0M-2Y-0B
6	Gemmeiza 9	Ald "S" / Huac // Cmh 74A. 630 / Sx CGM 4583-5GM-1GM-0GM
7	Sids 1	HD 2172 / Pavon "S" // 1158.57/ Maya 74 "S" Sd 46-4Sd-2Sd-1Sd-0Sd

The materials comprising 28 genotypes (7 parents+21 F<sub>1</sub>'s) were evaluated in a randomized complete block design with three replications during 2001/2002 wheat growing season. Each genotype was grown in a single row of 2m long, 30 cm apart and the plants were spaced 20 cm apart within the rows. The recommended package of cultural practices was followed. Data were recorded on five randomly selected plants per row in each of the three replications.

The studied characters were: number of days to heading (day), number of days to physiological maturity (day), grain filling period (day), plant height (cm), number of spikes per plant, number of kernels per spike, 100- kernel weight (g), grain yield per plant (g), and grain filling rate (g / day / plant).

Data obtained were statistically analyzed on plot mean basis. Analysis of variance was conducted to test the differences among various genotypes. The diallel cross analyses adopted by Hayman (1954 and 1958) were applied. Estimates of the genetic variation components were : components of variation due to additive gene effects (D), mean of covariance of additive and dominance effects over the arrays (F), component

of variation due to dominant gene effects ( $H_1$ ), dominance indicated a symmetry of positive and negative effects ( $H_2$ ), dominance effects as the algebraic sum over all loci in heterozygous phase in all crosses ( $h^2$ ) and component of variation due to environmental effect (E).

The above estimates were then used to compute the following proportions: the mean degree of dominance at each locus ( $H_1/D$ )<sup>1/2</sup>, the ratio of genes with positive and negative effects in the parents ( $H_2/4H_1$ ), the ratio of dominance and recessive genes in the parents (KD/KR), an estimator of groups number of genes which are involved in the performance of the trait and exhibit dominance to certain degree (K) and the coefficient of correlation between the parental order of dominance and parental measurement (r). Moreover, heritability values were also estimated.

## RESULTS AND DISCUSSION

The analysis of variance showed highly significant differences among various genotypes indicating that the parents were greatly different in all studied characters due to their partial different genetic backgrounds and origins as shown in Table 2.

Table 2. Analysis of variance of the studied characters in some bread wheat genotypes.

S.O.V.	df	MS								
		Days to heading (day)	Days to maturity (day)	Grain filling period (day)	Plant height (cm)	Spikes per plant	kernels per spike	100-kernel weight (g)	Grain yield/plant (g)	Grain filling rate (g/day)
Replicates	2	3.9	1.3	9.7	36.8	27.4	68.4	0.04	186.9	0.14**
Genotypes	27	52.4**	14.3*	36.7**	260.8**	69.7**	272.7**	0.80**	975.6**	0.41**
Error	54	5	4.4	5.1	26.7	8.1	22.9	0.17	55.3	0.02

\* and\*\* = Significant at 0.05 and 0.01 respectively.

Mean values of the parents and their  $F_1$  hybrids are given in Table 3. Wide variations were observed among parents and  $F_1$  hybrids. The genotypes having long period to heading usually require short grain filling period and vice versa. These results are in accordance with the findings of Menshaw (1996 and 2000) and Abdalla *et al.* (1997). It is of interest to note that  $F_1$  hybrid Giza 163 / Giza 168 which had the highest grain filling rate and high number of kernels / spike possessed the highest grain yield / plant,

which is in agreement with the data reported by Sharma (1994).

Table 3. Mean estimates of the studied characters in some bread wheat genotypes.

