

## **PEDIGREE SELECTION FOR EARLINESS, SPIKES NUMBER AND GRAIN WEIGHT IN TWO SEGREGATING POPULATIONS OF BARLEY (*Hordium vulgare* L.)**

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### **ABSTRACT**

Two cycles of pedigree selection were applied to the F<sub>3</sub> generation of two barley crosses. The objective of this investigation was to improve grain weight, spikes number/plant and days to heading using the pedigree selection. Highly significant differences among the F<sub>3</sub> families and sufficient genotypic coefficient of variability were detected for days to heading, spike length, number of spikes/plant, number of kernels/spike, 1000- kernel weight and grain weight/plant in both populations. Broad sense heritabilities were high for days to heading and moderate for number of spikes/plant and grain weight of both populations.

Heritability and predicted genetic gain upon selection decreased from F<sub>3</sub> to F<sub>5</sub> generation for the three selection criteria of both populations. The realized gains showed that days to heading was earlier by 4.16% in the first population and 2.76 % in the second one after two cycles compared to the bulk sample. Selection for more spikes/plant after two cycles increased the merit of selection by 10.88% in the first population and 5.07 % in the second population compared to the bulk of F<sub>3</sub> families. Direct selection for grain weight /plant showed realized response to selection reached to 7.57% and 7.60% from the bulk sample and accounted 6.59 and 2.41% from the best parent in population 1 and 2 , respectively. Family No. 66 in the first population yielded 13.07 % more than the bulk and was earlier than it by 5.58 % and family No. 92 in the second population could be considered the best selected family which had 6.45% increase in grain weight and was earlier than the bulk sample by 5.88%. Pedigree selection was an efficient selection procedure for increasing the mean of the character under selection and affected the other related characters.

**Keywords:** *Barley, Heritability, Predicted genetic advance-Realized gain.*

### **INTRODUCTION**

Barley is mainly used for animal feeding in Egypt. However, interest in using the crop for human consumption has recently renewed. Barley is the main cereal crop grown in the rainfed areas of Egypt. It occupies about 126,000 ha in the Northwest Coast and about 21,000 ha in North Sinai. Breeding for drought resistance through developing short season cultivars is nowadays widely adopted in different regions of the world where water supply is limited. When breeding for high productivity, the breeder is faced with three major decisions. The first is to identify the desirable germplasm which posses the desired attributes. Secondly, the breeder must determine the most efficient breeding method which could be adopted in handle the basic breeding populations.

In a breeding program, information on efficiency of early selection for superior yielding genotypes is especially important in making decisions dealing with population size and possible selection pressure. Löffler and Busch (1982) reported that no other selection criteria was effective in increasing grain yield as grain yield itself. In wheat, Mahdy (1988) found that selection based on grain yield *per se* was effective in improving grain yield itself and was accompanied by a sizeable significant increase in spike length, number of spikes/plant and grain numbers/spike. Kheiralla (1993) showed that direct selection for spike length, grain weight, grains/spike and spikes/plant was accompanied by an increase in grain yield which accounted 5.6, 5.9, 6.9 and 7.5 %, respectively, after two cycles of selection calculated as a deviation from mean of the best parent.

Therefore, the objective of this study was to compute the relative predicted genetic gain upon selection in two barley populations for two cycles started in the F<sub>3</sub> using the pedigree selection procedure in improving earliness, number of spikes/plant and grain weight and to measure direct and indirect response to selection for these traits.

### **MATERIALS AND METHODS**

This investigation was carried out during the three successive growing seasons, 1997/98 and 2001/02 at the Exp. Farm, Fac. of Agric., Tanta, Tanta University and 2002/03 at El- Eslahe, Nawag, Tanta, El-Gharbia Governorate, Egypt.

The breeding materials used in this study were 100 F<sub>3</sub>- families traced back to a random sample from F<sub>2</sub> single plants originated from each cross of:

(1) Giza 124 (Local) x ICRI (Hungary) (2) Plaisant (France) x ICRI.

The 100-F<sub>3</sub> families with the original parents along with F<sub>3</sub> bulked random sample were sown in 1997/98 season in separate experiments for each population in a randomized complete block design of three replications. Each plot was a single row 3 m long, 30 cm apart and 5 cm between plants within row. Days

to heading was recorded on a plot mean basis as days from sowing to 50% of the heads extruded from the flag leaf sheath. The earliest plant of each plot was labeled. At maturity, individual plants data were recorded on ten random plants from the middle portion of each plot.

Data were collected on each plant as follows:

- 1- Spike length of the main culm (cm).
- 2- Number of spikes /plant.
- 3- Number of kernels/spike.
- 4- 1000-Kernel weight (g).
- 5- Grain weight/plant (g).

Genotypic and phenotypic coefficients of variation were calculated on a plot mean basis as outlined by Miller *et al.* (1958). The best 20 plants from the best families from each population were selected for each of the selection criteria i.e., days to heading, number of spikes/plant and grain weight/plant and saved to give the F<sub>4</sub> family seeds (Family selection, C<sub>1</sub>).

