

GENETIC ANALYSIS OF YIELD, YIELD COMPONENTS, AND EARLINESS IN SOME BREAD WHEAT CROSSES

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(Manuscript received 18 September 2007)

Abstract

The present study was carried out at Sakha Agricultural Research Station, during the two winter wheat-growing seasons; 2004/2005 and 2005/2006. Six bread wheat genotypes namely; Gemmiza 9, Irena, Sakha 61, Line 1, Line 2 and Line 3 were used. These genotypes were crossed in a half diallel mating design to determine the genetic mechanism controlling earliness and grain yield characters. The parental genotypes and their F_1 's were planted in a randomized complete block design with three replications. The studied characters are: days to heading, days to physiological maturity, grain filling period, plant height, number of spikes/ plant, number of kernels/ spike, kernel weight, grain yield/ plant and grain filling rate/ plant. The results revealed that the additive and dominance gene actions were significant for most of the studied characters. Additive gene action played the major role in the inheritance of all studied characters. The mean degree of dominance (H_1/D)^{1/2} for all characters were less than one confirming the role of partial dominance gene effects in controlling the traits. The "F" values coupled with KD/KR ratio, indicated excess of dominant increasing alleles for all studied characters except for number of days to maturity, plant height and number of kernels/ plant. Narrow-sense heritability estimates were relatively high for all characters, indicating the importance of additive gene action.

Key words: Bread wheat, yield components, genetic analysis, heritability, diallel cross, gene action.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal crop in the world. It is the main staple food of the rapidly increasing population of Egypt, hence it occupies a prominent position in the cropping pattern of the country. Due to the limited cultivated area and irrigation water, to realize the demands of rapidly increasing population, we need to increase the grain production per unit area using available resources. Therefore, it is necessary to develop wheat cultivars, capable to produce high yield under a wide range of agro-climatic conditions. The diallel analysis technique illustrated by Hayman (1954 and 1958) provides a fairly reliable mechanism to properly understand the genetic system and gene action involved in the expression of important plant characters in early generations. So, the information on genetic control of yield and yield components is helpful in designing a breeding program (Shamsuddin and Abi-Antoun, 1986). For a sound breeding program, a plant breeder

needs to the relative importance of different gene actions involved in the inheritance of concerned characters.

Many wheat researchers observed partial dominance with additive type of gene action for days to heading (Subhani and Chowdhry, 2000), and grains per spike (Kashif and Khaliq, 2003). Similar results have been reported by Rahman *et al.* (2003) for number of spikes per plant, kernel weight and grain yield per plant.

Menshawy (2004) and El-Hag (2005) estimated the nature of gene action, and dominance was found to be predominant for number of days to maturity, number of kernels per spike, kernel weight, grain yield per plant and grain filling rate per plant.

In addition to gene effects, breeder would also like to know how much of the variation in a crop is due to genetic and to what extent this variation is heritable, because efficiency of selection mainly depends on additive genetic variation (Novoselovic *et al.*, 2004). Heritability values in narrow sense are important to the breeder since they quantify the expected improvement upon selection. However, grain yield is known to have low heritability and it is highly influenced by the environment. The present study was designed to achieve the following objectives: 1) to evaluate wheat genotypes for various characters, and 2) to estimate the nature of genetic mechanisms involved in the expression of some economic characters and earliness of wheat.

MATERIALS AND METHODS

The present research was carried out at Sakha Agricultural Research Station, Agricultural Research Center, Egypt, during the two wheat-growing seasons 2004-2005 and 2005-2006. Names and pedigrees of the wheat genotypes used are shown in Table 1.

Table 1. Names and pedigrees of the parental bread wheat genotypes

Names	Pedigrees	Source
Gemmiza 9	Ald "S" / Huac // Cmh 74A. 630 / Sx CGM 4583-5GM-1GM-0GM	Egypt
Irena	Buc/Fik//Myna/Vul CM91575- 28Y-0M-0Y-1M-0Y	CIMMYT
Sakha 61	Inia / RI 4220 // 7c / Yr "S" CM 15430 -2S-5S-0S-0S	Egypt
Line 1	Cazo/Kauz//Kauz CMBW90 Y3279-OTOPM-010M-010Y-3M-0SH	CIMMYT
Line 2	Skauza*2/ Srma CMBW91M02694F-OTOPY-7M-010Y-010M-010Y-0S	CIMMYT
Line 3	Sakha 12 /5/ Kvz //Cno 67 / Pj 62 /3/ Yd"S" Blo"S" /4/ K 134 (60) / Vee S.14665-4S -1S -0SY-0S	Egypt

In 2004-2005 half-diallel crosses were made among the six parents under field conditions.

