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Comparison of Bread Wheat Lines Performance Resulting From Early and Late Selection in the F6 and F7 Generation for Grain Yield and Its Attributes

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ESTIMATION of genetic variability parameters, correlation, and regression analyses are important statistical tools which can help breeders to Identify and select for desirable genotypes. The present study was carried out during the two successive seasons, i.e., 2022/2023 and 2023/2024, at Fac. Agric. Farm, Assiut University, Egypt. The material used comprised 10 bread wheat lines, resulting from early selection, and 10 lines resulting from late selection in addition to their two parents and bulk sample, evaluated in the F_6 and F_7 generations. The aim of this study was to evaluate some bread wheat lines resulting from early and late pedigree line selection for grain yield and select lines that perform high yield. Moreover, to determine the significant models of the components affecting grain yield via stepwise regression analysis. The relative performance for each genotype was accounted and phenotypic and genotypic coefficients of variation, heritability in the broad sense and correlation coefficients between grain yield and yield attributes were estimated. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits in both early and late generations. Magnitude of broad sense heritability was high (above 60%) in all 10 lines early and late selection under both F_6 and F_7 generations and ranged from 65.09% in 10 F_6 early lines selection for number of spikes/plant to 97.30% in 10 F_7 early lines selection for 100-grain weight and 72.80% in 10 F_7 late lines selection for grain yield/plant to 98.60% in 10 F_6 late lines selection for plant height. A positive correlation was found between grain yield/plant and each of the spike length, biological yield/plant, weight of spikes/ plant, 100- grain weight and harvest index in all 10 lines early and late selection under both F_6 and F_7 generations. Negative correlations of grain yield were observed with plant height, number of spike/ plant and number of spikelets/ spikes in all 10 lines early and late selection under both F_6 and F_7 generations. Stepwise regression analysis showed that, weight of spikes/plant, biological yield and harvest index as important traits affecting grain yield in wheat. These characters have to be ranked the first in any breeding program to improve wheat grain yield.

Keywords: Bread wheat, Heritability, Correlation, Stepwise regression.

Introduction

Wheat is one of the most important and commonly farmed cereal crops in Egypt and around the world, and its importance in ensuring long-term food security is generally recognized. In Egypt, the average cultivated area in the last ten years ranged from 2.8 to 3.6 million feddans. In 2022/23 growing season, about 3.6 million feddans were cultivated by wheat and yielded about 9.7 million tons **(FAO, 2023).** Wheat consumption in the local area increases year after year as the population grows. Wheat breeders' goal is to increase crop productivity in order to close the gap between national primary production and consumption. According to the statistics, local production is insufficient to meet annual requirements; thus, increasing wheat productivity is the most important way to close the production-consumption gap **(Gharib *et al.* 2016).** Various genetic and environmental factors greatly influence grain yield. As a result, breeding programs may be misdirected and hindered by focusing solely on yield selection. Understanding genetic variability and the connection between morpho-agronomic traits and grain yield is crucial for effectively selecting high-yielding genotypes **(Patpour *et al.* 2020).** Analyzing correlations between yield and its components is an essential technique for understanding how environmental factors affect productivity and yield potential. Understanding the type and strength of correlation coefficients helps breeders recognize selection criteria that can improve various traits in addition to yield. By

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calculating correlation coefficients among different wheat traits, it becomes possible to identify the most effective combinations of characteristics for achieving greater returns per unit area (**Abdurezake, *et al*. 2024**). Considering that the correlations between yield and its contributing characters is a basic and foremost endeavor to find out guidelines for plant selection. Stepwise multiple linear regression aims to create a regression equation that includes the variables that account for the greatest share of the overall yield variation. **Abd El-Mohsen and Abd El-Shafi, 2014** reported that, according to stepwise multiple linear regression analysis, four traits, i. e., the number of grains/spike, the number of tillers/plant, harvest index and the 1000-grain weight and possessed R^2 value of 97. 29%, eflecting the important role for these traits in improving the grain yield/plant., and **Mohamed (2005)** discovered that the spike length, number of spikes/m^2, and the weight of 1000 grains were significant contributors to the overall variation in wheat plant grain yield. The aim of this study was to evaluate performance of some bread wheat lines resulting from early and late pedigree line selection for grain yield and select lines that perform high yield. Moreover, to determine the significant models of the components affecting grain yield via stepwise regression analysis. The relative performance for each genotype was accounted and phenotypic and genotypic coefficients of variation, heritability in the broad sense and correlation coefficients between grain yield and yield attributes were estimated.

Materials and Methods

Plant Material and Experimental Design

The present study was carried out during the two successive seasons, i.e., 2022/2023 and 2023/2024, at Fac. Agric. Farm, Assiut University, Egypt. The material used comprised 10 bread wheat lines, resulting from early selection, and 10 lines resulting from late selection in addition to their two parents and bulk sample, evaluated in the F_6 and F_7 generations. These lines were produced from only two parents, Misr2 and Sakha94. The parents along with their pedigree and origin are shown in **Table 1**. The lines along with their parents and bulk sample were grown in a randomized complete block design (RCBD) with three replications. In both seasons, sowing was made during the last week of December. Each genotype was grown in two rows, each row 2 meters long and 20 cm apart. Plants within rows were 5 cm distant. All recommended agricultural practices were applied from planting to harvest in two seasons.

Table 1. Pedigree and origin of the two parental genotypes used in the present.

Parent No.	Name	Pedigree	Origin
P_1	Misr2	SKAUZ/BAV 92	Egypt
P_2	Sakha94	Opts / Rayon // KAVZ	Egypt

Studied traits

Data were recorded on five randomly plants for the following characters: 1- Plant height (PH), cm. 2- Spike length (SL), cm. 3- Number of spikes/plant (NSP). 4- Number of spikelets/spike (NSES). 5- Weight of spikes/plant (WSP), g. 6- Biological yield/plant (BYP), g. 7- grain yield/plant (GYP), g. 8- 100-Grain weight (100GW), g. 9- Harvest index % (HI).

Statistical and genetic analyses

1- The analysis of variance was done as outlined by **Steel** and **Torrie (1980)**. The correlation coefficients between each pair of traits were calculated in accordance with **Snedecor** and **Cochran (1981)**. The SPSS-PC program of **Nie *et al.* (1975)** was used to estimate stepwise regression in the respective generations and coefficient of determination (R^2) on the obtained data to determine the significance of the independent variables influencing grain yield.

