

## Efficiency of Two Cycles of Pedigree Line Selection in Bread Wheat (*Triticum aestivum* L) under Late Sowing Date

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### Summary

The current study aimed to assess the efficiency of two cycles of pedigree line selection in bread wheat (*Triticum aestivum* L) in late sowing date during four successive seasons from 2011/2012 to 2014/2015 at Fac. Agric. Farm, Assiut University, Egypt. The genetic materials were two segregating bread wheat populations *i.e.* Debeira x Sahel and Giza 165 x Sakha 93.

The genotypic (gcv) and phenotypic (pcv) coefficients of variation for grain yield/plant decreased from 14.90 and 17.12 in base population (F<sub>4</sub>) to 3.98 and 6.16% after two cycles (F<sub>6</sub>) of selection in population I and from 21.93 and 22.65 (F<sub>4</sub>) to 2.68 and 8.85% (F<sub>6</sub>) in population II, respectively. The same trend could be found for correlated traits in both populations. Grain yield/plant and number of spikes/plant in the two populations showed low heritability after two cycles of selection compared to their values in base populations.

After two cycles of pedigree line selection for grain yield/plant, selections mean in the F<sub>6</sub> was 17.82 g for population I compared to their parents Debeira (15.83 g) and Sahel (11.94 g) as well as the bulk sample (13.38 g). Also, the selections of population II averaged 18.78 g compared to the less values of 12.41, 15.09 and 14.19 g for both parents Giza 165, Sakha 93 and the bulk sample; respectively. The selected families in the F<sub>6</sub> surpassed the better parent and unselected bulk sample for number of spikes/plant, biological yield/plant, weight of spikes/plant, plant height, spike length and number of spikelets/spike.

The observed direct responses of pedigree line selection for grain yield/plant (selection criterion) were 33.18 and 32.35; 12.57 and 24.45; and 36.58 and 28.39% over two cycles of selection as accounted from unselected bulk sample, better parent and mid parents in population I and II, respectively.

The results revealed that the mean of family score for selection response (FSSR) over all selected F<sub>6</sub> family of Model 1 recorded the highest value (34.57 and 36.19%), followed by Model 2 (31.50 and 33.12%) and Model 7 (29.52 and 31.12%) in population I and II, respectively.

In general, the obtained results revealed that the direct pedigree line selection for grain yield/plant in wheat scaled to be powerful tool in late sowing date for improving the grain yield and be effective to get high yielding lines.

### Introduction

Wheat is the world's most important crop that excels all other cereal crops both in area and production, thereby providing about 20.0 percent of total food calories for the people of the

world (Vamshikrishna *et al.*, 2013). Moreover, wheat (*Triticum aestivum* L.) is the strategic cereal crop not only in Egypt, but also all over the world. Egypt produces about 8.2 M tons and consumes 17.9 M tons. The gap between total pro-

duction and consumption is met by imports (USDA, 2014). Also, demand of wheat is increasing with increasing population. Consequently, the maximum crop yield is an important objective in most breeding program and the major emphasis in wheat breeding is on the development of improved varieties (Fellahi *et al.*, 2013). The extent of genetic variability has been considered as an important factor which is an essential prerequisite for a successful wheat improvement program aimed to produce high yielding progenies. Selection is one of the important tools in crop improvement. It should not only be used to grain yield, but other components correlated to it must also be considered. Meanwhile, the success of selection procedure depends on the choice of selection criteria for improving grain yield (Samonte *et al.*, 1998).

In self-pollinated crops, breeders often select directly for grain yield. Many breeders of wheat indicated that pedigree selection was effective in improving grain yield of wheat (Ismail *et al.*, 1996; Ismail, 2001; Ahmed, 2006; Mahdy *et al.*, 2012a and Mostafa, 2015). Also, Loffler and Busch (1982) indicated that direct selection for grain yield was effective for increasing grain yield. Selection for yield components in some investigations resulted in yield increase. Since, efficient selection of genetically superior individuals requires adequate variance in the base population and sufficient high heritability (Vamshikrishna *et al.*, 2013).

The objective of the current study was to estimate the efficiency of single trait selection to increase the grain yield/plant through two successive generations in two segregating populations of bread wheat.

#### Materials and Methods

The current study was carried out during the four successive seasons *i.e.*, 2011/2012, 2012/2013, 2013/2014 and

2014/2015 at Fac. Agric. Farm, Assiut University, Egypt.

**Genetic materials:** The basic genetic materials were a bulk sample in F<sub>3</sub>-generation of two segregating bread wheat populations. The first population were produced from the cross Debeira x Sahel and the other one from the cross Giza 165 x Sakha 93

#### Field procedures:

**In 2011/2012 season (F<sub>3</sub>);** each population was sown in non-replicated trail on Dec. 25<sup>th</sup> (2011). Each plot (3.5x 3.5 m<sup>2</sup>) included 10 rows, 1.5 m long, 30 cm apart and 5 cm between grains within row. The recommended cultural practices for wheat populations were used during the growing season. At harvest, 537 and 250 guarded plants for population I and II, respectively, along with 60 plants from each parent were used to measure the following characters:

1-Plant height (PH) in cm. 2-Spike length (SL) in cm. 3- Number of spikes/plant (NS/P). 4- Number of spikelets/spike (NSE/S). 5- Weight of spikes/plant (WS/P) in g. 6- Biological yield (biomass)/plant (BY/P) in g. 7- Grain yield/plant (GY/P) in g. 8- Harvest index % (HI). 9- Threshing index % (TI) = (GY/P)/(WS/P).

**In 2012/2013 season (F<sub>4</sub>);** the F<sub>3</sub>-plants which gave sufficient grains for replicated trials in F<sub>4</sub> were 497 and 210 for population I and II, respectively. Both populations along with their respective parents as well as unselected bulk sample were sown on Dec. 25<sup>th</sup>, 2012 in randomized complete block design (RCBD) of three replications. An unselected bulk sample was consisted of a mixture of equal number of grains from each F<sub>3</sub>family for each population. The plot size was one row, 1.5 m long, 30 cm apart and 5 cm between grains within a row. At harvest, the previous traits were measured on 10 random guarded plants in each plot (row)/replicate.

The analysis of variance for each population was done on plot mean basis as outlined by Steel and Torrie, 1980.

Single trait selection was practiced based on grain yield/plant. The best 20% of the families (100 and 50 families for population I and II; respectively) were marked for grain yield/plant based on the family means.