In 2005/2006 season, the six parental genotypes and their 15 F₁'s were planted in a randomized complete block design with three replications. Each replicate consisted of 21 rows (15 F₁'s and parents), 2.8 m long and 30 cm apart with 20 cm between plants. Fifteen seeds were planted in each row.

The data were collected on five guarded plants from each experimental plot. The studied characters were; number of days to heading, number of days to physiological maturity, grain filling period (day), (days from heading to maturity), 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 per plant (g/day) was taken as the grain yield divided by grain filling period.

The collected data were subjected to analysis of variance technique. Plant characters which showed significant differences among genotypes were further analyzed by using diallel technique developed by Hayman (1954 and 1958). This analysis provides estimates of the following components of genetic variation: Variation due to additive gene effects (D), covariance of additive and dominance effects (F), variation due to dominant gene effects (H₁), dominance effect adjusted by gene frequency (H₂), dominance variation over all heterozygous loci (h²), variation due to environmental effect (E). Hayman's analysis also provides estimates of following proportions: The mean degree of dominance at each locus (H₁/D)^{1/2}, the ratio of genes with positive and negative effects in the parents (H₂/4H₁), the ratio of dominance and recessive genes in the parents (KD/KR), an estimator of number of gene groups exhibiting dominance involved in the inheritance of the trait (K), the coefficient of correlation between the parental order of dominance and parental measurement (r) and heritability in narrow sense (h²_{ns}).

RESULTS AND DISCUSSION

Statistical analysis of variance revealed highly significant differences among the tested wheat genotypes for all studied characters (Table 2). The significance of the genotypic differences indicates the presence of diversity in the studied materials.

Table 2. Analysis of variance mean squares for some traits in bread wheat genotypes.

Source of variance	d.f	MS								
		Days to heading	Days to maturity	Grain filling period	Plant height	Spikes per plant	Kernels per spike	100- kernel weight	Grain yield/plant	Grain filling rate /plant
Rep.	2	2.14*	26.59**	24.12**	7.05**	1.36	215.37**	0.09	99.82**	0.05**
Genotypes	20	165.35**	32.59**	66.42**	79.85**	26.43**	294.63**	0.76**	317.42**	0.14**
Error	40	0.58	3.47	3.18	1.34	1.86	27.71	0.07	14.76	0.005

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

Mean performance of the parental genotypes and their F_1 's is presented in Table 3. Line 1 and 3 and their cross ($P_4 \times P_6$) were the earliest genotypes in both days to heading and maturity. The shortest grain filling period were observed in P_5 (47.0 days) followed by P_1 (50.3 days) and their cross (49.3 day). The crosses; $P_2 \times P_4$ and $P_1 \times P_5$ exhibited the highest mean values for plant height (116.3 and 116.5 cm, respectively). On the other hand, the parent P_3 and the cross $P_3 \times P_6$ showed the highest mean values for number of spikes per plant; 26.7 and 21.5, respectively. Moreover, the parent P_6 and its cross $P_1 \times P_6$ recorded the same value (5.8 g) for 100-kernel weight. On the other hand, the parent P_2 and the cross $P_1 \times P_3$ recorded the highest mean values of grain yield per plant (72.2 g and 62.7 g) and grain filling rate per plant (1.3 g/day and 1.1 g/day).