The phenotypic (σ^2p) and genotypic (σ^2g) variance were calculated from ANOVA table according to the following formula:

$\sigma^2 g = M_2 - M_1/r$ and $\sigma^2 p = \sigma^2 g + \sigma^2 e$

2- Heritability in broad sense (H^2) was estimated as the ratio of genotypic ($\sigma^2 g$) to the phenotypic ($\sigma^2 p$) variance according to **Walker (1960).**

Heritability: $H^2_{b.s} = \sigma^2 g / \sigma^2 p \times 100$

3- The phenotypic and coefficients of variability were estimated using the formula developed by **Burton (1952)** as:

a) Phenotypic coefficient of variability (P.C.V) $= \frac{\sqrt{\sigma 2p}}{\bar{x}} \times 100$

b) Genotypic coefficient of variability (G.C.V) $= \frac{\sqrt{\sigma 2G}}{\bar{x}} \times 100.$

Where; σ^2p and σ^2g are the phenotypic and genotypic variances of the lines' mean, respectively, and $\overline{X}$ is the lines mean for a given trait.

4- The phenotypic (r_{pij}) correlation was calculated among the studied traits as outlined by **Walker (1960).**

$rp_{ij} = Cov.\ p_{ij} / \sigma^2_{pi}\ x\ \sigma^2_{pj}$

Where;

Cov.pij: the phenotypic covariance between *i* and *j* traits,

σ^2_{pi} and σ^2_{pj} are the phenotypic variance of the trait *i* and *j*, respectively.

5- Mean comparisons were calculated using Revised Least Significant Difference (RLSD) as described by **El Rawi** and **Khalafalla (1980)** as follows: $R.L.S.D._{\alpha} = t_{\alpha} \sqrt{\frac{2MSe}{r}}$

Results and Discussion:

Mean performance and estimation of genetic variability parameters for grain yield and yield components characters of wheat early and late selected lines:

The analyses of variance of both all 10 lines of both early and late in F_6 and F_7 for yield and its components are presented in Tables 2 and 3. These analyses were done twice, i.e., without parents and bulk sample (only selected Lines) and with their parents and bulk sample (all Genotypes) for all previous cases. The results of statistical analysis of variance presented showed a considerable variation among all wheat genotypes or early and late selected lines regarding the studied traits in both seasons. Similar results have been reported by **Ashmawy (2010) and Mostafa (2015).**

The mean performance for genotypes and 10 lines (early and late selection), variance types, heritability estimates, genotypic (g.c.v.%) and phenotypic (p.c.v.%) coefficients of variability for grain yield/plant and its components in F_6 and F_7 generation are presented in **Tables 4, 5, 6, 7 and 8.**

Table 2. Mean squares for genotypes and 10 early and late selected lines for grain yield/plant and its components in F_6 generation.

	S.O.V.	d.f.	PH	SL	NSP	NSES	BYP	WSP	GYP	100GW	HI
	F_6 Early										
Genotypes	**Reps.**	2	36.10	0.39	0.07	0.38	28.20	8.04	5.59	0.03	19.64
	Genotypes	12	182.60**	3.46**	5.21**	5.49**	239.58**	60.68**	54.20**	0.22**	35.12**
	Error	24	5.57	0.14	0.29	0.31	30.96	10.24	7.14	0.06	9.14
Lines	**Reps.**	2	38.69	0.33	0.12	0.52	48.06	10.23	6.24	0.04	13.32
	Lines	9	227.44**	4.27**	5.66**	6.24**	157.94**	48.43**	40.80**	0.25**	38.24**
	Error	18	6.76	0.15	0.29	0.32	36.98	12.77	8.76	0.05	10.53
	F_6 Late										
Genotypes	**Reps.**	2	2.29	0.07	0.63	0.51	13.11	16.31	2.95	0.01	0.50
	Genotypes	12	64.14**	1.70**	2.67**	3.74**	62.72**	31.30**	23.42**	0.21**	22.51**
	Error	24	5.76	0.22	0.17	0.14	13.81	4.22	2.68	0.02	3.31
Lines	**Reps.**	2	5.91	0.03	0.42	0.24	12.72	20.99	2.04	0.03	0.14
	Lines	9	84.80**	2.07**	1.33**	1.79**	58.30**	23.71**	19.03**	0.27**	13.54**
	Error	18	3.47	0.25	0.15	0.13	16.09	4.02	2.57	0.01	3.52

*, **: Significant at 0.05 and 0.01 levels of probability; respectively.

Table 3. Mean squares for genotypes and 10 early and late selected lines for grain yield/plant and its components in F_7 generation.

	S.O.V.	d.f.	PH	SL	NSP	NSES	BYP	WSP	GYP	100GW	HI
	F_7 Early										
Genotypes	Reps.	2	7.96	0.32	0.01	0.01	38.12	9.94	15.61	0.03	33.36
	Genotypes	12	83.28**	2.13**	5.18**	5.19**	70.72**	53.94**	54.27**	0.41**	77.15**
	Error	24	6.42	0.26	0.47	0.39	10.24	5.06	6.40	0.02	10.03
Lines	Reps.	2	10.54	0.58	0.04	0.03	35.38	13.38	15.98	0.01	30.06
	Lines	9	106.11**	2.30**	5.93**	6.18**	67.82**	39.92**	40.49**	0.46**	46.65**
	Error	18	7.46	0.26	0.59	0.51	12.52	5.65	8.05	0.02	12.16
	F_7 Late										
Genotypes	Reps.	2	3.58	0.03	0.09	0.03	75.94	16.68	3.08	0.01	6.45
	Genotypes	12	19.33**	2.35**	4.56**	4.83**	70.62**	26.11**	22.45**	0.23**	40.19**
	Error	24	3.46	0.25	0.29	0.25	14.71	2.91	3.10	0.02	6.58
Lines	Reps.	2	5.70	0.07	0.22	0.10	112.28	23.28	7.07	0.03	6.47
	Lines	9	24.73**	2.10**	4.24**	4.83**	74.86**	10.54**	12.60**	0.27**	29.79**
	Error	18	3.58	0.29	0.28	0.22	13.20	2.35	3.43	0.01	7.22

*, **: Significant at 0.05 and 0.01 levels of probability; respectively.

