

**GENETIC ANALYSIS, RESPONSE TO SELECTION  
AND PREDICTION OF NEW RECOMBINANT  
LINES IN BREAD WHEAT  
(*Triticum aestivum* L.)**

Awaad, H. A.

Agron. Dept., Fac. Agric., Zagazig Univ., Zagazig, Egypt.

*Received 26 / 8 / 2002*

*Accepted 28 / 9 / 2002*

**ABSTRACT:** Six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub>) of four wheat crosses, namely 1) Sakha 69 x Sahel1, 2) Sakha 69 x ACSAD 945, 3) Sids 1 x F134-71/ Crow 'S' and 4) Gemmeiza 5 x Giza 168, were raised in a randomized complete block design during the three successive seasons of 1999/2000, 2000/2001 and 2001/2002 at the Experimental Farm, Faculty of Agriculture, Zagazig Univ., Zagazig, Egypt. The materials were subjected to determine the adequacy of genetic model, gene action, response to selection and prediction by the new recombinant lines for days to heading, flag leaf area, leaf chlorophyll content, grain yield/plant and its components as well as grain protein content.

Scaling test, provide evidence of non-allelic interaction in controlling days to heading in 2<sup>nd</sup> and 4<sup>th</sup> crosses; flag leaf area, leaf chlorophyll content and grain yield/plant in all crosses and grain protein content in 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses. Whereas, the simple genetic model was adequate for explaining the inheritance of days to heading in 1<sup>st</sup> and 3<sup>rd</sup> crosses as well as 1000-grain weight and grain protein content in 1<sup>st</sup> one. The additive gene effect (d) was more important in the genetic system controlling days to heading in 1<sup>st</sup> and 3<sup>rd</sup> crosses and 1000-grain weight and grain protein content in 1<sup>st</sup> cross. The additive (d) and its digenic interaction type additive x additive (i) were significant and involved in the inheritance of days to heading and number of spikes/plant in 2<sup>nd</sup> cross; leaf chlorophyll content and grain yield/plant in 1<sup>st</sup> cross and flag leaf area in 1<sup>st</sup> and 3<sup>rd</sup> crosses. However, the dominance (h) and dominance x dominance (l) were involved in the genetic control of flag leaf area, number of spikes/plant and grain yield/plant in 1<sup>st</sup> and 2<sup>nd</sup> crosses and grain protein content in 3<sup>rd</sup> and 4<sup>th</sup> crosses. The additive x dominance (j) was significant for grain protein content in 2<sup>nd</sup> and 4<sup>th</sup> crosses.

Duplicate type of epistasis has been reported for flag leaf area, number of spikes/plant and grain yield/plant in 1<sup>st</sup> and 2<sup>nd</sup> crosses; number of grains/spike in 2<sup>nd</sup> cross and grain protein content in 3<sup>rd</sup> and 4<sup>th</sup> crosses. Whereas, complementary

type was detected for number of grains/spike in 1<sup>st</sup> cross. The additive genetic variance (D) was the prevailed type controlling days to heading, flag leaf area, number of grains/spike, 1000-grain weight and grain protein content in most cases. Whereas, the dominance genetic variance (H) was more important in the inheritance of grain yield/plant in all crosses.

Narrow sense heritability was high (> 50%) for days to heading, flag leaf area, leaf chlorophyll content, number of grain/spike, 1000-grain weight and grain protein content in most cases, and ranged from low (24.49%) to moderate (44.59%) for grain yield/plant.

The results of correlated response in F<sub>2</sub> generation revealed that, the importance of the studied characters slightly varied according to the cross, and in general over crosses, indicated that the maximum genetic change in wheat grain yield was attributed to number of spikes/plant followed by number of grains/spike, 1000-grain weight, leaf chlorophyll content and flag leaf area.

Prediction results indicated that, it is feasible to expect transgressive segregants which out perform parental range and those likely to exceed F<sub>1</sub> hybrid for days to heading and leaf chlorophyll content in 4<sup>th</sup> cross; grain yield/plant in 2<sup>nd</sup> and 4<sup>th</sup> crosses as well as grain protein content in 1<sup>st</sup> and 3<sup>rd</sup> ones.

The best inbred lines (P max) displayed all favorable alleles have been reported for days to heading, leaf chlorophyll content and grain yield/plant in 2<sup>nd</sup> and 3<sup>rd</sup> crosses as well as 1000-grain weight and grain protein content in 3<sup>rd</sup> and 4<sup>th</sup> crosses. These results indicate the importance of these crosses as a source to produce new promising lines.

### INTRODUCTION

Increasing wheat potentiality through breeding programs is the cheapest and quickest solution to minimize the gap between the Egyptian production and consumption. Since, decision making about the effective breeding procedure to be used is mainly dictated by the type of gene action controlling the economic characters. Such information is helpful for the breeder to predict in early generations of

wheat breeding program, by the potential of new recombinant lines that could be derived followed a series of selfing generations. Since, the genetic information obtained from multigeneration are reliable compared with those based on one generation, thus six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub>) are considered the one which may give detailed information for the employed genotypes.

Assessment the type of gene

action in wheat have been studied by many investigators, and they reported that epistasis and non-additive gene effects contributed an important role in the inheritance of days to heading and grain yield (Ketata *et al.*, 1976); number of spikes/plant, number of grains/spike, 1000-grain weight and grain yield/plant (Pawar *et al.*, 1988 and Hendawy, 1994) and days to heading and number of grains/spike (Hassan, 1993 and Awaad, 1996). Additive and dominance gene action and their digenic interactions, (additive x additive), (additive x dominance) and (dominance x dominance) were more important in the inheritance of number of spikes/plant and grain yield/plant (Singh *et al.*, 1985) and grain yield/plant only (Awaad, 1996).

Whereas, the predominant of non-additive gene action controlling leaf chlorophyll content, kernel weight, flag leaf area and grain yield/plant reflected in moderately low narrow sense heritability (Ismail *et al.*, 2000 and Awaad, 2001) as well as for yield and its attributes (Hassan, 2002). However, additive genetic variance was found to be the prevailed type controlling the inheritance of days to heading, flag leaf area, number

of grains/spike reflecting high heritability estimates in narrow sense (Salem *et al.*, 2000). Moreover, both additive and dominance gene action were involved in the inheritance of grain protein content, with the predominant of additive gene effect reflected in high "Tn" values (Khalifa, 1982 and Dhaliwal *et al.*, 1994).

The response to selection provide the breeder knowledge about the kinds of association between genes of selected and unselected characters i.e. those between favorable combinations and those of retarding ones. This knowledge may give the breeder a courage for rightful decision making about the most effective characters to be used in wheat breeding programs. In this respect, many investigators studied response to selection and recorded substantial progress in wheat grain yield when selection was practiced for different attributes (Guptal and Ziauddin Ahmed 1982, Awaad, 1992, Mou *et al.*, 1994 and Gebre-Mariam and Larter, 1996).

Prediction in early generations, is useful to identify the most promising crosses which may produce the best yield of lines exceeding parental range,  $F_1$

hybrid or the best inbred (P max). In this regard, Snap and Parker (1986), Kuldip Singh and Bhullar (1989), Eissa and Awaad (1993) and Awaad (1996) mentioned that it could be possible to obtain proportion of new recombinant lines falling outside the parental range and those likely to exceed  $F_1$  hybrid for morphophysiological and yield contributing characters.

The present work was designated to determine the adequate genetic model and types of gene action controlling yield and some related characters, also to identify the most selection criteria for improving grain yield and to predict in early generations of breeding program, by the properties of recombinant lines that could be derived following a series of selfing generations of  $F_2$  population.