In 2001/02 season, the best 20 F<sub>4</sub> families of both populations (C<sub>1</sub>), F<sub>3</sub> bulk families (C<sub>0</sub>) and parents were individually evaluated for the three traits as have been carried out in 1997/98 season. At harvest, the best ten plants from the best 10 families were selected for each of the three traits as in 1997/98 season to give the F<sub>2</sub> family seeds (Family selection, C<sub>2</sub>).

In 2002/03 season, the F<sub>3</sub> bulk families (C<sub>0</sub>), parents and the ten selected families (C<sub>2</sub>) were sown. The data of the two experiments for the two populations were recorded as in the first season.

The analysis of variance, the expected mean squares and heritability in broad sense were calculated as outlined by Miller *et al.*(1958). The realized gain from selection as a deviation percentage from the bulk sample and the best parent for the selection criteria and the correlated traits were also calculated. Expected genetic advance (G<sub>a</sub>) upon selection assuming a selection intensity of 10 % (K=1.76) and predicted genetic advance (G<sub>a</sub>%) were calculated according to Allard (1960) as follows:

$$G_a \% = [ 1.76 ( \sigma_{ph} )(H^2/x) \times 100$$

## **RESULTS AND DISCUSSION**

The analysis of variance (Table 1) indicate highly significant differences among F<sub>3</sub> families (base population ) in both cross populations for days to heading, spike length, number of spikes/plant, number of kernels/spike, 1000-kerenl weight and grain weight/plant.

Estimates of the phenotypic and genotypic coefficients of variation indicate the presence of sufficient variability for most studied traits. The obtained variabilities suggest that selection among F<sub>3</sub> families would be effective changes in the two populations. The genetic variability was sufficient for effective selection in the base population for the three selection criteria i.e., days to heading, number of spikes/plant and grain weight/plant in both populations. In addition great response to selection can be achieved from selection in both populations having a large amount of phenotypic and genotypic variance. Similar results were obtained by Kheiralla (1993) and Ismail (1995) in wheat.

The genetic components of variance, genotypic ( G.C.V.% ) and phenotypic (P.C.V.%) coefficients of variability, heritability in broad sense and predicted genetic gain upon selection for the two cycles of selection in both populations are shown in Table 2. It appears that the F<sub>3</sub> families possessed considerable amount of genetic variability more than the F<sub>4</sub> families (C<sub>1</sub>) for the three selection criteria in both populations. O'Brien *et al* (1978) stated that although response to selection will be greater in populations with great genetic variance, the highest yielding lines may be derived from populations with less genetic variance but with a higher initial mean yield. Both P.C.V % and G.C.V.% decreased rapidly after two cycles of selection for the three selection criteria in both populations. Consequently, small genetic variance, low heritability and small selection progress could be expected after the second cycle. Predicted genetic gain upon selection (G<sub>a</sub>%) was relatively high to moderate for all the studied traits except, days to heading of both populations (Table 1). Also, predicted genetic gain upon selection (G<sub>a</sub>%) and the heritability estimates decreased rapidly after two cycles of selection for the three selection criterion in population 1 and 2 and decreased from F<sub>3</sub> to F<sub>5</sub> generation (Table 2). Broad sense heritabilities for all traits studied were high to moderate of both populations except, grain weight/plant of both populations and number of spikes/plant in the second population. Higher values of genetic advance under selection along with high estimates of heritability indicate that these characters were largely controlled by the additive gene effects and the improvement of such traits could be achieved through phenotypic selection. Johanson *et al* (1955) suggested that heritability estimates along with genetic advance are normally more helpful in predicting gain under phenotypic selection than the use of heritability estimates alone. These results indicate that two cycles of selection for these traits were enough to identify the performance of the promising genotypes. It is clear that phenotypic coefficient of variation decreased from the base population as homogeneity increased from cycle to cycle (Table 2).

Falconer (1989) found that selection reduces the variance. High estimates of broad sense heritability indicate that the environmental effects were small compared to the genetic effects. High heritability were found for days to heading of both populations and moderate for number of spikes/plant in the first population compared with those obtained for grain weight/plant of both populations and number of spikes/plant of the second population. Several investigators reported high estimates of heritability for days to heading, such as El-Seidy and Hamada (1997), Moustafa *et al* (1998), Awaad (2001), Kheiralla *et al* (2001), Abd El-Aty and Katta (2002) and El-Seidy (2003). On the other hand, grain yield/plant has been extensively reported by many workers to be highly affected by environmental conditions as low heritability values were detected, of those; Kheiralla and Sherif (1992), El-Seidy and Hamada (1997), Moustafa *et al* (1998), Kheiralla *et al* (2001) and El-Seidy (2002). It is of interest to note that heritability estimates decreased from  $F_3$  (base population) to  $F_5$  ( $C_2$ ) generation for the three selection criteria at both populations. The reduction of heritability is due to the decrease in the amount of genetic variability. These results are in line with those reported by Kheiralla (1993) and Ismail (1995).