The analysis of variance indicated that plant height varied significantly in different early and late wheat lines in F_6 and F_7 generation. The average of plant height **(Table 4)** for 10 F_6 and F_7 early selected lines surpassed significantly their parents and unselected bulk sample by 5.07, 4.33 and 3.35% in F_6 and 1.66, 0.11 and 3.67% in F_7 generation, respectively. On the other hand, plant height for late selected lines average responses reduced significantly compared to the unselected bulk sample in F_6 and F_7 generation exceeded by 1.38% in F_6 and 1.18 in F_7 generation. For an average in spike length in 10 F_6 early and late lines surpassed significantly their parents and unselected bulk sample by 4.89, 2.23 and 7.17 % in 10 F_6 early line generation and 4.11, 2.55 and 4.59 %, respectively, in 10 F_6 late line generation. Moreover, the parent Sakha94 in **Table 4**, surpassed significantly the line average in F_7 early and late generation by 3.88 and 0.71% in both generations, respectively. For a number of spikes/plant and number of spikelets/spike **(Table 5),** the parents Sakha94, Misr2 and unselected bulk sample surpassed significantly the lines average in early and late selection in both generations, except the average of number of spikes/plant and number of spikelets/spike in 10 F_6 early lines surpassed significantly on the unselected bulk sample by 20.58 and 15.99% respectively. The average of biological yield/plant for 10 early and late selected lines in F_6 and F_7 generations **(Table 6)** surpassed significantly their parents and unselected bulk sample by 30.24, 21.79 and 32.75%, in 10 F_6 early and 0.08, 2.09 and 18.32% in 10 F_7 early to 12.14, 7.15 and 9.96% in 10 F_6 late and 12.98, 6.89 and 5.41% respectively, in 10 F_7 late. In the same way the average of weight of spikes/plant surpassed significantly their parents and unselected bulk sample by 27.30, 20.63 and 35.47% and 29.45, 21.28 and 29.68%, to 18.96, 27.01 and 10.00% and 20.00, 32.94 and 15.05%, respectively, in 10 early and late selected lines in F6 and F7 generations, respectively. In **Table 7,** the mean of grain yield/plant over the 10 early and late selected lines in F_6 and F_7 generations ranged from 23.75 and 24.74 to 23.82 and 23.92% in both F_6 and F_7 generations, respectively. The average of grain yield/plant for 10 F_6 and F_7 early and late lines surpassed significantly their parents and unselected bulk sample by 26.06, 25.86 and 55.73% in 10 F_6 early and 33.72, 31.42 and 40.40% in 10 F_7 early to 13.53, 32.62 and 6.19% in 10 F_6 late and 23.93, 27.26 and 15.50 in 10 F_7 late, respectively. For 100-grain weight, the parents Sakha94, Misr2 and unselected bulk sample surpassed significantly the lines average in 10 early and late selected lines in F_6 and F_7 generations, except the 10 F_7 late lines surpassed significantly on the parents and unselected bulk sample by 7.12, 4.11 and 1.26 respectively **(Table 7)**. The mean of harvest index over the 10 early and late lines **(Table 8)** ranged from 36.25 and 40.92 to 37.55 and 39.89 in both F_6 and F_7 generations, respectively. The average of harvest index for 10 F_7 early and late lines surpassed significantly their parents and unselected bulk sample by 32.51, 27.71 and 17.51% to 10.40, 24.77 and 9.58%, respectively. But, the parent Misr2 surpassed the lines average in early F_6 generation by 3.78%. On the other hand, the unselected bulk sample exceeded the lines average in late F_6 generation by 2.82%

Genetic variability

Coefficients of variation of different traits (genetic variability (σ^2g), phenotypic variability (σ^2p), phenotypic coefficient of variability% (PCV), genotypic coefficient of variability% (GCV), and heritability in broad sense are presented in **Tables 4, 5, 6,7** and **8.** Generally, the value of PCV was generally higher than that of GCV for grain yield/plant and all studied traits, in both early and late generations, which is in line with the findings of **El-Degwy (2013), Bayisa *et al.* (2020),** and **Hassani *et al.* (2022).** The genotypic (gcv) and phenotypic (pcv) coefficients of variation for grain yield/plant were decreased from 13.76 and 15.52% for 10 F_6 early lines to 13.29 and 14.84% for 10 F_7 early lines selection after one generation **(Table 7).** The same trend, the genotypic (gcv) and phenotypic (pcv) coefficients of variation decreased from 9.82 and 10.53% for 10 F_6 late lines to 7.30 and 8.55% for 10 F_7 late lines selection after one generation. The results agree with **Abd El-Kader 2011, Nukasani *et al.*, 2013** and **Hussain *et al.*, 2014.** The same way, all other attributes followed the same direction where decreased the genotypic (gcv) and phenotypic (pcv) coefficients of variation for all attributes in both early and late generations. Except number of spikes/plant, the values of the genotypic (gcv) coefficients were increased from 14.73 % for 10 F_6 early lines to 15.07 for 10 F_7 early lines and the values of the genotypic (gcv) and phenotypic (pcv) coefficients were increased from 8.03 and 8.53% for 10 F_6 late lines to 14.06 and 14.53% for 10 F_7 late lines selection after one generation **(Table 5).** The same way the values of the genotypic (gcv) and phenotypic (pcv) coefficients were increased in the F_6 and F_7 late generation in biological yield/plant and harvest index from 5.92 and 6.95% to 7.51 and 8.28% and 4.86 and 6.95% to 6.87 and 7.89 under both generations, respectively **(Tables 6** and **8).**

Heritability in broad senses are presented in **Tables 4, 5, 6, 7** and **8**. In general, the values of broad sense heritability for all studied traits were high (above 60%) in all 10 early and late selected lines in F_6 and F_7 generations and ranged from 65.09% in 10 F_6 early lines selection for number of spikes/plant to 97.30% 10 F_7 early lines selection for 100 - grain weight and 72.80% in 10 F_7 late lines selection for grain yield/plant to 98.60% in 10 F_6 late lines selection for plant height. In general, heritability values in broad sense were high for all studied traits, revealing that most of the phenotypic variability was due to genetic effects. These results are consistent with **El-Morshidy *et al.*, (2010)** and **Mahdy *et al.*, (2012).**

Table 4. Mean performance for genotypes and lines, variance types, heritability estimates, genotypic (g.c.v.%) and phenotypic (p.c.v.%) coefficients of variability for plant height (cm) and spike length (cm), of 10 early and late selected lines in F_6 and F_7 generations.

