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Genetic Analysis of Earliness and Yield Component Traits in Five Barley Crosses

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THE PRESENT investigation was carried out at Sakha Agricultural Research Station during 2013/014 to 2015/016 seasons to estimate genetic variance components and type of gene action controlling earliness and yield components of five barley crosses. These crosses used six-population model to determine the intra - and inter-allelic gene interactions controlling the inheritance of earliness and yield traits in five crosses of barley. Mean effect was highly significant for all traits in all crosses. Dominance × dominance was greater in magnitude than other components in most studied traits, indicating that these traits were greatly affected by dominance and its non-allelic interactions. Significant and highly significant desirable percentages of heterosis relative to mid and better parent were exhibited for grain filling period in crosses no. 1, 3 and 5, plant height in crosses no. 1 and 5, no. of grains/spike in crosses no. 1 and 4, no. of spikes/plant in crosses no. 2, 3 and 4 and grain yield/plant in cross no. 4. Broad-sense heritability values were high in all crosses for all studied traits. Narrow-sense heritability and genetic advance ranged from low to medium in most cases due to the opposite directions of dominance and dominance x dominance effects. Generally, the most promising crosses were the two crosses 1 and 5 for earliness and crosses no. 2, 3 and 4 for grain yield found to be higher in magnitude, which had high genetic advance associated with high heritability and would be of interest in breeding programs for improving barley.

Keywords: Barley, Early mature, Six-parameter model, Gene action, Heterosis, Heritability, Genetic advance

Introduction

Barley (*Hordeum vulgare* L.) is considered one of the most important cereal crops ranking the fourth in the world cereal crop production. It has a high tolerance to abiotic stresses such as salinity, drought, frost and heat. It is used mainly for animal feeding, brewing malts and human food in some countries. Barley in Egypt planted in the old land after harvesting vegetables grown for exporting has increased. Developing early-maturing barley is important for increasing cultivated area of barley. Early maturing cultivars are also preferable to escape disease, pests, drought, heat and other stress injuries that occur at the end of growing season. Breeding early-maturing cultivars is an important objective in barley breeding programs. Information about the inheritance of early-maturing and its attributes, as well as yield and its components are very scanty to barley breeders in developing short duration cultivars. Successful breeding programs need continuous information about the genetic variation and systems governing earliness attributes, as well as grain yield and its components (Abdel-Nour, 2011). Contradictory results were obtained by several authors with respect to genetic systems governing these characteristics. Reports are conflicting as to the effect of early vs. late heading genotypes on grain filling. Several researchers indicated that the final grain yield was more related to the rate of grain filling (Mou et al., 1994). Meanwhile, Gebeyehou et al. (1982) reported that grain filling duration was more important than the grain filling rate.

Therefore, it has become necessary to develop early- maturing and high-yielding barley genotypes. The present work was undertaken to study the role of different intra and inter-allelic gene interactions, controlling the inheritance of earliness and yield traits in five barley crosses.

Materials and Methods

The present investigation was carried out at the experimental field of Sakha Agricultural Research

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Stations, Agricultural Research Center (ARC), during three successive seasons from 2013/2014 to 2015/2016. Six barley genotypes representing a wide range of variability in earliness and grain yield traits were used as parents of five crosses in this study (Table 1).

In the first season (2013/2014) five crosses; 1 (Giza 126 × Sico), 2 (Giza 126 × Line-1), 3 (Giza 126 × Line-2), 4 (Giza 132 × Line-2) and 5 (Rihane-03 × Sico) were hand made to obtain their F_1 seeds. In the second season (2014/2015), the hybrid seeds were sown and F_1 plants of each cross were backcrossed to their respective parents to produce the two backcrosses (BC1's and BC2's). At the same time, the F_1 plants were selfed to produce F_2 seeds. In the third season (2015/2016), the obtained seeds of these populations, i.e. P_1's, P_2's, F_1's, F_2's, BC_1's and BC_2's for the five crosses were sown in the field using a randomized complete blocks design (RCBD) with three replications. Rows were 1.5m long, 30cm width and the space from plant to plant in a row was 10cm. Each plot consisted of two rows for each P_1, P_2, F_1, ten rows for F_2 and three rows for each of BC_1, BC_2 in each replicate. All agricultural practices were followed according to the growing barley recommendations. Data were recorded on 30 individual guarded plants in each P_1, P_2 and F_1, 90 plants in each BC_1 and BC_2 and 300 plants in each F_2 for days to 50% heading, days to 50% physiological maturity, grain filling period (days), grain filling rate (g/days), plant height (cm), spike length (cm), number of grains/spike, number of spikes/plant, 100 kernel weight (g) and grain yield/plant (g). Heterosis (%) was calculated as the percentage increase of F_1 over the mid- and better parent values.

