

## ESTIMATION OF SOME GENETIC PARAMETERS FOR YIELD AND ITS COMPONENTS IN SOME BARLEY GENOTYPES

AMER, KH. A., A. A. EID, M. M. A. EL-SAYED and A. A. EL-AKHDAR

Barley Dept., Field Crops Res. Institute, ARC, Egypt

---

### Abstract

This investigation was carried out at Sakha Agricultural Research Station, ARC, Egypt during the two growing seasons (2009/2010 and 2010/011). Four lines and three testers were used to develop barley hybrids for yield and its components. Through this study, general and specific combining ability, genetic parameters, heritability and genetic advance from selection were studied for plant height, spike length, no. of spikes/plant, no. of grains/spike, 100-grain weight and grain yield/plant. Data revealed that most of the variance due to the lines, testers and line x testers were highly significant for most studied traits. On the other hand, positive and negative heterosis over better parent and mid-parent were detected for most traits indicating that parental genotypes were genetically diverse. Potence ratio estimates showed partial and over dominance in most traits. The parents L4 considered as good combiners for plant height, no. of grains/spike, 100-grain weight and grain yield/plant. Also, the parent L3 is considered as good combiner for spike length, no. of spikes/plant, no. of grains/spike and grain yield/plant. Heritability in broad sense values were found to be high in magnitude for most of the studied characters on the other side, heritability in narrow sense were found to be low to moderate of these traits. From the results, it could be concluded that the two crosses: (L1 x T3) and (L3 x T3) are the best for yield and most of its components. So using these crosses in breeding programs for high yielding production would be useful.

### INTRODUCTION

Barley (*Hordeum Vulgare* L.) has a great adaptation potential in many regions of the world. It has a good tolerance to biotic stresses such as salinity, drought, frost and heat. It is considered one of the most important crops ranking the fourth in the world cereal crops production. Its economic importance is due to its usage it for animal feeding, brewing malts and human food in some areas. In Egypt, barley is mainly used as animal feed (grain and straw) and sometimes for bread making by Bedouins.

In Egypt barley is a minor winter cereal crops grown mainly in rainfed areas where limited water supply is as in the Northwest Coastal region and North of Sinai.

Also it is grown over wide range of soil variability and under many diverse climatic conditions compared with many other grain crops. So, it can be grown in irrigated saline lands and poor soil conditions. It has also been grown in the newly reclaimed lands as well as the old land (Amer 2011).

Therefore, the main objective of this study is the production of promising barley genotypes having high yield potentially through the following:-

- 1- Identification of superior parents and their crosses from a 4 line × 3 tester of barley parental genotypes.
- 2- Estimation of heterosis and combining ability effects for grain yield and some related agronomic traits.
- 3- Estimation the heritability and genetic advance from selection for yield and some related agronomic traits.

## MATERIALS AND METHODS

The present investigation was carried out at the experimental farm of Sakha Agricultural Research Station ,Kafr El-sheikh, Egypt, during the two successive seasons 2009/2010 and 2010/2011. Four barley lines; L<sub>1</sub>, L<sub>2</sub>, L<sub>3</sub> and L<sub>4</sub> and three testers T<sub>1</sub> (Giza 117), T<sub>2</sub> (Giza 123) and T<sub>3</sub> (Giza 125) of barley were used, the names and pedigrees of which are presented in Table (1).

Table 1. Names and pedigrees of parental barley genotypes.

No	Genotypes	Pedigree
	Lines	
1	L <sub>1</sub>	Alanda/5/Aths/4/Pro/TolI//Cer*2/TolI/3/5106/6/Baca'S/3/AC253//CI08887/CI05761
2	L <sub>2</sub>	Arizona5908/Aths//Avt/Attiki/3/S.T.Barley/4/Aths/Lignee686/5/Aths/Lignee686/3/DeirAlla106/Lignee527//Asl
3	L <sub>3</sub>	ACSAD 1182/4/Alanda//Lignee527/Arar/3/Centinel/ 2*Calicuchima
4	L <sub>4</sub>	STANDER-BAR/CABUYA
	Testers	
5	T <sub>1</sub> (Giza 117)	
6	T <sub>2</sub> (Giza 123)	Giza117/FAO86
7	T <sub>3</sub> (Giza 125)	Giza117/Bahteem52//Giza118/FAO86.Line366.16.2

In 2009/2010 season, the three testers were crossed with the four lines to produce F<sub>1</sub> hybrids of 12 top cross. In 2010/2011 season, 12 F<sub>1</sub> hybrids, three testers and four lines were sown in randomized complete block design with three replications.

