

## EFFICIENCY OF LATE AND EARLY SELECTION FOR GRAIN YIELD UNDER DIFFERENT SELECTION CRITERIA AND DNA MARKER POLYMORPHISM IN WHEAT (*Triticum aestivum* L.)

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**Abstract:** Two cycles of early selection (F4 & F5) and one cycle of late direct selection (F5) were used for grain yield to study the efficiency of pedigree line selection for grain yield in a population (multi-cross) of wheat at the Experimental Farm of Assiut University, Egypt. Early selection was carried out under different selection criteria. The results revealed high significant differences among F3 families for all studied traits, reflecting the genetic variability among obtained families of base population. The genotypic coefficient of variation was decreased from the base population due to the increasing of homogeneity among families after selection from cycle to another. It decreased from 28.86 % in the base population to 15.82 and 3.08 % in grain yield/plant (as a selection criteria) after second cycle of early selection and late selection, respectively. The response to selection in grain yield was 25.51 % in late selection compared to 17.76 %, 2.44, 16.80 and 12.49 % with grain yield/plant, biological yield/plant, number of spikes/plant and harvest

index as selection criteria in early selection, respectively, after second cycle of selection. It is clear from these results that the late selection gave the highest values of selection response (25.51) followed by early selection (17.76 %) for grain yield/plant as selection criteria. The high positive coefficient of genotypic correlation between grain yield/plant and each of number of spike/plant, biological yield and harvest index in base population is still in the same direction after second cycle of selection under different selection criteria, consequently, these traits could be used as selection criteria next to direct selection to improve grain yield in wheat. Late direct selection matched early direct one for grain yield/plant and indirect for number of spikes/plant for only the highest family (No. 100) among selections which yielded 21.81 g for grain yield/plant. Results of EST marker indicated that the obtained lines have wide range of genetic variation as revealed by the molecular DNA marker level.

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**Key words:** late, early selection, grain yield, wheat.

## Introduction

Developing high-yielding wheat varieties has been a major factor in lessening world hunger as well as satisfying the fast growing population needs in Egypt. Usually, higher yields allow farmers to plant the same area of land and end up with more food harvested and reduce the need for more lands. The main objective of most wheat breeding programs is to develop high yielding varieties with good qualities. Pedigree selection for yielding potential in wheat and other cereal crops assumes selection in the F<sub>2</sub> generation of individual plants spaced apart to enable their evaluation. Then selection from F<sub>3</sub> to F<sub>6</sub> generation is practiced among and within families following evaluation in row plots and/or in yield trials (Poelhman and Sleper, 1995). Selection for yield from early generation based on single plant evaluation is mostly interesting and should be initiated in the F<sub>2</sub> generation (Shebeski, 1967; Sneep, 1977). Wheat breeders improve grain yield through selection by using grain yield itself as a selection criteria (Loffler and Busch, 1982). Mahdy (1988) reported that selection based on grain yield *per se* was effective in improving grain yield as well as increased spike length, number of spikes/plant and grain number/spike. The goal of early generation selection is to increase breeding efficiency through

the early identification of superior heterogeneous populations.

Kheiralla (1993) reported that direct selection for spike length, 1000 kernal weight, number of kernels /spike and number of spike/plant resulted in an increase in grain yield after two cycles of selection.

The early elimination of inferior populations and subsequent concentration of selection efforts within superior populations is assumed to result in increased efficiency. The concept of early generation testing in self-pollinating species as a means to identify superior bulk hybrid populations was first described by Immer (1941) and has been used in various crops with varying success. Numerous variants of early generation selection have been developed and employed. Harlan *et al.* (1940) used F<sub>2</sub> bulks to identify superior barley (*Hordeum vulgare* L.) populations. The evaluation in all generations gave similar yield gains and therefore the F<sub>2</sub> families selected from the F<sub>1</sub> generation would be the most advantageous for selection (Cregan and Busch, 1977; Singh *et al.*, 1990; Singh *et al.*, 1998; Martin and Geraldi, 2002). Otherwise, Fowler and Heyne (1955) reported poor predictive results from bulk hybrid tests of hard red winter wheat (*Triticum aestivum* L.). Selection for quantitative traits with low heritability must be delayed until

later generations (Frederikson and Kronsted, 1985). Furthermore, late pedigree selection started in the F5 for one cycle increased grain yield/plant in wheat by 13.06 % compared to 7.6 % from the bulk sample after three cycles of selection started early in the F3 (Ismail *et al.*, 1996).

