

Genetic Improvement of Agronomic Traits and Quality Properties of Five Bread Wheat Cultivars

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ABSTRACT

Five bread wheat genotypes; Sakha 93, Sakha 94, Giza 168, Gemmiza 9 and Gemmiza 10 were crossed in 5 x 5 half diallel mating design. The field experiment was planted during 2005/06 and 2006/07 growing seasons at Sakha Agric. Res. Station and the laboratory experiment was achieved at Food Science and Technology., Fac. of Agriculture, Kafr El-Sheikh. The objective of the present study was to estimate the genetic components for eight agronomic characters and six quality traits. The superior genotypes in protein content were chosen to determine the rheological properties of dough and protein quality of the flour. Partial dominance gene effects played a role in inheritance of days to heading, days to maturity, days to anthesis, plant height, protein and gluten content. Meanwhile, number of kernels per spike, 100-kernel weight, grain yield, moisture, fat, ash and fiber were controlled by over dominance. Most of agronomic and quality characters recorded moderate to high heritability estimates in narrow sense. However, number of kernels per spike, fat, ash and fiber had low heritability estimates. The nutritional quality and physical properties of some genotypes were investigated by different methods. The results showed that Giza 168 had the highest content of crude protein, while gluten content was high in Gemmiza 9, water absorption was high in Giza 168 x Gemmiza 9 while dough development (mixing time) was high in Giza 168. Giza 168 x Gemmiza 10 contained the highest amount of indispensable amino acids, computed protein efficiency ratio (C-PER) and biological value (BV). Lysine was the first limiting indispensable amino acid for all wheat genotypes.

Key words: *Bread wheat, Agronomic traits, Quality characters, Heritability, Gene action.*

INTRODUCTION

Wheat is the most widely grown crop in the world and approximately one sixth of the total arable land in the world is cultivated with it (Abdul Sattar *et al.*, 2003). Also, it is the most

grown cereal world-wide. FAO's latest estimate of world cereal production was 2065 million tons in 2004 to 2005 (FAO 2005). The breeders and geneticists have always been making efforts to improve its productivity to the level of self-sufficiency. However, the success of any breeding programme depends on the presence of genetic variation in the breeding materials. High heritable characters can easily be found with simpler selection procedure resulting in quick progress. The magnitude of such estimates also suggests the extent to which improvement is possible through selection.

High yield and good breadmaking quality are important features in today's wheat market. Hence, improving the end-use quality of wheat is a key target for many breeding programmes. The knowledge concerning the genetic control of wheat quality traits is somewhat limited (Kuchel *et al.*, 2006). In this respect, understanding of the inheritance and type of gene action are important in the inheritance of quantitative traits in bread wheat. Additive and dominance gene effects play an essential role in the inheritance of days to heading, days to maturity, plant height (Abd EL-Rahman, 2004). However, additive and dominance gene effects were significant and involved in the inheritance of number of spikes per plant, number of kernels per spike and grain yield per plant (Hammad and Abd El-Aty, 2007). On the other hand, partial dominance type of gene action for protein content was reported by Akram *et al.* (2007).

Heritability estimates are used to indicate the relative degree to which a character is transmitted from parent to offspring. Earlier studies pertaining to heritability have yielded sufficient knowledge about the inheritance of many agronomic characters; e.g. Novoselovic *et al.* (2004) reported of high heritability estimates for grain yield per plant and plant height and intermediate heritability estimates for number of spikes per plant. Hammad and Abd El-Aty (2007) found high heritability estimates for days to heading, days to anthesis and days to maturity.

Wheat flour is the major constituent in bakery and bread industries. In the developing countries, bread represents about 70 percent of the total caloric values as well as similar ratio of the total protein intake (Yassen, 1985). The protein content of wheat is depending on the production environment especially, soil fertility, water and grain yield (Al-Eid, 2006). Grain protein is of primary importance in determining the breadmaking quality of wheat flour. Gluten imparts physical properties to wheat doughs that are lacking in other cereal grain doughs (Amal *et al.*, 2005). Conventional

mixograph parameters have been used for quality evaluation including mixing time, water absorption and mixing tolerance of wheat breeding lines (Chung *et al.*, 2001). Anjum *et al.* (2005) analyzed the amino acids content of 44 spring wheat varieties and found significant differences in certain genotypes. In the varieties analysed, they found considerable variability in Lys (lysine), Leu (leucine), Ile (isoleucine), Thr (threonine), Val (valine), Met (methionine), His (histidine), Arg (arginine), Ala (alanine), Asp (aspartic acid), Glu (glutamic acid), Gly (glycine), Pro (proline), Ser (serine) and Tyr (tyrosine) contents. Boila *et al.* (1996) analyzed protein and amino acid contents of wheat varieties and found significant differences in protein concentrations, such findings were similar to those in certain amino acids.