Each parent and  $F_1$  was represented by two rows per replicate. Each row was 1.5 m long, and spaces between rows were 30 cm with 15 cm between plants. All the recommended agronomic practices for barley production were applied at the proper time. Ten guarded plants were randomly taken from each entry to collect data on plant height, spike length, number of spikes/plant, number of grains /spike, 100-grain weight and grain yield /plant.

### Statistical analysis:

Line x tester analysis was performed according to Kempthorne (1957), Singh and Chaudhary (1977). The heterosis estimates over mid and better parent was determined according to Mather and Jinks (1971). Potence ratio was calculated according to Wigan (1944) and Mather and Jinks (1971). Heritability in broad ( $H^2$ ) and narrow ( $h^2$ ) senses were calculated according to Allard (1960) and Mather (1949). The phenotypic and genotypic coefficients of variation were estimated using the formulae developed by Burton (1952). Expected ( $\Delta g$ ) and predicted  $\Delta g$  (%) genetic advance were calculated as suggested by Borthakur and Poehlman (1970)

## RESULTS AND DISCUSSION

### Mean performance of genotype (parents and crosses):

The mean performance of the four lines, three testers and their 12 top crosses for all the studied traits are presented in Table (2).

Table 2. Mean performance of the barley genotypes for all studied traits.

Genotypes	Plant height (cm)	Spike length (cm)	No. of spikes/plant (cm)	No. of grains/spike	100-grain weight (g)	Grain yield/plant (g)
Lines						
L <sub>1</sub>	123.33	8.67	14.00	66.00	4.46	39.78
L <sub>2</sub>	113.33	6.33	13.67	50.00	4.17	33.14
L <sub>3</sub>	108.33	6.67	13.67	52.00	5.29	39.71
L <sub>4</sub>	111.67	7.67	14.00	58.00	4.98	44.43
Testers						
T <sub>1</sub>	105.00	7.33	13.67	56.00	5.11	38.17
T <sub>2</sub>	106.67	7.67	14.00	58.00	5.21	37.68
T <sub>3</sub>	105.00	6.67	12.67	52.00	5.04	30.12
Crosses						
L <sub>1</sub> x T <sub>1</sub> (1)	113.33	8.33	13.00	62.00	5.17	35.61
L <sub>1</sub> x T <sub>2</sub> (2)	126.67	10.67	14.33	80.00	6.14	46.76
L <sub>1</sub> x T <sub>3</sub> (3)	105.00	8.00	17.33	60.00	5.50	49.45
L <sub>2</sub> x T <sub>1</sub> (4)	110.00	8.33	16.33	64.00	4.89	46.58
L <sub>2</sub> x T <sub>2</sub> (5)	118.33	7.67	16.67	60.00	5.06	40.27
L <sub>2</sub> x T <sub>3</sub> (6)	103.33	7.33	15.33	56.00	4.25	38.04
L <sub>3</sub> x T <sub>1</sub> (7)	103.33	10.33	18.33	76.00	4.91	50.17
L <sub>3</sub> x T <sub>2</sub> (8)	120.00	8.33	15.33	62.00	5.17	48.51
L <sub>3</sub> x T <sub>3</sub> (9)	115.00	10.33	17.00	77.33	5.38	58.82
L <sub>4</sub> x T <sub>1</sub> (10)	120.00	9.67	15.33	76.00	5.46	56.92
L <sub>4</sub> x T <sub>2</sub> (11)	126.00	9.33	16.33	74.00	5.55	51.64
L <sub>4</sub> x T <sub>3</sub> (12)	113.33	8.67	17.00	68.00	5.39	47.84

Data indicated that the parental line-1 gave the highest values for plant height, spike length and no. of grain/spike; while, line-3 gave the heaviest 100-grain weight, for line-4 gave the highest values for no. of spikes/plant and grain yield/plant. For testers;  $T_2$  gave the highest values for all studied traits. For crosses; top crosses ( $L_1 \times T_2$ ) for plant height, spike length, no. of grain/spike and 100-grain weight, ( $L_1 \times T_3$ ) for no. of spikes/plant and ( $L_3 \times T_3$ ) for grain yield/plant gave the highest values for these traits.

#### Analysis of variance:

The estimation of the analysis of variance as shown in Table (3), revealed highly significant differences among genotypes for all studied traits. These results indicated that genotypic differences between genotypes are presented. Therefore, the genetic analysis was felt valid to be undertaken to reveal the inheritance and gene action controlling the characters studied.