## MATERIALS AND METHODS

### Crossing technique and experimental layout.

The present investigation was conducted during the three winter growing seasons; 1999/2000, 2000/2001 and 2001/2002 at the Experimental Farm, Faculty of Agriculture, Zagazig Univ., Zagazig, Egypt. Four wheat crosses have been used in the present

study derived from seven diverse parental bread wheat genotypes (Table 1). These genotypes were used to obtain the following four crosses; 1) Sakha 69 x Sahel 1, 2) Sakha 69 x ACSAD 945, 3) Sids 1x F134-71/Crow 'S' and 4) Gemmeiza 5 x Giza 168.

In the first season of 1999/2000, the seven parental wheat genotypes were evaluated in a randomized complete block design with three replications, at the meantime, pair crosses were performed to obtain  $F_1$ 's grains. In the second season, 2000/2001, four  $F_1$  cross grains were sown to produce  $F_1$  plants. Each of the  $F_1$  plants were crossed back to their respective parents to produce first ( $F_1 \times P_1$ ) and second ( $F_1 \times P_2$ ) backcrosses. In the meantime, pair crosses were made to produce more  $F_1$  grains, also the  $F_1$  plants were selfed to produce  $F_2$  grains. In the third season, 2001/2002, the obtained grains of six populations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $B_1$  and  $B_2$ ) for each of the four crosses were evaluated using a randomized complete block design with three replications. Wheat grains were sown in 21<sup>st</sup> November. Row was 2m long, row to row and plant to plant spacings were 20 and 5cm, respectively

Table (1): Name, origin and pedigree of the parental wheat genotypes.

No.	Genotype name	Origin	Pedigree
1	Sakha 69	Egypt	Inia/ RL 4220// 7c/ Yr "S" CM 15430-25-65-0s-0s
2	Sahel 1	Egypt	N.S.732/Plm//Veery "S" D735-4sd-1 sd-Osd.
3	Sids 1	Egypt	HD2172/Pavon "S"//1158.57/Maya 74"S"
4	Gemmeiza 5	Egypt	Vec"S"/SWM6525CGM4017-1GM-6GM-3GM-OGM
5	Giza 168	Egypt	MIL/BUK//Seri: CM93046-8M-OY-OM-2Y-OB
6	F134-71/Crow 'S'	Syr/Mex	SWM 11147-1AP-2AP-4AP-1AP-0AP.
7	ACSAD 945	Syria	Mon 's'/Ald 's'//Deir Alla 4 ACS-W-8211-11Z-71Z-11Z-olZ.

The normal agricultural practices for wheat production were performed. The following data were recorded on 10 guarded plants for each parent and  $F_1$ , 30 for each backcross and 70 plants for  $F_2$  generation in every replicate to study, days to heading and flag leaf area at the time of full emergence of main spike, also flag leaf chlorophyll content was estimated using SPAD-502 apparatus (Castelli *et al.*, 1996) and at harvest for number of spikes/plant, number of grains/spike, 1000-grain weight and grain yield/plant. Moreover, grain protein content was estimated.

#### Biometrical assessment:

A regular analysis of variance was firstly performed for the studied characters of the four wheat crosses.

#### Testing the genetic model:

The A, B and C scaling tests as outlined by Mather and Jinks (1982) were applied to test the presence of non-allelic interactions

as follows;  $A = 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1$ ,  $B = 2\bar{B}_2 - \bar{P}_2 - \bar{F}_1$  and  $C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$ . Joint scaling test proposed by Cavalli (1952) as indicated by " $\chi^2$ " was applied for testing the goodness of fit of the adequacy genetic model controlling the studied characters. Due to unknown biased effect of non-allelic interaction, the simple genetic model {m, d and h} was applied when epistasis was absent. Whereas, in the presence of non-allelic interaction, the analysis was proceeded to compute the interaction types involved using the six-parameters genetic model according to Jinks and Jones (1958). The significance of the genetic components were tested using the "t" test, where:

$$\pm t = \frac{\text{Effect}}{\sqrt{\text{Variance of effect}}}$$

#### Components of the genetic variance:

The components of genetic variance for each character in the studied crosses were partitioned

into additive (D), dominance (H) genetic variances and environmental (E) one using Mather and Jinks (1982) formulae as follows:

$$E = (1/3)(VP_1 + VP_2 + VF_1)$$

$$D = 4 VF_2 - 2(VB_1 + VB_2) \text{ and}$$

$$H = 4 (VF_2 - 1/2 VD - E).$$

The genetic components of variance were used further to compute average degree of dominance  $(H/D)^{1/2}$  and heritability in narrow sense (Tn)

$$Tn = \frac{1/2D}{1/2D + 1/4H + E}$$

#### Response to selection:

The correlated response or the expected genetic change in an unselected character "grain yield/plant" resulting from the selection of the other character in F<sub>2</sub> generation was calculated using the formula suggested by Johanson *et al.* (1955) as follows:

Expected genetic change in an unselected character

$$= \frac{g_{1*2}}{Ph_1} * K \text{ where:}$$

$g_{1*2}$  = Genotypic covariance between the selected and unselected character.

$Ph_1$  = The phenotypic standard deviation of the selected character.

K = The selection differential at (10%) selection intensity.

The values of expected genetic change expressed as percentage from the mean value of the unselected character.

#### Predicting the properties of new recombinant lines:

The properties of new recombinant lines which fall outside parental range and those exceeding F<sub>1</sub> hybrid following a number of selfing generations of a cross between two inbred lines were calculated using Jinks and Pooni (1976) formulae, where:

Proportion of inbreds falling

outside parental range =  $d/\sqrt{D}$   
Proportion of inbreds exceeding F<sub>1</sub>

hybrid =  $h/\sqrt{D}$ .

Also, the best inbred (P max)

$$= m + h/\sqrt{H/D}$$

was calculated according to Hayward *et al.* (1993), where:

$$m = 1/2 (\bar{p}_1 + \bar{p}_2)$$

$$[d] = 1/2 (\bar{p}_1 - \bar{p}_2)$$

$$[h] = \bar{F}_1 - m$$

The proportion of recombinant lines corresponding to the probability level were obtained using Fisher and Yates (1963) Tables.

## RESULTS AND DISCUSSION

### 1. Mean performance:

The reliability of the genetic parameters estimates depends mainly on the magnitude of genetic

variability existed among the tested genotypes. Thus, before proceeding to the biometrical assessments, "t" statistical test was applied for the studied genotypes of the different characters. The results indicated significant differences between parental wheat genotypes, suggesting the presence of high degree of genetic variability valid for further biometrical analysis. Data of mean performance (Tables 2 and 3) showed that the  $F_1$  was closed to the earlier parent and exceeded the high performing one for flag leaf area in 2<sup>nd</sup> and 4<sup>th</sup> crosses; leaf chlorophyll content, number of spikes/plant and grain protein content in 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses, number of grains/spike in 1<sup>st</sup> and 2<sup>nd</sup> crosses; 1000-grain weight in 3<sup>rd</sup> cross and grain yield/plant in 2<sup>nd</sup> one. Also the  $F_1$  was tended towards the high yielding parent in the 3<sup>rd</sup> cross.

The obtained results providing evidence of the predominant of desirable alleles responsible of earliness and yield contributing characters in aforementioned crosses.

## 2. Adequacy genetic model and gene effects.

Scaling tests (A, B and C) in Tables (4 and 5), provide evidence

for the failure of a simple genetic model to explain the genetic mechanism controlling days to heading in 2<sup>nd</sup> and 4<sup>th</sup> crosses; flag leaf area, leaf chlorophyll content and grain yield/plant in all crosses; number of spikes/plant and number of grains/spike in 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> crosses as well as 1000-grain weight and grain protein content in 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses. These results indicate the presence of epistasis, and the digenic model was adequate to explain the genetics of the abovementioned characters in the corresponding crosses. Similar findings were reported for yield contributing characters by Hassan (1993) and Awaad (1996).