The objectives of the present study were to estimate the nature of gene action determining the inheritance of some agronomic characters and quality traits in bread wheat genotypes, in addition to the farinograph properties of some wheat genotypes; flour, dough and its chemical composition. This information may assist wheat breeders to release cultivars with better quality and high yield.

MATERIALS AND METHODS

A field investigation was conducted at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt through two wheat growing seasons, 2005/06 and 2006/07. The laboratory investigations were carried out at the Food and Technology Dept., Fac. of Agriculture, Kafr El-Sheikh University.

1- Field experiment:

Five cultivars; Sakha 93, Sakha 94, Giza 168, Gemmiza 9 and Gemmiza 10, were crossed in a half diallel mating scheme during 2005/06 season to produce their F_1 's. Table 1, illustrates commercial names and pedigree of these cultivars. The five parents and their ten F_1 's were planted in a randomized complete block design with three replications during 2006/07 wheat growing season. Each genotype was grown in a single row; 2.8 m long, 30 cm apart and 20 cm between plants. Data was collected on six guarded plants from each genotype. The studied characters were; days to heading (DH), days to physiological maturity (DM), days to anthesis (Anth.), plant height (PH), number of spikes per plant (SP^{-1}), number of kernels per spike (KS^{-1}), 100- kernel weight (KW) and grain yield per plant (GYP^{-1}). The diallel cross analysis adopted by Hayman (1954) was applied. This analysis provides estimates of the following components of

genetic variation: Variation due to additive gene effects (D), variation due to dominant gene effects (H_1), dominance effect adjusted by gene frequency (H_2), covariance of additive and dominance effects (F), dominance variation over all heterozygous loci (h^2) and variation due to environmental effect (E). Hayman's analysis also provides estimates of following proportions: The mean degree of dominance at each locus $(H_1/D)^{1/2}$, 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 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 estimates in narrow sense (h^2_{ns}).

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

Parent	Pedigree
Sakha 93 (P ₁)	Sakha 92/ Tr 810328 S 8871 - 1S-2S - 1S - 0S
Sakha 94 (P ₂)	Opata / Rayon // Kauz CMBW 90Y3180 - 0TOPM - 3Y - 010M - 10M - 010Y- 6M - 0S
Giza 168 (P ₃)	Mri / Buc // Seri CM93046 - 8M - 0Y - 0M - 2Y - 0B
Gemmiza 9 (P ₄)	Ald "S" / Huac // Cmh 74A. 630 / Sx CGM 4583-5GM-1GM-0GM
Gemmiza 10 (P ₅)	Maya 74 "S" / On//1160 - 147/3/Bb/GII/4/ Chat "S" /5/ Crow "S". CGM 5820 - 3GM - 1GM - 2GM - OGM.

Data obtained from ten progenies and five parents were subjected to basic analysis of variance (Steel and Torrie, 1990). Gene action and genetic components of variation were determined according to Hayman (1954) and Jinks (1955).

2- Laboratory experiment:

Chemical composition including moisture, crude protein, fat, ash and crude fiber were determined in samples from the five parents and their ten F₁'s according to A.O.A.C. (1990). Carbohydrates content was calculated by difference i.e., Carbohydrates% = 100-[Protein% + Fat% + Ash% + Fiber%]. Gluten content (%) was determined by the hand washing method (A.A.C.C. 1995). Data of the Chemical composition were also analyzed using Hayman's procedure (1954).

Five superior genotypes in protein content were chosen to study the rheological properties of dough. The characteristics of dough prepared from wheat genotypes were measured by means of farinograph according to the methods described in A.A.C.C. (1995). Determination of amino acids composition was carried out using Beckman amino acid analyzer according to Sadasivam and Manickam (1992) method. Tryptophan was determined colourimetrically after sufficing sample to alkaline hydrolysis as outlined by Miller (1967). Chemical score of indispensable amino acids was calculated using the equations of Pellett and Young (1980). Computation procedure for protein efficiency ratio (C-PER) of five wheat genotypes was calculated as described by Alsmeyer *et al.* (1974) using the following equation:

$C-PER = -1.816 + 0.435 (\text{Methionine}) + 0.780 (\text{leucin}) + 0.211 (\text{histidine}) - 0.944 (\text{tyrosine})$. Biological values were calculated using the following equation as reported by Farag *et al.* (1996):

$\text{Biological value (B.V.)} = 49.9 + 10.53 \text{ C-PER}$

RESULTS AND DISCUSSION

The mean squares of analysis of variance presented in Tables 2a and 2b indicated that genotypic differences were significant ($P \leq 0.01$) for all the characters except for total carbohydrates. These results indicated that the parents were diverse for most of characters and this diversity was transmittable to the offspring.

Table 2a. Mean squares of eight agronomic characters for the studied genotypes.