Table 3. Observed mean squares from ordinary analysis of variance for the studied traits.

S.O.V	df	Plant height (cm)	Spike length (cm)	No. of spikes/plant	No. of grains/spike (g)	100-grain weight (g)	Grain yield/plant (g)
Rep.	2	13.596	2.05**	2.05	41.33*	0.01	0.44
Genotypes	18	177.1**	4.91**	8.16**	260.30**	0.65**	183.8**
Parents (P)	6	126.98**	1.94**	0.67	88.00**	0.52**	66.03**
Crosses (C)	11	200.19**	3.77**	6.27**	205.93**	0.63**	144.8**
P vs. C	1	223.73**	35.28**	73.94**	1892.25**	1.60**	1319.29**
Lines (L)	3	146.99**	5.88**	6.25**	301.44**	1.34**	281.03**
Testers (T)	2	643.75**	1.08*	3.69	62.11*	0.52**	9.59 *
L x T	6	78.94**	3.60**	7.14**	206.11**	0.32**	121.76**
Error	36	14.52	0.33	1.24	15.11	0.06	3.82

(\* ) and (\*\* ) significant at 0.05 and 0.01 levels probability, respectively.

Partitioning sum of squares due to genotypes (Table 3) revealed highly significant differences among parents, crosses and parents vs. crosses for all studied traits, except no. of spikes/plant for parents. However, the crosses was further partitioned into lines, testers and line x testers interaction. The mean squares of lines, testers and line x testers showed significant for all studied traits, except no. of

spikes/plant for testers These results indicated that both lines and testers had great diversity and they performed differently in there crosses.

#### **Estimation of heterosis and potence ratio:**

It is known fact that the phenomena of heterosis (hybrid vigor) is of common occurrence in both cross pollinated and self pollinated crops. There are three important genetic factors affecting heterosis, (i) the genetic diversity of the parents, where the heterotic effect increased with increasing the genetic divergence in morphological characters, and also with respect to widest geographical origin of parents, (ii) the genetic base of parents and (iii) the wider adaptability of the parents. However, there are three possible genetic causes of heterosis, partial, complete dominance and over-dominance particular with the dominance interactions.

From this point of view, heterosis would be of economical value when the  $F_1$  hybrid exceeds its better parents, therefore, if the breeder planned a program of selection in the advanced segregating generation from such superior specific hybrids, the expected improvement would be fruitful.

With regard to heterosis percentage as a deviation of  $F_1$  from either mid parent or better parent, the results of the 6 traits are presented in Table (4). The differences between the two estimates of heterosis varied from one cross to another according to the performance of the parents. On the other hand, the importance of heterosis relative to better parent for the breeder is that reflects the importance of the non-additive gene action in the genetic constitution. This type of heterosis is very desirable for the plant breeder from the practical point of view for production of superior elite breeding materials. On the other side, heterosis relative to mid parent is also important where it reflect the type of dominance which cause the heterotic effects.

Positive significant or highly significant heterosis over mid and better parent values were obtained for; plant height in crosses 8, 9, 10 and 11; spike length and number of grain/spikes in crosses 2, 4, 7, 9, 10, 11 and 12; number of spikes/plant in crosses 3, 4, 5, 7, 9, 11 and 12; 100-grain weight in cross 2 and cross 3 and for grain yield/plant in all crosses except for cross 1 and cross 5. These results are agreement with those obtained by Budak (2000), El-Seidy and Khattab (2000), Sharma et al (2002), El-Bawab (2003), El-Sayed (2007), El-shawy (2008), Amer (2010) and Eid (2010).

Potence ratio refer to over dominance for; plant height in all crosses where its values were exceeded unity except for cross 1 and cross 4 were less than unity

indicating partial dominance in these crosses. For spike length and number of grain/spikes all crosses refer to over dominance except for crosses 1, 3 showed that partial dominance, 9 and 11 showed no dominance; number of spikes/plant all crosses showed over dominance except for crosses 2, 4, 7, and 11; 100-grain weight all crosses showed over dominance except for crosses 4, 5, and 6 showed no dominance and for grain yield/plant all crosses showed over dominance. These results agreed with those obtained by El-Seidy (1997b), Yadav et al (2002b) and El-Bawab (2003), El-Sayed (2007) and El-Shawy (2008)

Table 4. Heterosis percent relative to mid-parent (MP), better parent (BP) and potence ratio (PR) for plant height, spike length and no. of spikes/plant.