Plant height (cm)							Spike length (cm)					
Earle line. No	**10 Early F6**		**10 Early F7**	**Late line. No**	**10 Late F6**	**10 Late F7**	**Earle line. No**	**10 Early F6**	**10 Early F7**	**Late line. No**	**10 Late F6**	**10 Late F7**
1	122.60		112.40	**130**	106.20	103.33	**1**	**11.6**	12.53	**130**	13.40	14.67
131	97.80		96.93	**131**	99.53	99.60	**131**	**14.13**	13.27	**131**	14.27	13.93
140	114.87		105.33	**140**	113.27	107.67	**140**	**14.87**	14.47	**140**	14.33	14.60
141	115.67		113.20	**250**	95.00	98.67	**141**	**12.8**	12.67	**250**	14.27	14.13
250	96.47		99.60	**321**	108.00	105.87	**250**	**13.87**	14.13	**321**	11.80	12.07
321	119.20		114.20	**373**	107.67	104.60	**321**	**11.53**	12.33	**373**	14.47	13.87
373	113.60		110.93	**380**	106.80	103.13	**373**	**14.13**	12.87	**380**	13.67	14.13
440	109.93		109.00	**431**	109.00	106.47	**440**	**14.27**	14.67	**431**	12.80	13.07
455	108.33		105.67	**440**	108.13	101.93	**455**	**12.13**	12.40	**440**	13.93	14.53
461	104.00		102.67	**500**	110.40	103.27	**461**	**13.6**	13.53	**500**	13.80	14.73
Bulk	106.67		103.20	**Bulk**	107.87	104.67	**Bulk**	**12.4**	12.13	**Bulk**	13.07	12.73
P1	104.93		105.33	**P1**	106.60	104.93	**P1**	**12.67**	13.00	**P1**	13.13	12.53
P2	105.67		106.87	**P2**	106.07	103.93	**P2**	**13**	13.80	**P2**	13.33	14.07
σ^2_E	2.25		2.48	σ^2_E	1.15	**1.19**	σ^2_E	0.05	**0.09**	σ^2_E	0.083	**0.097**
σ^2_G	73.56		32.88	σ^2_G	81.33	**7.05**	σ^2_G	1.37	**0.68**	σ^2_G	0.60	**0.603**
σ^2_P	75.81		35.36	σ^2_P	82.48	**8.24**	σ^2_P	1.42	**0.77**	σ^2_P	0.69	**0.70**
GCV %	7.78		5.36	**GCV %**	8.47	**2.56**	**GCV %**	8.8	**6.20**	**GCV %**	5.67	**5.56**
PCV%	7.90		5.56	**PCV%**	8.53	**2.77**	**PCV%**	8.97	**6.60**	**PCV%**	6.07	**5.9**
H%	97.03		92.98	**H%**	98.60	**85.56**	**H%**	96.47	**88.31**	**H%**	86.95	**86.14**
Average	110.25		106.99	**Average**	106.40	**103.45**	**Average**	13.29	**13.29**	**Average**	13.67	**13.97**
Genotype. R.L.S.D	**0.05**	**3.54**	**3.95**	**0.05**	**3.74**	**2.23**	**0.05**	**0.58**	**0.84**	**0.05**	**0.76**	**0.81**
	0.01	**4.70**	**5.27**	**0.01**	**4.99**	**3.93**	**0.01**	**0.78**	**1.07**	**0.01**	**0.99**	**1.06**
Lines. R.L.S.D	**0.05**	**3.95**	**4.32**	**0.05**	**2.95**	**3.13**	**0.05**	**0.59**	**0.85**	**0.05**	**0.83**	**0.89**
	0.01	**5.30**	**5.62**	**0.01**	**3.83**	**4.29**	**0.01**	**0.80**	**1.15**	**0.01**	**1.13**	**1.22**

Table 5. Mean performance for genotypes and lines, variance types, heritability estimates, genotypic (g.c.v.%) and phenotypic (p.c.v.%) coefficients of variability for number of spikes/plant and number of spikelets/spike, of 10 early and late selected lines in F_6 and F_7 generations.

Number of spikes/plant						Number of spikelets/spike					
Earle line. No	**10 Early F6**	**10 Early F7**	**Late line. No**	**10 Late F6**	**10 Late F7**	**Earle line. No**	**10 Early F6**	**10 Early F7**	**Late line. No**	**10 Late F6**	**10 Late F7**
1	10.13	9.47	**130**	7.53	7.60	**1**	10.47	9.80	**130**	7.87	8.07
131	8.00	8.00	**131**	6.87	7.87	**131**	8.13	8.27	**131**	7.13	8.20
140	8.60	7.73	**140**	8.33	7.27	**140**	9.07	8.00	**140**	8.73	7.87
141	11.20	9.87	**250**	6.53	7.00	**141**	11.47	10.60	**250**	6.73	7.40
250	7.07	7.07	**321**	8.67	10.40	**250**	7.27	7.47	**321**	9.40	11.07
321	10.20	10.87	**373**	8.40	9.87	**321**	10.80	11.33	**373**	8.60	10.53
373	8.53	8.00	**380**	8.00	7.13	**373**	8.87	8.67	**380**	8.33	7.80
440	7.67	7.27	**431**	7.87	9.07	**440**	8.00	8.00	**431**	8.07	9.67
455	8.80	9.47	**440**	7.80	7.73	**455**	9.13	9.93	**440**	8.27	8.20
461	10.60	10.73	**500**	7.73	7.73	**461**	11.07	11.27	**500**	8.47	8.00
Bulk	7.53	9.53	**Bulk**	9.47	8.33	**Bulk**	8.13	10.13	**Bulk**	9.87	8.87
P1	10.27	10.53	**P1**	9.67	10.53	**P1**	10.60	10.67	**P1**	10.67	10.87
P2	9.33	9.33	**P2**	9.27	9.07	**P2**	9.87	9.93	**P2**	9.93	9.60
σ^2_E	0.97	0.19	σ^2_E	**0.05**	**0.09**	σ^2_E	0.106	**0.17**	σ^2_E	0.043	**0.073**
σ^2_G	1.79	1.78	σ^2_G	**0.39**	**1.32**	σ^2_G	2.18	**1.89**	σ^2_G	0.55	**1.53**
σ^2_P	2.76	1.97	σ^2_P	**0.44**	**1.41**	σ^2_P	2.29	**2.06**	σ^2_P	0.59	**1.60**
GCV %	14.73	15.07	**GCV %**	**8.03**	**14.06**	**GCV %**	15.66	**14.73**	**GCV %**	9.08	**14.25**
PCV%	18.26	15.85	**PCV%**	**8.53**	**14.53**	**PCV%**	16.05	**15.38**	**PCV%**	9.41	**14.57**
H%	65.09	90.35	**H%**	**88.6**	**93.6**	**H%**	95.19	**91.75**	**H%**	93.2	**95.44**
Average	9.08	8.85	**Average**	**7.77**	**8.17**	**Average**	9.43	**9.33**	**Average**	8.16	**8.68**
Genotype. R.L.S.D 0.05	**0.84**	**1.07**	**0.05**	**0.64**	**0.84**	**0.05**	**0.87**	**0.97**	**0.05**	**0.56**	**0.78**
Genotype. R.L.S.D 0.01	**1.1**	**1.43**	**0.01**	**0.86**	**1.12**	**0.01**	**1.15**	**1.30**	**0.01**	**0.74**	**1.04**
Lines. R.L.S.D 0.05	**0.85**	**1.2**	**0.05**	**0.64**	**0.84**	**0.05**	**0.90**	**1.13**	**0.05**	**0.57**	**0.74**
Lines. R.L.S.D 0.01	**1.1**	**1.58**	**0.01**	**0.88**	**1.09**	**0.01**	**1.16**	**1.47**	**0.01**	**0.74**	**0.98**

Table 6. Mean performance for genotypes and lines, variance types, heritability estimates, genotypic (g.c.v.%) and phenotypic (p.c.v.%) coefficients of variability for biological yield/plant and weight of spikes/plant, of 10 early and late selected lines in F_6 and F_7 generations.