**In 2013/2014 season ( $F_5$ );** all the selected families, respective parents and bulk sample for each population were sown in separate trails on Dec. 25<sup>th</sup>. The same procedures and experimental design of the previous season were followed for each trail.

The twenty and ten superior families out of previous selections for population I and II were saved for evaluation in the  $F_6$  generation.

In 2014/2015 season ( $F_6$ ); the same experimental design of the previous season was followed.

#### Statistical analysis

Estimates of genotypic and phenotypic variances and covariance, as well as heritability were calculated from the Expected Mean Square (EMS) of the variance and covariance components of the selected families for separate analysis (Steel and Torrie, 1980).

Heritability in broad sense "H" was estimated as the ratio of genotypic ( $\sigma_g^2$ ) to the phenotypic ( $\sigma_p^2$ ) variance according to Walker (1960).

The phenotypic and genotypic coefficients of variation were estimated using the formula developed by Burton (1952) as:

a) Phenotypic coefficient of variability (P.C.V.)=  $(\sigma_p^2/\bar{X}) \times 100$

b) Genotypic coefficient of variability (G.C.V.)=  $(\sigma_g^2/\bar{X}) \times 100$

Where;  $\sigma_p$  and  $\sigma_g$  are the phenotypic and genotypic standard deviations of the families mean, respectively, and  $\bar{X}$  is a families mean also for a given trait.

The observed response to selection was measured as the deviation percentage of the mean of selected families from mid-parent, better parent and bulk sample. Comparing the observed response to selection was calculated using R.L.S.D.

Family score for selection response (FSSR) was calculated as a mean of selection responses for each selected  $F_6$  family in different models, which mainly included grain yield/plant beside other different trait/s, according the following formula:

$$FSSR \% = \frac{\sum_{i=1}^n (SR_1 \% + \dots + SR_n \%)}{n}$$

Where,

$SR_1$  %: selection response for trait 1,  $SR_n$  %: selection response for trait n, n: number of traits involved in the model, and i: number of trait.

These models were designed as follows:

**a- Model 1** includes all studied traits, **b- Model 2** includes GY/P and BY/P,

**c- Model 3** includes GY/P and NS/P, **d- Model 4** includes GY/P and WS/P,

**e- Model 5** includes GY/P and SL,

**f- Model 6** includes GY/P, BY/P, NS/P and WS/P, **g- Model 7** includes GY/P, BY/P and WS/P, and **h- Model 8** includes GY/P, NS/P

and WS/P.

#### Results and Discussion

The current study was designed to achieve two cycles of pedigree line selection for improving grain yield/plant using two segregating populations of bread wheat (*Triticum aestivum* L.) in the  $F_4$ -generation.

##### 1- Description of the base population

The two base populations were represented by 497 and 210  $F_4$  replicated families for population 1 and 2, respectively along with their parents and the unselected bulk sample.

##### 1.1- Variance and means:

The analysis of variance for each trait of each population was performed twice, the first for families to calculate pcv, gcv and heritability, and the second one for the families, parents and bulk sample to compare their means. The analyses of variance (Tables 1 & 2) showed that the F<sub>4</sub>-families possessed high significant differences for all the studied traits in the two base populations. These results reflect the genetic differences among the F<sub>4</sub>-families for the studied traits in the two base populations, consequently, the presence of sufficient genetic variation pedigree line selection. Similar results were observed by Ferdous *et al.* (2011), Subhani *et al.* (2011) and Mostafa (2015). High values of genotypic gcv (Table 3) were recorded for plant height (14.89 and 12.15%), spike length (11.97 and 13.20%), number of spikes/plant (12.05 and 18.39%), number of spikelets/spike (7.01 and 12.92%), biological yield/plant (14.51 and 20.47%), weight of spikes/plant (14.84 and 23.13%), grain yield/plant (14.90 and 21.93%), harvest index (11.86 and 8.64% and threshing index (10.43 and 11.57%) in population I and II, respectively. These results accompanied with high estimates of heritability in broad sense which were more than 70.0 and 84.0% for all studied traits in population I and II, respectively, except for number spikes/plant, harvest index and threshing index were moderate (58.76, 58.66 and 56.43%, respectively) in population I.

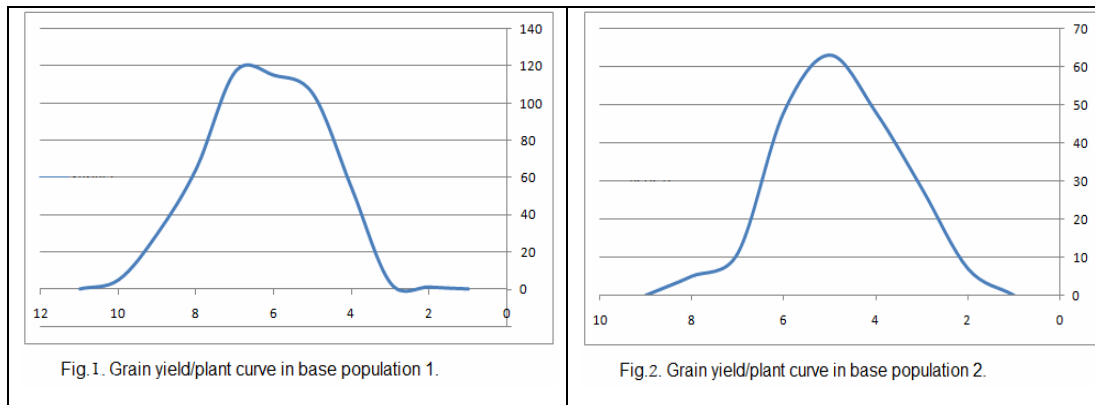
The high estimates of heritability obtained could be due to evaluation at one site and one year which inflated the genetic variance by confounding effects of years and locations. The values of genotypic coefficients of variation coupled with the estimates of heritability only would seem to give the best picture of the amount of genetic advance expected from selection (Burton, 1952 and Sanghi *et al.*, 1964).

Moreover, heritability of a metric character is one of its most important properties. It expresses the proportion of the total variance that is attributable to the average effects of genes, and this is what determines the degree of resemblance between relatives. Only the phenotypic values of individuals can be directly measured, but it is the breeding value that determines their influence on the next generation. Therefore, if the breeder chooses individuals to be parents according to their phenotypic values, the success in changing the characteristics of the population can be predicted only from the degree of correspondence between phenotypic value and breeding value, which is measured by the heritability. Consequently, in experimental populations, the individuals may be selected on the basis of the character whose heritability is being estimated, or other character correlated with it (Falconer, 1989).