The insignificancy of non allelic interaction tests for days to heading in 1<sup>st</sup> and 3<sup>rd</sup> crosses; number of spikes/plant and number of grains/spike in 4<sup>th</sup> cross and 1000-grain weight and grain protein content in 1<sup>st</sup> cross, indicating that the simple additive-dominance genetic model proved to be satisfactory in explaining the inheritance of the foregoing characters. Similar results were reported for yield attributes (Ketata *et al.*; 1976, and Eissa and Awaad, 1993) and for grain protein content (Dhaliwal *et al.*, 1994).

Table (2): Mean  $\pm$  S.E. for the six populations for days to heading, flag leaf area, leaf chlorophyll content and number of spikes/plant in four wheat crosses.

Character Cross Population	Days to heading (day)				Flag leaf area (cm <sup>2</sup> )			
	1	2	3	4	1	2	3	4
P <sub>1</sub>	88.662 $\pm$ 0.207	88.662 $\pm$ 0.207	78.500 $\pm$ 0.251	86.033 $\pm$ 0.364	48.279 $\pm$ 0.336	48.279 $\pm$ 0.336	55.439 $\pm$ 0.308	53.317 $\pm$ 0.342
P <sub>2</sub>	83.300 $\pm$ 0.245	87.345 $\pm$ 0.244	88.509 $\pm$ 0.325	90.059 $\pm$ 0.270	52.439 $\pm$ 0.286	45.520 $\pm$ 0.282	53.209 $\pm$ 0.315	42.118 $\pm$ 0.346
F <sub>1</sub>	86.153 $\pm$ 0.197	87.030 $\pm$ 0.161	87.882 $\pm$ 0.223	87.194 $\pm$ 0.225	48.820 $\pm$ 0.314	53.306 $\pm$ 0.272	48.002 $\pm$ 0.336	53.700 $\pm$ 0.268
F <sub>2</sub>	86.387 $\pm$ 0.329	82.881 $\pm$ 0.365	86.000 $\pm$ 0.586	85.439 $\pm$ 0.479	43.998 $\pm$ 1.138	43.717 $\pm$ 1.227	45.365 $\pm$ 1.443	48.098 $\pm$ 1.522
B <sub>1</sub>	87.726 $\pm$ 0.279	86.314 $\pm$ 0.322	84.210 $\pm$ 0.572	86.054 $\pm$ 0.461	49.803 $\pm$ 0.863	48.428 $\pm$ 1.093	54.410 $\pm$ 1.428	46.706 $\pm$ 1.152
B <sub>2</sub>	85.040 $\pm$ 0.313	84.733 $\pm$ 0.356	86.891 $\pm$ 0.561	86.030 $\pm$ 0.409	53.230 $\pm$ 0.975	50.046 $\pm$ 1.023	44.172 $\pm$ 0.962	51.438 $\pm$ 1.491
	Leaf chlorophyll content				Number of spikes \ plant			
	1	2	3	4	1	2	3	4
P <sub>1</sub>	74.336 $\pm$ 0.325	74.336 $\pm$ 0.325	69.578 $\pm$ 0.309	70.933 $\pm$ 0.350	4.548 $\pm$ 0.089	4.548 $\pm$ 0.089	3.787 $\pm$ 0.172	4.500 $\pm$ 0.146
P <sub>2</sub>	68.578 $\pm$ 0.303	64.713 $\pm$ 0.330	70.947 $\pm$ 0.354	67.738 $\pm$ 0.336	4.202 $\pm$ 0.137	4.833 $\pm$ 0.145	4.201 $\pm$ 0.064	4.700 $\pm$ 0.151
F <sub>1</sub>	71.860 $\pm$ 0.344	75.850 $\pm$ 0.270	74.733 $\pm$ 0.270	72.091 $\pm$ 0.262	4.032 $\pm$ 0.138	6.030 $\pm$ 0.137	5.088 $\pm$ 0.173	5.263 $\pm$ 0.158
F <sub>2</sub>	65.327 $\pm$ 1.672	61.393 $\pm$ 2.242	61.028 $\pm$ 2.167	61.653 $\pm$ 2.150	4.104 $\pm$ 0.305	5.818 $\pm$ 0.311	4.550 $\pm$ 0.219	4.498 $\pm$ 0.329
B <sub>1</sub>	66.666 $\pm$ 1.271	64.116 $\pm$ 1.938	56.907 $\pm$ 2.109	65.428 $\pm$ 2.105	6.020 $\pm$ 0.268	4.973 $\pm$ 0.265	4.455 $\pm$ 0.197	4.811 $\pm$ 0.239
B <sub>2</sub>	71.250 $\pm$ 1.415	65.600 $\pm$ 1.989	63.989 $\pm$ 2.121	64.439 $\pm$ 2.101	5.806 $\pm$ 0.300	4.067 $\pm$ 0.270	5.100 $\pm$ 0.209	4.682 $\pm$ 0.261

Table (3): Mean  $\pm$  S.E. for the six populations for number of grains\spike, 1000-grain weight, grain yield\plant and grain protein content in four wheat crosses.

Character Cross Population	Number of grains\spike				1000-grain weight (g.)			
	1	2	3	4	1	2	3	4
P <sub>1</sub>	49.887 $\pm$ 0.649	49.887 $\pm$ 0.649	56.247 $\pm$ 0.528	60.061 $\pm$ 0.909	51.677 $\pm$ 0.337	51.677 $\pm$ 0.337	48.900 $\pm$ 0.357	48.734 $\pm$ 0.339
P <sub>2</sub>	52.633 $\pm$ 0.796	47.010 $\pm$ 0.676	64.467 $\pm$ 0.466	57.324 $\pm$ 1.101	38.900 $\pm$ 0.301	42.787 $\pm$ 0.341	47.349 $\pm$ 0.306	40.232 $\pm$ 0.281
F <sub>1</sub>	53.178 $\pm$ 0.754	50.300 $\pm$ 0.935	54.267 $\pm$ 0.567	50.079 $\pm$ 0.529	40.793 $\pm$ 0.302	45.469 $\pm$ 0.328	50.240 $\pm$ 0.336	45.931 $\pm$ 0.245
F <sub>2</sub>	45.821 $\pm$ 1.273	46.976 $\pm$ 1.961	53.889 $\pm$ 1.707	51.600 $\pm$ 2.237	42.448 $\pm$ 1.449	40.509 $\pm$ 1.624	37.770 $\pm$ 1.352	36.540 $\pm$ 0.877
B <sub>1</sub>	47.414 $\pm$ 0.609	42.694 $\pm$ 0.899	54.634 $\pm$ 1.488	51.206 $\pm$ 1.728	43.932 $\pm$ 1.190	34.461 $\pm$ 1.352	34.096 $\pm$ 1.019	33.689 $\pm$ 0.752
B <sub>2</sub>	50.313 $\pm$ 0.999	42.344 $\pm$ 0.842	50.188 $\pm$ 1.806	53.355 $\pm$ 1.784	39.505 $\pm$ 1.414	41.179 $\pm$ 1.395	36.987 $\pm$ 1.304	41.421 $\pm$ 0.854
	Grain yield\plant (g.)				Grain protein content (%)			
	1	2	3	4	1	2	3	4
P <sub>1</sub>	8.338 $\pm$ 0.325	8.338 $\pm$ 0.325	7.627 $\pm$ 0.309	10.686 $\pm$ 0.251	10.544 $\pm$ 0.332	10.544 $\pm$ 0.332	11.616 $\pm$ 0.147	10.733 $\pm$ 0.233
P <sub>2</sub>	6.627 $\pm$ 0.282	7.193 $\pm$ 0.315	11.424 $\pm$ 0.284	8.586 $\pm$ 0.211	12.075 $\pm$ 0.205	10.275 $\pm$ 0.264	12.188 $\pm$ 0.177	12.138 $\pm$ 0.409
F <sub>1</sub>	5.250 $\pm$ 0.202	10.864 $\pm$ 0.313	9.893 $\pm$ 0.184	8.989 $\pm$ 0.234	10.221 $\pm$ 0.487	11.667 $\pm$ 0.234	12.891 $\pm$ 0.132	12.244 $\pm$ 0.232
F <sub>2</sub>	5.365 $\pm$ 1.378	9.419 $\pm$ 0.787	7.338 $\pm$ 0.639	6.258 $\pm$ 0.435	11.415 $\pm$ 1.729	11.825 $\pm$ 0.948	10.540 $\pm$ 1.078	11.325 $\pm$ 1.243
B <sub>1</sub>	10.076 $\pm$ 0.933	6.635 $\pm$ 0.784	6.967 $\pm$ 0.615	5.998 $\pm$ 0.427	10.825 $\pm$ 0.942	12.075 $\pm$ 0.773	11.974 $\pm$ 0.474	10.105 $\pm$ 0.743
B <sub>2</sub>	7.599 $\pm$ 1.191	7.271 $\pm$ 0.774	5.569 $\pm$ 0.632	5.985 $\pm$ 0.433	11.775 $\pm$ 1.208	10.725 $\pm$ 0.872	12.790 $\pm$ 0.813	9.725 $\pm$ 0.843