Biological yield/plant							Weight of spikes/plant					
Earle line. No	10 Early F6		10 Early F7	Late line. No	10 Late F6	10 Late F7	Earle line. No	10 Early F6	10 Early F7	Late line. No	10 Late F6	10 Late F7
1	50.48		49.05	130	62.78	67.34	1	20.87	20.37	130	28.12	28.05
131	65.33		61.61	131	70.78	58.76	131	32.55	31.91	131	32.84	29.52
140	67.09		56.38	140	66.88	58.32	140	32.73	28.46	140	32.33	29.19
141	77.79		62.72	250	65.38	69.21	141	33.91	31.37	250	32.55	32.24
250	63.81		62.58	321	57.70	53.40	250	31.40	32.91	321	26.56	26.43
321	59.94		60.44	373	66.01	61.14	321	26.44	30.52	373	32.17	28.74
373	71.00		61.49	380	60.33	55.77	373	32.51	30.88	380	27.14	28.08
440	70.40		61.96	431	55.98	57.31	440	28.86	31.03	431	25.46	31.97
455	63.12		57.82	440	63.57	63.24	455	26.52	27.27	440	28.27	31.31
461	64.35		66.54	500	63.95	58.63	461	28.92	31.58	500	28.18	30.23
Bulk	49.21		50.76	Bulk	57.60	57.21	Bulk	21.71	22.64	Bulk	26.69	25.71
P1	50.16		60.01	P1	56.48	53.38	P1	23.15	22.68	P1	24.68	24.65
P2	53.64		58.83	P2	59.11	56.42	P2	24.43	24.43	P2	23.10	22.25
σ^2_E	12.32		4.17	σ^2_E	5.36	4.4	σ^2_E	4.25	1.88	σ^2_E	1.34	0.78
σ^2_G	40.32		18.43	σ^2_G	14.07	20.55	σ^2_G	11.88	11.42	σ^2_G	6.56	2.73
σ^2_P	52.64		22.60	σ^2_P	19.43	24.95	σ^2_P	16.13	13.30	σ^2_P	7.90	3.51
GCV %	9.71		7.15	GCV %	5.92	7.51	GCV %	11.69	11.51	GCV %	8.72	5.64
PCV%	11.10		7.91	PCV%	6.95	8.28	PCV%	13.63	12.42	PCV%	9.57	6.30
H%	76.60		81.55	H%	74.41	82.36	H%	73.65	85.86	H%	83.03	77.70
Average	65.33		60.06	Average	63.34	60.31	Average	29.47	29.36	Average	29.36	29.58
Genotype. R.L.S.D	0.05	9.08	5.22	0.05	6.46	6.67	0.05	5.22	3.50	0.05	3.35	2.78
	0.01	11.26	6.77	0.01	8.83	9.11	0.01	6.77	4.68	0.01	4.34	3.86
Lines. R.L.S.D	0.05	10.67	6.20	0.05	7.53	6.38	0.05	6.71	3.94	0.05	3.52	2.70
	0.01	15	8.03	0.01	10.70	8.24	0.01	8.81	5.40	0.01	4.55	3.78

Table 7. Mean performance for genotypes and lines, variance types, heritability estimates, genotypic (g.c.v.%) and phenotypic (p.c.v.%) coefficients of variability for grain yield/plant and 100 - grain weight, of 10 selected early and late lines in F_6 and F_7 generations.

Grain yield/plant						100 - Grain weight					
Earle line. No	10 Early F6	10 Early F7	Late line. No	10 Late F6	10 Late F7	Earle line. No	10 Early F6	10 Early F7	Late line. No	10 Late F6	10 Late F7
1	15.49	15.21	130	22.14	21.61	1	4.03	3.88	130	4.21	4.42
131	26.51	28.01	131	26.96	23.90	131	4.94	4.91	131	4.81	5.02
140	27.08	23.96	140	25.67	23.96	140	4.80	4.81	140	4.75	4.96
141	27.43	26.97	250	26.93	29.09	141	4.40	4.16	250	5.01	5.21
250	25.69	26.54	321	21.83	21.92	250	5.05	5.18	321	4.46	4.67
321	21.75	25.61	373	26.92	23.66	321	4.77	4.74	373	4.53	4.74
373	26.43	26.58	380	21.90	23.19	373	4.62	4.39	380	4.11	4.32
440	22.18	26.44	431	20.49	24.81	440	4.65	4.34	431	4.78	4.99
455	21.69	22.78	440	22.24	23.60	455	4.58	4.35	440	4.95	5.15
461	23.22	25.29	500	23.15	23.44	461	4.53	4.32	500	4.46	4.66
Bulk	15.25	17.62		22.43	20.71	Bulk	4.98	4.18	Bulk	4.78	4.75
P1	18.84	18.50	P1	20.98	19.30	P1	4.86	4.56	P1	4.68	4.49
P2	18.87	18.87	P2	17.96	18.01	P2	4.69	4.92	P2	4.62	4.62
σ^2_E	2.92	2.68	σ^2_E	0.85	1.14	σ^2_E	0.018	0.006	σ^2_E	0.003	0.003
σ^2_G	10.68	10.81	σ^2_G	5.48	3.05	σ^2_G	0.067	0.14	σ^2_G	0.086	0.086
σ^2_P	13.6	13.49	σ^2_P	6.3	4.19	σ^2_P	0.085	0.15	σ^2_P	0.089	0.08
GCV %	13.76	13.29	GCV %	9.82	7.30	GCV %	5.80	8.47	GCV %	6.36	6.13
PCV%	15.52	14.84	PCV%	10.53	8.55	PCV%	6.48	8.58	PCV%	6.47	6.23
H%	78.53	80.13	H%	86.98	72.80	H%	80.04	97.3	H%	96.63	96.67
Average	23.75	24.74	Average	23.82	23.92	Average	4.46	4.51	Average	4.61	4.81
Genotype. R.L.S.D 0.05	4.36	4.13	0.05	2.67	2.87	0.05	0.45	0.22	0.05	0.23	0.22
Genotype. R.L.S.D 0.01	5.65	5.35	0.01	3.46	3.72	0.01	0.64	0.29	0.01	0.30	0.29
Lines. R.L.S.D 0.05	5.19	4.98	0.05	2.66	3.48	0.05	0.39	0.22	0.05	0.16	0.16
Lines. R.L.S.D 0.01	7.30	6.44	0.01	3.64	4.94	0.01	0.55	0.29	0.01	0.20	0.20

Table 8. Mean performance for genotypes and lines, variance types, heritability estimates, genotypic (g.c.v.%) and phenotypic (p.c.v.%) coefficients of variability for harvest index of 10 selected lines in F_6 and F_7 generations.