Genotypes	Characters								
	Days to heading (day)	Days to maturity (day)	Grain filling period (day)	Plant height (cm)	Spikes per plant	Kernels per spike	100-kernel weight (g)	Grain yield / plant (g)	Grain filling rate (g/day)
Parents									
Sakha 61 (P <sub>1</sub> )	93.7	153.0	56.3	93.3	18.4	58.9	4.1	37.5	0.7
Sakha 93 (P <sub>2</sub> )	104.0	155.3	51.3	93.3	19.9	63.2	4.1	43.9	0.9
Giza 163 (P <sub>3</sub> )	115.3	157.3	42.0	120.0	23.2	64.5	3.8	34.4	0.8
Giza 164 (P <sub>4</sub> )	108.7	155.3	46.7	110.0	19.5	81.2	3.9	38.3	0.8
Giza 168 (P <sub>5</sub> )	100.7	156.0	55.3	105.0	28.5	88.6	4.7	86.3	1.6
Gemmeiza 9 (P <sub>6</sub> )	110.0	157.3	47.3	100.0	27.2	86.4	5.1	66.7	1.4
Sids 1 (P <sub>7</sub> )	106.0	156.3	50.3	121.7	28.6	70.9	4.8	48.9	1.0
Hybrids									
P <sub>1</sub> X P <sub>2</sub>	97.0	151.0	54.0	98.3	17.2	54.3	5.2	31.9	0.6
P <sub>1</sub> X P <sub>3</sub>	107.0	150.7	43.7	103.3	13.9	66.9	5.4	39.9	0.9
P <sub>1</sub> X P <sub>4</sub>	105.3	151.0	45.7	102.7	15.0	62.8	5.5	40.7	0.9
P <sub>1</sub> X P <sub>5</sub>	100.0	154.3	54.3	98.3	19.9	73.4	4.4	45.5	0.8
P <sub>1</sub> X P <sub>6</sub>	106.3	155.0	48.7	93.3	27.7	81.5	4.8	56.4	1.2
P <sub>1</sub> X P <sub>7</sub>	103.0	151.3	48.3	103.3	25.1	64.1	5.0	60.6	1.3
P <sub>2</sub> X P <sub>3</sub>	106.7	155.3	48.7	100.0	18.1	75.6	5.1	45.9	0.9
P <sub>2</sub> X P <sub>4</sub>	106.0	155.0	49.0	105.0	17.4	63.6	4.9	48.8	1.0
P <sub>2</sub> X P <sub>5</sub>	104.3	155.7	51.3	100.0	17.4	68.4	5.2	56.8	1.1
P <sub>2</sub> X P <sub>6</sub>	107.7	155.7	48.0	96.7	22.1	70.2	5.7	39.3	0.8
P <sub>2</sub> X P <sub>7</sub>	102.0	154.3	52.3	108.3	20.9	65.3	4.7	48.9	0.9
P <sub>3</sub> X P <sub>4</sub>	111.0	155.7	44.7	106.7	19.2	69.6	4.6	37.1	0.8
P <sub>3</sub> X P <sub>5</sub>	105.0	151.0	46.0	113.3	26.4	89.1	5.1	93.5	2.0
P <sub>3</sub> X P <sub>6</sub>	112.7	157.3	44.7	110.0	26.4	66.7	6.0	65.4	1.5
P <sub>3</sub> X P <sub>7</sub>	106.3	156.3	50.0	130.0	28.3	79.5	5.0	81.9	1.6
P <sub>4</sub> X P <sub>5</sub>	104.9	154.5	49.6	122.4	26.7	89.7	5.0	84.1	1.7
P <sub>4</sub> X P <sub>6</sub>	109.7	156.0	46.3	106.7	20.3	73.5	5.2	75.5	1.6
P <sub>4</sub> X P <sub>7</sub>	105.3	155.7	50.3	116.7	28.1	82.2	5.1	83.0	1.7
P <sub>5</sub> X P <sub>6</sub>	107.7	157.3	49.7	110.0	16.6	79.7	5.1	58.0	1.2
P <sub>5</sub> X P <sub>7</sub>	108.0	158.3	50.3	110.0	19.9	71.0	4.7	51.9	1.0
P <sub>6</sub> X P <sub>7</sub>	106.3	156.7	50.3	110.0	30.1	75.5	5.5	73.5	1.5
New LSD 0.05	3.4	3.8	3.6	7.9	4.4	7.3	0.7	11.2	0.2

Results in Table 4, indicate that  $t^2$  values were not significant for all studied characters except for days to maturity. Accordingly, the major assumptions postulated for diallel analysis appeared to be valid except for days to maturity. The regression coefficients are expected to be significantly different from zero but not from unity if all assumptions are correct. This was true for days to heading and grain filling period, confirming further validity of diallel assumptions. The other characters, which are significantly differed from unity and / or insignificantly differed from zero, showed a partial failure of the assumptions.

Table 4. Values of  $t^2$ , regression coefficient of covariance ( $W_r$ ) on variance ( $V_r$ ) and t-values for  $b = 0$  and  $b = 1$ .

Characters	$t^2$	Regression coefficient	t value for $b=0$	t value for $b=1$
Days to heading (day)	0.268	0.91± 0.313	2.910*	0.278
Days to maturity (day)	2.872*	0.149± 0.218	0.682	3.900**
Grain filling period (day)	0.082	0.835± 0.310	2.695*	0.532
Plant height (cm)	0.164	0.669± 0.261	2.560	1.269
Kernels per spike	0.067	0.802± 0.324	2.477	0.611
Spikes per plant	0.083	0.483± 0.453	1.065	1.140
100- kernel weight (g)	0.049	0.530± 0.338	1.572	1.391
Grain yield/plant (g)	0.025	0.601± 0.327	1.839	1.219
Grain filling rate (g/day)	0.353	0.466± 0.294	1.584	1.814

$b = 0$  and  $b = 1$  indicate difference of regression coefficient value from 0 and 1 (unit), respectively.