Source of Variation	D.F	DH	DM	Anth.	PH	SP ⁻¹	KS ⁻¹	KW	GYP ⁻¹
		MS							
Blocks	2	1.35	2.92	6.07*	39.32**	74.37**	0.93	0.39**	77.04*
Genotypes	14	61.83**	18.34**	69.68**	157.42**	8.83**	272.09**	1.18**	245.72**
Error	28	0.64	1.52	2.19	3.44	2.70	16.22	0.11	15.06

* and ** indicate significant at $p \leq 0.05$ and $p \leq 0.01$, respectively.

DH = Days to heading, DM = Days to physiological maturity, Anth. = Days to anthesis, PH = Plant height and SP⁻¹ = Number of spikes per plant, KS⁻¹ = Number of kernels per spike, KW = 100-kernel weight, GYP⁻¹ = Grain yield per plant.

Table 2b. Mean squares of seven bread wheat traits for the studied genotypes.

Source of Variation	D.F	Moisture	Protein	Gluten	Fat	Ash	Fiber	Total carbohydrates
Blocks	2	0.01	0.001	0.49	0.06**	0.01	0.003	2.13
Genotypes	14	1.52**	0.41**	6.26**	0.24**	0.05**	0.09**	2.11
Error	28	0.01	0.02	0.25	0.01	0.01	0.01	2.21

** indicate significant at $p \leq 0.01$.

Mean performances of the parents and their ten F_1 's for the agronomic characters and quality traits are presented in Tables 3a and 3b, respectively. Concerning agronomic characters, Sakha 93 was the earliest one, where it needed 93.94, 101.67 and 150.50 days to heading, days to anthesis and days to maturity, respectively. While Sakha 94 was the best parent for days to maturity, plant height, number of spikes per plant, number of kernels per spike and grain yield per plant. On the other hand, Gemmiza 9 had the highest weight for 100-kernel which recorded 5.38 g. Regarding the mean values of crosses, the crosses $P_1 \times P_3$ and $P_1 \times P_4$ were the earliest and recorded the same value for days to heading and days to anthesis; 95.94 and 104.67 days, respectively. These results may be attributed to Sakha 93 (the earliest parent used in these crosses). On the other hand, the crosses $P_2 \times P_3$, $P_2 \times P_4$, $P_1 \times P_2$ and $P_2 \times P_5$ were the earliest in maturity; 148.00, 149.50, 149.50 and 150.00 days, respectively. These crosses included the earliest maturing parent; Sakha 94. For plant height, the cross $P_2 \times P_4$ was the tallest cross. While, crosses $P_2 \times P_3$, $P_2 \times P_5$, $P_1 \times P_2$ and $P_2 \times P_4$ scored the highest mean number of spikes per plant (19.22, 18.94, 17.06 and 16.56, respectively). The crosses $P_3 \times P_5$ (77.33), $P_1 \times P_2$ (64.13) and $P_4 \times P_5$ (63.92) were the highest mean number of kernels per spike.

Table 3a. Mean performances of the agronomic characters for parents and their F₁'s.

Genotype	DH (day)	DM (day)	Anth. (day)	PH (cm)	SP ⁻¹	KS ⁻¹	KW (g)	GYP ⁻¹ (g)
Sakha 93 (P ₁)	93.94	150.50	101.67	100.28	15.61	64.17	5.11	36.43
Sakha 94 (P ₂)	104.33	149.50	112.00	118.33	19.39	73.17	4.93	54.06
Giza 168 (P ₃)	94.39	151.00	105.33	108.61	18.06	71.56	4.28	51.57
Gemmiza 9 (P ₄)	107.11	156.67	116.67	114.44	15.50	70.92	5.38	35.31
Gemmiza 10 (P ₅)	105.61	154.67	116.67	94.17	18.11	60.22	3.98	28.58
P ₁ × P ₂	98.17	149.50	107.67	109.17	17.06	64.13	5.82	51.64
P ₁ × P ₃	95.94	152.00	104.67	107.50	15.56	50.50	5.73	58.22
P ₁ × P ₄	95.94	152.00	104.67	112.50	13.83	60.17	6.30	49.80
P ₁ × P ₅	98.17	153.67	108.00	99.72	15.17	58.43	5.80	38.37
P ₂ × P ₃	97.28	148.00	107.67	114.72	19.22	49.75	5.23	48.86
P ₂ × P ₄	105.26	149.50	114.33	120.28	16.56	47.67	6.22	43.26
P ₂ × P ₅	100.94	150.00	111.00	109.44	18.94	53.50	5.33	38.44
P ₃ × P ₄	100.94	152.00	112.33	111.94	15.22	49.25	5.40	39.74
P ₃ × P ₅	100.84	151.00	112.00	102.78	16.22	77.33	5.25	39.95
P ₄ × P ₅	106.67	155.50	116.33	105.00	15.39	63.92	5.48	29.15
Mean	100.37	151.70	110.07	108.59	16.66	60.98	5.35	42.89
LSD 0.05	1.34	2.06	2.47	3.10	2.75	6.73	0.55	6.49
LSD 0.01	1.80	2.78	3.34	4.18	3.71	9.09	0.75	8.75
CV %	0.80	0.81	1.34	1.71	9.86	6.60	6.25	9.05

DH = Days to heading, DM = Days to physiological maturity, Anth. = Days to anthesis, PH = Plant height and SP⁻¹ = Number of spikes per plant, KS⁻¹ = Number of kernels per spike, KW = 100-kernel weight, GYP⁻¹ = Grain yield per plant.