Statistical and genetic analysis

To determine the presence or absence of non- allelic interactions, scaling test as outlined by Mather (1949) was used. Generation mean analysis was performed according to Mather and Jinks (1982). Genetic analysis of generation means to give estimates of the types of gene action was performed using the relationships given by Gamble (1962). Heritability estimates were computed in both broad (H^2) and narrow (h^2) senses for F_2 generation according to Allard (1960) and Mather (1949). The expected genetic advance from selection (G_a) was calculated according the formulae proposed by Johnson et al. (1955), using the selection differential (k) equal 2.06 for 5% selection intensity and heritability in narrow sense. The predicted genetic advance from selection was expressed as percentage of F_2 mean (G_a%) according to Miller et al. (1958).

Results and Discussion

Mean performance

Means and variances of the studied traits in the six crosses for the six populations P_1, P_2, F_1, F_2, BC_1 and BC_2 are presented in Table 2. The F_1 mean values exceeded the mid values of the two parental means for most of studied traits in the six crosses.

The F_2 population mean performance values were intermediate between the two parents and less than F_1 mean performance in most studied traits, indicating the importance of non-additive components of genetic variance for the studied traits. However, the two populations (BC_1 and BC_2) mean performance values varied in each trait tended towards the mean of its recurrent parent. The high means of BC_1 for days to heading and days to maturity are due to lateness of the first parent (P_1), while the low means of BC_2 are due to the earliness of the second parent (P_2). The highest magnitude of variance was reported by the F_2 generation for all studied earliness and yield traits in all crosses (Table 2) followed by that of backcross generations (BC'$_1$s and BC'$_2$s), while the lowest S^2 magnitude was exhibited by P_1, P_2 and F_1 genotypes, which is also logic from the breeding point of view, due to the homogeneity of such genotypes.

TABLE 1. Name and pedigree of the six parental barley genotypes used in this study

Pedigree	Genotype	No
BaladiBahteem/SD729-por12762-Bc	Giza 126	1
Rihane-05//AS46/Athes*2Athe/Lignee686	Giza 132	2
As 46//Avt/Aths	Rihane-03	3
Exotic variety	Sico	4
Cen/Bglo'S'//Kataf-01	Line-1	5
Apm/ HC 1905// Robur/ 3/ Arar/ 4/ Arar /3/ Mari/ Aths *2// M - Att - 73- 337 - 1	Line-2	6

TABLE 2. Mean ($\bar{X}$) and variance (S^2) of the six populations of the five crosses for days to heading, days to maturity, grain filling period and grain filling rate

Trait	Cross	Statistical Parameter	P1	P2	F1	F2	BC1	BC2
Days to heading (day)	1	$\bar{X}$	81.10	69.20	80.30	75.32	79.44	73.04
		S^2	0.69	0.58	0.42	26.47	23.25	20.71
	2	$\bar{X}$	82.01	73.20	80.90	77.70	80.16	78.12
		S^2	0.72	0.37	0.71	17.40	14.43	13.54
	3	$\bar{X}$	81.66	65.11	76.40	76.02	79.24	74.44
		S^2	0.81	0.77	1.28	29.85	25.89	24.63
	4	$\bar{X}$	89.10	64.80	79.30	76.58	82.16	75.76
		S^2	0.88	0.79	0.42	18.06	13.35	15.83
	5	$\bar{X}$	87.10	68.94	80.40	77.93	79.84	75.36
		S^2	0.93	0.58	1.08	15.88	12.97	11.69
Days to maturity (day)	1	$\bar{X}$	120.30	103.50	113.23	107.38	108.92	103.84
		S^2	1.20	1.43	2.36	27.16	22.45	24.62
	2	$\bar{X}$	119.70	104.60	113.63	111.58	113.48	109.56
		S^2	1.25	2.21	1.59	20.74	18.52	18.22
	3	$\bar{X}$	120.07	103.01	114.00	114.23	115.16	105.20
		S^2	1.32	1.82	1.86	29.44	22.76	27.57
	4	$\bar{X}$	122.60	102.55	116.20	113.42	115.96	109.04
		S^2	2.73	1.65	2.03	39.88	33.36	32.85
	5	$\bar{X}$	122.10	103.50	114.80	116.53	115.28	110.40
		S^2	2.58	2.25	1.20	28.14	19.42	25.62
Grain filling period (day)	1	$\bar{X}$	39.20	34.30	32.93	32.07	29.48	30.80
		S^2	3.25	2.28	2.27	34.58	26.25	30.97
	2	$\bar{X}$	37.69	31.40	32.73	33.88	33.32	31.44
		S^2	3.25	3.23	2.29	45.25	38.06	34.76
	3	$\bar{X}$	38.41	37.90	37.60	38.22	35.92	30.76
		S^2	3.26	2.25	2.24	60.61	51.99	55.97
	4	$\bar{X}$	33.50	37.75	36.90	36.83	33.80	33.28
		S^2	2.26	2.23	1.27	53.10	49.16	44.99
	5	$\bar{X}$	35.00	34.56	34.40	38.60	35.44	35.04
		S^2	2.29	2.28	2.24	47.87	32.49	37.85
Grain filling rate (g/day)	1	$\bar{X}$	0.55	0.61	0.75	0.70	0.68	0.57
		S^2	0.005	0.003	0.004	0.07	0.06	0.05
	2	$\bar{X}$	0.55	0.48	0.67	0.62	0.52	0.49
		S^2	0.006	0.002	0.003	0.08	0.06	0.06
	3	$\bar{X}$	0.56	0.30	0.60	0.54	0.49	0.44
		S^2	0.005	0.004	0.005	0.09	0.08	0.07
	4	$\bar{X}$	0.46	0.32	0.52	0.50	0.43	0.40
		S^2	0.002	0.004	0.004	0.11	0.09	0.10
	5	$\bar{X}$	0.55	0.59	0.75	0.66	0.55	0.49
		S^2	0.002	0.003	0.003	0.08	0.07	0.07