Harvest index						
Earle line. No		10 Early F6	10 Early F7	Late line. No	10 Late F6	10 Late F7
1		30.44	31.33	130	35.25	32.24
131		40.89	45.48	131	37.97	40.56
140		40.22	42.03	140	38.44	41.29
141		35.01	42.96	250	41.18	42.15
250		40.11	42.35	321	37.75	41.07
321		36.30	42.25	373	40.76	38.56
373		37.34	43.09	380	36.21	41.54
440		31.37	42.39	431	36.55	43.46
455		34.77	39.29	440	34.97	37.77
461		36.05	37.99	500	36.37	40.27
Bulk		31.28	34.82	Bulk	38.61	36.40
P1		37.62	30.88	P1	37.07	36.13
P2		35.39	32.04	P2	30.38	31.97
σ^2_E		3.51	4.05	σ^2_E	1.17	2.40
σ^2_G		9.23	11.49	σ^2_G	3.34	7.52
σ^2_P		12.74	15.54	σ^2_P	4.51	9.92
GCV %		8.38	8.28	GCV %	4.86	6.87
PCV%		9.84	9.63	PCV%	5.65	7.89
H%		72.45	73.94	H%	74.05	75.80
Average		36.25	40.92	Average	37.55	39.89
Genotype. R.L.S.D	0.05	5.60	5.17	0.05	2.97	4.18
	0.01	7.67	6.70	0.01	3.85	5.42
Lines. R.L.S.D	0.05	6.09	6.55	0.05	3.52	4.71
	0.01	8.66	9.34	0.01	5.00	6.62

Phenotypic correlation for the studied traits of 10 early and late selected lines in both F_6 and F_7 generations.

The coefficients of phenotypic correlation between each pair for studied traits of all 10 early and late selected lines in F_6 and F_7 generations for grain yield/plant are presented in **Tables 9** and **10**. Grain yield/plant showed positive and high phenotypic correlateion with each of spike length (0.69, 0.31, 0.74 and 0.11), biological yield/plant (0.81, 0.87, 0.86 and 0.48), weight of spikes/ plant (0.99, 0.97, 0.98 and 0.76), 100- grain weight (0.64, 0.57, 0.41 and 0.68) and harvest index (0.76, 0.93, 0.80 and 0.51) in all 10 early and late selected lines in F_6 and F_7 generations (**Tables 9** and **10**). **Aycicek** and **Yildirim, (2006)** and **Khan *et al.* (2015)** and **Milkessa (2022)**, reported similar results between grain yield, spikes number and number of grains per spike. Negative correlateion of grain yield were observed with Plant height (-0.45, -0.33, -0.48 and -0.49), number of spike/ plant (-0.24, -0.25, -0.42 and -0.35) number of spikelets/ spikes (-0.26, -0.20, -0.43 and -0.36) in all 10 early and late selected lines in F_6 and F_7 generations, respectively (**Tables 9** and **10**). These results are consistent with **Kilic** and **Yagbasanlar (2010).** In addition to grain yield/plant, other characteristics also showed various trends of associations among themselves. Among those characteristics, biological yield/plant was highly positively correlated with weight of spikes/plant (0.85, 0.93, 0.91 and 0.46) in all 10 early and late selected lines in F_6 and F_7 generations, respectively and harvest index in 10 F_7 early lines selection, and highly negatively correlated with plant height (-0.57) and harvest index (-0.51) in 10 F_7 late lines selection. Meanwhile, weight of spikes/ plant was highly positively correlated with 100 - grain weight (0.59 and 0.61) and harvest index (0.69 and 0.71) in 10 F_6 and F_7 early lines selection respectively. In 10 F_6 late lines selection weight of spikes/ plant was highly positively correlated with, spike length

(0.80) and harvest index (0.71) and 100 - grain weight (0.74) in 10 F_7 late lines selection, and negative correlateion with, plant height, number of spike/ plant and number of spikelets/ spikes in all 10 early and late selected lines in F_6 and F_7 generations, respectively. In the end these obtained results revealed that the most effective yield components in grain yield of wheat would be both of biological yield/plant, weight of spikes/ plant and harvest index, whereas spike length and 100-grain weight had a minor effect. It is concluded that those traits can be used for wheat grain yield improvement.

Table 9. Phenotypic correlation coefficients for all studied traits of 10 early selected lines in F_6 (above diagonal) and F_7 (below diagonal).

	PH	SL	NSP	NSES	BYP	WSP	GYP	100GW	HI
PH	1	-0.51	0.59	0.61	-0.19	-0.44	-0.45	-0.69	-0.58
SL	-0.46	1	-0.59	-0.59	0.54	0.74	0.69	0.55	0.54
NSP	0.43	-0.70	1	0.996	-0.05	-0.25	-0.24	-0.67	-0.38
NSES	0.48	-0.69	0.99	1	-0.07	-0.27	-0.26	-0.65	-0.38
BYP	-0.33	0.26	0.03	0.08	1	0.85	0.81	0.28	0.24
WSP	-0.39	0.36	-0.21	-0.16	0.93	1	0.99	0.59	0.69
GYP	-0.33	0.31	-0.25	-0.20	0.87	0.97	1	0.64	0.76
100GW	-0.63	0.43	-0.46	-0.50	0.35	0.61	0.57	1	0.81
HI	-0.29	0.29	-0.39	-0.36	0.64	0.85	0.93	0.65	1

Table 10. Phenotypic correlation coefficients for all studied traits of 10 late selected lines in F_6 (above diagonal) and F_7 (below diagonal).