Crosses	Plant height (cm)			Spike length (cm)			No. of spikes/plant		
	M.P	B.P	PR	M.P	B.P	PR	M.P	B.P	PR
L <sub>1</sub> × T <sub>1</sub> (1)	-0.73	-8.11**	-0.09	4.13	-3.92	0.49	-6.04	-7.14	-5.06
L <sub>1</sub> × T <sub>2</sub> (2)	10.15**	2.71	1.40	30.60**	23.07**	5.00	2.36	2.36	0.00
L <sub>1</sub> × T <sub>3</sub> (3)	-8.03**	-14.9**	-1.00	4.30	-7.73	0.33	29.96**	23.79**	6.01
L <sub>2</sub> × T <sub>1</sub> (4)	0.76	-2.94	0.20	21.96**	13.64**	3.00	19.46**	19.46**	0.00
L <sub>2</sub> × T <sub>2</sub> (5)	7.57**	4.41	2.50	9.57	0.00	1.00	20.49**	19.07**	17.18
L <sub>2</sub> × T <sub>3</sub> (6)	-5.35*	-8.82**	-1.40	12.77*	9.90	4.88	16.40**	12.14	4.32
L <sub>3</sub> × T <sub>1</sub> (7)	-3.13	-4.59	-2.00	47.57**	40.93**	10.09	34.09**	34.09**	0.00
L <sub>3</sub> × T <sub>2</sub> (8)	11.63**	10.80**	15.06	16.18**	8.60	2.32	10.81	9.50	9.06
L <sub>3</sub> × T <sub>3</sub> (9)	7.81**	6.19*	5.01	54.87**	54.87**	0.00	29.08**	24.36**	7.66
L <sub>4</sub> × T <sub>1</sub> (10)	10.77**	7.46*	3.50	28.93**	26.08**	12.76	10.81	9.50	9.06
L <sub>4</sub> × T <sub>2</sub> (11)	16.03**	13.43**	7.00	21.64**	21.64**	0.00	16.64**	16.64*	0.00
L <sub>4</sub> × T <sub>3</sub> (12)	4.61	1.49	1.50	20.92**	13.04*	3.00	27.48**	21.43**	5.51

(\*) and (\*\*) significant at 0.05 and 0.01 levels probability, respectively.

Table 4. cont.

Crosses	No. of grains/spike			100-grain weight (g)			Grain yield/plant (g)		
	M.P	B.P	PR	M.P	B.P	PR	M.P	B.P	PR
L <sub>1</sub> × T <sub>1</sub> (1)	1.64	-6.06	0.20	8.05*	1.17	1.18	-8.63*	-10.48*	-4.18
L <sub>1</sub> × T <sub>2</sub> (2)	29.03**	21.21**	4.50	26.99**	17.85**	3.48	20.73**	17.55**	7.65
L <sub>1</sub> × T <sub>3</sub> (3)	1.69	-9.09	0.14	15.79**	9.13*	2.59	41.49**	24.31**	3.00
L <sub>2</sub> × T <sub>1</sub> (4)	20.75**	14.29*	3.67	5.39	-4.31	0.53	30.64**	22.03**	4.34
L <sub>2</sub> × T <sub>2</sub> (5)	11.11*	3.45	1.50	7.89*	-2.88	0.71	13.72**	6.87	2.14
L <sub>2</sub> × T <sub>3</sub> (6)	9.80	7.69	5.00	-7.71*	-15.67**	-0.82	20.27**	14.79**	4.25
L <sub>3</sub> × T <sub>1</sub> (7)	40.74**	35.71**	11.0	-5.58	-7.18	-3.22	28.84**	26.34**	14.58
L <sub>3</sub> × T <sub>2</sub> (8)	12.73*	6.90	2.33	-1.52	-2.27	-2.00	25.37**	22.16**	9.67
L <sub>3</sub> × T <sub>3</sub> (9)	48.71**	48.71**	0.00	4.16	1.70	1.72	68.47**	48.12**	4.99
L <sub>4</sub> × T <sub>1</sub> (10)	33.33**	31.03**	19.00	8.23*	6.85	6.38	37.82**	28.11**	4.99
L <sub>4</sub> × T <sub>2</sub> (11)	27.59**	27.59**	0.00	8.93*	6.53	3.96	25.78**	16.23**	3.14
L <sub>4</sub> × T <sub>3</sub> (12)	23.64**	17.24**	4.33	7.58*	6.94	12.67	28.34**	7.67*	1.48

(\* and \*\*) significant at 0.05 and 0.01 levels probability, respectively.