The adequacy of genetic model (Tables 4 and 5) indicated that the additive gene effect (d) was the main type controlling the inheritance of days to heading in 1<sup>st</sup> and 3<sup>rd</sup> crosses and 1000-grain weight and grain protein content in 1<sup>st</sup> cross. Meanwhile, the additive (d) and additive x additive (i) interaction type were important in the genetic system controlling days to heading and number of spikes/plant in 2<sup>nd</sup> cross; flag leaf area in 1<sup>st</sup> and 3<sup>rd</sup> crosses; leaf chlorophyll content and grain yield/plant in 1<sup>st</sup> cross and grain protein content in 3<sup>rd</sup> one. These results indicated that, the superior genotypes could efficiently identified from its phenotypic expression, therefore phenotypic selection was more effective for improving these characters in those crosses. Similar results were reported by many investigators (Pawar *et al.*, 1988; Mosaad, 1991 and Awaad, 1996).

The dominance (h) and its digenic interaction type dominance x dominance (l) were significant and involved in the inheritance of flag leaf area, number of spikes/plant and grain yield/plant in 1<sup>st</sup> and 2<sup>nd</sup> crosses; number of grains/spike in 2<sup>nd</sup> cross as well as grain protein content in 3<sup>rd</sup> and 4<sup>th</sup>

crosses. The considerable amount of non-fixable gene action type displayed by these characters in the corresponding crosses may suggest that improving these characters could be achieved through hybrid breeding method. Similar findings were detected by Pawar *et al.* (1988), Hassan (1993) and Hassan (2002).

Meanwhile, the interaction type additive x dominance (j) was positive and significant for days to heading in 4<sup>th</sup> cross; flag leaf area, number of grains/spike and grain yield/plant in 3<sup>rd</sup> cross; number of spikes/plant in 2<sup>nd</sup> cross and grain protein content in 2<sup>nd</sup> and 4<sup>th</sup> crosses. Suggesting that increasing alleles were more frequent than the decreasing ones, and vice versa was recorded for flag leaf area in 2<sup>nd</sup> and 4<sup>th</sup> crosses; leaf chlorophyll content in 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> crosses; 1000-grain weight in 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses and grain yield/plant in 4<sup>th</sup> one, which showing more frequent of decreasing alleles over increasing ones. Also, the interaction types of (j) and (l) were highly significant for grain yield/plant in 3<sup>rd</sup> and 4<sup>th</sup> crosses.

It is worth noting that the dominance (h) and its digenic interaction dominance x dominance (l) were significant and

have different signs for flag leaf area, number of spikes/plant and grain yield/plant in 1<sup>st</sup> and 2<sup>nd</sup> crosses; number of grains/spike in 2<sup>nd</sup> cross as well as grain protein content in 3<sup>rd</sup> and 4<sup>th</sup> crosses. Indicating that interaction is predominantly of duplicate type (Mather and Jinks, 1982).

Whereas the sign of (h) and (l) was similar in number of grains/spike in 1<sup>st</sup> cross, indicating that interaction is predominantly of complementary type. Similar result was reported by Jedynski (1988).

### 3. Components of the genetic variance and heritability:

The results given in Tables (4 and 5) clearly indicate that, additive genetic variance (D) was the predominant type controlling days to heading in 1<sup>st</sup>, 2<sup>nd</sup> and 4<sup>th</sup> crosses; flag leaf area and grain protein content in all crosses; leaf chlorophyll content in 1<sup>st</sup> and 2<sup>nd</sup> crosses; number of spikes/plant in 2<sup>nd</sup> cross; number of grains/spike in 1<sup>st</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses; 1000-grain weight in 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> crosses, resulting in  $(H/D)^{1/2}$  ratio was less than unity, suggesting the effectiveness of phenotypic selection for improving the foregoing characters in the corresponding crosses. Similar conclusion was reported for days

to heading, flag leaf area and yield components (Eissa and Awaad 1993 and Salem *et al.* 2000) and for grain protein content (Dhaliwal *et al.*, 1994).

The dominance genetic variance was the prevailed type controlling the inheritance of days to heading in 3<sup>rd</sup> cross; leaf chlorophyll content in 3<sup>rd</sup> and 4<sup>th</sup> crosses; number of grains/spike in 2<sup>nd</sup> cross; 1000-grain weight in 4<sup>th</sup> cross and grain yield/plant in all crosses, resulting in  $(H/D)^{1/2}$  more than unity. Indicating the effectiveness of using hybrid breeding method when commercial seed production of wheat is feasible. In this respect, dominance gene effect played an important role in the inheritance of leaf chlorophyll content and kernel weight (Ismail *et al.*, 2000); number of spikes/plant, 1000-grain weight and grain yield/plant (Hassan, 1998) as well as 1000-grain weight and grain yield/plant (Kheiralla *et al.*, 2001).

Heritability estimates depends on the magnitude of its portions, additive and dominance genetic components to the phenotypic variance. In this respect, narrow sense heritability "Tn" reflects the fixable type of gene action transmissible from the parents to

Table (4): Non-allelic interaction tests (A, B and C), adequacy genetic model, genetic components of variance and heritability for days to heading, flag leaf area, leaf chlorophyll content and number of spikes/plant in four wheat crosses.