TABLE 2. Cont. Mean ($\bar{X}$) and variance (S^2) of the six populations of the five crosses for plant height, spike length, number of grains/spike and number of spikes/plant

Trait	Cross	Statistical Parameter	P1	P2	F1	F2	BC1	BC2
Plant height (cm)	1	$\bar{X}$	103.50	99.00	111.00	108.02	102.04	111.44
		S^2	16.12	22.55	14.48	97.95	89.71	80.41
	2	$\bar{X}$	105.60	90.50	106.50	108.04	106.32	104.28
		S^2	17.83	23.36	16.81	120.84	101.82	112.61
	3	$\bar{X}$	107.80	64.10	79.30	82.32	88.00	75.76
		S^2	17.68	13.75	21.80	130.31	120.32	113.54
	4	$\bar{X}$	90.10	64.90	82.00	94.86	88.00	74.20
		S^2	20.64	14.78	18.97	182.73	164.51	162.92
	5	$\bar{X}$	83.80	96.30	103.00	100.70	103.16	101.88
		S^2	19.61	24.01	13.45	127.98	120.22	114.89
Spike length (cm)	1	$\bar{X}$	6.70	7.00	7.50	7.18	6.12	6.22
		S^2	0.13	0.12	0.17	1.79	1.16	1.57
	2	$\bar{X}$	6.90	6.80	7.50	6.52	7.24	7.04
		S^2	0.11	0.18	0.16	1.87	1.73	1.42
	3	$\bar{X}$	6.50	5.60	7.20	5.70	6.12	5.72
		S^2	0.14	0.15	0.18	1.49	1.33	1.58
	4	$\bar{X}$	7.70	5.90	7.60	6.58	7.04	5.88
		S^2	0.12	0.13	0.16	1.97	1.42	1.46
	5	$\bar{X}$	5.40	7.30	8.10	5.86	7.32	5.72
		S^2	0.15	0.11	0.11	1.92	1.41	1.74
Number of grains / spike (grain)	1	$\bar{X}$	56.80	56.40	62.40	56.01	56.28	55.92
		S^2	3.82	3.94	3.74	42.26	31.80	34.21
	2	$\bar{X}$	57.60	55.80	62.40	51.12	56.64	54.72
		S^2	3.24	3.82	3.39	42.02	36.50	33.47
	3	$\bar{X}$	57.00	43.80	57.60	43.92	44.88	46.32
		S^2	4.31	5.22	4.33	48.31	38.30	42.82
	4	$\bar{X}$	58.20	43.40	59.40	53.64	53.52	49.04
		S^2	3.82	5.30	5.70	67.05	52.31	59.28
	5	$\bar{X}$	51.00	57.00	61.20	49.92	57.36	48.96
		S^2	4.31	3.76	3.96	55.54	49.91	47.07
Number of spikes / plant (spike)	1	$\bar{X}$	14.10	12.20	14.90	13.34	14.00	12.16
		S^2	1.46	1.24	1.16	27.79	25.05	22.43
	2	$\bar{X}$	14.40	16.10	16.70	15.52	15.06	13.60
		S^2	1.51	1.13	2.01	39.67	35.90	30.42
	3	$\bar{X}$	14.70	15.20	17.20	16.40	17.08	13.76
		S^2	1.49	1.42	1.17	35.48	28.13	28.91
	4	$\bar{X}$	11.60	15.10	16.50	17.56	15.28	14.84
		S^2	1.46	1.36	1.74	33.78	28.18	27.62
	5	$\bar{X}$	15.30	12.30	19.50	16.54	14.96	16.24
		S^2	1.53	1.22	2.05	30.49	25.44	27.27