CV = Coefficient of variation

Regarding 100-kernel weight, the crosses P₁ × P₅, P₂ × P₄, P₁ × P₂ and P₁ × P₃ recorded the highest values; 5.80, 6.22, 5.82 and 5.80 g, respectively. The cross P₁ × P₃ had the highest grain yield per plant

(58.22 g). Generally, the best crosses included the best parents in days to heading, days to anthesis, days to maturity, plant height and number of spikes per plant.

Chemical composition of the wheat genotypes presented in Table 3b indicated that, Giza 168 contained the highest content of crude protein (11.71 %) followed by the cross $P_3 \times P_5$ (11.65%), while the lowest was Sakha 93. The highest gluten content was found in Gemmiza 9 (33.90 %) followed by $P_3 \times P_4$ (32.90 %), while the lowest content was detected in Sakha 93 (28.80 %). The cross $P_1 \times P_4$ had the highest fat content (1.86 %) compared with the other wheat genotype. The highest content of ash was recorded for the genotype $P_4 \times P_5$ (1.48 %) followed by $P_2 \times P_3$ (1.45 %) while, the cross $P_3 \times P_5$ had the lowest value; 1.05 %.

Table 3 b. Mean chemical composition of flour for parents and their F_1 's (g/ 100 g on dry weight basis).

Genotype	Moisture %	Protein %	Gluten %	Fat %	Ash %	Fiber %	Total carbohydrates %
Sakha 93 (P_1)	13.10	10.31	28.80	1.25	1.31	1.34	85.79
Sakha 94 (P_2)	11.75	10.88	29.00	1.55	1.25	1.04	85.28
Giza 168 (P_3)	12.50	11.71	31.60	1.33	1.10	1.14	84.72
Gemmiza 9 (P_4)	12.15	11.30	33.90	1.41	1.15	1.00	85.14
Gemmiza 10 (P_5)	11.91	11.11	31.00	1.07	1.28	1.25	81.96
$P_1 \times P_2$	11.50	11.20	29.00	1.19	1.34	1.27	85.00
$P_1 \times P_3$	11.60	11.00	30.10	1.70	1.37	1.19	84.74
$P_1 \times P_4$	13.46	10.77	30.70	1.86	1.26	1.23	84.88
$P_1 \times P_5$	12.41	10.89	30.30	1.04	1.36	1.60	85.11
$P_2 \times P_3$	12.34	10.70	30.40	1.60	1.45	1.36	84.89
$P_2 \times P_4$	13.31	11.00	30.80	1.53	1.17	1.47	84.83
$P_2 \times P_5$	12.65	11.15	29.70	1.80	1.19	1.17	84.69
$P_3 \times P_4$	11.57	11.44	32.90	1.62	1.18	1.52	84.24
$P_3 \times P_5$	11.11	11.65	31.50	1.00	1.05	1.43	84.87
$P_4 \times P_5$	12.90	11.35	32.00	1.15	1.48	1.19	84.83
Mean	12.28	11.10	30.78	1.41	1.26	1.28	84.73
LSD 0.05	0.20	0.21	0.83	0.15	0.13	0.13	2.49
LSD 0.01	0.27	0.29	1.12	0.20	0.18	0.17	3.36
C.V. %	0.98	1.15	1.61	6.29	6.31	5.90	1.76

CV = Coefficient of variation

Results also revealed that the cross $P_1 \times P_5$ had the highest fiber content (1.60 %) followed by $P_3 \times P_4$ (1.52 %). While the lowest was Gemmiza 9 (1.00 %). The highest carbohydrates content was found in Sakha 93 (85.79 %) compared with Gemmiza 10 which had the lowest content (81.96 %). The aforementioned results coincided with those obtained by Simic *et al.* (2006).

The validity of Hayman's assumptions was tested using r^2 test. The r^2 values (Table 4) were not significant for all studied characters

except for number of spikes per plant and number of kernels per spike that were significant and highly significant, respectively. Accordingly, the major assumptions postulated for diallel analysis by Hayman (1954) appeared to be valid except for these two traits.