Character Cross Estimate	Days to heading				Flag leaf area				Leaf chlorophyll content				Number of spikes/plant			
	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4
<b>Scaling test</b>																
A	0.637	-3.064**	2.038	-1.119	2.507	-4.729*	5.379	-13.605**	-12.864**	-21.954**	-30.497**	-12.168**	3.460**	-0.632	0.035	-0.141
B	0.627	-4.909**	-2.609	-5.193**	5.201**	1.266	-12.867**	7.058*	2.062	-9.363*	-17.702**	-10.951**	3.378**	-2.729**	0.911*	-0.599
C	1.280	-18.543**	1.227	-8.724**	-22.366**	-25.543**	-23.192**	-10.443	-25.326**	-45.177**	-45.879**	-36.241**	-0.398	1.831	0.036	-1.734
$\chi^2$	N.S.	**	N.S.	**	**	**	**	**	**	**	**	**	**	*	*	N.S.
<b>Adequacy genetic model</b>																
m	85.997**	82.881**	85.303**	85.439**	46.998**	46.717**	45.365**	48.098**	65.327**	61.393**	61.028**	61.653**	4.104**	5.818**	4.550**	3.606*
d	2.681**	1.581**	-5.005**	0.024	-3.427**	-1.618	13.238**	-4.732*	-4.584*	-1.484	-7.082**	0.989	0.214	0.906*	-0.645**	-0.100
h	1.404	9.597**	0.211	1.560	28.535**	28.487**	9.382	9.879	14.927*	20.186*	2.151	15.878	6.893**	-3.853**	2.004	1.911
i		10.570**		2.412	30.074**	22.080**	15.704*	3.896	14.524*	13.860	-2.320	13.122	7.236**	-5.192**	0.910	
j		0.923		2.037**	-1.345	-2.998*	9.123**	-10.332**	-7.463**	-6.296*	-6.398*	-0.609	0.041	1.059**	-0.438	
l		-2.597		3.900	-37.782**	-18.617*	-8.216	2.651	-3.722	17.457	50.519**	9.997	-14.074**	8.553**	-1.856	
<b>Components of genetic variance</b>																
D	7.662	7.182	17.674	12.266	108.682	104.088	194.408	169.488	281.598	381.772	293.350	203.804	4.178	7.054	2.118	3.972
H	2.248	2.700	29.668	6.004	29.656	33.548	48.020	65.264	26.840	64.776	411.596	414.424	9.836	0.256	2.688	11.06
E	1.440	1.305	2.246	2.668	3.048	2.788	3.187	3.236	3.340	4.042	3.982	3.184	0.471	0.491	0.569	0.449
$\sqrt{H/D}$	0.542	0.613	1.296	0.699	0.522	0.568	0.497	0.621	0.308	0.411	1.185	1.426	1.534	0.191	1.127	1.669
Tn%	65.68	64.46	47.77	59.53	83.86	82.32	86.48	81.25	93.34	90.42	57.85	48.95	41.62	86.40	46.04	38.19

\*, \*\* Significant and highly significant at 0.05 and 0.01 probability levels, respectively.

Table (5): Non-allelic interaction tests (A, B and C), adequacy genetic model, genetic components of variance and heritability for number of grains/spike, 1000-grain weight, grain yield/plant and grain protein content in four wheat crosses.

Character Cross Estimate	Number of grains/spike				1000-grain weight				Grain yield/plant				Grain protein content (%)			
	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4
<b>Scaling test</b>																
A	-8.237**	-14.799**	-1.246	-7.728	-4.606	-28.224**	-30.948**	-27.287**	6.564*	-5.932*	-3.586*	-7.679**	0.885	1.939**	-0.559	-2.767**
B	-5.185	-12.622**	-18.358**	-0.693	-0.683	-5.898*	-23.615**	-3.321*	3.321	-3.515*	-10.179**	-5.605**	1.254	-0.492	0.501	-4.932**
C	-25.592**	-9.593	-13.692*	-11.143	-2.371	-7.366	-13.649**	-16.644**	-4.005	-0.417	-9.485**	-12.218**	2.599	3.147**	-7.428**	-2.059
$\chi^2$	**	**	**	N.S.	N.S.	**	**	**	**	**	**	**	N.S.	**	**	**
<b>Adequacy genetic model</b>																
m	45.821**	46.976**	53.889**	55.971**	48.207**	40.509**	37.770**	36.540**	5.365**	9.419**	7.338**	6.258**	11.769**	11.825**	10.540**	11.325**
d	-2.899	0.350	4.446**	1.369	6.389*	-6.718**	-2.891	-7.732**	2.477*	-0.636	1.398*	0.013	-0.766**	1.350**	-0.816**	0.380
h	14.088**	-15.977**	-12.002	17.209	-15.621	-12.519	-6.799	5.508	11.658*	-6.766*	-3.913	-1.713	0.131	-0.443	8.357**	-4.832**
l	12.170**	-17.828**	-5.912			-10.756	-8.914	4.060	13.890*	-9.864**	-4.280	-1.066		-1.700	7.368**	-5.640**
j	-1.526	-1.089	8.556**			-11.163**	-3.667*	-11.983**	1.622	-1.209	3.297**	-1.037*		1.216**	-0.530	1.083**
l	1.252	45.249**	25.516**			44.878**	63.477**	26.548**	-23.775**	19.311**	18.045**	14.350**		0.253	-7.310**	13.339**
<b>Components of genetic variance</b>																
D	65.362	128.588	238.764	72.632	181.536	194.566	172.164	32.742	5.440	12.252	8.676	7.568	6.738	1.938	2.36	3.800
H	37.472	240.988	123.152	60.664	78.288	41.144	36.464	62.480	9.364	59.064	14.508	11.864	0.140	1.896	0.352	1.976
E	9.865	10.724	7.179	8.518	3.129	3.213	3.458	2.660	2.349	3.142	2.147	1.737	0.539	0.533	0.363	0.606
$\sqrt{E/D}$	0.757	1.369	0.718	0.914	0.656	0.459	0.460	1.381	1.312	2.195	1.293	1.252	0.144	0.989	0.386	0.721
Tb%	62.95	47.53	75.87	60.53	79.99	87.82	87.26	47.25	36.71	25.49	42.89	44.59	85.44	49.04	72.35	63.33

\*, \*\* Significant and highly significant at 0.05 and 0.01 probability levels, respectively.

the progeny or from generation to another, was high (>50%) for days to heading in 1<sup>st</sup>, 2<sup>nd</sup> and 4<sup>th</sup> crosses; flag leaf area in all crosses, leaf chlorophyll content and 1000-grain weight in 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> crosses; number of spikes/plant in 2<sup>nd</sup> cross and number of grains/spike and grain protein content in 1<sup>st</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses. These results allowing for considerable progress from selection. In this connection, high "Tn" values have been reported for days to heading, flag leaf area and number of grains/spike (Salem *et al.*, 2000) as well as number of grains/spike and 1000-grain weight (Awaad, 1996). Whereas, low to moderate "Tn" estimates were reported for grain yield/plant and the remaining crosses for the various characters. Similar results were recorded for days to heading (Mosaad, 1991); leaf chlorophyll content and grain yield (Ismail *et al.*, 2000 and Awaad, 2001) and for yield and its attributes (Awaad, 2002).

#### 4. Response to selection:

The results of response to selection or correlated response (Table 6) provide evidence for the maximum and significant expected genetic change in the unselected character, "grain yield/plant", was

recorded when selection was imposed to number of spikes/plant followed by late heading, 1000-grain weight, grain protein content and leaf chlorophyll content in 1<sup>st</sup> cross as well as number of spikes/plant followed by 1000-grain weight, leaf chlorophyll content, number of grains/spike, early heading and flag leaf area in 2<sup>nd</sup> cross. Whereas, in 3<sup>rd</sup> cross, five characters i.e., number of spikes/plant followed by number of grains/spike, grain protein content, flag leaf area and leaf chlorophyll content were accounted for high expected genetic change in the unselected character "grain yield/plant". However, substantial genetic progress in grain yield/plant has been occurred in 4<sup>th</sup> cross by selecting number of spikes/plant followed by number of grains/spike, late heading, grain protein content, flag leaf area and leaf chlorophyll content. In this connection, selection based on number of productive tillers/plant, number of grains/spike and 1000-grain weight (Guptal and Ziauddin Ahmad, 1982 and Awaad, 1992) resulted in high correlated response in grain yield.