TABLE 2. Cont. Mean ($\bar{X}$) and variance (S^2) of the six populations of the five crosses for 100-grain weight and grain yield / plant

Trait	Cross	Statistical Parameter	P1	P2	F1	F2	BC1	BC2
100-grain weight (g)	1	$\bar{X}$	4.72	5.25	5.87	4.69	4.69	4.60
		S^2	0.05	0.03	0.04	0.57	0.46	0.49
	2	$\bar{X}$	4.68	5.44	5.73	4.98	4.61	4.97
		S^2	0.04	0.02	0.03	0.62	0.50	0.55
	3	$\bar{X}$	4.71	3.76	4.89	4.29	4.25	4.17
		S^2	0.04	0.04	0.04	0.63	0.58	0.54
	4	$\bar{X}$	4.93	3.82	4.76	4.57	4.90	4.47
		S^2	0.03	0.04	0.03	0.55	0.48	0.46
	5	$\bar{X}$	4.57	5.20	5.82	4.62	4.76	4.55
		S^2	0.05	0.03	0.05	0.50	0.46	0.45
Grain yield / plant (g)	1	$\bar{X}$	21.58	20.81	24.66	20.76	19.93	17.46
		S^2	4.29	5.59	3.09	52.25	47.94	42.48
	2	$\bar{X}$	20.60	15.16	21.95	18.48	18.35	15.18
		S^2	4.33	4.87	3.95	59.04	49.05	50.05
	3	$\bar{X}$	21.65	11.40	22.41	17.85	17.76	13.51
		S^2	4.35	3.46	3.40	60.73	52.04	54.25
	4	$\bar{X}$	15.48	11.95	19.05	18.82	17.75	16.53
		S^2	4.68	3.42	3.60	54.78	48.00	44.35
	5	$\bar{X}$	19.25	20.52	25.73	21.08	19.40	17.31
		S^2	3.97	5.53	3.06	69.69	63.97	62.86

Gene effects

These data were used to calculate the scaling test and six parameters according to Gamble procedure (1962). At least, one of the scales (A, B and C) was significant in the six crosses for all studied traits. However, the significance of any one of the scales reveals the presence of non-allelic interaction as pointed out in Table 3.

Estimates of gene effects calculated from the six-parameter model of the generation mean analysis are presented in Table 3. Desirable values of additive gene effects were obtained from crosses no. 3 and 4 for plant height, 3, 4 and 5 for spike length, 2, 4 and 5 for number of grains/spike, 3 for number of spikes/plant, 4 for 100-grain weight and 1, 2 and 3 for grain yield/plant. This assures the enhancing effect of additive variance in the inheritance of these traits. These results indicated the potentiality of improving the performance of these traits using pedigree selection as reported by Mansour (2012) and Mansour et al. (2014).

However, dominance plays greater role in inheritance of grain filling period, spike length and no. of grains/spike, additive x additive plays greater role in inheritance of grain filling period, additive x dominance plays greater role in inheritance of days to heading and maturiety and dominance x dominance plays greater role in inheritance of most yeild traits. It could be observed that when additive effects are larger than non-additive ones, it is suggested that selection would be effective in early segregating generations, while if the non-additive portion are larger than additive ones, the improvement of the characters need intensive selection in the later generations. However, when epistatic effect was significant for a trait, the possibility of obtaining desirable segregates through inter-mating in early segregating generations by breaking undesirable linkage could be available or it is suggested to adopt recurrent selection for handling the above crosses for rapid improvement. These conclusions are in the same line with those reported by Zeng et al. (2001), Eid (2006), Munir et al. (2007), Khattab et al. (2010), Aykuttonk et al. (2011), Mansour (2012), Amin (2013), Ljaz et al. (2013), Mansour et al. (2015), Abaas et al (2016) and Mansour (2016).