The range and averages of the F<sub>4</sub>-families as well as means of both parents and bulk sample for population I and II were presented in Table 3. The results exhibited that the ranges of all traits of the F<sub>4</sub> families fell outside the means of both parents and bulk sample in both populations and seem to be in normal distribution as exhibited for grain yield/plant (Figs. 1 and 2). Moreover, the bulk sample was closed to the average of all traits and slightly exceeded it in both populations, except plant height, spike length and number of spikelets/spike in population II which were slightly less. The harvest index of bulk sample (47.23%) surpassed significantly the average of F<sub>4</sub>-families (43.38%) in population II. Meanwhile, the average of the F<sub>4</sub>-families surpassed the better parent for number of spikes/plant in population I and II, and number of spikelets/spike in population I by 3.01, 2.85 and 1.35%, respectively. Mostly, the averages of F<sub>4</sub>-families were pointed between the means

of their two parents as revealed for biological yield/plant, weight of spikes/plant and grain yield/plant in both populations and spike length in population I and plant height in population II. In all cases the differences were not significant between the average of F<sub>4</sub>-families and their parents. The obtained results revealed that nearly and may be complete dominance towards the better parent for number of spikes/ plant, biological yield/plant, weight of spikes/plant and grain yield/plant in the two populations, spike length and num-

ber of spikelets/spike in population I and plant height in population II. The others cases (harvest index, threshing index in both populations, plant height in population I, spike length and number of spikelets/spike I population II) were correlated to the less parent. Mostafa (2015) found non-additive effects and/or transgressive segregation for grain yield/plant and biological yield/plant, as well as the complete dominance towards the better parent for harvest index and partial dominance for number of gains/spike and weight grains/spike of bread wheat.



**Table 1. Analysis of variance for studied traits of population I in the F<sub>4</sub> generation.**

**a- Entries:**

S.O.V.	d.f	PH	SL	NS/P	NSe/S	BY/P	WS/P	GY/P	HI	TI
<b>Reps.</b>	2	2291.72	10.71	103.57	9.88	1095.73	192.70	420.13	211.38	2780.83
<b>Treat</b>	499	343.29**	8.24**	5.87**	17.21**	154.59**	51.84**	27.00**	70.35**	215.45**
<b>Error</b>	998	51.05	1.00	2.43	1.54	43.96	13.16	6.58	13.01	19.52
<b>b-families</b>										
<b>Reps</b>	2	1878.26	9.49	104.18	5.21	1075.75	190.79	413.41	110.11	2553.1
<b>Treat</b>	496	670.30**	7.68**	5.89**	9.19**	154.67**	51.91**	27.05**	128.31**	307.05**
<b>Error</b>	992	151.28	2.55	2.43	1.55	43.74	13.10	6.55	53.05	133.8

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

**Table 2. Analysis of variance for studied traits of population II in the F<sub>4</sub> generation.**

**a- Entries:**

S.O.V.	d.f	PH	SL	NS/P	NSe/S	BY/P	WS/P	GY/P	HI	TI
<b>Reps</b>	2	118.99	2.58	2.40	3.34	58.16	42.42	17.34	9.47	135.57
<b>Treat</b>	212	446.26**	6.89**	8.72**	27.73**	310.21**	100.08**	44.18**	105.43**	289.01**
<b>Error</b>	424	83.67	0.38	1.29	1.03	15.42	6.05	3.19	5.49	11.77
<b>b- families</b>										
<b>Reps</b>	2	130.99	2.63	2.64	3.20	59.01	39.11	17.64	8.88	132.82
<b>Treat</b>	209	551.67**	7.24**	8.28**	28.96**	226.24**	87.06**	47.96**	47.67**	266.04**
<b>Error</b>	418	84.61	0.38	1.29	1.04	14.44	5.66	2.96	5.53	11.90

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

**Table 3. Range, average of genotypes, genotypic and phenotypic variances, coefficients of variation and heritability in broad sense for the studied traits of the base population (F<sub>4</sub> families) of population I and II.**

		PH; cm	SL; cm	NS/P	NSe/S	BY/P ; g	WS/P ; g	GY/P ; g	HI	TI
<b>Population 1 (F<sub>4</sub> generation)</b>										
Family's range	Min	73.10	8.95	5.85	20.40	24.43	13.22	<b>8.59</b>	30.41	57.06
	Max	102.47	14.00	18.20	25.93	75.21	43.35	<b>30.39</b>	48.48	81.81
Average		<b>88.33</b>	<b>10.92</b>	<b>8.91</b>	<b>22.56</b>	<b>41.90</b>	<b>24.24</b>	<b>17.54</b>	<b>42.22</b>	<b>72.72</b>
Bulk		94.38	11.27	9.21	23.17	48.43	28.41	<b>20.77</b>	43.38	73.72
Debeira		95.05	11.13	8.65	22.26	43.69	25.31	<b>19.15</b>	43.80	75.93
Sahel		90.21	9.56	7.13	21.69	32.09	19.67	<b>15.14</b>	47.53	77.35
Mid-parents		<b>92.63</b>	<b>10.35</b>	<b>7.29</b>	<b>21.98</b>	<b>37.19</b>	<b>22.49</b>	<b>17.15</b>	<b>45.67</b>	<b>76.64</b>
$\sigma_E^2 =$		50.43	0.85	0.81	0.52	14.58	4.37	<b>2.18</b>	17.68	44.59
$\sigma_G^2 =$		173.01	1.99	1.15	2.55	36.98	12.94	<b>6.83</b>	25.05	57.75
$\sigma_P^2 =$		223.44	2.84	1.96	3.07	51.56	17.30	<b>9.02</b>	42.77	102.3 4
GCV %		14.89	11.97	12.05	7.01	14.51	14.84	<b>14.90</b>	11.86	10.43
PCV %		16.92	15.43	15.72	7.79	17.14	17.16	<b>17.12</b>	15.49	13.91
H %		77.43	70.07	58.76	83.06	71.72	74.77	<b>75.79</b>	58.66	56.43
R.L.S.D. (Entries)	0.05	11.14	1.56	2.93	1.85	11.59	6.34	<b>4.21</b>	9.92	6.60
	0.01	14.53	2.03	3.84	2.42	15.16	8.29	<b>5.51</b>	7.75	8.62
<b>Population 2 (F<sub>4</sub> generation)</b>										
Family's range	Min	87.48	10.13	5.60	21.27	26.47	13.67	<b>11.52</b>	37.85	73.64
	Max	163.53	12.87	11.67	26.33	66.53	36.07	<b>27.35</b>	48.33	86.94
Average		<b>102.69</b>	<b>11.46</b>	<b>8.30</b>	<b>23.61</b>	<b>41.04</b>	<b>22.52</b>	<b>17.66</b>	<b>43.38</b>	<b>79.55</b>
Bulk		96.14	11.06	8.46	23.07	41.31	24.00	<b>19.41</b>	47.23	82.20
Giza. 165		97.94	11.56	8.07	24.33	37.08	20.68	<b>16.55</b>	45.05	80.72
Sakha 93		105.01	12.29	7.60	24.31	42.19	23.70	<b>19.51</b>	46.56	83.32
Mid-parents		<b>101.48</b>	<b>11.93</b>	<b>7.84</b>	<b>24.32</b>	<b>39.64</b>	<b>22.19</b>	<b>18.03</b>	<b>45.81</b>	<b>82.02</b>
$\sigma_E^2 =$		28.20	0.13	0.43	0.35	4.81	1.89	<b>0.99</b>	1.84	3.97
$\sigma_G^2 =$		155.69	2.29	2.33	9.31	70.60	27.13	<b>15.00</b>	14.05	84.71
$\sigma_P^2 =$		183.89	2.42	2.76	9.66	75.41	29.02	<b>15.99</b>	15.89	88.68
GCV %		12.15	13.20	18.39	12.92	20.47	23.13	<b>21.93</b>	8.64	11.57
PCV %		13.21	13.57	20.02	13.16	21.16	23.99	<b>22.65</b>	9.19	11.84
H %		84.66	93.63	84.42	96.38	93.62	93.49	<b>93.81</b>	88.42	95.52
R.L.S.D. (Entries)	0.05	15.01	0.92	1.77	1.47	5.87	3.68	<b>2.67</b>	3.50	5.13
	0.01	19.64	1.20	2.31	1.91	7.66	4.80	<b>3.49</b>	4.57	6.69