Several molecular markers were used to study the genetic variability and relationship among wheat germplasm (Zhang *et al.*, 2000; Cao *et al.*, 2000; Taghian and Abo-Elwafa, 2003). ESTs “Expressed Sequence Tags” are derived from coding DNA, which generally has a high degree of sequence conservation, they are more likely to be transportable across pedigree and species boundaries than are markers derived from non-expressed sequences (Lazo *et al.* 2004). Therefore, ESTs can be used in studying genetic variability, QTL analysis, map-based cloning and synteny analysis among related species.

The objective of the current study was to estimate the efficiency of pedigree line selection in late and early generations for grain yield using different selection criteria. Furthermore, EST marker was used to detect the genetic variability under the molecular level among some F5 families compared to their parents.

## **Materials and Methods**

This study was carried out during 2001/02, 2002/03, 2003/04 and 2004/05 seasons on clay-loam soil at Assiut University experimental Farm, Egypt.

### **Genetic materials**

The genetic materials used in this study were the F2, F3, F4 and F5 segregating generations of one multiple cross population of five wheat parents (Fig. 1). The five parents were as follows; P1; Tokowe, P2; Giza 164, P3; Sonora 64, P4; Giza 155, P5; Sakha 69.

### **Field procedures**

In 2001/02 season; the F2 seeds were grown in non-replicated trail in rows, 4 m long, 30 cm apart and 5 cm between seeds to get the F3 seeds.

In 2002/03 season; (Base population) part of seed for 186 F3-families of the studied population were evaluated in a Randomized Complete Block Design with three replications. The experimental unit was single row, 4 m long, 30 cm apart and 5 cm between hills. One plant per/hill was left after complete emergence. The following traits were measured on 10 random guarded plants for each plot; 1- plant height, cm; 2- main spike length, cm; 3- number of spikes/plant; 4- biological yield/plant, g; 5- grain yield/plant, g; 6- harvest index, % and seed index (100 kernel weight), g.



The F3-family means provided the base of pedigree line selection, the 37 superior families (selection intensity 20%) were selected for each of grain yield/plant, biological yield, number of spikes/plant and harvest index as early selection criteria. The superior plant/family was saved to initiate the first cycle of pedigree line selection. The choice of previous four traits was done based on their high variability (G.C.V. and P.C.V.) as well as high genotypic correlation between grain yield/plant and each of the other three traits.

In 2003/04 season; selection was repeated using all procedures of those in 2002/03 season. Means of selections were ranked to initiate the second cycle of pedigree line selection for each selection criteria.

In 2004/05 season; 10 superior families for each selection criteria (second cycle) were generated in the same way of the first cycle of selection.

All families (186) were grown in each season for two purposes; *First*, to calculate the generation mean for base (F3), first cycle (F4) and second cycle (F5) of selection, and *Second*, to initiate late selection for grain yield/plant only in F5 as a selection criteria as follow: other part of F3 seeds was grown in bulk across the F3 and F4, respectively. Then, seeds of F5 families were grown in same way for pedigree line selection. The comparison among

all early and late selections was done over the obtained data.

### **Statistical analysis**

The analysis of variance through base population and the two cycles of selection for each selection criteria was performed according to Gomez and Gomez (1984). Genotypic correlation between grain yield/plant and each of other studied traits in base and all selection criteria of both cycles of selection was done using the method of Walker 1960. Moreover, direct and indirect response to selection over the generation mean with all selection criteria were calculated for first and second cycles of selection.

The phenotypic and genotypic coefficient of variability were calculated according to Burton (1952).

### **Fingerprinting using EST marker**

Four parents (Sonora 69, Giza 164, Sakha 69 and Tokowe) and fifteen F5 lines were chosen randomly to conduct fingerprinting and screening the polymorphisms among studied lines under molecular level. Genomic DNA was extracted and purified from fresh leaf samples using Dneasy<sup>plant</sup> Minikit (QIAGEN). Purified DNA was quantified using Agarose mini gel electrophoresis.

On the basis of sequence of wheat EST (P04G09860, actin binding protein, putative), PCR

primer pair was designed and used for screening the polymorphism. The primers sequences were as follow:

For:5'

ACCTTCTCAACGGGTTGATTC 3'

Rev:5' GCTTCTTTATCCTCGGCTTCT 3'

PCR was carried out under the following conditions; one initial strand separation cycle at 94 °C for 4 min followed by 32 cycles including a denaturation step at 94 °C for 30 sec, an annealing step at 52 °C for 30 sec and polymerization step at 72 °C for 1 min, with final extension step at 72 °C for 5 min. Reactions were performed in total volume of 25 µl. DNAs of PCR products were digested with two restriction enzymes *RsaI* and *ApaI*.