Heterosis, potence ratio and inbreeding depression

Heterosis over mid-parent and better parent, potence ratio and inbreeding depression, are presented in Table 4. Significant and highly significant desirable percentages of heterosis relative to mid and better parent with insignificant values for inbreeding depression were exhibited for grain filling period in crosses no. 1, 3 and 5, plant height in crosses no. 1 and 5, no. of grains/spike in crosses no. 1 and 4, no. of spikes/plant in crosses no. 2, 3 and 4 and grain yield/plant in cross no. 4.

TABLE 3. Scaling test and type of gene action estimated by generation means of the five crosses for days to heading, days to maturity, grain filling period, grain filling rate and plant height

Trait	Cross	Scaling test			Type of gene action					
		A	B	C	(m)	(a)	(d)	(aa)	(ad)	(dd)
Days to heading	1	-2.52*	-3.42**	-9.63**	75.32**	6.40**	8.84**	3.69	0.45	2.25
	2	-2.59**	2.14*	-6.21**	77.70**	2.04**	9.05**	5.76**	-2.37**	-5.31*
	3	0.42	7.37**	4.50**	76.02**	4.80**	6.31**	3.29	-3.48**	-11.08**
	4	-4.08**	7.42**	-6.17**	76.58**	6.40**	11.86**	9.51**	-5.75**	-12.85**
	5	-7.82**	1.38	-5.11**	77.93**	4.48**	1.05	-1.33	-4.60**	7.77**
Days to maturity	1	-15.69**	-9.05**	-20.73**	107.38**	5.08**	-2.68	-4.01*	-3.32**	28.76**
	2	-6.37**	0.89	-5.23**	111.58**	3.92**	1.23	-0.25	-3.63**	5.74
	3	-3.75**	-6.61**	5.85**	114.23**	9.96**	-13.75**	-16.21**	1.43	26.57**
	4	-6.88**	-0.67	-3.88*	113.42**	6.92**	-0.04	-3.67	-3.11**	11.22**
	5	-6.34**	2.50*	10.93**	116.53**	4.88**	-12.77**	-14.77**	-4.42**	18.61**
Grain filling period	1	-13.17**	-5.63**	-11.10**	32.07**	-1.32	-11.52**	-7.71**	-3.77**	26.51**
	2	-3.78*	-1.25	0.98	33.88**	1.88	-7.82**	-6.01*	-1.27	11.05**
	3	-4.17*	-13.98**	1.36	38.22**	5.16**	-20.06**	-19.51**	4.91**	37.66**
	4	-2.80	-8.09**	2.28	36.83**	0.52	-11.90**	-13.17**	2.65*	24.06**
	5	1.48	1.12	16.04**	38.60**	0.40	-13.82**	-13.44**	0.18	10.84*
Grain filling rate	1	0.05	-0.22**	0.15*	0.70**	0.11**	-0.14	-0.31**	0.14**	0.48**
	2	-0.18**	-0.17**	0.11	0.62**	0.03	-0.30**	-0.46**	0.00	0.81**
	3	-0.17*	-0.02	0.10	0.54**	0.06	-0.13	-0.29**	-0.08	0.48*
	4	-0.12	-0.03	0.19*	0.50**	0.03	-0.21	-0.34**	-0.04	0.49*
	5	-0.20**	-0.35**	0.01	0.66**	0.05	-0.38**	-0.56**	0.08	1.11**
Plant height	1	-10.42**	12.88**	7.58**	108.02**	-9.40**	4.63	-5.12	-11.65**	2.66
	2	0.54	11.56**	23.06**	108.04**	2.04	-2.51	-10.96**	-5.51**	-1.14
	3	-11.10**	8.12**	-1.22	82.32**	12.24**	-8.41	-1.76	-9.61**	4.74
	4	3.90	1.50	60.44**	94.86**	13.80**	-50.54**	-55.04**	1.20	49.64**
	5	19.52**	4.46	16.70**	100.70**	1.28	20.23**	7.28	7.53**	-31.26**

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

TABLE 3. Cont. Scaling test and type of gene action estimated by generation means of the five crosses for spike length, number of grains / spike, number of spikes / plant, 100-grain weight and grain yield / plant