## 2- Pedigree line selection for grain yield/plant

**2.1- Estimates of variability and heritability:** The analyses of variance of all entries (selected families, their parents and unselected bulk sample) as well as only selected families in F<sub>6</sub> generations (cycle two of selection) for grain yield/plant and its correlated traits of population I and II are presented in Table 4. All entries as well as selected families after two

cycles (F<sub>6</sub>) of pedigree line selection showed highly significant differences for grain yield/plant (selection criterion) and its correlated traits in both segregating populations, except the number of spikes/ plant (entries & families) in population I and spike length (families) in population II were only significant. These results indicate the presence of variability for further cycles of selection. Similar results were observed by Eissa

(1996), Ismail (2001), Hassan *et al.* (2004), Ahmed (2006), Mangi *et al.* (2007), Memon *et al.* (2007), Mobarok (2007), Ali *et al.* (2008), Hamam (2008), Kumar *et al.* (2009), El-Morshidy *et al.* (2010), Ali (2012),

Mahdy *et al.* (2012a), Abd El-Shafi (2014), Ahmed *et al.* (2014) and Mostafa (2015). Nearly, normal distribution could be found for the  $F_6$  selected families in both populations (Figs. 3, 4).

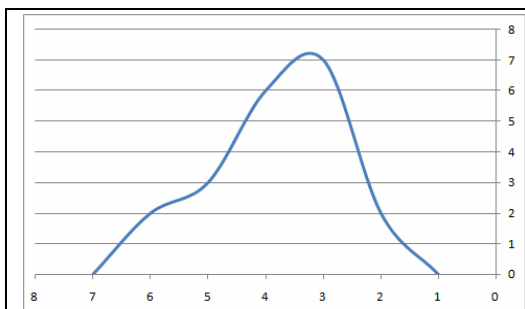


Fig. 3 . Grain yield/plant curve of selected families after two cycles of pedigree line selection in population 1.

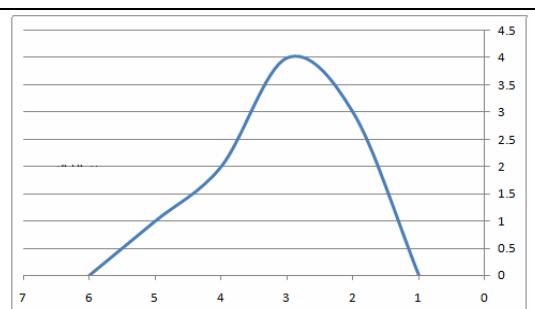


Fig. 4 . Grain yield/plant curve of selected families after two cycles of pedigree line selection in population 2.

The genotypic (gcv) and phenotypic (pcv) coefficients of variation for grain yield/plant decreased from 14.90 and 17.12 in base population ( $F_4$ ) to 3.98 and 6.16% after two cycles ( $F_6$ ) of selection in population I (Tables 3 and 4). Also, the viewed values decreased from 21.93 and 22.65 ( $F_4$ ) to 2.68 and 8.85% ( $F_6$ ) in population II (Tables 3 and 4). The same trend could be found for correlated traits in both populations. Ahmed (2006) reported that gcv 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 criterion) after second cycle of early and late selection, respectively. Also, Abd El-Kader (2011) found that the gcv decreased rapidly after two cycles of pedigree selection for number of spikes/plant from 26.2 to 4.70 and grain yield/plant from 28.60 to 3.80% in population I in  $F_3$

and  $F_5$ -generation, respectively, and the same trend was observed in population 2 of wheat. Moreover, the low differences between the pcv and gcv indicated low environmental influences in expression of grain yield and its components of wheat (Majumder *et al.*, 2008; Mukherjee *et al.*, 2008 and Mostafa, 2015). Falconer (1989) stated that the loss of genetic variance should lead to a reduced phenotypic variance. But, sometimes, the phenotypic variance increasing by selection, this may be due to *first* the phenotypic variance is correlated with means when the mean changes by selection the variance consequently changes with it, and *second* the homozygotes produced with selection are sometimes more variable than heterozygotes under environmental effects.