\* and \*\* Significant at 0.05 and 0.01, respectively.

The estimates of genetic and environmental components of variation for the studied characters are given in Table 5. The data showed that the additive component (D) and the dominance components ( $H_1$  and  $H_2$ ) were significant for all studied characters. These results indicate the importance of both additive and dominance gene effects in the inheritance of these characters. Comparison between magnitude of additive and dominance values revealed that the additive gene effects were more important than dominant ones for days to heading, plant height and grain filling period. Whereas, the dominance genetic variance was the prevailing in the other characters. Moreover, values of  $H_2$  were relatively smaller than those of  $H_1$ , indicating that the

positive and negative alleles, at the loci of the character in question, are not equal in proportion to the parents.

Table 5. Estimates of genetic components of variation for the studied characters of certain bread wheat cultivars.

Characters	D	F	H <sub>1</sub>	H <sub>2</sub>	h <sup>2</sup>	E
Days to heading (day)	36.63** ±1.83	13.22** ±4.39	13.99** ±4.40	11.18** ±3.89	-0.79 ±2.61	1.66* ±0.65
Days to maturity (day)	-	-	-	-	-	-
Grain filling period (day)	23.68** ±2.61	11.64 ±6.26	15.60* ±6.28	11.96* ±5.54	2.38 ±3.72	1.76 ±0.92
Plant height (cm)	126.83** ±11.24	-8.13 ±26.96	74.48** ±2.75	72.89** ±23.84	-2.91 ±16.01	9.02** ±3.97
Spikes per plant	17.01* ±6.65	-2.12 ±15.96	56.56** ±16.02	52.28** ±14.11	9.01 ±9.48	2.93 ±2.35
Kernels per spike	134.93** ±9.58	50.95* ±22.97	174.56** ±23.05	152.79* ±20.31	-1.63 ±13.64	8.18* 3.39
100- kernel weight (g)	0.19* ±0.08	0.23 ±0.19	0.80** ±0.20	0.68** ±0.17	1.61** ±0.12	0.05 ±0.03
Grain yield / plant (g)	339.80** ±101.00	230.94 ±242.30	961.03** ±243.16	746.54** ±214.26	141.96 ±143.91	20.13 ±35.71
Grain filling rate (g/day)	0.10* ±0.04	0.04 ±0.10	0.40** ±0.10	0.32** ±0.09	0.09 ±0.06	0.01 ±0.02

Similar results were also obtained by Awaad (2002) and Abd El-Aty and Katta (2002) for days to heading, plant height, number of spikes / plant, number of kernels/ spike, 100 – kernel weight and grain yield / plant.

The F value was positive and significant for days to heading and number of kernels/ spike, reflecting that dominant genes were more frequent than recessive ones among the parental genotypes. However, the insignificant values of F for the other characters may indicate the equality in the relative frequencies of dominant and recessive genes in the parents. Estimates of h<sup>2</sup> values were found to be significant and positive for 100-kernel weight indicating the prevalence of positive genes controlling this character and suggesting that dominance was unidirectional. The estimates of h<sup>2</sup> values were found to be not significant for all other studied characters in spite of significant of H<sub>1</sub> and H<sub>2</sub> that could be due to the presence of considerable amount of cancel-

ing dominance effects in the parental materials.

Several ratios and proportions were obtained using the estimates of genetic and environmental components of variation to provide further genetic information about each studied character as presented in Table 6. Mean degree of dominance  $(H_1/D)^{1/2}$  indicated the presence of over dominance for number of kernels / spike, number of spikes / plant, 100-kernel weight, grain yield / plant and grain filling rate. Meanwhile, partial dominance was observed for the other characters. In this connection, similar conclusions were reported by several researchers; Eissa *et al.* (1994) for the number of kernels / spike and number of spikes / plant and Abd El-Aty and Katta (2002) and Awaad (2002) for days to heading, 100 – kernel weight and grain yield / plant.

The proportion of genes with negative and positive effects in the parent  $(H_2/4H_1)$  was equal or near to one quarter for most of the studied characters, indicating that the negative and positive alleles were equally distributed among the parents.

The ratio of dominant to recessive genes (KD/KR) was found to be more than unity for all characters except for plant height and number of spikes / plant, confirming the existence of more dominance than recessive genes in the parents (Table 6).

Regarding number of gene block (K), the data showed that one gene blocks governed all studied characters except 100-kernel weight which is governed by two gene blocks.

Table 6. Proportions of genetic components for the studied characters.