Digested DNAs were loaded on 2 % Agarose gel.

## Results and discussions

### Base population

One hundred eighty six F<sub>3</sub> families (base population) of multiple cross were grown in 2002/2003 season on clay-loam soil at Assiut Experimental Farm. They were evaluated for their performance. The results in Table 1 revealed that there were highly significant differences among the F<sub>3</sub>-families for plant height, spike length, number of spike/plant, biological yield/plant, grain yield/plant, harvest index and 100 kernel weight, reflecting the genetic differences among obtained F<sub>3</sub>-families.

**Table(1):** Analysis of variance for studied traits in F<sub>3</sub>-families (base population) of wheat.

S.O.V.	d.f.	Plant height	Spike length	No. of spikes/plant	Biological yield/plant	Grain yield/plant	Harvest index	Seed index
Rep	2	18.25	0.64	5.54	186.5	25.80	4.70	0.64
Families	185	543.94**	3.27**	23.35**	140.91**	193.98**	32.01**	3.27**
Error	370	30.56	0.30	4.70	102.55	17.45	5.02	0.30

The averages of 115.00 cm, 9.71 cm, 9.55, 50.95 g, 15.58 g, 30.59 % and 4.71 g were exerted for previous characters, respectively (Table 2). Also, high phenotypic (PCV) and genotypic (GCV) coefficients of variation were recorded for all studied traits. The highest values of

P.C.V. and G.C.V. were obtained for number of spikes/plant (19.17 & 17.14), biological yield/plant (23.21 & 22.35), grain yield/plant (30.25 & 28.86) and harvest index (18.57 & 17.05%), respectively (Table 2).



Highly significant differences among the F3 families and sufficient of variability were obtained for spike length, number of spikes/plant, 100 kernel weight and grain yield/plant in wheat (Kheiralla, 1993).

Moreover, high genotypic correlation coefficients were found

between grain yield/plant and each of number of spikes/plant (0.747), biological yield/plant (0.867) and harvest index (0.611) in base population (Table 3). Therefore, these four traits could be used for pedigree line selection as selection criteria in early generation such (F3-families).

**Table(3):** Genotypic correlation between grain yield/plant and each of other studied traits in base population, both cycles of selection under different selection criteria and late selection.

Selection Criteria		Plant height	Spike length	No. of spikes/plant	Biological yield/plant	Harvest index	Seed index		
Base population		0.184	-0.196	0.747	0.867	0.611	-0.196		
Early selection	Biological yield/plant	C1	-0.120	-0.020	0.673	0.682	0.772	0.151	
		C2	-0.149	-0.574	0.385	0.297	0.503	0.688	
	No. of spikes/plant	C1	-0.552	-0.136	0.792	0.673	0.761	0.262	
		C2	-0.578	0.364	0.651	0.840	0.405	-0.579	
	Harvest index	C1	-0.453	-0.212	0.861	0.767	0.852	0.144	
		C2	0.726	-0.338	0.642	0.932	0.490	0.201	
	Grain yield/plant	C1	-0.286	-0.263	0.813	0.692	0.603	0.215	
		C2	0.365	-0.218	0.713	0.897	0.362	-0.093	
	Grain yield/plant (LS*)		C2	0.761	-0.259	0.842	0.637	0.266	-0.362

\*(LS), Selection in late generation (F5)

### **Selection criteria**

#### **Means, P.C.V and G.C.V.**

The means, P.C.V. and G.C.V. for all studied traits in both cycles (2003/04 and 2004/05 seasons) of selection under different selection criteria were presented in Table 2.

The results of genotypic coefficient of variability (Table 2) indicated that the direct and indirect selection had the most deleterious effect on the genetic variability of the selection criteria. For example, the g.c.v. of grain yield/plant decreased from 28.86% in the base population to



15.82 and 3.08% for this trait (as a selection criteria), after the second cycle of early and late selection, respectively. This means that the late selection could reduce the genetic variability among selections more than early selection after two cycles of selection for grain yield/plant. The little variability in late selection was also revealed as insignificant differences among those selections for grain yield/plant (Table 5). Moreover, the genetic variability was decreased after the second cycle of selection in other criteria and correlated traits of

different selection criteria (Table 2). Consequently, small genetic variance and little selection progress could be expected after the second cycle for early selection. This result is clear with late selection for grain yield/plant. Similarly, it is clear that phenotypic coefficient of variation was decreased from the base population due to the increasing of homogeneity among families after selection from cycle to another. Similar results were obtained by Mahdy et al. (1996) and Kheiralla, (1993).