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

Character	r^2	Regression Coefficient	t value for $b=0$	t value for $b=1$
Days to heading	0.14	1.02 ± 0.11	9.10**	-0.20
Days to maturity	0.01	0.99 ± 0.07	15.09**	0.19
Days to anthesis	0.01	0.95 ± 0.15	6.37**	0.31
Plant height	0.27	0.84 ± 0.19	4.47*	0.87
Spikes per plant	3.81*	0.71 ± 0.12	5.99**	2.50
Kernels per spike	6.60**	-0.21 ± 0.17	-1.25	7.17**
100- kernel weight	0.11	0.91 ± 0.15	6.21**	0.58
Grain yield per plant	0.20	0.38 ± 0.41	0.94	1.52
Moisture %	0.29	0.48 ± 0.36	1.34	1.46
Protein %	1.91	1.17 ± 0.76	1.54	-0.22
Gluten %	0.04	1.01 ± 0.06	16.66**	-0.10
Fat %	1.17	0.49 ± 0.26	1.87	1.98
Ash %	5.98**	0.27 ± 0.17	1.58	4.25*
Fiber %	0.64	0.19 ± 0.89	0.22	0.90
Total carbohydrates %	2.73	1.15 ± 0.11	10.72**	-1.39

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

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

The regression coefficients are expected to be significantly different from zero, but not from unity if all assumptions are correct. This held true for all characters except kernels per spike, grain yield per plant, moisture (%), fat (%) and ash (%) confirming further validity of diallel assumptions. These characters, which showed insignificant b values differed from unity and from zero, showing partial failure of the assumptions.

Estimation of the genetic components of variation for the agronomic characters and quality traits are presented in Table 5. The additive component "D" was highly significant for all characters except for number of spikes per plant, number of kernels per spike, grain yield per plant, moisture (%), gluten (%), fat (%), ash (%) and fiber (%).

The dominance components effects (H_1 and H_2) were significant to highly significant for all characters. These significant estimates indicate that additive and dominance gene effects play an essential role in the inheritance of these characters. The dominance variance " H_1 " was larger than that of " H_2 " for most of the studied characters, indicating that the positive and negative alleles, at the loci of the character in question, are not equal in proportion among the parents. This result indicates that improving these characters through selection might be more effective in early generations. Similar results were obtained by Abd EL-Rahman (2004) for days to heading, days to maturity, plant height, number of spikes per plant, number of kernels per spike and grain yield per plant.

The "F" values were highly significant and positive for days to heading and gluten percentage indicating that the dominant alleles are more frequent than the recessive ones among the parental genotypes. Meanwhile, the insignificant "F" values for the other characters may be a sign of equality in the relative frequencies of dominant and recessive genes in the parent.

The estimates of (h^2) values which refer to the dominance effects over all heterozygous loci were found to be significant and positive for days to maturity, plant height, number of spikes per plant, number of kernels per spike, 100-kernel weight and fiber content. This result indicating the predominance of positive genes controlling these characters and suggesting that dominance was unidirectional. Meanwhile, the estimates of h^2 values were not significant for the remaining studied characters, indicating the absence of dominance over all loci in heterozygous phase.

The mean degree of dominance (H_1/D)^{1/2} is less than unity for days to heading (Table 6) , days to maturity, days to anthesis, plant height, protein and gluten contents. These results confirm the role of partial dominance gene effects in controlling these traits. Meanwhile, number of kernels per spike, 100-kernel weight, grain yield per plant, moisture (%), fat (%), ash (%) and fiber (%) were controlled by overdominance suggesting early selection for good improvement of these traits.

Table 5. Estimates of genetic components of variation for agronomic and quality characters of the studied genotypes.

Character	D	H ₁	H ₂	F	h ²	E
Days to heading	40.57** ±1.07	14.04** ±2.88	12.69** ±2.61	7.49** ±2.66	2.74 ±1.76	0.23 ±0.43
Days to maturity	8.79** ±0.27	6.27** ±0.74	4.71** ±0.67	0.43 ±0.68	3.04** ±0.45	0.54** ±0.11
Days to anthesis	44.94** ±1.38	10.99** ±3.73	10.28** ±3.39	5.30 ±3.45	0.40 ±2.29	0.81 ±0.56
Plant height	97.11** ±1.42	8.37* ±3.82	9.01** ±3.47	-2.39 ±3.54	10.47** ±2.34	1.94** ±0.58
Spikes per plant	0.43 ± 0.25	-3.76** ±0.67	-2.89** ±0.61	-5.20** ±0.62	1.05* ±0.41	2.49** ±0.10
Kernels per spike	25.69 ±54.40	463.68** ±146.92	384.27** ±133.25	92.31 ±135.89	281.20** ±89.97	5.07 ±22.21
100- kernel weight	0.30** ±0.02	0.72** ±0.07	0.72** ±0.06	-0.02 ±0.06	2.14** ±0.04	0.04** ±0.01
Grain yield per plant	116.01 ±15.41	122.34 ±41.61	78.51 ±37.74	29.43 ±38.49	12.62 ±25.48	6.40 ±6.29
Moisture %	0.28** ±0.10	2.51** ± 0.27	1.81** ± 0.25	0.60* ± 0.25	-0.003 ± 0.17	0.005 ± 0.04
Protein %	0.26** ±0.06	0.28 ±0.16	0.25 ±0.14	0.16 ±0.14	0.004 ±0.10	0.005 ±0.02
Gluten %	4.29** ±0.04	0.20 ±0.11	0.16 ±0.10	0.44** ±0.10	-0.02 ±0.07	0.09** ±0.02
Fat %	0.03 ±0.02	0.28** ±0.04	0.27** ±0.04	0.04 ±0.04	0.039 ±0.03	0.004 ±0.01
Ash %	0.01 ±0.01	0.06** ±0.02	0.06** ±0.02	0.001 ±0.02	0.010 ±0.01	0.002 ±0.003
Fiber %	0.02 ±0.01	0.13** ±0.03	0.12** ±0.03	0.02 ±0.03	0.09** ±0.02	0.002 ±0.005