Means of three selection criteria over the selected families in two cycles ( $C_1$  and  $C_2$ ) and the best parents for population 1 and 2 presented in Table 3. The overall family means for cycle 1 and cycle 2 selection exceeded the mean of the  $F_3$  families and the best parent for the three selection criteria at both populations. The response to selection was coined by Falconer (1989) as the difference between mean phenotypic values of the offspring of the selected parents and the generation mean of these parents. The bulk sample mean could be considered as the parent generation mean before selection. As well as, in the additive genetic model, the parental mean equals the generation mean before selection.

Realized gain from direct selection for the three selection criteria and correlated response with the other correlated traits in both populations measured as the deviation percentage of the overall cycle mean from the bulk sample and the best parent are shown in Tables 4 and 5. The results indicate that direct selection for early heading resulted in earlier families. Days to heading was earlier by 2.3 and 3.5 days from the bulk of  $F_3$  families which were 2.7 % and 4.16 % earlier than the base population ( $C_0$ ) in the first population after  $C_1$  and  $C_2$ , respectively, and 1.9 and 2.3 days which equivalent 2.24 % and 2.76 % in the second population after  $C_1$  and  $C_2$ , respectively. Likewise, the reduction in heading time reached 2.1 and 3.2 days in the first cross and 1.3 and 1.8 days in the second cross after  $C_1$  and  $C_2$  selection as compared to the earliest parent, respectively.

However, deleterious effects on the other correlated traits accompanied earliness after two cycles of selection, and accounted -8.99,-4.76,-1.29,-2.08 and -2.98 % relative to the base population ( $C_0$ ) in the first population for spike length, number of spikes/plant, number of kernels/spike, 1000-kernel weight and grain weight /plant, respectively, and -3.33, -0.32 and -2.53 % in the second population for spike length, number of kernels/spike and grain weight/plant, respectively. However, the percentages of reduction ranged from -2.45 % for 1000-kernel weight to - 6.9% for spike length in the first population and ranged from -0.39 for 1000-kernel weight to -7.24 % for grain weight/plant in the second population compared to the best parent after two cycles of selection.

Selection for more spikes/plant after the two cycles of pedigree selection increased the mean by 10.88 and 5.07 % in the first and second population after two cycles of selection compared to the bulk  $F_3$  families and increased by 9.4 and 2.11% in the first and the second population after two cycles of selection over the best parent. Such increase in number of spikes caused increment in grain weight/plant in both populations with values of 2.75 and 6.68% compared to the bulk  $F_3$  families and 1.82 and 1.54 % over the best parent after two cycles of selection in both populations, respectively. The other correlated traits behaved differently in the two cycles and populations. Afiah (1999), Afiah and Abdel-Hakim (1999) and Afiah and Darwish (2003) demonstrated that number of spikes/plant and number of grains/spike had the most prominent indirect positive effects on grain weight/plant. Positive values were detected between number of spikes/plant and grain weight/plant. This finding under present study, indicates that selection for number of spikes/plant would be accompanied by high yielding ability. El-Seidy (1997) in barley and El-Seidy (2002) in wheat found that spikes number/plant was good character for indirect selection for yield improvement, whereas the other yield components were intermediate.

Direct selection for grain weight/plant showed realized response to selection reached 7.57 and 7.60% compared to the bulk sample and accounted 6.59 and 2.41% from the best parent in population 1 and 2, respectively after two cycles of selection.

The correlated traits caused increment in all traits studied in both populations, except days to heading which had positive values towards lateness compared to mean of the bulk  $F_3$  families ( $C_0$ ) and the earliest parent and differed in magnitude from one trait to another and from one population to another. This could be indicate that response and correlated response to selection depend upon gene pool. Kheiralla (1993) and Ismail (1995) reported that selection based on grain yield *per se* was the most effective for improving such complicated trait. In pedigree selection, the breeder concerned with the performance of individual selected families. This could be due to that the overall mean masked the individual family means.

The results in Tables 6 and 7 show that the effect of pedigree selection for early heading was found in family No. 66 for the first population which was earlier than the bulk sample and better parent by 5.58 and

5.24% and was higher in grain weight by 13.07 and 12.05 %, respectively after the second cycle in the first population. For the second population, family No. 92 was earlier than the bulk by 5.88 and outyielded it by 6.45% after the second cycle. As well as, more spikes/plant resulted in families 50 and 63 which increased by 27.89 and 34.69% relative to C<sub>0</sub> after C<sub>2</sub> and the former outyielded the bulk sample by 3.21 and 12.61%, respectively, in the first population. For the second population, No. 6 had more spikes than the F<sub>3</sub> bulk by 29.71% and also outyielded it by 11.06% after the second cycle. Pedigree selection for grain weight/plant resulted in four high yielding families i.e., No. 36, 53, 60 and 62 which outyielded the bulk sample by 13.99, 13.99, 21.33 and 14.22 % in the first population and resulted two high yielding families in the second population i.e., No. 9 and 77 which outyielded the bulk sample by 16.59 and 15.67 %, respectively after the second cycle.