**Table(4):** Direct and correlated response of selection for studied traits of both selection cycles under different selection criteria.

Criteria		Plant height	Spike length	No. of spikes/plant	Biological yield/plant	Grain yield/plant	Harvest index	Seed index
Biological yield/plant	C1	0.81	0.61	0.28	<b>3.52</b>	3.23	-0.83	3.17
	C2	2.23	-2.25	-1.62	<b>2.49</b>	2.44	-0.24	-6.98
No. of spikes/plant	C1	-1.89	-2.50	<b>4.09</b>	5.44	9.18	3.44	1.77
	C2	-0.17	1.39	<b>-0.42</b>	12.77	16.80	2.63	-11.46
Harvest index	C1	-1.80	-1.89	1.49	1.80	4.52	<b>1.81</b>	1.77
	C2	-4.96	-5.28	-1.73	-10.65	12.49	<b>14.99</b>	-5.32
Grain yield/plant	C1	-0.36	-0.09	2.70	6.30	<b>9.71</b>	3.72	3.77
	C2	-2.25	-2.25	-3.15	4.86	<b>17.76</b>	10.67	-6.48
Grain yield/plant (LS)*	C2	-3.85	-1.24	14.21	25.81	<b>25.51</b>	9.44	-9.64

\*(LS), Selection in late generation (F5)

The means of grain yield/plant for selections after second cycle were increased compared to the generation mean even under early selection of different criteria or with late selection for grain yield/plant.

The late selection subjected to be the best and gave the highest mean of 18.35 g compared with 17.22, 14.98, 17.08 and 16.45 g for grain yield/plant with selection criteria of grain yield/plant, biological

yield/plant, number of spikes/plant and harvest index in early selection (Table 2).

### **Response of selection and genotypic correlation**

Response to selection is the mean deviation for offspring of selected parent from the population mean (Falconer, 1989). The results exhibited to give higher values for response of selection in grain yield 25.51 % in late selection of grain yield/plant compared to 17.76, 2.44, 16.80 and 12.49% for grain yield/plant, biological yield/plant, number of spikes/plant and harvest index as selection criteria in early selection, respectively, after second cycle of selection (Table 4). It is clear from this results that the late selection gave the highest response (25.51 %) of selection followed by early selection (17.76%) for grain yield/plant as a selection criteria. Thus, we can conclude that the direct selection in late generation is preferable way to improve grain yield in wheat based on our results. Also, Ismail et al. 1996, found that the late pedigree single trait selection was more effective than early selection in wheat. Moreover, Kheiralla (1993) concluded that selection based on yield *per se* was the most effective in increasing grain yield itself in wheat. The predicted direct response in grain yield reached to 20.81 % as a percent of the better parent (Kheiralla, 1993). The correlated

response of selection ranged from negative to positive values as shown in Table 4. For example, the correlated responses were (-9.64 and -6.48) for seed index (100 kernel weight) in late and early selection of grain yield/plant after second cycle of selection, respectively, (Table 4). This result expressed the less values for seed index of 5.44 and 5.63 g in late and early selection under grain yield/plant as a selection criteria compared to 6.01 g of generation mean after second cycle of selection (Table 2). Also, the genotypic correlation coefficients were negative between grain yield/plant and seed index in the same subjects. These results revealed that the high genotypes in grain yield possess less seed index. These results are confirmed with those were obtained by Mahdy, 1996.

On other hand, the high positive coefficients of genotypic correlation between grain yield/plant and each of number of spike/plant (0.747), biological yield (0.867) and harvest index (0.611) in base population still in the same direction after second cycle of selection under different selection criteria (Table 3). This means that these traits could be used as selection criteria next to direct selection to improve the grain yield/plant as shown and relative to direct and indirect response of selection in Table 4.

**Table(5):** The mean of grain yield/plant for the 10-superior families after second cycle of selection under different selection criteria.