When selection was imposed to late heading, a positive and

significant genetic change in grain yield/plant was observed in 1<sup>st</sup> and 4<sup>th</sup> crosses, suggesting that genes controlling late heading were associated with those increasing grain yield/plant and vice versa in 2<sup>nd</sup> cross. In this connection, maximum correlated response in wheat grain yield/plant was achieved through selection for late heading in F<sub>3</sub>'s families of wheat crosses C.B.35 x Giza 155 and Giza 157 x Giza 155 as well as for earliness in the cross C.B. cimmyt 48 x Sakha 61 (Awaad, 1992).

When selection was

performed based on grain protein content, positive and significant genetic change in grain yield/plant has been occurred in 1<sup>st</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses. Similar finding was observed by Mou *et al.* (1994). On the other hand, negative correlated response in this respect was detected in 2<sup>nd</sup> cross. This result is expected because of a high protein content can result from a relatively poor starch accumulation. Gebre-Mariam and Larter (1996) reported that a 1% increase in grain protein content from selection for protein level, depressed wheat grain yield.

**Table (6):** Response to selection in F<sub>2</sub> generation of the studied crosses.

Selected character	Expected genetic change in unselected character "grain yield/plant".			
	Cross 1	Cross 2	Cross 3	Cross 4
Days to heading	6.192**	-3.103*	0.389	5.680**
Flag leaf area	1.961	2.397*	3.063*	3.385*
Leaf chlorophyll content	2.392*	4.217**	2.708*	2.980*
No. of spikes/plant	10.869**	7.014**	12.613**	9.259**
No. of grains/spike	-0.635	3.405*	7.841**	6.174**
1000-grain weight	5.179**	4.763**	-1.039	1.469
Grain protein content	4.924*	-6.710**	3.398*	4.665**

##### 5. Predicting the properties of new recombinant lines:

Prediction results given in Table (7) reveal that it is feasible to expect transgressive segregants which out perform the parental range. The percentage of such segregants for days to heading was (40.129%) and grain yield/plant

(43.644%) in 2<sup>nd</sup> cross; flag leaf area (44.433%) and (46.812%); 1000-grain weight (37.448%) and (47.608%) and grain protein content (46.414%) and (42.465%) in 2<sup>nd</sup> and 3<sup>rd</sup> crosses, respectively; leaf chlorophyll content (48.405%) and (45.620%) in 3<sup>rd</sup> and 4<sup>th</sup> crosses, respectively; number of

**Table (7): Predicting the properties of new recombinant lines falling outside parental range for different characters in four wheat crosses.**

Parameter	[m]=F <sub>2</sub>	Range of inbreds $m \pm 2\sqrt{D}$	d	Probability $d/\sqrt{D}$	Proportion of inbreds falling outside parental range	[m]=F <sub>2</sub>	Range of inbreds $m \pm 2\sqrt{D}$	d	Probability $d/\sqrt{D}$	Proportion of inbreds falling outside parental range
<b>Cross</b>						<b>Days to heading</b>				
1	86.387	91.923-80.851	2.681	0.969	16.602	47.821	63.990-31.652	1.373	0.169	43.251
2	82.881	88.240-77.522	0.659	0.246	40.129	46.976	69.655-24.297	1.439	0.127	44.828
3	86.000	94.408-77.592	5.005	1.191	11.507	53.889	84.793-22.985	4.110	0.266	39.358
4	85.439	92.444-78.435	2.013	0.575	28.096	51.600	68.645-34.160	1.369	0.161	45.620
<b>Flag leaf area</b>						<b>1000-grain weight</b>				
1	43.998	64.848-23.148	2.080	0.199	42.465	42.448	69.395-15.501	6.389	0.474	31.918
2	43.717	64.122-23.312	1.379	0.135	44.433	40.509	68.406-12.612	4.445	0.319	37.448
3	45.365	73.251-17.479	1.115	0.079	46.812	37.770	64.012-11.528	0.776	0.059	47.608
4	48.098	74.136-22.061	5.599	0.430	33.360	36.540	47.984-25.096	4.251	0.743	22.965
<b>Leaf chlorophyll content</b>						<b>Grain yield/plant</b>				
1	65.327	98.889-31.765	2.879	0.172	43.251	5.365	10.029-0.700	0.856	0.367	35.569
2	61.393	100.471-22.315	4.812	0.246	40.129	9.419	16.419-2.419	0.573	0.163	43.644
3	61.028	95.283-26.773	0.685	0.039	48.405	7.338	13.229-1.447	1.899	0.645	25.785
4	61.653	90.205-33.101	1.598	0.112	45.620	6.258	11.759-0.756	1.050	0.382	35.197
<b>Number of spikes/plant</b>						<b>Grain protein content</b>				
1	4.104	8.192-0.016	0.173	0.085	46.414	11.415	16.607-6.223	0.766	0.295	38.591
2	5.818	11.129-0.506	0.143	0.054	48.006	11.825	14.609-9.041	0.135	0.097	46.414
3	4.550	7.461-1.639	0.207	0.142	44.433	10.540	13.612-7.468	0.286	0.186	42.465
4	4.498	8.484-0.513	0.100	0.050	48.006	11.325	15.224-7.426	0.703	0.361	35.942

spikes/plant (48.006%) and (48.006%) and number of grains/spike (44.828%) and (45.620%) in 2<sup>nd</sup> and 4<sup>th</sup> crosses, respectively. Indicating that these crosses are the promising ones. In this connection, the highest proportion of recombinants falling outside parental range were reported for days to heading (Kuldip Singh and Bhullar, 1989); number of spikes/plant, 1000-grain weight and grain yield/plant (Snape and Parker, 1986 and Eissa and Awaad, 1993) and flag leaf area, grain yield and its components (Awaad, 1996).

Concerning the potence ratio (Table 8), the results indicated that the highest values were detected for days to heading in 2<sup>nd</sup> and 3<sup>rd</sup> crosses; leaf chlorophyll content in 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> crosses; 1000-grain weight in 1<sup>st</sup> and 3<sup>rd</sup> crosses; grain yield/plant in 1<sup>st</sup> and 2<sup>nd</sup> crosses as well as flag leaf area, number of spikes/plant, number of grains/spike and grain protein content in all crosses. These results indicated dispersion of dominant genes which increase expression between the parents and ensure transgressive segregation for these characters should be occurred in F<sub>2</sub> generation. The overdominant type of genetical architecture is

commonly found for yield and its attributes in wheat (Khalifa *et al.*, 1998 and Awaad, 2002).

With respect to those recombinant lines derived from series of selfing generations and exceeding F<sub>1</sub> (Table 8), it could be noted that the higher proportion of inbreds have been recorded for days to heading (47.608%), flag leaf area (44.038%) and leaf chlorophyll content (49.202%) in 1<sup>st</sup> cross; number of spikes/plant (43.251%) and (44.828%) and number of grains/spike (40.517%) and (43.614%) in 1<sup>st</sup> and 2<sup>nd</sup> crosses, respectively; 1000-grain weight (44.828%) and (43.644%) in 2<sup>nd</sup> and 3<sup>rd</sup> crosses, respectively and grain yield/plant in 3<sup>rd</sup> (44.828%) cross as well as grain protein content (33.724%) in 1<sup>st</sup> and 4<sup>th</sup> crosses. Similar findings were obtained for yield contributing characters by Snape and Parker (1986), Eissa and Awaad (1993) and Awaad (1996).

The best inbred line (P max) (Table 8) will have all the favorable alleles was recorded for days to heading in all crosses; flag leaf area in 2<sup>nd</sup> and 4<sup>th</sup> crosses; leaf chlorophyll content and grain yield/plant in 2<sup>nd</sup> and 3<sup>rd</sup> crosses; number of spikes/plant in 2<sup>nd</sup> cross; 1000-grain weight and grain

Table (8): Predicting the properties of new recombinant lines exceeding  $F_1$  and the best inbred (P max) for different characters in four wheat crosses.