Table 3. Mean performance of the studied characters in 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-Kernels weight (g)	Grain yield/plant (g)	Grain filling rate/plant (g/day)
Parents									
(P_1) Gemmiza 9	107.0	158.0	50.3	113.3	19.3	86.3	4.5	56.4	1.1
(P_2) Irena	97.3	152.7	53.7	110.3	18.5	86.2	4.7	72.2	1.3
(P_3) Sakha 61	95.9	149.0	53.3	100.7	26.7	59.3	4.2	38.0	0.7
(P_4) line1	87.3	145.7	56.7	109.3	17.7	72.1	5.1	45.9	0.8
(P_5) line2	108.3	154.7	47.0	109.7	24.7	84.8	4.0	45.2	1.0
(P_6) line3	80.2	147.0	65.0	99.0	15.1	63.9	5.8	26.9	0.4
Hybrids									
$P_1 \times P_2$	102.0	153.3	50.0	114.0	20.4	89.3	5.3	52.7	1.0
$P_1 \times P_3$	98.7	154.7	55.7	112.3	21.4	74.2	5.2	62.7	1.1
$P_1 \times P_4$	95.5	151.3	55.7	115.3	17.5	72.0	5.5	47.2	0.8
$P_1 \times P_5$	105.0	155.0	49.3	116.0	18.9	68.9	5.1	45.9	0.9
$P_1 \times P_6$	92.0	151.0	58.3	109.0	14.3	66.3	5.8	35.8	0.6
$P_2 \times P_3$	95.4	152.0	55.6	111.0	19.6	81.0	4.7	49.5	0.9
$P_2 \times P_4$	92.7	148.3	54.7	116.3	17.1	79.4	5.2	50.7	0.9
$P_2 \times P_5$	101.0	153.3	53.0	113.3	18.3	91.3	4.7	49.9	1.0
$P_2 \times P_6$	90.2	148.0	56.3	106.0	17.7	77.4	5.4	45.3	0.8
$P_3 \times P_4$	90.0	147.0	55.7	106.7	20.3	60.5	5.0	41.5	0.7
$P_3 \times P_5$	95.7	153.0	58.0	102.5	20.8	78.4	4.5	42.2	0.7
$P_3 \times P_6$	86.0	148.7	61.7	102.3	21.5	59.1	5.1	32.5	0.5
$P_4 \times P_5$	93.6	150.7	57.0	113.3	18.5	79.4	5.2	54.5	1.0
$P_4 \times P_6$	83.7	146.7	62.3	106.3	15.9	65.3	5.7	34.7	0.6
$P_5 \times P_6$	90.0	149.7	58.0	105.3	16.4	76.2	5.2	46.7	0.8
New LSD 0.05	1.1	2.9	2.7	1.7	2.1	8.1	0.4	5.7	0.1
New LSD 0.01	2.1	3.7	3.5	3.1	2.7	10.6	0.5	7.4	0.1

Results in Table 4, show that t^2 values were not significant for all studied characters. Accordingly, the major assumptions postulated for diallel analysis by

Hayman (1954) appeared to be valid. The regression coefficients (b) are expected to be significantly different from zero but not from unity if all assumptions are correct. This was true for each of plant height, spikes per plant, kernels per spike, kernel weight, grain yield per plant and grain filling rate, confirming further validity of diallel assumptions for these traits.

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	0.014	0.798 ± 0.272	2.926*	0.739
Days to maturity	0.060	0.874 ± 0.312	2.805*	0.403
Grain filling period	0.247	0.708 ± 0.250	2.835*	1.167
Plant height	0.743	0.600 ± 0.239	2.511	1.675
Spikes per plant	0.0003	0.765 ± 0.326	2.345	0.719
Kernels per spike	0.072	0.549 ± 0.490	1.120	0.919
100- kernel weight	1.429	0.566 ± 0.210	2.691	2.064
Grain Yield/ plant	0.284	0.818 ± 0.450	1.815	0.405
Grain filling rate/ plant	0.023	0.662 ± 0.338	1.959	0.999

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

* Significant at 0.05 level of probability.

Estimation of the genetic components of variation for all studied characters are presented in Table 5. The additive component "D" was highly significant for all characters. In addition, the dominance components (H_1 and H_2) were highly significant for most of the studied characters. These significant values suggest that the additive and dominance gene effects play an important role in the inheritance of these characters. Moreover, the values of additive genetic variances (D) were greater than the dominance variances (H_1 and H_2) for all characters. This result indicated that selection for these characters might be more effective in early generations for improving such characters.

The results obtained from present study were in agreement with the finding of Abd El-Rahman (2004) who reported that the dominance components H_1 and H_2 were significant for number of spikes per plant, number of kernels per spike and grain yield in wheat indicating asymmetrical distribution of positive and negative alleles among parents. Also, Dere and Yildirim (2006) reported that the additive genetic variance was the main type of gene action controlling grain yield per plant.