The estimates of broad sense heritability calculated from the expected mean squares were high (more than 70.0%) for most the studied traits after two cycles of selection in

both segregating populations, except for grain yield/plant as selection criterion and its correlated traits of number of spikes/plant and harvest index were low and accounted 41.67, 41.55 and 48.67% in population I, respectively (Tables 4). Also, it is clear that grain yield/plant and number of spikes/plant in the two populations as well as harvest index in population I and spike length, number of spikes/plant, number of spikelets/spike, weight of spikes/plant and threshing index in population II had less heritability after two cycles of selection compared to their values in base populations. Other traits recorded high estimates compared to the two base populations (Tables 3 and 4). Abd El-Shafi (2014) noted that the different between genotypic and phenotypic variances for grain yield/plant were low suggesting that the directional selection appears to reduce the range and variability for grain yield/plant in the  $F_4$  and less affected by environmental factors and consequently this could be referring to the high estimates of broad sense heritability for two crosses in  $F_4$  generation of wheat. Moreover, Aydin *et al.* (2010) estimated low values of heritability for grain yield and plant height which accounted 46.05 and 43.69%, respectively. Consequently, both traits were the most affected traits across environmental condition on wheat. Otherwise, Assefa and Lemma (2009) reported that the highest genetic gain (69.7%) with high heritability (88.3%) for grain yield

indicated that grain yield is more reliance on direct selection. Zakaria *et al.* (2008) found heritability values of 85.2, 59.4 and 54.5% for grain yield in base population, cycle 1 and cycle 2 of selection, respectively. Meanwhile, high heritability estimates were observed for grain yield/plant, spike length, number of spikes/spike, harvest index, plant height (Moshref, 1996; Eid, 2009; Kumar *et al.*, 2009; Mohsin *et al.*, 2009; Ajmal *et al.*, 2009; El-Morshidy *et al.*, 2010; Laghari *et al.*, 2010 and Mahdy *et al.*, 2012b). Mukherjee *et al.* (2008) found that grain yield had high heritability with moderate genetic advance which attributed to non-additive gene action. But, Sharma and Sharma (2007) found high heritability (92.27%) for grain yield/plant, indicating that most of variation was due to additive gene effects. Meanwhile, Mostafa (2015) noted that the pcv and gcv in all traits under normal and drought stress were very close to each other, resulted in very high estimates of heritability. The high values of heritability could be attributed to two main reasons. *First*, the evaluation of the selected families at one site for one year inflated the families mean squares by the confound effects of the interactions of families with locations and years in families mean square. In consequence, large estimates of genetic variance were obtained. *Second*, the small error variances which cause the phenotypic variance tend to be very close to genotypic one.



**Table 4. Mean squares for entries and families, variance types, heritability estimates, genotypic (g.c.v.%) and phenotypic (p.c.v.%) coefficients of variability of selected families for grain yield/plant and correlated traits in F<sub>6</sub> generations of population I and II.**

	S.O.V.	d.f.	PH	SL	NS/P	NSe/S	BY/P	WS/P	GY/P	HI	TI
<b>Population I (F<sub>6</sub>- generation)</b>											
A- Entries	Reps.	2	76.44	0.53	2.39	0.47	56.60	15.00	<b>7.90</b>	30.26	2.61
	Entries	22	42.10**	1.94 **	2.65 *	3.40 **	45.75**	13.85**	<b>10.49**</b>	18.02 **	21.93**
	Error	44	8.21	0.42	1.43	0.50	2.56	2.67	<b>1.86</b>	9.69	9.46
B- Families	Reps.	2	63.41	0.93	0.89	0.79	6.76	15.82	<b>6.93</b>	43.19	12.09
	Families	19	43.63**	1.43 **	4.28 *	2.89 **	47.43 **	11.32**	<b>3.61 **</b>	18.10**	20.84**
	Error	38	8.04	0.41	2.51	0.45	2.65	2.68	<b>2.11</b>	9.37	8.15
	σ <sup>2</sup> <sub>FE</sub>		2.68	0.14	0.83	0.15	0.88	0.89	<b>0.70</b>	3.12	2.72
	σ <sup>2</sup> <sub>CE</sub>		11.86	0.34	0.59	0.81	14.93	2.88	<b>0.50</b>	2.91	4.23
	σ <sup>2</sup> <sub>PE</sub>		14.54	0.48	1.42	0.96	15.81	3.77	<b>1.20</b>	6.03	6.95
	GCV %		4.99	5.13	6.70	4.23	8.55	6.64	<b>3.98</b>	4.31	2.94
	PCV%		5.53	6.08	10.39	4.60	8.80	7.60	<b>6.16</b>	6.20	3.77
	H%		81.56	71.31	41.55	84.57	94.42	76.34	<b>41.67</b>	48.24	60.90
	Average		<b>69.02</b>	<b>11.34</b>	<b>11.46</b>	<b>21.31</b>	<b>45.18</b>	<b>25.56</b>	<b>17.82</b>	<b>39.59</b>	<b>69.84</b>
<b>Population II (F<sub>6</sub>- generation)</b>											
A- Entries	Reps.	2	2.74	0.93	4.44	0.97	6.68	5.04	<b>3.85</b>	1.34	0.20
	Entries	12	91.60**	2.78 **	9.03 **	7.35**	119.96**	54.51**	<b>24.25**</b>	13.94**	55.53**
	Error	24	2.56	0.49	1.51	0.60	2.18	3.58	<b>1.92</b>	1.78	1.98
B- Families	Reps.	2	9.83	1.52	4.96	1.55	2.57	1.40	<b>0.85</b>	4.84	1.82
	Families	9	82.64**	1.72*	9.09**	4.56**	84.70**	23.41**	<b>8.27 **</b>	16.50**	24.62**
	Error	18	1.81	0.51	1.51	0.70	2.24	3.69	<b>2.04</b>	1.45	1.66
	σ <sup>2</sup> <sub>FE</sub>		0.60	0.17	0.50	0.23	0.75	1.23	<b>0.68</b>	0.48	0.55
	σ <sup>2</sup> <sub>CE</sub>		26.94	0.40	2.53	1.29	27.49	6.57	<b>2.08</b>	5.02	7.65
	σ <sup>2</sup> <sub>PE</sub>		27.54	0.57	3.03	1.52	28.24	7.80	<b>2.76</b>	5.50	8.20
	GCV %		6.65	5.63	12.60	5.34	11.05	9.45	<b>2.68</b>	5.63	3.98
	PCV%		6.73	6.72	13.79	5.80	11.20	10.29	<b>8.85</b>	5.89	4.12
	H%		97.82	70.18	83.50	84.87	97.38	84.23	<b>75.36</b>	91.27	93.29
	Average		78.00	11.24	12.62	21.25	47.45	27.13	<b>18.78</b>	39.83	69.44

Entries: Selected families, their parents and unselected bulk sample.