Parameter	h	Potence ratio h/d	Probability $h/\sqrt{D}$	Proportion of inbreds exceeding $F_1$	P max	h	Potence ratio h/d	Probability $h/\sqrt{D}$	Proportion of inbreds exceeding $F_1$	P max				
<b>Cross</b>					<b>Days to heading</b>					<b>Number of grains/spike</b>				
1	0.172	0.128	0.062	47.608	86.299	1.918	1.397	0.237	40.517	53.793				
2	-0.974	2.954	0.363	35.942	86.415	1.852	1.287	0.163	43.644	49.802				
3	4.378	1.749	1.041	14.917	86.884	-6.090	1.482	0.394	34.827	51.877				
4	-0.852	0.846	0.243	40.517	86.828	-8.614	6.292	1.011	15.625	49.268				
<b>Flag leaf area</b>					<b>1000-grain weight</b>									
1	-1.539	1.479	0.148	44.038	47.413	-4.496	1.407	0.334	37.070	38.443				
2	6.407	9.292	0.628	26.435	58.184	-1.763	0.793	0.126	44.828	43.398				
3	-6.322	11.339	0.453	32.636	41.604	2.116	5.452	0.161	43.644	52.722				
4	5.983	2.137	0.459	32.276	57.359	1.448	0.681	0.253	40.129	45.531				
<b>Leaf chlorophyll content</b>					<b>Grain yield/plant</b>									
1	0.403	0.279	0.024	49.202	72.762	-2.233	5.216	0.957	16.853	5.781				
2	6.326	2.629	0.324	37.448	84.883	3.099	10.815	0.885	18.943	9.177				
3	4.471	13.053	0.261	39.743	74.038	0.367	0.193	0.125	44.828	9.809				
4	2.756	3.449	0.193	42.465	71.269	-0.647	0.616	0.235	26.763	9.119				
<b>Number of spikes/plant</b>					<b>Grain protein content</b>									
1	-0.343	3.965	0.168	43.251	4.151	-1.089	1.422	0.419	33.724	3.754				
2	1.339	18.734	0.127	44.828	11.719	1.258	9.319	0.904	18.406	11.681				
3	0.547	5.285	0.376	35.197	4.479	0.989	3.458	0.644	26.109	14.463				
4	0.663	13.260	0.333	37.070	4.997	0.809	1.151	0.415	33.724	12.558				

protein content in 3<sup>rd</sup> and 4<sup>th</sup> crosses as well as number of grains/spike in 1<sup>st</sup> and 3<sup>rd</sup> crosses. These results indicate that it should be possible to produce an inbred line which is at least as good, if not considerable better than the original heterotic F<sub>1</sub> (Hayward *et al.*, 1993)

#### REFERENCES

- Awaad, H.A. (1992). Breeding studies on some wheat crosses Ph.D. Thesis Fac. of Agric Zagazig Univ. Egypt.
- Awaad, H.A. (1996). Genetic system and prediction for yield and its attributes in four wheat crosses (*Triticum aestivum* L.). Annals of Agric. Sci. Moshtohor 34(3): 864-890.
- Awaad, H.A. (2001). The relative importance and inheritance of grain filling rate and period and some related characters to grain yield of bread wheat (*Triticum aestivum* L.). Proc. 2<sup>nd</sup> Pl. Breed. Conf. Assiut Univ. Oct. 2<sup>nd</sup> 2001, P. 181-198.
- Awaad, H.A. (2002). Assessment of some genetic parameters using diallel cross fashion and their implications in breeding programs of bread wheat (*Triticum aestivum* L.). Zagazig J. Agric. Res. 29(4): 1123-1141.
- Castelli, F.; R. Contillo and F. Miceli (1996). Non-destructive determination of leaf chlorophyll content in four crop species. J. Agronomy and Crop Science 177: 275-283.
- Cavalli, L.L.(1952). An analysis of linkage in quantitative inheritance. (ed. E.C.R. Rieve. And C.H. Waddington), PP 135-44, HMSO, London.
- Dhaliwal, L.S.; H. Singh; G.S. Nanda and H.S. Dhaliwal (1994). Inheritance of grain protein content in two high protein lines of wheat. Rachis 13:34-37.
- Eissa, M.M. and H.A. Awaad (1993). Prediction of new recombinant lines for earliness and some other traits using F<sub>3</sub> generation of ten wheat crosses (*Triticum aestivum* L.). Zagazig J. Agric. Res. 20: 1683-1693.
- Fisher, R.A. and F. Yates (1963). Statistical Tables for Biological, Agricultural and Medical Research. Edinburgh. Oliver and Boyd.
- Gebre-Mariam, H. and E.N. Larter (1996). Genetic response to index selection for grain yield, kernel weight and percent protein in four wheat crosses. Plant Breed. 115(6): 459-464.

- Guptal, R.R. and Ziauddin Ahmad (1982). Selection parameters for some developmental and component traits in durum wheat. *Indian J. Agric. Sci.* 52(5): 278-284.
- Hassan, E.E. (1993). Genetic analysis of some main spike characteristics in four wheat crosses (*Triticum aestivum* L.). *Zagazig J. Agric. Res.* 20: 611-621.
- Hassan, E.E. (1998). Components of genetic variance for some agronomic characters in wheat (*Triticum aestivum* L.). *Zagazig J. Agric. Res.* 25(1):45-58.
- Hassan, A.I.A. (2002). Gene action and heritability estimates of F<sub>3</sub> wheat families under saline condition at Ras Sudr. *Zagazig J. Agric. Res.* 29(2): 405-420.
- Hayward, M.D.; N.O., Bosemark and I. Romagosa (1993). *Plant Breeding, Principles and Prospects*. Chapman and Hall, London.
- Hendawy, F.A. (1994). Influence of location on heterosis and combining ability in bread wheat. *Menofya J. Agric. Res.* 19: 2201-2224.
- Ismail, T.A.; A.H. Fayed and R.M.F. Khalaf (2000). Diallel analysis for partitioning of genetic variance for some yield characters and chlorophyll content in wheat. *Zagazig J. Agric. Res.* 27(2): 487-500.
- Jedynski, S. (1988). Heritability and diallel analysis of several agronomic characters in winter wheat hybrids. *Zeszyty Naukowe Akademii Rolniczej We Wroclawinu, Rolnictwo*, 47:27-43 (C.F. *Plant Breed. Abst.*, 59: 1989, 4600).
- Jinks, J.L. and R.M., Jones (1958). Estimation of the components of heterosis. *Genetics* 43:223-224.
- Jinks, J.L. and H.S., Pooni (1976). Predicting the properties of recombinant inbred lines derived by single seed descent. *Heredity* 36:253-266.
- Johanson, H.W.; H.F. Robinson and R.E. Comstock (1955). Genotypic and phenotypic correlations in soybean and their implications in selections. *Agron. J.* 47: 477-485.
- Ketata, H.; I. H. Edwards and E.L. Smith (1976). Inheritance of eight agronomic characters in a winter wheat cross. *Crop Sci.* 16:19-22.
- Khalifa, M.A. (1982). Inheritance of protein content in some wheat crosses (*Triticum aestivum* L. em Thell.). *Assiut J. Agric. Sci.*