Trait	Cross	Scaling test			Type of gene action					
		A	B	C	(m)	(a)	(d)	(aa)	(ad)	(dd)
Spike length	1	-1.96**	-2.06**	0.02	7.18**	-0.10	-3.39**	-4.04**	0.05	8.06**
	2	0.08	-0.22	-2.62**	6.52**	0.20	3.13**	2.48**	0.15	-2.34**
	3	-1.46**	-1.36**	-3.70**	5.70**	0.40*	2.03**	0.88	-0.05	1.94*
	4	-1.22**	-1.74**	-2.48**	6.58**	1.16**	0.32	-0.48	0.26	3.44**
	5	1.14**	-3.96**	-5.46**	5.86**	1.60**	4.39**	2.64**	2.55**	0.18
Number of grains / spike	1	-8.64**	-8.96**	-13.96**	56.01**	0.36	2.16	-3.64	0.16	21.24**
	2	-6.72**	-8.76**	-33.72**	51.12**	1.92*	23.94**	18.24**	1.02	-2.76
	3	-24.84**	-8.76**	-40.32**	43.92**	-1.44	13.92**	6.72*	-8.04**	26.88**
	4	-10.56**	-4.72*	-5.84**	53.64**	4.48**	-0.84	-9.44**	-2.92*	24.72**
	5	2.52	-20.28**	-30.72**	49.92**	8.40**	20.16**	12.96**	11.40**	4.80
Number of spikes / plant	1	-1.00	-2.78*	-2.74*	13.34**	1.84*	0.71	-1.04	0.89	4.82
	2	-3.90**	-2.68*	-1.82	15.52**	-1.46	-3.31	-4.76*	-0.61	11.34**
	3	2.26	-4.88**	1.30	16.40**	3.32**	-1.67	-3.92	3.57**	6.54
	4	2.46	-1.92	10.54**	17.56**	0.44	-6.85**	-10.00**	2.19*	9.46*
	5	-4.88**	0.68	-0.44	16.54**	-1.28	1.94	-3.76	-2.78**	7.96*
100-grain weight	1	-1.22**	-1.91**	-2.94**	4.69**	0.08	0.70*	-0.19	0.35**	3.32**
	2	-1.19**	-1.23**	-1.66**	4.98**	-0.36**	-0.09	-0.76*	0.02	3.18**
	3	-1.11**	-0.32	-1.10**	4.29**	0.08	0.33	-0.32	-0.40**	1.75**
	4	0.12	0.37*	0.04	4.57**	0.43**	0.83**	0.45	-0.13	-0.94
	5	-0.88**	-1.92**	-2.92**	4.62**	0.21	1.06**	0.12	0.52**	2.68**
Grain yield / plant	1	-6.38**	-10.55**	-8.67**	20.76**	2.47*	-4.80	-8.26**	2.09	25.19**
	2	-5.85**	-6.75**	-5.74**	18.48**	3.17**	-2.79	-6.86*	0.45	19.46**
	3	-8.53**	-6.79**	-6.47**	17.85**	4.25**	-2.97	-8.86**	-0.87	24.18**
	4	0.98	2.05	9.75**	18.82**	1.23	-1.39	-6.72*	-0.54	3.70
	5	-6.17**	-11.63**	-6.90**	21.08**	2.09	-5.06	-10.90**	2.73*	28.70**

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

TABLE 4. Heterosis, inbreeding depression and potence ratio in five crosses for all studied traits

Trait	Cross	Heterosis		ID	PR%	Traits	Cross	Heterosis		ID	PR%
		MP	BP					MP	BP		
Days to heading	1	6.85**	16.04**	6.21	0.87	Spike length	1	9.49**	7.14**	4.27**	4.33
	2	4.25**	10.52**	3.96	0.75		2	9.49**	8.70**	13.07**	13.00
	3	4.11**	17.34**	0.50	0.36		3	19.01**	10.77**	20.83**	2.56
	4	3.05**	22.38**	3.43	0.19		4	11.76**	-1.30**	13.42**	0.89
	5	3.05**	16.62**	3.07	0.26		5	27.56**	10.96**	27.65**	1.84
Days to maturity	1	1.19**	9.40**	5.17	0.16	Number of grains / spike	1	10.25**	9.86**	10.24	29.00
	2	1.32**	8.64**	1.80	0.20		2	10.05**	8.33**	18.08**	6.33
	3	2.21**	10.67**	-0.20	0.29		3	14.29**	1.05**	23.75**	1.09
	4	3.22**	13.31**	2.40	0.36		4	16.93**	2.06**	9.70	1.16
	5	1.77**	10.92**	-1.51	0.22		5	13.33**	7.37**	18.43*	2.40
Grain filling period	1	-10.4**	-3.98**	2.63	-1.56	Number of spikes / plant	1	13.31**	5.67**	10.47*	1.84
	2	-5.24**	4.25**	-3.51	-0.58		2	9.51**	3.73**	7.07	1.71
	3	-1.45**	-0.79*	-1.64	-2.18		3	15.05**	13.16**	4.65	9.00
	4	3.58**	10.15**	0.18	0.60		4	23.60**	9.27**	-6.42	1.80
	5	-1.09**	-0.46**	-12.21	-1.73		5	41.30**	27.45**	15.18**	3.80
Grain filling rate	1	29.41**	23.42**	6.52**	6.06	100-grain weight	1	17.80**	11.85**	20.07**	3.35
	2	30.28**	22.69**	7.54**	4.90		2	13.22**	5.29**	13.09**	1.76
	3	37.91**	5.76**	9.40**	1.25		3	15.44**	3.82**	12.32**	1.38
	4	32.60**	11.72**	3.15**	1.74		4	8.78**	-3.49**	3.82**	0.69
	5	30.77**	25.95**	11.74**	8.03		5	19.12**	11.92**	20.57**	2.97
Plant height	1	9.63**	7.25**	2.68	4.33	Grain yield / plant	1	16.35**	14.27**	15.82*	9.00
	2	8.62**	0.85	-1.45	1.12		2	22.75**	6.55**	15.81*	1.50
	3	-7.74**	-26.4**	-3.81	-0.30		3	35.63**	3.53**	20.35*	1.15
	4	5.81**	-8.99**	-15.68	0.36		4	38.90**	23.06**	1.21	3.02
	5	14.38**	6.96**	2.23	2.07		5	29.38**	25.37**	18.06*	9.18