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

## 2.2- Means and selection response for grain yield/plant and correlated traits

### 2.2.1- Mean of cycle two selection for grain yield/plant (F<sub>6</sub>).

Range and averages of selections as well as means of their parents and bulk sample over the cycle II of pedigree line selection for grain yield/plant for population I and II are given in Table 5. After two cycles of pedigree line selection for grain yield/plant, the selected families of population I ranged from 16.39 to

19.92 with an average of 17.82 g compared to their parents Debeira (15.83) and Sahel (11.94) as well as bulk sample (13.38 g). Also, the selections of population II varied from 16.66 to 22.03 with an average of 18.78 g compared to 12.41, 15.09 and 14.19 g for both parents Giza 165, Sakha 93 and bulk sample; respectively (Table 5). It is clear that the selections of both populations surpassed their respective parents and unselected bulk sample in cycle 2

(F<sub>6</sub>) of pedigree line selection for grain yield/plant.

The averages of F<sub>6</sub> selections in population I for correlated traits such as plant height, spike length, number of spikes/plant, number of spikelets/spike, biological yield/plant, weight of spikes/plant, harvest index and threshing index were 69.02, 11.34, 11.46, 21.31, 45.18, 25.56, 39.59, and 69.84, respectively. Also, the same trend could be seen for population II. The averages of selected families were 78.00, 11.24, 12.62, 21.25, 47.45, 27.13, 39.83, and 69.44 for plant height, spike length, number of spikes/plant, number of spikelets/spike, biological yield/plant, weight of spikes/plant, harvest index and threshing index in F<sub>6</sub> (Table 5). It is clear that the selected families in F<sub>6</sub> for both populations surpassed the better parent and unselected bulk sample for number of spikes/plant, biological yield/plant, weight of spikes/plant, plant height, spike length and number of spikelets/spike in F<sub>6</sub>. Meanwhile, the average of F<sub>6</sub> selections surpassed the bulk sample for harvest index and threshing index in population I.

### **2.2.2- Mean observed direct response over two cycles of pedigree selection for grain yield/plant (F<sub>6</sub>).**

The observed direct responses of pedigree line selection for grain yield/plant (selection criterion) in population I were 33.18, 12.57, and 28.39% over two cycles of selection as accounted from unselected bulk sample, better parent and mid parents; respectively. These direct responses were 32.35, 24.45, and 36.58% for same respective items in

population II (Table 6). It is clear that the direct response for grain yield/plant in cycle two (F<sub>6</sub>) was large in both populations indicating to the effectiveness of direct pedigree selection for grain yield in both the studied populations of bread wheat. These results are in line with those obtained by Ahmed (2006), Talaat (2006), Ali (2011) and Mostafa (2015) who found that the observed gain increase in grain yield/plant over the bulk sample was more than 25.00%. Also, Mahdy *et al.* (2012b), Hamam (2008) and Zakaria *et al.* (2008) noted that observed gain from the better parent was 11.00 ~ 20.21 % after two cycles of selection for grain yield. Consequently the pedigree selection procedure has been proposed in wheat as an effective breeding method for developing high yielding genotypes. Meanwhile, Assefa and Lemma (2009) noted genetic gain of 69.7% for grain yield indicating that grain yield is more reliance on direct selection. Also, Abd El-Kader (2011) found realized gain in F<sub>5</sub> in relative to the bulk of 17.39 and 36.41% for grain yield/plant in population I and II, respectively. Moreover, Abd El-Shafi (2014) stated that actual gains in grain yield/plant and its components were higher than the predicted one through cycle 1 and 2 for two populations which indicate that the dominance gene effects are involved in the inheritance of yield and its components.

### **2.2.3- Mean correlated responses over two cycles of pedigree selection for grain yield/plant (F<sub>6</sub>)**

The correlated responses on other traits after cycle two (F<sub>6</sub>) of pedigree selection for grain

yield/plant in percentage of the unselected bulk sample, better parent and mid parents for population I and II are shown in Table 6. It is clear that the three traits i.e. number of spikes/plant, biological yield/plant and weight of spikes/plant had the highest positive values of correlated response in and cycle two ( $F_6$ ) in both populations. The estimates were 22.83, 21.01 and 23.62% in population I, and 37.47, 28.91 and 30.37% in population II for number of spikes/plant; 22.61, 15.20 and 24.77% in population I, and 36.51, 28.98 and 39.44% in population II for biological yield/plant and 27.04, 13.45 and 29.75% in population I, and 34.44, 31.70 and 42.12% in population II for weight of spikes/plant as relative to the bulk, better parent and mid parents, respectively. The correlated responses for plant height and spike length were positive and less than 11.0% (population I) and 14.0% (population II) in cycle 2 ( $F_6$ ). This result may be due to the direction of selection was in one way for these traits. Otherwise, the negative values of correlated responses were found for harvest and threshing index in cycle two in population II and some cases in population I. Last negative results may be due to the direct increase of grain yield for selections are less compared to the correlated increases biological yield and weight of spike in cycle two ( $F_6$ ) in both populations (Table 6).

Some researchers found different correlated response for various traits when selection was done for grain yield/plant in wheat. Kumar *et al.* (2009) reported that the genetic advance ranged from 2.05 to 18.61% for plant height, spike length, number of spikelets/spike and harvest index. This range was from 22.67 to 47.45% for the same traits (Vamsikrishna *et al.*, 2013). Talaat (2006) found correlated response of 2.44 and 16.20% for biological yield/plant and number of spikes/plant, respectively. Meanwhile, Mostafa (2015) found correlated response for biological yield/plant, number of spikes/plant and harvest index of 30.42 and 31.85, 59.7 and 15.03, and 29.99 and 15.24 with drought stress in relative to bulk and better parent, respectively. Also, correlated responses for plant height were 7.49% (Kashif & Khaliq, 2009), 25.29% (Ajmal *et al.*, 2009), 18.89 (Assefa and Lemma, 2009) and 13.09% (Ali, 2011). Moreover, number of spikes/plant accounted correlated response more than 5.0 % in two wheat populations (Abd El-Kader, 2011). High correlated genetic advance was recorded for spike length (Eid, 2009). Otherwise, pedigree selection for grain yield/plant in wheat proved to be an efficient selection method in increasing grain yield with adverse effects on some correlated traits (Eissa, 1996; Ismail *et al.*, 1996; Mahdy *et al.*, 1996 and Ali, 2012).