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

Characters	D	H ₁	H ₂	F	h ²	E
Days to heading	119.92** ±1.25	12.41** ±3.18	8.13** ±2.84	22.50** ±3.06	10.01**±1. 91	0.21± 0.47
Days to maturity	21.18 **±0.36	-0.41 ±0.92	-0.40 ±0.82	1.63 ±0.89	-0.56 ±0.55	1.52** ±0.14
Grain filling period	47.75** ±1.24	17.55** ±3.15	10.71** ±2.82	19.73**±3. 03	6.23** ±1.89	1.39** ±0.47
Plant height	33.04** ±2.33	20.87** ±5.91	19.06** ±5.28	-12.64* ±5.69	23.60** ±3.55	0.54 ±0.88
Spikes per plant	19.22** ±0.87	10.50** ±2.21	8.39** ±1.97	10.21** ±2.12	8.43** ±1.33	0.61 ±0.33
Kernels per spike	132.55** ±19.68	95.61 ±49.97	72.05 ±44.64	-5.04 ±48.09	-4.75 ±30.04	12.22 ±7.44
100- kernel weight	0.43**±0. 02	0.25** ±0.05	0.19** ±0.04	0.14** ±0.04	0.58** ±0.02	0.02** ±0.01
Grain Yield/ Plant	235.63** ±18.53	168.38**± 47.03	138.78**± 42.01	141.87**± 45.26	1.31 ±28.28	6.27 ±7.00
Grain filling rate/ plant	0.10** ±0.01	0.04** ±0.01	0.03** ±0.01	0.03** ±0.01	0.010 ±0.007	0.002 ±0.002

The "F" values were highly significant and positive for most of the studied characters, indicating that the dominant alleles are more frequent than the recessive ones among the parental genotypes. Significant and negative F value was recorded for plant height. Meanwhile, the insignificant "F" values for days to maturity and number of kernels per spike may be a sign of equality in the relative frequencies of dominant and recessive genes in the parents.

The dominance effect "h²" estimates, which is a measure of heterozygous loci, were highly significant and positive for each of days to heading, grain filling period, plant height, spikes per plant and 100-kernel weight. The observed positive and significant "h²" values indicated that the dominant effects of these characters were due to heterozygosity and dominance seemed to be acting in positive direction (unidirectional). In contrast, the h² values for grain yield and grain filling rate were not significant indicating that it could be due to the presence of considerable amount of canceling the dominant effects in the parents. These results agreed with Kashif, *et al.*

(2003) for plant height and grain yield per plant in durum wheat and El-Hag (2005) for number of kernels per spike in bread wheat.

Estimation of the proportions of genetic components for the studied characters are shown in Table 6. The values of average degree of dominance $(H_1/D)^{1/2}$ is less than one confirming the role of partial dominance gene effects in all characters. These results are in accordance with those of Habib and Khan (2003), Rahman *et al.* (2003) for number of kernels per spike and grain yield per plant and Menshawy (2004) for number of days to heading, grain filling period and plant height.

The proportion of genes with positive and negative effects in parents $(H_2/4H_1)$ was equal to or close to the ratio 0.25 for number of days to maturity (Table 6). This result confirms equal frequencies of positive and negative genes among parents. While for the other characters the ratio ranged from 0.15 to 0.23 indicating unequal frequencies of positive and negative genes among parents. These results are in accordance with those of Awaad (1996) who recorded unequal frequencies of positive and negative genes among parents for days to heading, plant height, number of spikes per plant, number of kernels per spike and grain yield per plant in F_1 generation.

The proportion of dominant and recessive alleles in the parents (KD/KR) were found to be unequal with more dominant than recessive alleles for all the characters, except for plant height and number of kernels per spike (Table 6). Similar results were obtained by Awaad (1996) for number of spikes per plant and grain yield per plant and Dere and Yildirim (2006) for grain yield per plant.

Concerning number of effective factors (K) that control the trait and show dominance to certain degree, the data showed one gene block governing grain filling period, number of kernels per spike, grain yield per plant and grain filling rate. While, two genes blocks control days to heading, days to maturity and plant height. One hundred kernel weight was regulated by four genes blocks.