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

For potence ratio, results showed over dominance for all studied traits in all crosses except for days to heading and matureity in all crosses, grain filling period in crosses no. 2 and 4, plant height in crosses no 3 and 4, spike length and 100-grain weight in cross no. 4. Similar findings were also reported by Mahmoud, Badeaa (2006), Eid (2006), Munir et al. (2007), El-Akhdar (2011), Amin (2013), El-Refaey and Abd El-Razek (2013) Mansour et al. (2015), Abaas et al (2016) and Mansour (2016).

Heritability in broad and narrow-senses and genetic advance

Heritability in broad and narrow-senses and genetic advance, are presented in Table 5. Broad sense heritability values (H^2) estimates were generally higher than the corresponding narrow-sense heritability (h^2), indicating the presence of non-additive gene action. Broad-sense heritability values were high in all crosses for all studied traits and ranged from 82.74 to 98.00% in cross no. 1 for plant height and days to heading, respectively.

Narrow-sense heritability ranged from low to medium in most cases due to the opposite directions of dominance and dominance x dominance effects with values; 5.17 to 53.96% for spike length in crosses no. 3 and 4, respectively. Genetic advance from selection ranged from 1.92% in cross no. 2 for days to maturity to 49.27% in cross no. 2 for grain filling rate. High percentage of expected genetic advance would help breeder in improving the trait of interest via few cycles of selection. These results are in good agreement with those reported by Eid (2006), Munir et al. (2007), Khattab et al. (2010), El-Akhdar (2011), Aykuttonk et al. (2011), Mansour (2012), Amin (2013), El-Refaey & Abd El-Razek (2013), Mansour et al. (2015), Abaas et al (2016) and Mansour (2016).

Generally, the most promising crosses were the two crosses 1 and 5 for earliness and crosses no. 2, 3 and 4 for grain yield and were found to be higher in magnitude, which expressed high genetic advance associated with high heritability and would be of interest in breeding programs for improving the studied traits in barley.

TABLE 5. Heritability percentage in broad (H^2) and narrow (h^2) senses and expected genetic advance from selection (Δg) of the five crosses for all studied traits