**Table 5. Range and means of selections ( $F_6$ ), their parents and bulk sample after the cycle II of pedigree line selection for grain yield/plant in population I and II.**

		PH; cm	SL; cm	NS/P	NSe/S	BY/P; g	WS/P; g	GY/P; g	HI	TI	
Population I	F <sub>6</sub> - Selections	Min.	62.15	10.00	10.13	19.77	39.69	23.14	16.39	36.28	65.44
		Max.	75.27	12.60	15.07	23.67	53.38	29.73	19.92	43.49	74.03
		Mean	69.02	11.34	11.46	21.31	45.18	25.56	17.82	39.59	69.84
	Bulk	67.20	11.03	9.33	20.47	36.85	20.12	13.38	36.31	68.74	
	Debeira	68.13	10.53	9.47	20.13	39.22	22.53	15.83	40.36	70.26	
	Sahel	63.40	9.97	9.07	19.00	33.20	16.86	11.94	35.96	70.82	
	Mid. Parents	65.27	10.25	9.27	19.57	36.21	19.70	13.88	38.16	70.46	
Population II	F <sub>6</sub> - Selections	Min.	70.80	10.27	10.5	20.6	40.26	23.73	16.66	35.89	65.09
		Max.	89.40	12.20	15.4	22.87	56.05	32.51	22.03	42.88	73.05
		Mean	78.00	11.24	12.62	21.25	47.45	27.13	18.78	39.83	69.44
	Bulk	71.22	10.53	9.18	20.27	34.76	20.18	14.19	40.82	70.32	
	Giza 165	68.00	9.80	9.56	19.80	31.32	17.58	12.41	39.62	70.60	
	Sakha 93	73.67	9.93	9.79	19.93	36.79	20.60	15.09	41.07	73.24	
	Mid. Parents	70.83	9.87	9.68	19.87	34.03	19.09	13.75	40.34	71.92	

**Table 6. Mean observed direct and correlated response after the cycle II ( $F_6$ ) of pedigree line selection for grain yield/plant percentage from the mid parents, better parent and bulk sample in population I and II.**

		PH	SL	NS/P	NSe/S	BY/P	WS/P	GY/P	HI	TI
Population I	Bulk	2.71	2.81	22.83	4.10	22.61	27.04	33.18	9.03	1.60
	Bet. Parent	1.31	7.69	21.01	5.86	15.20	13.45	12.57	-1.91	-1.38
	Mid. Parents	5.75	10.63	23.62	7.97	24.77	29.75	28.39	3.75	-0.88
Population II	Bulk	9.52	6.74	37.47	4.83	36.51	34.44	32.35	-2.43	-1.25
	Bet. Parent	5.88	13.19	28.91	6.62	28.98	31.70	24.45	-3.02	-5.19
	Mid. Parents	10.12	13.88	30.37	6.95	39.44	42.12	36.58	-1.26	-3.45

#### 2.2.4- The direct responses for selected ( $F_6$ ) families (cycle two) of pedigree selection for grain yield/plant

Means, direct and correlated response of the studied traits for the selected families in cycle two ( $F_6$ ) in percentage of the better parent, mid parents and bulk sample in population I and II are shown in Tables 7 and 8, respectively. Direct response to pedigree line selection for grain yield/plant in population I revealed that all selections (20- $F_6$  families) in cycle two of selection exceeded sig-

nificantly the mid parents and unselected bulk sample. The direct response for grain yield/plant ranged from 18.08 to 43.52 with an average of 28.39% over the mid parents; and from 3.54 to 25.84 with an average 12.57% over the better parent and from 22.50 to 48.88 with an average of 33.18% over the bulk sample. All the largest values of direct response were recorded for the Fam. no. 536. Otherwise, the lowest one was Fam. no. 289. Moreover, seven and five families among all  $F_6$  families surpassed significantly and highly sig-

nificantly the mean of better parent. These last superior families number were 28, 41, 108, 296, 460, 518 and 536 and accounted direct response of 15.35, 19.27, 14.97, 21.98, 22.05, 24.13 and 25.84% over the better parent (Debeira), respectively (Table 7).

The direct response for grain yield/plant in population II were in the same trend as in population I, and all the selected  $F_6$  families surpassed significantly the mid parents and bulk sample. Moreover, eight and six selected families out of the ten families were exceeded significantly and highly significantly the better parent, respectively. The direct response for grain yield/plant ranged from 21.16 to 60.22 with an average of 36.58% over the mid parent; from 10.40 to 45.99 with an average of 24.45 over the better parent and from 17.41 to 55.25 with an average of 32.35% over the bulk sample. The highest values of direct response were recorded to the Fam. no. 249. But, the lowest values attached with Fam. 279. The superior families surpassed significantly in rank the better parent (Sakha 93) in values of 45.99 (no. 249), 32.94 (no. 1), 32.60 (no. 70), 29.89 (no. 289), 23.06 (no. 192), 21.47 (no. 266), 20.34 (no. 236) and 16.04% (no. 154) (Table 8).

The obtained results revealed that the direct pedigree line selection for grain yield/plant in wheat could be a powerful tool for improving the grain yield and effective to get high yielding lines. Same conclusion was proven by many authors such as Whan *et al.* (1982), Kheiralla (1993), Hamam (2008), Zakaria *et al.* (2008), Ajmal *et al.* (2009), Assefa and

Lemma (2009), El-Morshidy *et al.* (2010), Ali (2011), Ali (2012), Ahmed *et al.* (2014) and Mostafa (2015). Also, Alexander *et al.*, (1984), Mahdy (1988), Nanda *et al.*, (1990) and Ismail (1995) obtained realized genetic gain of 12.9 ~ 44.02% for grain yield/plant after two cycles of direct selection in wheat.

### **2.2.5- The correlated responses for selected $F_6$ families (cycle two) of pedigree selection for grain yield/plant**

The correlated responses for selected  $F_6$  families (cycle two) of pedigree selection for grain yield/plant in percentage of the bulk sample, better parent and mid parents for population I and II are presented in Tables 7 and 8, respectively.