Both families No. 66 in the first population and family 92 in the second population were earlier and higher in yield and would be recommended for further evaluation. Fortunately, some early families still had more spikes/plant and high grain weight.

Finally, it can be concluded that, pedigree selection is an efficient method for improving the selection criterion, and the response to selection depends upon the gene pool and these results enhance the chances of using these high yielding early lines in developing new varieties.

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O'Brien , L. ; R.J. Baker and L.E. Evans (1978). Response to selection for yield in F<sub>3</sub> of four wheat crosses. Crop. Sci., 18:1029-1033.

### الانتخاب المنسب لصفات التبكير وعدد السنابل ووزن الحبوب في عشيرتين إنزالييتين لمحصول الشعير السيد حامد الصعيدى قسم المحاصيل - كلية الزراعة بطنطا - جامعه طنطا

تم إجراء هذا البحث في ثلاث مواسم 98/1997 ، 02/2001 ، 03/2002 حيث أجريت دورتي إنتخاب على الجيل الثالث لهجينين من الشعير ، وكان الهدف من الدراسة هو تحسين صفة وزن الحبوب ، عدد السنابل على النبات والتبكير في الطرد وذلك بإستخدام طريقة الإنتخاب المنسب.

1-أوضحت النتائج أن هناك إختلافات عالية المعنوية بين العائلات في الجيل الثالث حيث أشارت تقديرات معاملى الإختلاف المظهري والوراثي إلى وجود إختلافات مرضية للصفات المدروسة وهى تاريخ الطرد ، طول السنبله، عدد السنابل على النبات، عدد الحبوب فى السنبله ، وزن الألف حبة ووزن الحبوب للنبات.

2- أشارت النتائج أن درجة التوريث بمعناها الواسع عالية لصفه تاريخ الطرد ومتوسطه لصفتي عدد السنابل ومحصول الحبوب للعشيرتين المستخدمتين حيث إنخفضت درجة التوريث والتقدم الوراثي المتوقع من الجيل الثالث إلى الجيل الخامس للصفات الإنتخابية الثلاثة تحت الدراسة للعشيرتين المستخدمتين.

3- أظهرت النتائج بعد دورتين إنتخابيتين إلى التحسين الحقيقى للتبكير فى الطرد بمقدار 4.16 % فى العشيرة الأولى، 2.76 % فى العشيرة الثانية مقارنةً بمتوسط عائلات الجيل الثالث . لقد أدى التحسين إلى زيادة فى عدد السنابل بمقدار 10.88 % فى العشيرة الأولى ، 5.07 % فى العشيرة الثانية مقارنةً بمتوسط عائلات الجيل الثالث (Bulk) وكذلك زاد وزن الحبوب للنبات بمقدار 7.57 % ، 7.6 % مقارنةً بمتوسط عائلات الجيل الثالث ، 6.59 % ، 2.41 % بالمقارنة بالأب الأفضل فى العشيرتين على الترتيب وذلك بعد دورتي إنتخاب.

3- أوضحت النتائج أن أفضل عائله فى العشيرة الأولى نتيجة للإنتخاب المنسب هى العائلة رقم 66 والتي أعطت محصولاً أعلى من متوسط عائلات الجيل الثالث بمقدار 13.07 % مصحوبةً بتبكير بلغ 5.58 %، وأن العائلة رقم 92 فى العشيرة الثانية كانت الأفضل محصولياً حيث أعطت محصولاً بلغ 6.45 % أعلى من متوسط عائلات الجيل الثالث وكانت مبكرة بمقدار 5.88 % .

من نتائج هذه الدراسة يمكن القول أن طريقة الإنتخاب المنسب فعالة فى زيادة الصفات الإنتخابية الثلاث(وزن الحبوب - عدد السنابل على النبات و التبكير فى الطرد) لمحصول الشعير فى دورتين إنتخابيتين.

**Table 6: Means of ten selected families for three selection criteria in the first and second cycles of selection in the first population.**