#### Combining ability analysis:

Analysis of variance for combining ability and estimates of variance due to GCA and SCA are presented in Table (5).

General combining ability (GCA) expressed main effects and specific combining ability (SCA) expressed interactions. GCA/SCA ratio was used as a measure to understand the nature of gene action involved. The ratio of GCA/SCA were lesser than unity for all studied traits which mean that non-additive gene effects played an important role in the inheritance of these traits. In such cases, a bulk method would be fruitful to eliminate the effect of dominance in the advanced generation. These results agreed with those obtained by Amer (2010), Eid (2010) and Amer *et al* (2011).

Table 5. Mean squares from the analysis of variance for general (GCA), specific (SCA) combining ability and GCA/SCA.

Characters	$\sigma^2$ GCA	$\sigma^2$ SCA	Error term	$\sigma^2$ GCA/ $\sigma^2$ SCA
Plant height (cm)	5.795	21.47	4.84	0.006
Spike length (cm)	0.185	1.09	0.11	0.009
No. of spikes/plant (spike)	0.245	1.967	0.41	-0.012
No. of grains/spike (grain)	1.1625	63.667	5.04	-0.007
100-grain weight (g)	0.07	0.086	0.02	0.084
Grain yield/plant (g)	2.0845	39.314	1.27	0.002

Estimates of general combining ability effects (GCA):

The data of general combining ability effects for all traits are presented in Table (6).

General combining ability effects varied from one parent to another giving negative or positive values. The significant values of GCA for any genetic variance plays a major role in the positive direction of the desired trait in all the crosses in which the gene type is involved. The negative and significant ones indicated that the flexible portion of genetic variance responses well in the positive direction of desired character in some crosses and negative direction in the other crosses that having the gene type in question as a constant parent. The non-significant GCA indicated that the genotypes have no important effects in the crosses in which they will be involved, but in some cases, they may show important response in specific cross which could be estimated by the SCA.

The parental line-1 exhibited desirable significant positive GCA for 100-grain weight. Meaning that, this genotype could be considered as good combiner for these traits. The parental line-3 gave highly significant positive GCA for spike length, no. of spikes/plant, no. of grains/spike and grain yield/plant. So, it could be used as parent for the development of desirable hybrids. The parental line-4 exhibited significant positive GCA for plant height, no. of grains/spike, 100-grain weight and grain yield/plant. These results are in good agreement with those obtained by Amer (2010), Eid (2010) and Amer *et al.* (2011) where they observed significant and positive GCA for these traits in their respective studies. For testers; the parental tester-2 showed desirable significant positive GCA for plant height and 100-grain weight.

Table 6. Estimates of general combining ability effects for the studied traits.

Parents	Plant height (cm)	Spike length (cm)	No. of spikes/plant	No. of grains/spike	100-grain weight (g)	Grain yield/plant (g)
Lines						
L <sub>1</sub>	0.42	0.08	-1.14**	-0.61	0.36**	-3.61**
L <sub>2</sub>	-4.03**	-1.14**	0.08	-7.94**	-0.51**	-5.92**
L <sub>3</sub>	-1.81	0.75**	0.86*	3.83**	-0.09	4.95**
L <sub>4</sub>	5.42**	0.31	0.19	4.72**	0.23**	4.59**
LSD 0.05	2.57	0.39	0.75	2.63	0.17	1.32
0.01	3.44	0.52	1.01	3.51	0.22	1.77
Testers						
T <sub>1</sub>	-2.92*	0.25	-0.28	1.56	-0.13	-0.23
T <sub>2</sub>	8.33**	0.08	-0.36	1.06	0.24**	-0.76
T <sub>3</sub>	-5.42**	-0.33	0.64	-2.61*	-0.11	0.99
LSD 0.05	2.23	0.34	0.65	2.27	0.14	1.14
0.01	2.98	0.45	0.87	3.04	0.19	1.53

(\*) and (\*\*) significant at 0.05 and 0.01 levels probability, respectively.



**Estimates of specific combining ability effects (SCA):**

The data of specific combining ability effects of the top crosses for all traits are presented in Table (7).