	Cross	Heritability		Genetic advance		Traits	Cross	Heritability		Genetic advance	
		H^2	h^2	Δg	Δg %			H^2	h^2	Δg	Δg %
Days to heading	1	98.00	33.92	3.59	4.77	Spike length	1	91.76	47.62	1.31	18.28
	2	96.38	39.25	3.37	4.34		2	91.84	31.94	0.90	13.80
	3	96.53	30.76	3.46	4.55		3	89.13	5.17	0.13	2.28
	4	96.52	38.36	3.36	4.39		4	92.77	53.96	1.56	23.71
	5	94.24	44.68	3.67	4.71		5	93.75	35.68	1.02	17.38
Days to maturity	1	93.23	26.68	2.86	2.67	Number of grains / spike	1	90.98	43.80	5.87	10.47
	2	91.99	22.85	2.14	1.92		2	91.77	33.48	4.47	8.75
	3	94.17	29.06	3.25	2.84		3	90.59	32.11	4.60	10.47
	4	94.71	33.95	4.42	3.89		4	92.35	33.59	5.67	10.56
	5	93.58	39.96	4.37	3.75		5	92.80	25.38	3.90	7.81
Grain filling period	1	92.72	34.53	4.18	13.04	Number of spikes / plant	1	95.48	29.12	3.16	23.71
	2	93.89	39.06	5.41	15.98		2	95.80	32.82	4.26	27.44
	3	95.88	21.88	3.51	9.18		3	96.30	39.24	4.81	29.36
	4	96.69	22.68	3.40	9.24		4	95.34	34.81	4.17	23.74
	5	95.27	53.07	7.56	19.60		5	94.38	27.14	3.09	18.66
Grain filling rate	1	94.29	49.17	0.27	38.28	100-grain weight	1	92.98	33.33	0.52	11.05
	2	95.55	52.85	0.31	49.27		2	94.89	31.37	0.51	10.22
	3	94.72	33.33	0.21	38.15		3	93.65	22.22	0.36	8.47
	4	96.82	27.27	0.19	37.27		4	94.09	29.09	0.44	9.72
	5	96.56	22.35	0.13	19.73		5	91.00	18.00	0.26	5.67
Plant height	1	82.74	26.32	5.37	4.97	Grain yield / plant	1	92.32	26.95	4.01	19.33
	2	84.52	22.55	5.11	4.73		2	92.76	32.15	5.09	27.54
	3	85.61	20.54	4.83	5.87		3	93.98	24.98	4.01	22.47
	4	89.96	20.81	5.79	6.11		4	93.02	31.42	4.79	25.45
	5	86.22	16.29	3.80	3.77		5	94.40	18.01	3.10	14.69

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التحليل الوراثى لصفات التبكير ومكونات المحصول فى خمسة هجن من الشعير

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الخلاصة

أجريت هذه الدراسة بمزرعة محطة البحوث الزراعية بسخا خلال الثلاثة مواسم 14/2013، 15/2014 و16/2015 لدراسة مكونات التباين الوراثي وتأثير الفعل الجيني المتحكم فى وراثة التبكير والمحصول ومكوناته باستخدام نظام العشائر الست (الأب الأول، الأب الثاني، الجيل الأول، الجيل الثاني، الهجين الرجعى الأول والهجين الرجعى الثاني) لخمسة هجن من الشعير وهى: الهجين الأول (جيزة 126 × سايكو), الهجين الثاني (جيزة 126 × سلالة1-), الهجين الثالث (جيزة 126 × سلالة2-), الهجين الرابع (جيزة 132 × سلالة2-) و الهجين الخامس (ريحان3- × سايكو). أظهرت النتائج أن متوسطات الأجيال كانت عالية المعنوية بالنسبة لكل الصفات فى كل الهجن. تشير النتائج أيضا بصورة عامة إلى وجود تفاعل بين العوامل غير الأليلية بالنسبة لكل الصفات فى كل الهجن, كما أشارت النتائج إلى أهمية تأثيرات كل من الفعل الوراثي المضيف والسيادي والتي اختلفت تبعا للصفات والهجن. أما بالنسبة لمكونات التفاعل فإن التفاعل السيادي × السيادي كان ذو تأثير أكبر من تأثير الفعل الوراثي المضيف × المضيف و المضيف × السيادي فى معظم الصفات تحت الدراسة. تم الحصول على تقديرات عالية المعنوية مرغوبة لقوة الهجين بالمقارنة بمتوسط الأبوين والأب الأفضل مع عدم وجود معنوية للتدهور الناتج عن التربية الداخلية بالنسبة لصفة فترة امتلاء الحبوب فى الهجن: 1, 3 و 5, صفة طول النبات فى الهجينين: 1 و 5, صفة عدد الحبوب فى السنبلة فى الهجينين: 1 و 4, صفة عدد السنابل للنبات فى الهجن: 2, 3 و 4 وصفة محصول الحبوب للنبات فى الهجين رقم 4. كانت كفاءة التوريث بالمعنى الواسع مرتفعه فى كل الهجن بالنسبة للصفات المدروسة. بالنسبة للتقديرات الخاصة بكفاءة التوريث بالمعنى الضيق والتحسين الوراثي المتوقع نتيجة الانتخاب فتراوحت من منخفضة إلى متوسطة وذلك بالنسبة لكل الصفات فى معظم الهجن. وبصفة عامة كانت أفضل الهجن المبشرة هي الهجينين: 1 و 5 بالنسبة لصفة التبكير والهجن: 2, 3 و 4 بالنسبة لصفة المحصول حيث أعطت قيماً عالية للتحسين الوراثي المتوقع نتيجة للانتخاب وكذلك كفاءة التوريث، مما يشير إلى أهمية هذه الهجن فى برامج التربية لتحسين هذه الصفات فى الشعير فى هذه الدراسة.