Selection criterion	C <sub>2</sub> Fam.		Days to heading		Spike length		No. of spikes/plant		No. of kernels/spike		1000-kernel weight		Grain weight/plant	
			C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>
		Bulk sample	85.2	84.2	8.6	8.9	13.7	14.7	61.7	61.8	51.9	52.9	42.6	43.6
		Best parent	85.0	83.9	8.2	8.7	13.8	14.9	62.0	62.7	52.3	53.1	43.0	44.0
Days to heading (days)	3		81.7	81.9	10.2	6.3	14.0	13.4	65.8	60.4	51.9	53.6	46.6	41.7
	18		81.6	80.8	8.8	8.7	14.0	14.8	60.0	58.4	50.2	50.8	41.7	42.7
	22		84.3	79.7	6.5	10.0	11.6	9.9	58.4	60.7	49.8	51.4	32.8	30.6
	36		83.4	82.9	7.9	9.5	15.4	12.4	59.2	62.8	48.2	53.2	43.2	40.8
	39		84.7	79.8	8.2	8.0	12.0	13.9	60.0	65.3	52.4	52.8	37.3	42.1
	45		82.9	79.9	6.0	6.7	12.2	15.8	64.1	61.2	53.8	50.2	40.4	46.0
	66		83.9	79.5	7.7	8.4	15.5	16.7	58.1	60.0	44.6	49.3	38.0	49.3
	73		82.8	82.4	8.4	7.9	14.1	13.8	59.6	62.4	52.0	51.4	43.8	44.3
	85		82.8	78.4	7.9	9.0	10.0	15.3	64.6	60.0	51.2	51.1	32.4	46.7
93		80.9	81.7	8.4	6.5	13.2	14.0	51.2	58.8	49.9	54.2	33.8	38.8	
		Average	82.9	80.7	8.0	8.1	13.2	14.0	60.1	61.0	50.4	51.8	39.0	42.3
		LSD <sub>0.05</sub>	2.02	2.1	1.6	1.7	2.2	2.1	2.4	2.5	1.8	1.7	3.5	3.3
Number of spikes/ plant (spike)	11		84.6	84.3	9.6	9.7	15.0	15.7	61.3	65.4	50.4	51.7	45.3	45.3
	17		86.2	85.9	9.0	8.9	17.0	14.2	60.3	66.3	50.7	51.2	47.2	41.8
	33		85.4	83.0	9.4	10.8	15.2	17.2	58.4	58.4	53.7	48.6	46.3	48.6
	41		85.6	86.7	8.8	9.5	16.6	16.3	63.4	62.8	49.8	51.1	47.0	40.2
	46		83.7	87.3	10.3	9.9	15.2	17.1	56.7	57.3	52.8	48.9	40.6	47.5
	50		87.0	84.8	7.9	8.7	14.0	18.8	56.8	59.7	49.0	50.4	38.2	45.0
	63		85.4	86.7	8.4	7.8	13.1	19.8	63.7	61.4	50.2	48.8	40.8	49.1
	72		86.3	87.3	8.2	9.6	16.8	15.7	58.2	63.1	50.9	55.6	49.3	48.2
	83		86.8	85.4	7.6	8.3	17.4	11.8	61.0	65.2	50.1	50.4	44.0	38.3
87		82.0	87.6	9.8	9.8	17.7	16.4	57.2	65.4	50.4	52.3	40.3	44.0	
		Average	85.3	85.9	8.9	9.3	15.8	16.3	59.7	62.5	50.8	50.9	43.9	44.8
		L.S.D. <sub>0.05</sub>	1.8	1.4	1.4	1.2	1.9	1.7	2.0	1.8	1.9	1.6	3.6	3.7
Grain weight/plant (g)	8		87.1	83.7	9.8	9.9	11.7	16.0	65.4	68.7	53.1	57.7	40.3	41.7
	12		86.2	85.7	10.4	9.9	12.9	14.3	64.2	65.8	54.3	58.8	42.3	46.6
	21		85.0	89.4	10.7	9.4	14.3	17.2	65.0	64.8	55.4	56.6	43.6	47.7
	36		85.3	82.6	8.3	9.5	15.7	18.3	65.8	62.3	54.4	55.3	48.8	49.7
	40		87.7	89.4	9.8	10.8	13.8	17.6	69.2	65.5	55.2	58.6	45.8	41.6
	53		88.9	86.0	9.7	7.3	15.9	14.7	60.4	62.7	52.8	58.2	44.0	49.7
	60		85.3	86.3	7.8	10.3	14.7	17.0	64.3	65.6	52.9	52.4	48.9	52.9
	62		89.8	88.8	9.5	10.6	16.3	14.6	65.2	66.9	52.2	56.3	50.2	49.8
	73		86.7	83.9	10.5	11.0	13.8	14.9	64.1	64.9	50.0	54.2	40.7	46.7
97		87.0	82.2	10.5	9.3	15.9	15.4	60.4	61.8	53.7	55.9	43.4	42.6	
		Average	86.9	85.8	9.7	9.8	14.5	16.0	64.4	64.9	53.4	56.4	44.8	46.9
		LSD <sub>0.05</sub>	1.4	1.7	1.6	2.1	2.4	2.3	2.1	2.3	1.7	1.4	2.9	3.1

**Table 7: Means of ten selected families for three selection criteria in the first and the second cycles of selection in the second population.**