- 13 (5): 163-175.
- Khalifa, M.A.; A.A., Ismaiel; G.R., EL-Nagar and I.M., Amin (1998). Genetical studies of earliness, grain yield and it's components of bread wheat. Assuit J. Agric. Sci. 29 (5): 59-69.
- Kheiralla, K. A.; M.A. EL-Morshidy and M.M. Zakeria (2001). Inheritance of earliness and yield in bread wheat under favourable and late sowing dates. Proc. 2<sup>nd</sup> Pl. Breed. Conf. Assuit Univ. Oct. 2<sup>nd</sup> 2001 PP 219-239.
- Kuldip Singh, and G.S., Bhullar (1989). Prediction of recombinant lines in durum wheat crosses. Crop Improv. 16(2): 129-132.
- Mather, K. and J. L. Jinks (1982). Biometrical Genetics, 3<sup>rd</sup> ed. Chapman and Hall, London.
- Mosaad, M.G. (1991). Genetic architecture of morpho-physiological traits in Durum wheat. Egypt J. Appl. Sci. 6:186-195.
- Mou, B.; W.E. Kronstad and N.N. Saulescu (1994). Grain filling parameters and protein content in selected winter wheat populations:II. Associations. Crop Sci. 34: 838-841.
- Pawar, I.S.; S., Singh; R.S. Paroda and I. Singh (1988). An analysis of generation means for yield and its component traits in bread wheat. Indian J. Genet. 48(3): 317-319.
- Salem, A.H.; S.A. Nigem; M.M. Eissa and H.F. Oraby (2000). Type and magnitude of gene action for some quantitative characters and their implication in applied wheat breeding. Zagazig J. Agric. Res. 27(4): 805-818.
- Singh, G.; G.S. Bhullar and K.S. Gill (1985). Inheritance of some plant characters in an intervarietal cross of bread wheat. Crop Improv. 12:179-183.
- Snap, J. and B., Parker (1986). Cross prediction in wheat using F<sub>3</sub> data. Proc. 6<sup>th</sup> Meeting of Eucarpia selection. Biometrics in Plant breeding 359-369 Birmingham U.K.

## التحليل الوراثي والإستجابة للإنتخاب والتنبؤ بالإتحادات الوراثية الجديدة

في قمح الخبز.

حسن عوده عواد

قسم المحاصيل-كلية الزراعة-جامعة الزقازيق-مصر

أجريت هذه الدراسة بالمزرعة التجريبية بكلية الزراعة-جامعة الزقازيق في الموسم الشتوي لأعوام ١٩٩٩/٢٠٠٠، ٢٠٠١/٢٠٠٠ و ٢٠٠٢/٢٠٠١ مستخدماً نظام الستة عشائر لأربعة هجن من قمح الخبز هي (١ سخا  $\times$  ٦٩ ساحل، ٢ سخا  $\times$  ٦٩ أكساد ٣، ٩٤٥) سدس  $\times$  ١-F134 '71/Crow'S' و ٤) جميزة  $\times$  ٥ جميزة ١٦٨ بهدف معرفة النظام الوراثي وطبيعة الفعل الجيني ودراسة الإستجابة للإنتخاب والتنبؤ بالتراكيب الوراثية المباشرة لصفات ؛ عدد الأيام حتى طرد السنابل، مساحة ورقة العلم، محتوى كلوروفيل الورقة، محصول حبوب النبات ومكوناته ومحتوي الحبوب من البروتين. ويمكن تلخيص أهم النتائج فيما يلي:

أظهرت نتائج اختبار المقياس (A, B and C) أن المودل الوراثي المعقد هو الملائم لتفسير وراثية صفات؛ عدد الأيام حتى طرد السنابل في الهجينين الثاني والرابع؛ مساحة ورقة العلم، محتوى كلوروفيل الورقة ومحصول حبوب النبات في جميع الهجن؛ ومحتوي الحبوب من البروتين في الهجين الثاني والثالث والرابع. في حين كان المودل الوراثي البسيط هو الملائم لتفسير وراثية صفات؛ عدد الأيام حتى طرد السنابل في الهجينين الأول والثالث؛ ووزن الألف حبة ومحتوي الحبوب من البروتين في الهجين الأول فقط. وكان الفعل الجيني المضيف أكثر أهمية في وراثية صفة عدد الأيام حتى طرد السنابل في الهجينين الأول والثالث ووزن الألف حبة ومحتوي الحبوب من البروتين في الهجين الأول. كما كان الفعل الجيني المضيف والتفاعل {مضيف  $\times$  مضيف} ذو أهمية في وراثية صفات عدد الأيام حتى طرد السنابل وعدد سنابل النبات في الهجين الثاني؛ محتوى كلوروفيل الورقة ومحصول حبوب النبات في الهجين الأول ومساحة ورقة العلم في الهجينين الأول والثالث. بينما كان الفعل الجيني السيادة والتفاعل {سيادة  $\times$  سيادة} هو المتحكم في وراثية صفات مساحة ورقة العلم، عدد سنابل النبات ومحصول حبوب النبات في الهجينين الأول والثاني ومحتوي الحبوب من البروتين في الهجينين الثالث والرابع، في حين كان التفاعل {مضيف  $\times$  سيادة} معنوياً في صفة محتوى الحبوب من البروتين في الهجينين الثاني والرابع.

كان التفاعل غير الأليلي من النوع المضاعف Duplicate هو السائد لصفات؛ مساحة ورقة العلم، عدد سنابل النبات ومحصول حبوب النبات في الهجينين الأول والثاني؛ عدد حبوب السنبل في الهجين الثاني ومحتوي الحبوب من البروتين في الهجينين الثالث والرابع. بينما كان طراز التفاعل من النوع المكمل Complementary أكثر وضوحاً لصفة عدد حبوب السنبل في الهجين الأول.

كان التباين الوراثي المضيف هو المكون الأعظم المتحكم في وراثته صفات؛ عدد الأيام من السزراعة حتى طرد السنابل، مساحة ورقة العلم، عدد حبوب السنبله، وزن الألف حبة ومحتوي الحبوب من البروتين في معظم الحالات، بينما كان التباين الوراثي السيادة أكثر أهمية في وراثته محصول حبوب النبات في جميع الهجن.

كانت كفاءة التوريث في المعنى المحدود عالية (< ٥٠%) لصفات عدد الأيام حتى طرد السنابل، مساحة ورقة العلم، محتوى كلورفيل الورقة، عدد حبوب السنبله، وزن الألف حبة ومحتوي الحبوب من البروتين في معظم الهجن، ومنخفضة (٢٥,٤٩%) إلى متوسطة (٤٤,٥٩%) لمحصول حبوب النبات.

وتشير نتائج الإستجابة للإختاب في الجيل الثاني إلى الإختلاف النسبي في أهمية الصفات المدروسة في تحسين محصول الحبوب من هجين إلى آخر، وبصفة عامة كان لصفة عدد سنابل النسب أكبر الأثر في تحسين محصول الحبوب يليها عدد حبوب السنبله، وزن الألف حبة، محتوى كلورفيل الورقة ومساحة ورقة العلم.

أشارت نتائج التنبؤ، أن أعلى نسبة من التراكيب الوراثية المباشرة التي تفوق حدود الأبوين وكذلك الجيل الأول الهجين كانت لصفات؛ عدد الأيام حتى طرد السنابل ومحتوي كلورفيل الورقة في الهجين الرابع؛ محصول حبوب النبات في الهجينين الثاني والرابع ومحتوي الحبوب من البروتين في الهجينين الأول والثالث.

وكانت أعلى نسبة من السلالات الجديدة المباشرة التي تحتوي على الأليلات المرغوبة لصفات عدد الأيام حتى طرد السنابل، محتوى كلورفيل الورقة و محصول حبوب النبات في الهجينين الثاني والثالث ووزن الألف حبة ومحتوي الحبوب من البروتين في الهجينين الثالث والرابع. مشيراً إلى أهمية هذه الهجن كمادة وراثية يمكن عزل سلالات نقيه مباشرة.