For plant height, the top cross ( $L_3 \times T_3$ ) expressed significant and positive SCA. However, the combinations showed significant positive SCA may be useful in exploitation of heterosis due to their desirable plant height. For spike length and no. of grains/spike the top cross; ( $L_1 \times T_2$ ) and ( $L_3 \times T_3$ ) showed significant positive value for SCA. Regarding no. of spikes/plant, significant positive SCA were demonstrated by cross; ( $L_1 \times T_3$ ) where it gave the highest no. of spikes/plant.

Table7. Estimates of specific combining ability effects for the studied traits.

Crosses	Plant height (cm)	Spike length (cm)	No. of spikes/plant	No. of grains/spike	100-grain weight (g)	Grain yield/plant (G)
$L_1 \times T_1$	1.25	-0.92**	-1.61*	-6.89**	-0.30*	-8.10**
$L_1 \times T_2$	3.33	1.58**	-0.19	11.61**	0.30*	3.58**
$L_1 \times T_3$	-4.58*	-0.67*	1.81**	-4.72*	0.01	4.52**
$L_2 \times T_1$	2.36	0.31	0.50	2.44	0.29*	5.18**
$L_2 \times T_2$	-0.56	-0.19	0.92	-1.06	0.09	-0.61
$L_2 \times T_3$	-1.81	-0.11	-1.42*	-1.39	-0.38**	-4.58**
$L_3 \times T_1$	-6.53**	0.42	1.72*	2.67	-0.11	-2.10
$L_3 \times T_2$	-1.11	-1.42**	-1.19	-10.83**	-0.23	-3.24**
$L_3 \times T_3$	7.64**	1.00**	-0.53	8.17**	0.34*	5.33**
$L_4 \times T_1$	2.92	0.19	-0.61	1.78	0.13	5.02**
$L_4 \times T_2$	-1.67	0.03	0.47	0.28	-0.16	0.26
$L_4 \times T_3$	-1.25	-0.22	0.14	-2.06	0.03	-5.28**
L.S.D. 0.05	4.46	0.67	1.30	4.55	0.29	2.29
0.01	5.96	0.90	1.74	6.08	0.38	3.06

(\*) and (\*\*) significant at 0.05 and 0.01 levels probability, respectively.

For 100-grain weight, three top crosses namely ( $L_1 \times T_2$ ), ( $L_2 \times T_1$ ) and ( $L_3 \times T_3$ ) expressed significant positive SCA. With respect to grain yield/plant, positive and significant SCA for grain yield/plant were revealed by five top crosses; ( $L_1 \times T_2$ ), ( $L_1 \times T_3$ ), ( $L_2 \times T_1$ ), ( $L_3 \times T_3$ ) and ( $L_4 \times T_1$ ). These results indicated that; non-additive gene effects were predominant in these particular combinations of barley hybrids for grain yield/plant due to the presence of considerable inter and intra-allelic interactions. Therefore, these crosses could be utilized for increasing grain yield/plant following approach of gene accumulation for the characters. These results are in general

agreement with those reported by Bhatnagar and Sharma (1997), Sharma *et al* (2003), Mahmoud (2006), El-Sayed (2007), Katta *et al* (2009), Amer (2010), Eid (2010) and Amer *et al* (2011).

#### Coefficients of variability:

Phenotypic (P.C.V) and genotypic (G.C.V) coefficients of variability were estimated for the studied traits as presented in Table (8).

Table 8. Estimates of the genetic variance components, heritability and genetic advance for all studied traits.

Parameter traits	$\sigma^2_{ph}$	$\sigma^2_G$	$\sigma^2_E$	$\sigma^2_A$	$\sigma^2_D$	PCV%	GCV%	H <sup>2</sup>	h <sup>2</sup>	$\Delta g$	$\Delta g\%$
Plant height	37.90	33.06	4.84	11.59	21.47	5.44	5.09	87.23	30.58	3.88	3.43
Spike length	1.57	1.46	0.11	0.37	1.09	15.07	14.53	92.99	23.57	0.61	7.32
No. of spikes/plant	2.87	2.46	0.41	0.49	1.97	11.17	10.34	85.70	17.09	0.60	3.93
No. of grains/spike	71.03	65.99	5.04	2.33	63.67	13.26	12.78	92.90	3.27	0.57	0.89
100-grain weight	0.25	0.23	0.02	0.14	0.09	9.70	9.30	91.87	56.91	0.58	11.37
Grain yield/plant	44.75	43.48	1.27	4.17	39.31	15.25	15.03	97.16	9.32	1.28	2.93

It could be concluded that the (PCV and GCV) were low in magnitude for plant height and 100-grain weight. While, it was observed that the phenotypic (PCV) and genotypic (GCV) coefficients of variability were high in magnitudes for spike length, no. of spikes/plant, no. of grains/spike and grain yield/plant. These results are in general agreement with those reported by El-Sayed (2012).