Selection criterion	C <sub>2</sub> .Fam.		Days to heading		Spike length		No. of spikes/plant		No. of kernels/spike		1000-kernel weight		Grain weight/plant	
			C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>1</sub>	C <sub>2</sub>
		Bulk sample best parent	84.9	83.4	8.9	9.0	13.2	13.8	61.3	61.9	50.8	51.1	41.0	43.4
			84.3	82.9	8.8	9.2	13.4	14.2	61.8	62.4	51.1	51.8	42.2	45.6
Days to heading (days)	15		81.6	80.4	8.6	8.3	14.0	12.7	59.9	61.4	54.3	54.3	46.2	40.7
	23		83.9	79.8	8.2	6.1	12.7	15.0	68.3	55.2	50.7	49.8	43.7	41.2
	35		82.7	80.5	7.7	10.7	16.3	16.0	62.9	58.4	51.1	51.4	51.3	47.9
	39		83.6	80.0	8.0	8.8	11.4	13.6	53.5	59.8	50.0	48.2	30.4	41.4
	46		85.8	79.7	9.0	9.1	11.0	11.7	56.2	68.2	49.8	55.8	30.3	42.3
	62		82.7	83.2	11.0	11.5	11.0	10.9	56.8	69.7	51.8	51.6	32.8	38.3
	71		84.3	80.7	7.5	6.8	16.9	14.8	58.4	56.0	44.8	53.3	44.9	40.9
	75		81.9	82.4	9.3	8.7	12.9	16.3	67.2	60.6	50.4	53.4	43.7	45.8
	81		81.6	85.8	6.2	10.7	14.5	14.2	54.1	59.8	46.8	48.0	37.3	38.3
	92		81.9	78.5	8.5	6.3	15.3	14.8	58.7	67.9	50.3	50.2	44.4	46.2
		Average	83.0	81.1	8.4	8.7	13.6	14.0	59.6	61.7	50.0	51.6	40.5	42.3
		LSD <sub>0.05</sub>	1.8	2.03	1.6	2.0	1.9	2.1	2.2	2.5	1.4	1.5	2.3	2.5
No. of spikes/plant (spike)	6		84.9	80.7	9.4	10.8	11.7	17.9	63.7	61.4	55.0	49.6	40.2	48.2
	9		85.3	79.4	7.8	9.5	13.6	16.9	61.7	66.0	53.6	50.2	44.3	47.1
	14		86.4	85.0	8.7	11.7	14.0	15.2	60.6	64.8	48.6	51.6	40.0	46.4
	17		86.1	80.1	11.0	11.5	14.1	14.4	58.4	58.9	53.2	54.8	43.7	45.7
	22		87.6	86.3	10.1	8.9	14.1	13.3	64.3	65.7	54.4	55.7	48.3	48.9
	30		83.7	80.1	9.3	9.5	14.7	16.6	56.1	65.2	51.6	56.1	40.9	46.3
	39		83.2	80.7	9.9	9.3	13.4	12.6	68.7	69.5	47.9	53.3	43.3	46.2
	62		86.3	79.6	10.3	8.6	12.2	12.2	65.2	69.4	55.0	56.4	41.9	45.8
	75		82.8	86.5	9.6	8.7	13.5	12.7	69.3	66.3	50.1	56.1	47.0	44.3
	84		81.7	80.6	8.9	9.5	16.7	13.2	61.0	67.8	48.6	50.2	49.4	44.1
		Average	84.8	81.9	9.5	9.8	13.8	14.5	62.9	65.5	51.8	53.4	43.9	46.3
		LSD <sub>0.05</sub>	2.0	2.1	1.5	1.8	2.0	1.8	2.1	2.2	1.7	1.8	2.1	2.2
Grain weight/plant (g)	3		84.5	89.3	8.7	10.0	15.3	12.6	70.5	72.8	50.4	57.3	46.2	48.1
	9		86.4	88.4	8.5	9.9	13.7	16.4	69.3	76.6	50.1	51.4	46.8	50.6
	22		85.0	80.0	7.6	8.4	14.2	11.8	68.9	69.7	55.3	59.0	44.9	48.4
	35		88.3	86.6	10.5	9.3	16.0	16.7	58.4	69.3	58.4	52.8	42.4	43.3
	38		86.7	85.8	11.0	8.5	13.9	14.1	71.1	70.3	53.6	55.6	50.8	42.8
	42		88.9	80.4	8.7	9.3	14.3	15.8	69.2	69.1	54.8	54.9	41.7	45.1
	63		88.4	86.3	8.4	8.7	13.6	14.7	69.4	69.7	57.9	56.1	48.3	45.4
	65		87.9	87.8	10.7	11.5	14.5	16.3	69.7	59.3	50.7	59.4	46.3	46.7
	77		86.6	83.1	10.5	13.4	10.8	16.6	68.3	73.8	56.0	56.2	39.0	50.2
	82		80.3	80.3	11.4	10.0	13.7	13.0	68.2	68.4	48.8	55.3	40.6	46.4
		Average	86.3	84.8	9.6	9.9	14.0	14.8	68.3	69.9	53.6	55.8	44.7	46.7
		LSD <sub>0.05</sub>	1.7	1.9	1.5	1.9	2.4	2.2	2.3	2.6	1.3	1.6	2.5	2.6

**Table 4: Direct and correlated gains from pedigree selection for days to heading, number of spikes/plant and grain weight/plant after the two cycles of selection in the first population as percent of F<sub>3</sub> means of bulk samples and best parent.**