	PH	SL	NSP	NSES	BYP	WSP	GYP	100GW	HI
PH	1	-0.24	0.84	0.84	-0.35	-0.43	-0.48	-0.34	-0.45
SL	-0.30	1	-0.42	-0.49	0.83	0.80	0.74	0.31	0.37
NSP	0.46	-0.80	1	0.97	-0.45	-0.40	-0.39	-0.42	-0.16
NSES	0.51	-0.81	0.99	1	-0.45	-0.45	-0.43	-0.43	-0.24
BYP	-0.57	0.55	-0.46	-0.48	1	0.91	0.86	0.32	0.39
WSP	-0.36	0.30	-0.38	-0.41	0.46	1	0.98	0.43	0.71
GYP	-0.49	0.11	-0.35	-0.36	0.48	0.76	1	0.41	0.80
100GW	-0.29	0.00	-0.09	-0.12	0.30	0.74	0.68	1	0.36
HI	0.10	-0.42	0.09	0.10	-0.51	0.32	0.51	0.37	1

Stepwise regression analysis

The correlation is proposing only the relationships degree among traits. While, the stepwise regression is used to estimate the value of a quantitative variable regarding its relationship with one or some other quantitative variables. This relationship is possible to predict other changes using one variable. Stepwise regression was used to remove the effects of ineffective or low impact on yield traits in the regression model. Different models were exerted using stepwise regression analysis through F_6 and F_7 generations of bread wheat as presented in **Table 11.** The coefficients of determination (R^2) and regression equations of stepwise regression analysis for all 10 early and late selected lines in F_6 and F_7 generations for grain yield/plant are presented in **Table 11**. The stepwise regression analysis revealed four fitted models for 10 F_6 early lines selection, including one (WSP), two (WSP and HI) and three (WSP, HI and BYP), four (WSP, HI, BYP and PH) as independent traits in model 1, model 2, model 3 and model 4, respectively. The contributions of these traits to predict the grain yield/plant were in major role from weight of spikes/plant and harvest index model 2 where R^2 accounted of 0.991 with an increase of 1.12% over model 1 which gave R^2 of 0.980 and including only weight of spikes/plant Moreover, there is an insignificant and almost non-existent difference (0.70%) between model 2 and model 3, which the latter contains three characteristics (weight of spikes/plant, harvest index and biological yield/plant) and possessed R^2 of 0.998. There is an insignificant and almost non-existent difference (0.1%) between model 3 and model 4, which the latter contains four characteristics (weight of spikes/plant, harvest index, biological yield/plant and plant height) and possessed R^2 of 0.999. Consequently, the plant height doesn't make sense over both biological yield/plant and harvest index for predicted grain yield/plant. In the same way four efficient models were released from 10 F_7 early lines selection. Model 1 (WSP), model 2 (WSP and HI) and model 3 (WSP, HI and BYP) model 4 (HI and BYP). The best of these models contributing to the grain yield/plant is model 4 (HI and BYP) which gave R^2 of 0.999 with an increase of over model 1(5.26%), (1.01) over model 2 and equal to Model 3. Reflecting the important role of the harvest index and biological yield/plant in improving the grain yield/plant. In the same way four efficient models were released from 10 F_6 late lines selection. Model 1 (WSP), model 2 (WSP and HI) and model 3 (WSP, HI and BYP) model 4 (HI and BYP). The best of these models contributing to the grain yield/plant is model 4, reflecting the important role of the harvest index and biological yield/plant in improving the grain yield/plant. But in 10 F_7 late lines selection one efficient model was released Model 1 (WSP) which accounted R^2 of 0.573, reflicting the important role of the weight of spikes/plant in improving the grain yield/plant these results are consistent with those reported **Fouad (2018).**

Table 11. Stepwise regression analysis in F_6 and F_7 of early and late pedigree selection for grain yield/plant.

Generation	Mod. no.	Independent trait(s)	R^2	Regression equation
(F6) Early lines	1	WSP	0.980	Ŷ = -3.026 + 0.908 WSP
	2	WSP + HI	0.991	Ŷ = -5.778 + 0.814 WSP +0.152 HI
	3	WSP + HI+ BYP	0.998	Ŷ = -15.308 + 0.307 WSP +0.445 HI + 0.213 BYP
	4	WSP + HI+ BYP + PH	0.999	Ŷ = -18.142 + 0.321 WSP +0.462 HI + 0.208 BYP + 0.19 PH
(F7) Early lines	1	WSP	0.949	Ŷ = - 4.338+ 0.981 WSP
	2	WSP + HI	0.989	Ŷ = -9.149 + 0.657 WSP + 0.352 HI
	3	WSP + HI+ BYP	0.999	Ŷ = -20.524 + 0.0.32 WSP + 0.577 HI + 0.3453 BYP
	4	HI + BYP	0.999	Ŷ = -21.059 + 0.589 HI + 0.361 BYP
(F6) Late lines	1	WSP	0.962	Ŷ = -1.975 + 0.879 WSP
	2	WSP + HI	0.983	Ŷ = -7.353+ 0.747 WSP + 0.246 H + 0.235 HI
	3	WSP + HI+ BYP	0.999	Ŷ = -23.412 + 0.32 WSP + 0.631 HI + 0.357 BYP
	4	HI + BYP	0.999	Ŷ = -24.107 + 0.648 HI +0.372 BYP
(F7) Late lines	1	WSP	0.573	Ŷ = -5.72 + 0.828 WSP

Actual and expected grain yield/plant for all models

Tables 12 and 13 shows the actual and expected grain yield/plant of all inference regression models for all 10 early and late selected lines in F_6 and F_7 generations. Furthermore, the expected grain yield/plant for all 10 early and late selected lines in F_6 and F_7 generations was calculated using their regression equations for all models. As well as, both actual and expected grain yield/plant of stepwise regression models for all 10 early and late selected lines in F_6 and F_7 generations were compared for their homogeneity using ***t-test*** and respective relationship using simple correlation coefficient (**r**), as presented in **Tables 12 and 13**. It is remarkable result that the powerful Models released from stepwise regression were that possessed traits with WSP, BYP and TI, exerted values equal to one and values close to unity for each of r, as well as insignificant value (less than unity) of ***t-test.*** These models are number **3** for WSP, BYP and TI in all 10 early and late selected lines in F_6 and F_7 generations and model number **4** for TI and BYP in 10 F_7 early and 10 F_6 late selections, respectively. The previous estimates (**r, and R^2**) for these models indicating that completely variance of grain yield/plant can be accounted by the linear combination of (WSP, BYP with TI) and (TI with BYP). Consequently, the scores of expected grain yield can estimated using their stepwise regression equations, model number 3 in 10 F_6 early selections (Ŷ = -15.308 + 0.307 WSP +0.445 HI + 0.213 BYP), model number 3 in 10 F_6 late selections (Ŷ = -23.412 + 0.32 WSP + 0.631 HI + 0.357 BYP) and model number 3 in 10 F_7 early selections (Ŷ = -20.524 + 0.0.32 WSP + 0.577 HI + 0.3453 BYP) and model number **4** in 10 F_7 early selections (Ŷ = -21.059 + 0.589 HI + 0.361 BYP) and model number **4** in 10 F_6 late selections (Ŷ = -24.107 + 0.648 HI +0.372 BYP). Accordingly, it is recommended to use stepwise regression by wheat breeders due to their efficient contributions in yield and equivalent to other models which have two traits, and also to save time and costs in selection programs.