* and ** indicate significant at $p \leq 0.05$ and $p \leq 0.01$, respectively.

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

Character	$(H_1/D)^{1/2}$	$H_2/4H_1$	KD/KR	h^2/H_2 (K)	r	h^2_{ms}
Days to heading	0.59	0.23	1.37	0.22	0.84	0.83
Days to maturity	0.84	0.19	1.06	0.65	0.98	0.74
Days to anthesis	0.49	0.23	1.27	0.04	0.66	0.86
Plant height	0.29	0.27	0.92	1.16	-0.66	0.92
Spikes per plant	-	0.19	-	-0.36	0.73	0.57
Kernels per spike	4.25	0.21	2.47	0.73	0.53	0.06
100- kernel weight	1.55	0.25	0.95	2.97	-0.86	0.42
Grain yield per plant	1.03	0.16	1.28	0.16	-0.08	0.71
Moisture %	2.98	0.18	2.10	-0.002	0.74	0.30
Protein %	1.04	0.22	1.82	0.02	0.45	0.52
Gluten %	0.21	0.21	1.63	-0.12	0.96	0.94
Fat %	3.18	0.24	0.73	0.14	-0.94	0.31
Ash %	3.29	0.25	1.08	0.16	-0.69	0.11
Fiber %	2.64	0.23	1.65	0.76	0.30	0.05

These results are in agreement with those reported by Rahman *et al.* (2003) for days to maturity, plant height and protein content, Sultan *et al.* (2006) for days to heading, days to maturity, plant height and 100-kernel weight, and Esmail (2007) for days to heading and plant height. Overdominance was found to be important in controlling grain yield and kernels per spike (Sharma *et al.*, 2005) and 1000-kernel weight (Hassani *et al.*, 2005).

The proportion of genes with negative and positive effects among the parent ($H_2/4H_1$) was equal or near to one quarter for most of the studied characters, reflecting unequal distribution of positive and negative alleles in the parents. These results are in accordance

with those obtained by **Dere and Yildirim (2006)** for grain yield and **Akram *et al.* (2007)** for protein.

The proportion of dominant and recessive alleles in the parents (KD/KR) were found to be unequal with more dominant alleles for most characters. The recessive alleles were more than dominant alleles for plant height and 100-kernel weight (Table 6). Similar results were obtained by **Dere and Yildirim (2006)** for grain yield per plant and **Hammad and Abd El-Aty (2007)** for days to heading, days to maturity, plant height, spikes per plant, kernels per spike and grain yield per plant and contrarily for protein content by **Akram *et al.* (2007)**.

Regarding number of effective factors (K) that control the trait and exhibit dominance to certain degree, the data showed that the gene blocks governed all studied characters except plant height which was governed by two gene blocks and 100-kernel weight by three blocks.

The correlation coefficient "r" between the parental order of dominance (W_r+V_r) and the parental measurement (y_r) were negative for plant height, 100 kernel weight and grain yield, moisture (%), fat (%), ash (%) and fiber (%). These results suggested that the parents contain most increasing genes and the dominant genes controlled 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 expression is an advantage in breeding program as it might facilitate fixation of the traits in the early generations.

Heritability estimates in narrow sense (h^2_{ns}) are presented in Table 6. In general, moderate to high heritability estimates in narrow sense for most characters indicating that most of the variation in these characters was due to additive gene effects. Hence, traits improvement could be possible through selection in the early segregating generations. However, number of kernels per spike, fat (%), ash (%) and fiber (%) had low heritability that may be attributed to non-additive gene. These characters can be improved through hybridization. Similarly, high heritability estimates were obtained by **Hammad and Abd El-Aty (2007)** for days to heading, days to anthesis and days to maturity.

Laboratory Experiment:**Rheological properties of dough:**

Rheological properties of dough prepared from flour of some wheat genotypes were measured by farinograph and the results are presented in Table (7).

Table 7. Rheological properties of flour (82% extraction) from some wheat genotypes.