#### Heritability estimates:

Heritability in both broad and narrow senses were computed and the obtained results are presented in Table (8). The estimates of broad-sense heritability determine as the relative proportion of genetic variance with respect to the phenotypic variance. The heritability estimates either in broad or in narrow sense are important to plant breeders since they judge the expected improvement that could be obtained through selection programs. Broad sense heritability values were found to be high in

magnitudes for all traits under investigation. High  $H^2$  ranged from 85.70% for no. of spikes/plant to 97.16% for grain yield/plant.

Narrow sense heritability was generally low to moderate and ranged from 3.27 for no. of grains/spike to 56.91 for 100-grain weight. The high difference between broad and narrow sense heritability estimates which was found for all traits studied was an expected due to more important of non-additive genes in the inheritance of these traits as it mentioned before. These results are in line with those reported by El-Sayed (2007), El-Shawy (2008) El-Sayed (2012).

#### **Genetic advance under selection:**

Genetic advance was calculated using phenotypic standard deviation and heritability in narrow sense (Table 8). Relatively high genetic advance was found in association with high PCV% and GCV% values for spike length and 100-grain weight. Therefore, selection for this trait could be more effective than the other traits because of its high expected ( $\Delta g\%$ ) genetic advance which reflected in high genetic variability. On the other hand, relative low genetic advance was associated with low heritability values for no. of grains/spike, indicating that selection for this trait would be less successful than for the former cases. These results agreed with those obtained by El-Sayed (2007), El-Shawy (2008) El-Sayed (2012).

### **REFERENCES**

1. Allard, A. M. 1960. Principles of Plant Breeding. Jon Wiley and Sons. Inc. NY, U. S. A., p. 92.
2. Amer, Kh. A. 2010. Inheritance of drought tolerance in some barley genotypes. Egypt. J. Agric. Res., (1) 88: 89-106.
3. Amer, Kh. A. 2011. Genetic Analysis of yield and its components under normal and drought conditions in some barley crosses. Egypt. J. Plant Breed (15) 2: 65:79.
4. Bhatnagar, V. K. and S. N. Sharma. 1997. Diallel analysis for grain yield and harvest index in barley under diverse environments. Rachis. publ. 16: 22-27.
5. Borthakur, D.N. and J.M. Poehlman. 1970. Heritability and genetic advance for kernel weight in barley. Crop Sci. 10: 452-453.

6. Budak, N. 2000 . Heterosis, general and specific combining ability estimates at F1 and F2 generations of a 8 x 8 diallel cross population of barley. Turkish J. of Field Crops. Society of Field Crop Sci., Izmir, Turkey. 5 (2): 61-70.
7. Burton, G.W. (1952). Quantitative inheritance in grasses. proc. 6th Int. Grassid Congr. 1: 270-283.
8. Eid, A. A. 2010. The genetic behavior for salinity tolerance in some barley genotypes. Egypt. J. Agric. Res., (1) 88: 67-86.
9. El-Bawab, A. M. O. 2003. Genetic studies on some characters in barley. Egypt. J. Agric., 81(2).
10. El-Sayed, M. M. A. 2007. Estimation of quantitative genetic statistical in diallel crosses of barley. M. Sc. Thesis Fac., Agric., Kafr El-Sheikh, Tanta Univ., Egypt.
11. El-Sayed, M. M. A. 2012. Genetical studies on some barley genotypes and its tolerance to drought. Ph. D. Thesis Fac., Agric., Tanta Univ., Egypt.
12. El-Seidy, E. S. H. 1997b. Inheritance of earliness and yield in some barley crosses. Annals of Agric. Sci., Moshtohor, 35 (2): 715-730.
13. El-Seidy, E. H. and A. B. Khattab 2000. Heterosis and combining ability in barley under drought conditions at different growth stages. Proc.9th., Agron. Conf. Minufiya, 1-2 Sept. 2000:167-182.
14. El-Shawy, E. E. A. 2008. Genetic analysis of some important traits of six-rowed barley in normal and saline affected fields. M. Sc. Thesis, Fac. Agric., Kafr El-Sheikh, Tanta Univ., Egypt.
15. Katta et al. 2009. Studies on tolerance of some hulless barley crosses to drought. 6th International Plant Bred. Conf., Ismailia, Egypt, 3-5 May 2009. 867:885.
16. Kempthorne, O. 1957. An introduction to genetic statistics. Iowa State Univ., John Wiley and Sons Inc., New York, USA. 545 pp.
17. Mather, K. 1949. Biometrical Genetics. Dover Publications, Inc., London.
18. Mather, K. and J.L. Jinks. 1971. Biometrical genetics. Cornell Univ. Proc. Ithaca, N.Y., 231 pp.
19. Mather, K., and J. L. Jinks. 1982. Biometrical Genetics 3rd ed. Chapman and Hall, London.