Table 12. Actual and expected (F6) 10 lines selected early and Late) grain yield for all obtained models of stepwise regression analysis, correlation coefficient and t test.

F_6 Early						F_6 Late					
Lines. No	Actual GYP	Expected GYP				Lines.No	Actual GYP	Expected GYP			
		Mod.1	Mod.2	Mod.3	Mod.4			Mod.1	Mod.2	Mod.3	Mod.4
1	15.49	15.93	15.84	15.40	36.42	130	22.14	22.75	22.33	30.24	22.09
131	26.51	26.53	26.93	26.79	43.37	131	26.96	26.89	26.52	36.33	26.83
140	27.08	26.69	26.98	26.93	46.73	140	25.67	26.45	26.26	35.06	25.68
243	27.43	27.77	27.15	27.25	47.07	250	26.93	26.64	27.10	36.33	26.90
250	25.69	25.48	25.88	25.77	42.07	321	21.83	21.37	21.78	29.51	21.82
321	21.75	20.98	21.26	21.73	42.23	373	26.92	26.30	26.70	36.17	26.86
373	26.43	26.50	26.36	26.41	45.90	380	21.90	21.88	21.83	29.65	21.80
440	22.18	23.18	22.49	22.51	41.15	431	20.49	20.40	20.66	27.79	20.40
455	21.69	21.05	21.09	21.75	40.15	440	22.24	22.88	22.37	30.40	22.20
490	23.22	23.24	23.25	23.32	40.94	500	23.15	22.79	22.64	31.38	23.25
R		0.990	0.995	0.999	0.914	R		0.980	0.991	0.999	1.000
T		0.47	0.42	0.24	0.00	*T*		0.47	0.48	0.00	0.04

Table 13. Actual and expected (F_7) 10 lines selected early and Late) grain yield for all obtained models of stepwise regression analysis, correlation coefficient and t test.

F_7 Early						F_7 Late		
Lines. No	Actual GYP	Expected GYP				Lines.No	Actual GYP	Expected GYP
		Mod.1	Mod.2	Mod.3	Mod.4			Mod.1
1	15.21	15.65	15.27	21.00	15.10	130	21.61	17.50
131	28.01	26.97	27.83	37.19	27.97	131	23.90	18.72
140	23.96	23.58	24.34	32.29	24.05	140	23.96	18.45
243	26.97	26.43	26.58	35.94	26.88	250	29.09	20.97
250	26.54	27.95	27.38	36.04	26.48	321	21.92	16.16
321	25.61	25.60	25.77	34.47	25.64	373	23.66	18.08
373	26.58	25.96	26.31	35.43	26.52	380	23.19	17.53
440	26.44	26.11	26.16	35.24	26.28	431	24.81	20.75
455	22.78	22.41	22.59	30.82	22.96	440	23.60	20.21
490	25.29	26.64	24.97	34.46	25.34	500	23.44	19.31
R		0.974	0.994	0.998	1.000	R		0.757
T		0.48	0.44	0.00	0.29	*T*		0.00

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مقارنة أداء سلالات قمح الخبز الناتجة من الإنتخاب المبكر والمتأخر في الجيل السادس والسابع لمحصول الحبوب ومكوناته

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يعتبر تقد ير مكونات التباين الوراثى وتحليل معامل الإرتباط والإنحدار أدوات إحصائية هامة فى مساعدة مربى النبات فى تحديد وإختيار التراكيب الوراثية المرغوبة. أجريت هذه الدراسة خلال موسمى 2023/2022 و 2024/2023. فى مزرعة كلية الزراعة، جامعة أسيوط، مصر. كانت المواد المستخدمة عبارة عن عشر سلالات من قمح الخبز الناتجة من الإنتخاب المبكر والمتأخر فى الجيلين السادس والسابع بالإضافة الى الأباء (مصر2 وسخا94) وعينة البلك. كان الهدف من هذه الدراسة هو تقييم أداء سلالات قمح الخبز الناتجة من الإنتخاب المبكر والمتأخر لمحصول الحبوب وإختيار أفضل السلالات التى حققت أعلى إنتاجية بالإضافة الى تحديد أفضل الموديلات التى تؤثر على محصول الحبوب عن طريق تحليل معامل الإنحدار التدريجى . تم حساب الأداء النسبى لكل السلالات وتقدير معاملات التباين الظاهرى (الكلى) والوراثى وكذلك تم تقدير درجة التوريث بالمعنى العريض (الواسع) ومعامل الأرتباط بين محصول الحبوب والصفات الأخرى. كان معامل التباين الظاهرى (PCV) أعلى من التباين الوراثى (GCV) لجميع الصفات فى كل من الأجيال المبكرة والمتأخرة، وكانت درجة التوريث بالمعنى الواسع عالية (أكبر من 60%) لجميع السلالات العشرة المختارة المبكرة والمتأخرة فى الجيل السادس والسابع، وتراوح من 65.09% فى العشر سلالات المبكرة للجيل السادس لعدد السنابل /النبات الى 97.30% للعشر سلالات المبكرة للجيل السابع لوزن ال100 حبة ومن 72.80% للعشر سلالات المتأخرة فى الجيل السابع لمحصول الحبوب /النبات الى 98.60% للعشر سلالات المتأخرة فى الجيل السادس لإرتفاع النبات. بالنسبة لمعامل الإرتباط كان هناك إرتباط إيجابى بين محصول الحبوب /النبات وكل من طول السنبلة، والمحصول البيولوجى/النبات، وزن السنبلة/النبات، ووزن ال100 حبة ومؤشر الحصاد فى جميع السلالات العشرة المبكرة والمتأخرة فى كل من الجيل السادس والسابع. ولوحظ أيضا وجود إرتباط سلبى بين محصول الحبوب/النبات وإرتفاع النبات عدد السنابل/النبات وعدد الأفرع لجميع السلالات العشرة المبكرة والمتأخرة فى كل من الجيل السادس والسابع. أظهر تحليل معامل الإنحدار التدريجى أن وزن السنابل/النبات والمحصول البيولوجى/النبات ومؤشر الحصاد من الصفات المهمة التى تؤثر على محصول الحبوب فى القمح ويجب أخذ هذه الصفات فى الأعتبار فى برامج التربية لتحسين محصول الحبوب فى القمح.