Selection Criteria	Biological yield/plant		No. of spikes/plant		Harvest index		Grain yield/plant		Grain yield/plant (LS)*	
1	(37)	19.20	(100)	21.81	(180)	19.81	(100)	21.81	(100)	21.81
2	(111)	16.99	(161)	21.37	(121)	19.02	(37)	19.20	(180)	19.81
3	(151)	16.81	(130)	20.24	(160)	18.52	(160)	18.52	(121)	19.02
4	(131)	16.64	(181)	18.78	(110)	17.86	(111)	16.99	(20)	18.67
5	(122)	15.71	(109)	18.33	(151)	16.81	(151)	16.81	(118)	18.30
6	(56)	13.89	(108)	15.91	(152)	16.31	(131)	16.64	(5)	17.41
7	(105)	13.74	(66)	15.34	(122)	15.71	(108)	15.91	(90)	17.31
8	(178)	13.57	(50)	15.30	(66)	15.34	(122)	15.71	(86)	17.28
9	(159)	13.23	(105)	13.74	(173)	14.18	(66)	15.34	(20)	18.67
10	(142)	9.98	(142)	9.98	(184)	10.94	(50)	15.30	(118)	18.30
Mean		14.98		17.08		16.45		17.22		18.35
LSD 0.05		2.29		1.98		4.18		4.09		-
LSD 0.01		3.14		2.71		5.73		5.60		-

\*(LS), Selection in late generation (F5)

### Means of superior selections;

Mean of grain yield/plant for the 10-superior families after second cycle of selection under different selection criteria are presented in Table 5. As it is mentioned before, the mean of direct selection over all selections under late selection ranked in first order (18.35 g) followed by early direct selection (17.22 g) for grain yield/plant. The number of spikes/plant is ranking in third order (17.08 g). Only the highest family (No. 100) among all selections yielded 21.81 g for grain yield/plant matched late direct selection with each of early direct one for grain yield/plant and indirect

for number of spikes/plant. Also, the two families nos. 121 and 180, which yielded 19.02 and 19.81 g, respectively, shared in late direct selection for grain yield/plant and early indirect one for harvest index. Both of the families (nos. 121 and 180) appear to be high in grain yield as mentioned before. On the other hand, four families (nos. 66, 122, 151, and 160) combined in early direct selection for grain yield/plant and harvest index. The early direct selection of grain yield/plant matched each of indirect one of biological yield/plant in five families (nos. 37, 111, 122, 131 and 151) and number of spikes/plant in four families (nos. 50, 66, 100 and

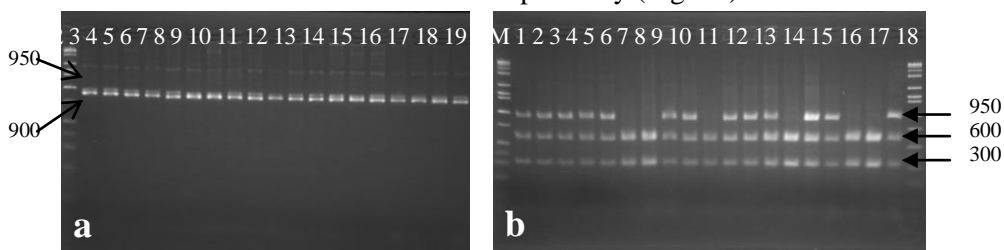
108). Finally, some selected families combined in three selection criteria in grain yield/plant after second cycle of selection such as no. 66 which was in early direct selection for grain yield/plant and indirect for number of spikes/plant and harvest index. Also, families nos. 122 and 151 included in early direct selection of grain yield/plant and each of indirect for biological yield/plant and harvest index. Moreover, family no 100 found to be in the same trend (combined in three selection criteria) as mentioned before.

These results confirmed the high positive genetic correlations between grain yield/plant and each of biological yield/plant, number of spikes/plant and harvest index (Table 3). It is clear from these results that the latter two traits could be used as indirect selection, which

gave response of selection of 16.80 and 12.49% for grain yield/plant, respectively, and ranked after direct late and early selection of grain yield in wheat. These results are on line with those were obtained by Taghian et al. 1998, who concluded that selection within the multi-parental crosses was more effective than that in bi-parental crosses.

### Detection of genetic variability by using EST marker

Double bands with sizes of 950 and 900 bp, could be amplified for the four parents and nine lines, while six lines showed single band with 900 bp size (Fig. 2a). Then, the PCR products have been digested with two restriction enzymes (*RsaI* and *ApaI*). However, the restriction enzymes could cut the smaller band of 900 bp into two fragments with the sizes of 600 and 300 bp, respectively (Fig. 2b).



**Fig.(2a):**Electrophoresis of PCR products amplified by EST (P04G09860) marker on an agarose gel (2% agarose), where M is wide range ladder DNA marker, lanes 1-4 are four parents (Sonora 69, Giza 164, Sakha 69 and Tokowe) and fifteen F5 lines were chosen randomly.