Genotype	Water absorption %	Arrival time (min)	Dough Development (min)	Dough Stability (min)	Dough weakening (B.U.)
P ₃	59.3	1.5	2.0	5.5	95
P ₄	59.0	1.0	1.5	5.0	80
P ₃ × P ₄	59.9	1.0	1.5	5.0	85
P ₃ × P ₅	59.7	1.5	2.0	5.5	90
P ₄ × P ₅	59.5	1.0	1.0	5.0	80

P₃ = Giza 168, P₄ = Gemmiza 9 and P₅ = Gemmiza 10.

Water absorption was higher in cross P₃ × P₄ than other genotypes which may be due to the increase in protein and fiber contents as reported by Abd El-Samad (2001). The wheat flour of P₄, P₃ × P₄ and P₄ × P₅ recorded the shortest arrival time; 1.0 min as earlier mentioned by Damir *et al.* (1982) which they found that short arrival time is generally associated with weak or/and low gluten content of the flour. Dough development (mixing time) was higher in P₃ and P₃ × P₅ than other genotypes. These results are in agreement with those obtained by El-Demiry (2005). She reported that the dough mixing time increased with increasing the protein content and gluten strength of the flour. Whereas, the increase in dough stability has been attributed to the pressure of low level energy of sulfhydryl groups in the protein which caused a softening or degradation action of the dough (Hamida, 1990).

Data in Table 7, also revealed that dough weakening low was low in P₄ and P₄ × P₅ compared with the other genotypes which could not form a strong gluten to hold and entrap gases during fermentation and baking as reported by Haber *et al.* (1976).

Protein quality of flour from some wheat genotypes:**1- Amino acids content:**

Amino acids content of flour of some wheat genotypes are presented in Table 8. All samples contained the detected indispensable amino acids. P₃ and the cross P₃ × P₅ contained the

highest total amount of all indispensable amino acids compared with other samples. Meanwhile, the flour of the wheat genotype $P_4 \times P_5$ contained the lowest amount of total indispensable amino acids. All samples of wheat genotypes contained more amounts of dispensable amino acids (64.59-64.99) than indispensable amino acids (28.05-28.47). The nutritive value of any protein depends primarily on its capacity to satisfy the need for indispensable amino acids for human being. Thus, the amino acids requirements are the logical factors by which protein quality can be measured (Bhushan, 1991).

Table 8. Amino acids content of flour from some wheat genotypes.

Amino acids	P_3	P_4	$P_3 \times P_4$	$P_3 \times P_5$	$P_4 \times P_5$
Indispensable amino acids:					
Leucine	5.69	5.59	5.64	5.62	5.58
Isoleucine	3.36	3.25	3.20	3.32	3.29
Lysine	2.55	2.50	2.45	2.53	2.43
Methionine	1.22	1.15	1.18	1.26	1.19
Cystine	1.48	1.61	1.54	1.57	1.50
<i>Meth. + Cyst.</i>	2.70	2.76	2.72	2.83	2.69
Phenylalanine	4.64	4.79	4.70	4.68	4.75
Tyrosine	1.82	1.84	1.86	1.79	1.81
<i>Phen. + Tyro.</i>	6.46	6.63	6.56	6.47	6.56
Threonine	2.14	2.10	2.21	2.01	1.98
Valine	4.40	4.38	4.36	4.43	4.32
* Tryptophan	1.17	1.15	1.26	1.23	1.20
Total indispensable amino acids	28.47	28.36	28.40	28.44	28.05
Dispensable amino acids:					
Alanine	3.30	3.27	3.25	3.19	3.22
Arginine	4.61	4.57	4.45	4.48	4.52
Aspartic acid	4.50	4.45	4.53	4.40	4.55
Glutamic acid	31.40	31.38	31.42	31.32	31.35
Glycine	3.64	3.61	3.57	3.66	3.67
Histadine	2.17	2.20	2.24	2.18	2.14
Proline	10.75	10.69	10.63	10.71	10.65
Serine	4.62	4.68	4.59	4.65	4.71
Total dispensable amino acids	64.99	64.85	64.68	64.59	64.81
Total amino acids	93.46	93.21	93.08	93.03	92.86

P_3 = Giza 168, P_4 = Gemmiza 9 and P_5 = Gemmiza 10.

2- Amino acid scores (A.A.S.):

The scores of the indispensable amino acid of flour of some wheat genotypes are given in Table (9). Data indicated that, lysine was found to be the first limiting indispensable amino acid followed by threonine.

Table 9. Chemical scoring * of flour from some wheat genotypes.