Selection criterion	Item		Days to heading		Spike length		No. of spikes/plant		No. of kernels/spike		1000-kernel weight		Grain weight/plant	
			Units	%	Units	%	Units	%	Units	%	Units	%	Units	%
Days to heading (days)	C <sub>1</sub>	Bulk sample	-2.3	-	-0.6	-	-0.5	-	-1.6	-	-1.5	-	-3.6	-
		Best parent	-2.1	2.70	-0.2	6.98	-0.6	3.65	-1.9	2.59	-1.9	2.89	-4.0	8.45
	C <sub>2</sub>	Bulk sample	-3.5	-	-0.8	-	-0.7	-	-0.8	-	-1.1	-	-1.3	-
		Best parent	-3.2	4.16	-0.6	8.99	-0.9	4.76	-1.7	1.29	-1.3	2.08	-1.7	2.98
				2.47		2.44		4.35		3.06		3.63		9.30
				3.81		6.90		6.04		2.71		2.45		3.86
Number of spikes/plant (spike)	C <sub>1</sub>	Bulk sample	0.1	0.12	0.3	3.49	2.1	15.33	-2.0	-	-1.1	-	1.3	3.05
		Best parent	0.3	0.35	0.7	8.54	2.0	14.49	-2.3	-	-1.5	-	0.9	2.09
	C <sub>2</sub>	Bulk sample	1.7	2.02	0.4	4.49	1.6	10.88	0.7	1.13	-2.0	-	1.2	2.75
		Best parent	2.0	2.38	0.6	6.90	1.4	9.40	-0.2	-	-2.2	-	0.8	1.82
										0.32		4.14		
										4.38		2.89		5.16
Grain weight/plant	C <sub>1</sub>	Bulk sample	1.7	2.0	1.1	12.79	0.8	5.84	2.7	4.38	1.5	2.89	2.2	5.16

nt (g)	C <sub>1</sub>	Best parent	1.9	2.24	1.5	18.29	0.7	5.07	2.4	3.87	1.1	2.10	1.8	4.19
	C <sub>2</sub>	Bulk sample	1.6	1.90	0.9	10.11	1.3	8.84	3.1	5.02	3.5	6.62	3.3	7.57
	C <sub>2</sub>	Best parent	1.9	2.26	1.1	12.64	1.1	7.38	2.2	3.51	3.3	6.21	2.9	6.59

Table 5: Direct and correlated gains from pedigree selection for days to heading, number of spikes/plant and grain weight/ plant after the two cycles of selection in the second population as percent of F<sub>3</sub> means of bulk samples and best parent.

Selection criterion	Item		Days to heading		Spike length		No. of spikes/plant		No. of kernels/spike		1000-kernel weight		Grain weight/plant	
			Units	%	Units	%	Units	%	Units	%	Units	%	Units	%
Days to heading (days)	C <sub>1</sub>	Bulk sample	-1.9	-2.24	-0.5	-5.62	0.4	3.03	-1.7	-2.77	-0.8	-1.57	-0.5	-1.22
	C <sub>1</sub>	Best parent	-1.3	-1.54	-0.4	-4.55	0.2	1.49	-2.2	-3.56	-1.1	-2.15	-1.7	-4.03
	C <sub>2</sub>	Bulk sample	-2.3	-2.76	-0.3	-3.33	0.2	1.45	-0.2	-0.32	0.5	0.98	-1.1	-2.53
	C <sub>2</sub>	Best parent	-1.8	-2.17	-0.5	-5.43	-0.2	-1.41	-0.7	-1.12	-0.2	-0.39	-3.3	-7.24
Number of spikes/plant (spike)	C <sub>1</sub>	Bulk sample	-0.1	-0.12	0.6	6.74	0.6	4.55	1.6	2.61	1.0	1.97	2.9	7.07
	C <sub>1</sub>	Best parent	0.5	0.59	0.7	7.95	0.4	2.99	1.1	1.78	0.7	1.37	1.7	4.03
	C <sub>2</sub>	Bulk sample	-1.5	-1.80	0.8	8.89	0.7	5.07	3.6	5.82	2.3	4.50	2.9	6.68
	C <sub>2</sub>	Best parent	-1.0	-1.21	0.6	6.52	0.3	2.11	3.1	4.97	1.6	3.09	0.7	1.54
Grain weight/plant (g)	C <sub>1</sub>	Bulk sample	1.4	1.65	0.7	7.87	0.8	6.06	7.0	11.42	2.8	5.51	3.7	9.02
	C <sub>1</sub>	Best parent	2.0	2.37	0.8	9.09	0.6	4.48	6.5	10.52	2.5	4.89	2.5	5.92
	C <sub>2</sub>	Bulk sample	1.4	1.68	0.9	10.0	1.0	7.25	8.0	12.92	4.7	9.20	3.3	7.60
	C <sub>2</sub>	Best parent	1.9	2.29	0.7	7.61	0.6	4.23	7.5	12.02	4.0	7.72	1.1	2.41



Table 1: Means, mean squares, genotypic (GCV%) and phenotypic (PCV%) coefficients of variability, broad sense heritabilities and predicted genetic gain upon selection (Ga%) of the six traits studied in the F<sub>3</sub> families and their parents in the two barley populations.