**Fig.(2b):**PCR products were digested with two restriction enzymes (*RsaI* and *ApaI*). Arrows indicate the sizes of bands in bp.

In total, after digestion three clear bands could be seen in the four parents Sonora 69, Giza 164, Sakha 69 and Tokowe as well as in nine lines of 5, 8, 9, 11, 12, 13, 15, 16 and 19. However, the other six lines no. 6, 7, 10, 14, 17 and 18 showed only two clear bands with sizes of 600 and 300 bp. These results clearly indicate that the polymorphic bands appeared only among the segregating lines while parents showed monomorphic bands. These findings prove that the studied lines have wide range of genetic variation even under molecular DNA marker level. Consequently, the EST analysis could be used to detect the genetic variability among studied F5 lines compared to their respective parents. ESTs were used widely to detect DNA polymorphism in different kind of plants such as Rice and Brassica (Sato and Nishio 2003, Inoue and Nishio 2004 and Shirasawa *et al.* 2004).

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## كفاءة الانتخاب المتأخر و المبكر لمحصول الحبوب تحت صفات انتخابية مختلفة ، و الاختلافات الوراثية باستخدام مثبرات الـ DNA فى القمح (*Triticum aestivum* L.)

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تم استخدام عشيرة أساسية (F3) و دورتين (F4 & F5) من الانتخاب المبكر و كذلك دورة واحدة من الانتخاب المتأخر و ذلك لدراسة كفاءة الانتخاب فى محصول الحبوب فى عشيرة (متعددة الهجن) من القمح فى المزرعة البحثية لجامعة أسيوط - مصر.

تم تنفيذ الانتخاب المبكر باستخدام صفات إنتخابية مختلفة ، بينما تم إجراء الانتخاب المتأخر مباشرة لمحصول الحبوب فى الجيل الخامس فقط . و يمكن تلخيص النتائج فيما يلى :-

أ. أظهرت النتائج وجود إختلافات معنوية عالية بين عائلات الجيل الثالث لجميع الصفات المدروسة مما يعكس التباين الوراثى بين تلك العائلات فى العشيرة الأساسية.

ب. إنخفض معامل الاختلاف الوراثى عما كان عليه فى العشيرة الأساسية بسبب زيادة الاصاله الوراثية بين العائلات بعد الانتخاب من دورة إنتخابية إلى اخرى ، حيث إنخفض من 28.86 % فى العشيرة الأساسية الى 15.82 و 3.08 % فى محصول النبات ( كصفة إنتخابية ) بعد دورتين من الانتخاب المبكر و المتأخر عل الترتيب .

ج. قيم الإستجابة للإنتخاب فى صفة محصول الحبوب كانت 34.61 % فى الانتخاب المتأخر مقارنة بـ 17.76 ، 2.44 ، 16.80 ، 12.49 % مع كل من الصفات الإنتخابية الاتية محصول الحبوب / نبات ، الوزن البيولوجى / نبات ، عدد السنابل / نبات و معامل الحصاد فى الانتخاب المبكر على الترتيب و ذلك بعد دورتين من الانتخاب . و يتضح من تلك النتائج أن الانتخاب المتأخر أعطى أعلى قيم للإستجابة للإنتخاب (25.51%) و تبعه الانتخاب المبكر ( 17.76 %) فى محصول حبوب النبات مباشرة كصفات إنتخابية .

د. معامل الارتباط الموجب بين محصول الحبوب / نبات و كل من عدد السنابل / نبات و الوزن البيولوجى و معامل الحصاد فى العشيرة الأساسية إستمر فى نفس الإتجاه بعد دورتين من الانتخاب تحت جميع الصفات الإنتخابية المختلفة ، و بالتالى يمكن استخدام هذه الصفات كصفات إنتخابية بجانب الانتخاب المباشر لتحسين محصول الحبوب فى القمح .

ه. هناك فقط أعلى عائلة محصولا ( رقم 100 ) بين المنتخبات و التى أعطت 2.81 جم محصول حبوب / نبات إشتراك فى الانتخاب المتأخر لمحصول الحبوب / نبات مباشرة و كل من الانتخاب المباشر المبكر لمحصول الحبوب / نبات و الانتخاب غير المباشر لصفة عدد السنابل / نبات .

و. أظهرت نتائج تحليل واسمات الـ EST أن السلالات المتحصل عليها فى الجيل الخامس بينها مدى واسع من التباين الوراثى على المستوى الجزيئى .