Amino acids	P ₃	P ₄	P ₃ × P ₄	P ₃ × P ₅	P ₄ × P ₅	Casein	FAQ/ WHO Pattern (g/16 gN)
Indispensable amino acids:							
Leucine	81.29	79.86	80.57	80.29	79.71	131.4	7.0
Isoleucine	84.00	81.25	80.00	83.00	82.25	126.2	4.0
Lysine	46.36	45.45	44.55	46.00	44.18	136.5	5.0
<i>Meth. + Cyst.</i>	77.14	78.86	77.71	80.86	76.86	84.5	3.5
<i>Phen. + Tyro.</i>	107.67	110.50	109.33	107.83	109.33	136.5	6.0
Threonine	53.50	52.50	55.25	50.25	49.50	85.7	4.0
Valine	88.00	87.60	87.20	88.60	86.40	108.4	5.0
Tryptophan	117.00	115.00	126.00	133.00	120.00	121	1.0

* Chemical scoring was calculated as a percentage according to FAQ/ WHO (1988) pattern. P₃ = Giza 168, P₄ = Gemmiza 9 and P₅ = Gemmiza 10.

3- The computed protein efficiency ratio (C-PER):

The computed protein efficiency ratio (C-PER) of different samples were lower than that of standard casein protein (PER=2.50) as given in Table (10). The lowest (C-PER) value was recorded in P₄ (1.77), while the highest value was detected in P₃ and P₃ × P₅ (1.89 %) genotypes.

Table 10. Computed protein efficiency ratio (C-PER) and biological value (B.V.) of flour from some wheat genotypes.

Genotype	C-PER	Biological value
P ₃	1.89	69.80
P ₄	1.77	68.54
P ₃ × P ₄	1.81	68.96
P ₃ × P ₅	1.89	69.80
P ₄ × P ₅	1.80	68.85
Casein	2.50	76.23

C-PER = Computed protein efficiency ratio and B.V.= Biological value. C-PER and B.V. of casein according to (FAO/ WHO pattern, 1988). P₃ = Giza 168, P₄ = Gemmiza 9 and P₅ = Gemmiza 10.

4- Biological value (B.V.):

The biological values of protein of different flour samples are presented in Table (10). Biological value is directly related to the concentration of the first limiting amino acid (Lysine) as reported by **Luh (1980)**. The results revealed that P_3 and $P_3 \times P_5$ genotypes had the highest biological value (69.80). These results are related to the (C-PER) which was the highest in P_3 and $P_3 \times P_5$ genotypes.

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الملخص العربي

التحسين الوراثي في الصفات المحصولية وصفات الجودة لخمسة أصناف من قمح الخبز

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تم تهجين خمسة أصناف من قمح الخبز وهي سخا ٩٣ و سخا ٩٤ و جيزة ١٦٨ وجميزة ٩ وجميزة ١٠ بنظام التهجين الدائري بدون الهجن العكسية. وقد أقيمت التجربة الحقلية خلال موسمي الزراعة ٢٠٠٥/٢٠٠٦ و ٢٠٠٦/٢٠٠٧ في محطة البحوث الزراعية بسخا. كما تم إجراء التجارب المعملية في معمل الصناعات الغذائية بكلية الزراعة بكفر الشيخ. وقد تم تقدير للمكونات الوراثية لسبعة صفات محصولية وستة صفات جودة. تم اختيار التراكيب الوراثية عالية المحتوى البروتيني لتحديد الصفات

الريولوجية للعجين وجودة البروتين وذلك باستخدام دقيق هذه التراكيب الوراثية. وقد أشار التحليل الوراثي للتراكيب الوراثية أن تأثيرات السيادة الجزئية لعبت دور في وراثية عدد الأيام حتى طرد السنابل وعدد الأيام حتى التزهير وعدد الأيام حتى النضج وطول النبات ومحتوى البروتين والجلوتين. كما أوضحت النتائج أن السيادة الكاملة تحكمت في وراثية كل من عدد حبوب السنبل ووزن المائة حبة ومحصول الحبوب ونسبة كل من الرطوبة والدهون والرماد والألياف. وقد أظهرت درجة التوريث بالمعنى الضيق قيم تتراوح ما بين متوسطة وعالية لأغلب الصفات المحصولية وصفات الجودة ماعدا كل من عدد حبوب السنبل ونسبة الدهن والرماد والألياف التي كانت منخفضة. كما تمت دراسة الجودة الغذائية والخواص الطبيعية لبعض أصناف القمح وهجنها وقد أعطى الصنف جيزة ١٦٨ أعلى محتوى من البروتين بينما سجل الصنف جيزة ٩ أعلى محتوى من الجلوتين. كما وجد أن أعلى نسبة للماء الممتص في الهجين جيزة ١٦٨ × جيزة ٩ بينما كان زمن الخلط في الصنف جيزة ١٦٨ و الهجين جيزة ١٦٨ × جيزة ٩ أعلى من باقي التراكيب الوراثية موضع الدراسة، كما أوضحت الدراسة أن الصنف جيزة ١٦٨ و الهجين جيزة ١٦٨ × جيزة ١٠ يحتويان على أعلى كمية من الأحماض الأمينية الأساسية وكذلك القيمة الحيوية للبروتين ومدى الاستفادة من البروتين بالمقارنة بباقي التراكيب الوراثية. وأن الليسين هو الحامض الأميني المحدد الأول في كل التراكيب الوراثية.