Characters	$(H_1/D)^{1/2}$	$H_2/4H_1$	KD/KR	$h^2/H_2$ (K)	r	h (sub)
Days to heading (day)	0.618	0.200	1.825	-0.071	-0.259	0.75
Days to maturity (day)	-	-	-	-	-	-
Grain filling period (day)	0.812	0.192	1.868	0.199	0.649	0.62
Plant height (cm)	0.766	0.245	0.920	-0.040	0.870	0.72
Spikes per plant	1.824	0.231	0.934	0.172	-0.349	0.42
Kernels per spike	1.137	0.219	1.398	-0.011	0.118	0.53
100- kernel weight (g)	2.059	0.211	1.825	2.365	-0.818	0.16
Grain yield (g)	1.682	0.194	1.506	0.190	-0.313	0.44
Grain filling rate (g/day)	1.957	0.201	1.218	0.278	-0.150	0.44



The correlation coefficient of  $(W_r+V_r)$  with parental measurements ( $Y_r$ ) was positive and high for plant height and grain filling period indicating that the dominance was unidirectional i.e. increasing alleles were associated with one parent, whereas, the decreasing alleles were presented in the second one. However, the correlation coefficient was found to be negative and high for 100-kernel weight suggesting that dominant genes controlling this character were unidirectional i.e. decreasing alleles were associated with one parent, while the increasing alleles were presented in the other one. The other characters were characterized by lower values suggesting that dominance is ambidirectional in the parents (Kearsey and Pooni 1996).

Moderate to high narrow sense heritability estimates were obtained for all studied characters except for 100-kernel weight, assuring the role of additive genes in controlling these traits (Table 6). Therefore, selection could be practiced in early segregating generations for such plant characteristics. These results agreed with those obtained by Shehab El-Dein (1997), Abd El-Aty (2002), Abd El-Aty and Katta (2002) and Awaad (2002).

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## التحليل الوراثى لحصول الحبوب وبعض الصفات المرتبطة به فى قمح الخبز

عبد السلام محمود محمد منشاوى

البرنامج القومي لبحوث القمح - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية

أجرى التحليل الوراثى لحصول الحبوب وبعض الصفات المرتبطة به فى محطة البحوث الزراعية بسخا خلال موسمى زراعة القمح ٢٠٠١/٢٠٠٠م و ٢٠٠٢/٢٠٠١م. وقد استخدمت ٧ أصناف من قمح الخبز متباينة وراثياً وهى سخا ٦١، سخا ٩٣، جيزة ١٦٣، جيزة ١٦٤، جيزة ١٦٨، جيزة ٩٦ و سدس ١. وقد أجريت التهجينات الممكنة تبعاً لنظام الـ Diallel لدراسة الأهمية النسبية لمكونات التباين الوراثى والنسب المتحصل عليها منها. وقد زرعت الآباء والجيل الأول الناتج منها فى تجربة على مسافات فى ثلاثة مكررات.

وأوضح تحليل البيانات وجود اختلافات وراثية بين التركيب الوراثية وكذلك صحة الفروض الأساسية الخاصة بهذه الطريقة و أظهرت النتائج أهمية كل من الفعل الجينى المضيف والسيادى فى وراثه كل الصفات المدروسة. كما أوضحت النتائج أن المكون المضيف كان المكون الرئيسى فى وراثه صفات عدد الأيام حتى طرد السنابل، طول النبات وفترة امتلاء الحبوب، مشيراً إلى فعالية الانتخاب المظهرى فى تحسين هذه الصفات. بينما كان التباين الوراثى السيادى المكون الرئيسى الذى يحكم وراثه صفات عدد الحبوب فى السنبله، وعدد السنابل / نبات، وزن الحبة ١٠٠ حبة، محصول الحبوب للنبات و معدل امتلاء الحبوب. وكان الفعل الجينى السيادى أكبر أهمية عن الفعل الجينى المضيف ويتضح ذلك من قيم متوسط درجة السيادة حيث كانت أعلى من الوحدة لكل الصفات المدروسة ماعدا صفات عدد الأيام حتى طرد السنابل، وطول النبات وفترة امتلاء الحبوب.

ارتبطت قيم F مع قيم KD/KR فى دلالة على زيادة تكرار الأليلات السائدة المتحكمة فى وراثه جميع الصفات المدروسة ماعدا صفتى طول النبات وعدد السنابل لكل نبات. كما أوضحت النتائج أن درجة التوريث بالمعنى الضيق تراوحت بين عالية نسبياً لصفات عدد الأيام حتى طرد السنابل، طول النبات وفترة امتلاء الحبوب مما يؤكد أهمية الفعل الجينى المضيف لهذه الصفات، بينما كانت متوسطة لصفات عدد الحبوب فى السنبله، عدد السنابل للنبات، محصول الحبوب للنبات ومعدل امتلاء الحبوب، فى حين كانت منخفضة لصفة وزن الحبة ١٠٠ حبة.