Trait	Pop. 1									Pop. 2								
	Mean			Mean Squares		Statistics				Mean			Mean squares		Statistics			
	F <sub>3</sub> Families	Giza 124	IC RI	Families	Error	GC V%	PC V%	H <sup>2</sup>	G <sub>a</sub> %	F <sub>3</sub> Families	Plaisant	IC RI	Families	Error	GC V%	PC V%	H <sup>2</sup>	G <sub>a</sub> %
Days to heading	87.7	85.2	93.0	39.79**	4.86	3.89	4.15	0.88	5.33	89.6	88.2	93.0	35.97**	5.4	3.56	3.86	0.85	4.79
Spike length (cm)	8.3	7.5	8.8	4.38**	0.62	13.49	14.56	0.86	18.5	8.9	8.5	8.8	3.47**	0.81	10.58	12.08	0.77	13.57
No. of spikes/plant	11.6	10.4	12.3	7.38**	2.36	11.15	13.52	0.68	13.4	14.1	14.4	12.3	6.87**	2.92	8.14	10.73	0.57	8.92
No. of kernels / spike	58.7	56.3	62.4	170.4**	37.6	11.33	12.84	0.78	14.0	63.9	66.1	62.4	160.8**	44.2	9.76	11.46	0.73	12.9
1000-kernel weight (g)	45.9	48.1	43.3	39.52**	9.73	6.87	7.91	0.75	8.65	42.6	41.3	43.3	82.4**	12.53	11.33	12.30	0.85	15.5
Grain weight/plant (g)	40.8	38.7	42.4	593.6**	267.4	25.56	34.48	0.55	27.5	45.2	47.6	42.4	200.2**	10.04	12.76	18.07	0.50	13.8

\*, \*\* Significant at 0.05 and 0.01 level of probability, respectively.

Table 2: Genotypic ( $\sigma^2_G$ ) and phenotypic ( $\sigma^2_P$ ) variances and their coefficients of variability and heritability in broad sense ( $H^2$ ) of the three selected traits in  $F_3$  before and after two cycles of selection in both populations of barley.

Traits	Selection cycle	Pop. 1						Pop. 2					
		$\sigma^2_G$	GCV%	$\sigma^2_P$	PCV%	$H^2$	$G_a\%$	$\sigma^2_G$	GCV%	$\sigma^2_P$	PCV%	$H^2$	$G_a\%$
Days to heading	Base pop. ( $F_3$ )	11.64	3.89	13.26	4.15	0.88	5.33	10.19	3.56	11.99	3.86	0.85	4.79
	$C_1$	3.11	2.13	4.84	2.65	0.64	2.48	4.62	2.59	5.98	2.95	0.77	3.31
	$C_2$	1.42	1.48	2.97	2.14	0.48	1.49	1.81	1.66	3.22	2.21	0.56	1.81
No. of Spikes/plant	Base pop. ( $F_3$ )	1.67	11.14	2.46	13.52	0.68	13.41	1.32	8.15	2.29	10.73	0.58	9.08
	$C_1$	0.41	4.05	0.86	5.87	0.48	4.11	0.22	3.40	0.53	5.28	0.42	3.23
	$C_2$	0.19	2.67	0.43	4.02	0.44	2.58	0.12	2.39	0.30	3.78	0.40	2.20
Grain weight /plant	Base pop. ( $F_3$ )	108.73	25.56	197.86	34.48	0.55	27.65	33.27	12.76	66.74	18.07	0.50	13.18
	$C_1$	11.73	7.64	23.84	10.90	0.49	7.79	10.02	7.08	24.97	11.18	0.40	6.52
	$C_2$	5.07	4.80	10.98	7.07	0.46	4.74	4.13	4.35	11.41	7.23	0.36	3.80

Table 3: Means of days to heading, number of spikes/plant and grain weight/ plant over all selected families in the  $C_1$  and  $C_2$  of selection.

Item	Pop. 1			Pop.2		
	Days to heading	Number of spikes /plant	Grain weight /plant	Days to heading	Number of spikes /plant	Grain weight /plant
First Cycle ( $C_1$ )	82.9	15.8	44.8	83.0	13.8	44.7
$F_3$ Bulk ( $C_0$ )	85.2	13.7	42.6	84.9	13.2	41.0
Best parent	85.0	13.8	43.0	84.3	13.4	42.2
Second Cycle ( $C_2$ )	80.7	16.3	46.9	81.1	14.5	46.7
$F_3$ Bulk ( $C_0$ )	84.2	14.7	43.6	83.4	13.8	43.4
Best parent	83.9	14.9	44.0	82.9	14.2	45.6