The correlation coefficient values "r" between the parental order of dominance (W_r+V_r) and the parental measurement (yr) were negative for grain filling period, plant height, number of kernels per spike and 100 kernel weight revealed (Table 6). These results suggested that the parents contains most increasing genes have the lowest values of $W_{r_i} + V_{r_i}$, and thus contain most dominant genes controlling these characters. However, correlation coefficient was found to be positive for the remaining values indicating that high mean expression is associated with recessive genes. The possession of recessive gene with high expressing is an advantage in breeding program as it might facilitate fixation of the traits in the early generations.

Narrow-sense heritabilities (h^2_{ns}) estimates ranged from 0.60 to 0.96 for the studied characters (Table 6). These results revealed that the additive component played the major role in the inheritance of these characters. Thus, phenotypic selection would be an effective procedure for improving those characters. Similar moderate heritability in narrow sense were estimated by Darwish and Ashoush (2003) for number of spikes per plant. The high estimates of heritability agreed with those obtained by Abd El Rahman (2004) for days to heading, days to maturity and plant height and Menshawy (2004) for plant height.

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^2_{ns}
Days to heading	0.32	0.16	1.82	1.23	0.80	0.96
Days to maturity	-	0.25	-	1.39	0.18	0.87
Grain filling period	0.61	0.15	2.03	0.58	-0.59	0.81
Plant height	0.80	0.23	0.61	1.24	-0.28	0.82
Spikes per plant	0.74	0.20	2.12	1.01	0.42	0.67
Kernels per spike	0.85	0.19	0.96	-0.07	-0.66	0.73
100- kernel weight	0.77	0.19	1.54	3.03	-0.80	0.71
Grain Yield/ plant	0.85	0.21	2.11	0.01	0.28	0.60
Grain filling rate	0.62	0.23	1.70	0.27	0.14	0.76

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التحليل الوراثي لمكونات التبكير وبعض صفات محصول الحبوب في قمح الخبز

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أجريت هذه الدراسة في مزرعة محطة البحوث الزراعية بسخا خلال موسمي ٢٠٠٤-٢٠٠٥ م و ٢٠٠٥-٢٠٠٦ م. وقد استخدمت ستة تراكيب وراثية من قمح الخبز ما بين أصناف وسلالات وهي جميزة ٩، إرينا، سخا ٦١، سلالة ١، سلالة ٢ و سلالة ٣. وتم التهجين فيما بينها طبقاً لنظام الـ Diallel الهجن الدورية لتحديد ميكانيكية التحكم الوراثي في مكونات التبكير وبعض صفات محصول الحبوب. تمت زراعة التراكيب الوراثية الأبوية والجيل الأول لها بنظام القطاعات التامة العشوائية. وتم تسجيل وتحليل البيانات لكل من صفة عدد الأيام حتى طرد السنابل، عدد الأيام حتى النضج الفسيولوجي، فترة امتلاء الحبة، طول النبات، عدد السنابل للنبات، وزن حبوب السنبل، وزن الـ ١٠٠ حبة، محصول الحبوب للنبات و معدل امتلاء الحبة.

أظهرت النتائج معنوية كل من الفعل المضيف والسيادي لأغلب الصفات المعنية بالدراسة. كما أوضحت الدور الرئيسي الذي يلعبه المكون المضيف في وراثية كل الصفات. ويتضح ذلك من قيم متوسط درجة السيادة $(H_1/D)^{1/2}$ حيث كانت أقل من الواحد الصحيح لكل الصفات، حيث يؤكد ذلك دور التأثيرات، الجينية للسيادة الجزئية في التحكم في هذه الصفات. ارتبطت قيم F مع نسبة KD/KR موضحة زيادة تكرار الأليلات السائدة المتحركة في وراثية جميع الصفات المدروسة ما عدا صفة عدد الأيام حتى النضج، طول النبات و عدد حبوب السنبل. كما أوضحت النتائج أن درجة التوريث بالمعنى الضيق كانت عالية نسبياً لكل الصفات تحت الدراسة مما يدل على أن أغلب هذه الصفات يمكن الإنتخاب لها في الأجيال الإنعزالية المبكرة.