20. Mahmoud, Badeaa A. M. 2006. Genetic evaluation of some barley traits in crosses under saline and non-saline conditions. M. Sc. thesis, Fac. Agric., Kafr El-Sheikh, Tanta Univ., Egypt.
21. Sharma, Y., S. N. Sharma., P. Joshi and R. S. Sain. 2002. Combining ability analysis for yield and yield contributing characters in six-rowed barley. *J. of Breed. and Genet.* 34 (2): 55-63.
22. Sharma, Y., S. N. Sharma., P. Joshi and R. S. Sain. 2003. Combining ability in the F1 and F2 generations of a diallel cross in six rowed barley (*Hordeum vulgare* L.). *Acta Agron. Hungaricae.*, 51: 281-288.
23. Singh, R.K. and B.D. Chaudhary. 1977. Biometrical methods in quantitative genetic analysis. Kalyani, Publishers, Daragnai, New Delhi.
24. Wigan, L.G. 1944. Balance and potence in natural populations. *J. Genet.* 46: 150-160.
25. Yadav, V. K., R. Kumar and L. Ram. 2002b. Genetic analysis of malt yield and some of its components in barley. *Plant Archives.* 2 (2): 269-273. (Cited after CAB Abs. 2002/08-2003/07).

## تقدير بعض الثوابت الوراثية للمحصول ومكوناته في بعض التراكيب الوراثية من الشعير

خيري عبدالعزيز عامر، علاء على عيد، محمد منصور عبدالعاطي السيد ،

عمار عبد العظيم الاخضر

قسم بحوث الشعير- معهد بحوث المحاصيل الحقلية- مصر

أجريت هذه الدراسة بمزرعة محطة البحوث الزراعية بسخا خلال الموسمين ٢٠١٠/٢٠٠٩ و ٢٠١١/٢٠١٠م. تم التهجين بين أربع سلالات وثلاث كشافات للحصول على الحبوب الهجينة التي تم تقييمها في الموسم الثاني. تم تقدير قوة الهجين، القدرة العامة والخاصة على الانتلاف، معامل التوريث بمعناه الواسع والضيق والتحسين الوراثي المتوقع وذلك بالنسبة لصفات: طول النبات، طول السنبل، عدد السنابل للنبات، عدد الحبوب في السنبل، وزن المائة حبة ومحصول الحبوب للنبات. كانت أهم النتائج المتحصل عليها كالآتي:

أظهرت النتائج أن الاختلافات الراجعة إلى السلالات، الكشافات والسلالات  $\times$  الكشافات كانت عالية المعنوية في معظم الصفات المدروسة. كما أظهرت قوة الهجين قيما سالبة وموجبة للصفات المدروسة بالنسبة لمتوسط الأبوين والأب الأفضل، كما إتضح من نتائج القدرة على التألف أن السلالة-٤ كانت أب مشارك جيد بالنسبة لصفات: طول النبات، عدد الحبوب في السنبل، وزن المائة حبة ومحصول الحبوب للنبات، كما أن السلالة-٣ كانت أب مشارك جيد بالنسبة لصفات: طول السنبل، عدد السنابل للنبات، عدد الحبوب في السنبل ومحصول الحبوب للنبات. كما أوضحت النتائج أن قيمة معامل التوريث بمعناها الواسع تراوحت بين متوسطة إلى عالية في معظم الصفات ، في حين تراوحت قيم معامل التوريث بمعناه الضيق بين منخفضة إلى متوسطة. من النتائج السابقة يتضح أن الهجينان (L1 x T3) و (L3 x T3) كانت أفضل الهجن تحت الدراسة وذلك بالنسبة للمحصول ومكوناته ولذلك نوصى بإدخالهما في برامج التربية للمحصول العالي تحت الظروف الطبيعية.