The  $F_6$ -families of the three traits i.e. number of spikes/plant, biological yield/plant and weight of spikes/plant showed the highest and positive correlated response. In population I, the correlated responses for number of spikes/plant ranged from 9.28 to 62.57 with an average of 23.62% over the mid parent, and varied from 6.97 to 59.13 with an average of 21.01% over the better parent. Also, it ranged from 8.57 to 61.52 with an average of 22.83% over the bulk sample. The highest correlated response matched the family no. 41. There were five families (nos. 41, 291, 474, 518 and 536) surpassed in highly significant means the mid parents, better parent and bulk sample. These five families surpassed the better parent and bulk sample by 59.13 and 61.52, 42.87 and 45.02, 35.16 and 37.19, 28.62 and 30.55, and 28.83 and 30.76%, respectively. In population II, the correlated re-

sponses for number of spikes/ plant ranged from 8.47 to 59.09 with an average of 30.37% over the mid parents, and varied from 7.25 to 57.30 with an average of 28.91% over the better parent. It also, ranged from 14.38 to 67.76 with an average of 37.47% over the bulk sample. There were six out of the ten selected families i.e. No. 59, No.154, No.192, No.236, No.249 and No.289 highly significant exceeded the bulk sample, better parent and mid parents. The values of correlated response of the above families in number of spike/plant over the bulk sample and better parent were 35.08 and 26.66, 37.25 and 28.70, 67.76 and 57.30, 42.37 and 33.50, 58.28 and 48.42, and 44.55 and 35.55%, respectively.

The correlated response for biological yield/plant in *population I* revealed that the means of all the twenty selected  $F_6$  families were significantly surpassed the bulk sample and mid parent, eighteen of these families were highly significant. Also, there were fourteen  $F_6$  families surpassed highly significant the better parent. The values of correlated response ranged from 9.61 to 47.42 with an average of 24.77% over the mid parent and varied from 1.20 to 36.10 with an average of 15.20 over the better parent. Meanwhile, it ranged from 7.71 to 44.86 with an average of 22.61% over the bulk sample. The highest correlated response was for Fam. no. 536 over the three scales. The highest ten superior  $F_6$  families in respective rank surpassed highly significant the better parent by 36.10 (no. 536), 34.40 (no. 41), 25.75 (no. 401), 24.66 (no. 28), 22.03 (no. 460), 20.86 (no. 261),

18.84 (no. 518), 18.41 (no. 291), 18.03 (no. 296), and 16.37% (no. 313) in biological yield/plant. In *population II*, the means of all the ten  $F_6$  families were exceeded the bulk sample, mid parents and better parent in highly significant differences. The correlated response for biological yield/plant varied from 18.31 to 64.71 with an average of 39.44% over the mid parent, and ranged from 9.43 to 52.35 with an average of 28.98% over the better parent. In addition to, it ranged from 15.82 to 61.25 with an average of 36.51% over the bulk sample. The family no. 249 had the highest correlated response over the three scales. The ten selected  $F_6$  families were exceeded in highly significant differences the better parent and recorded values in respective rank of 52.35 (no. 249), 48.90 (no. 1), 40.07 (no. 192), 31.39 (no. 289), 26.64 (no. 226), 26.61 (no. 70), 22.48 (no. 236), 20.01 (no. 59), 11.96 (no. 154) and 9.43 (no. 279).

Means of selected  $F_6$  families in *population I* for weight of spikes/plant exhibited that all families exceeded significant or high significantly the bulk sample and mid parents. Moreover, two and seven families surpassed in high significant and significant differences the better parent (Table 7). The correlated response ranged from 15.01 to 47.76 with an average of 27.04% over the bulk sample, and varied from 17.46 to 50.91 with an average of 29.75% over the mid parents. Moreover, it ranged from 2.71 to 31.96 with an average of 13.45% over the better parent. The nine families surpassed significantly the better parent showed by 31.96 (no. 536), 26.59 (no. 460),

26.28 (no. 41), 23.70 (no. 28), 20.73 (no. 518), 19.62 (no. 401), 17.49 (no. 296), 13.14 (no. 108) and 12.21% (no. 261). For population II, the ten selected F<sub>6</sub> families exceeded significantly or highly, significantly the bulk sample, mid parents and better parent for weight of spikes/plant (Table 8). The correlated response ranged from 17.59 to 61.10 with an average of 34.44% over the bulk sample and from 24.31 to 70.30 with an average of 42.12% over mid parent. Likewise, it ranged from 15.19 to 57.82 with an average of 31.70 over the better parent. The ten selected F<sub>6</sub> families surpassed the better parent for weight of spikes/plant by 57.82 (no. 249), 49.90 (1), 34.85 (no. 289), 34.08 (no. 192), 32.82 (no. 70), 27.52 (no. 226), 24.61 (no. 59), 22.38 (no. 236), 17.72 (no. 154) and 15.19% (no. 279). Concerning the other correlated response for the rest studied traits were less or adverse trend for some families.

In general, in population I, the family no. 536 has the highest values of both direct response for grain yield/plant and correlated responses for spike length, biological yield/plant and weight of spikes/plant. Likewise, in population II, the family no. 249 has the highest value of direct response for grain yield/plant as well as correlated responses for spike length, spikelets

number/spike, biological yield/plant and weight of spikes/plant. These results revealed that the superiority in grain yield/plant was depending on selection for grain yield *per se* or with these correlated traits. Ali *et al.* (2008) found high genetic advance for plant height, number of spikelets/spike, spike length and yield/plant. Also, high genetic advance obtained for plant height, harvest index and grain yield (Majumder *et al.*, 2008). Otherwise, low genetic advance was recorded for plant height (Eid, 2009). The observed response of selection was 20.21% for grain yield/plant after two cycles of pedigree selection over better parent. Direct pedigree selection for grain yield was effective to get high yielding lines (Zakaria *et al.*, 2008). Range of 2.05-18.61% of genetic advance was reported for plant height, length of spike, number of spikelets/spike, grain yield and harvest index (Kumar *et al.*, 2009). The best family resulted from pedigree selection surpassed the bulk for grain yield by 21.43 - 44.02% in two populations (Whan *et al.*, 1982 and Ismail, 1995). Also, Ismail (1995) concluded that the increase of yield was accompanied with adverse effect on the correlated traits. Moreover, Hamam (2008) concluded that pedigree selection procedure was effective breeding tool for developing high yielding genotypes of wheat.

**Table 7. Observed direct and correlated responses in cycle two (F<sub>6</sub>) of pedigree line selection for grain yield/plant in percentage better parent, mid parents and bulk sample in population I.**

Fam. No.	Plant height, cm				Spike length, cm				Spikes number/plant			
	Mean	Bulk	Better. parent	M.-parents	Mean	Bulk	Better. parent	M.-parents	Mean	Bulk	Better. parent	M.-parents
28	71.87	6.95	5.49	10.11	12.60	14.23	19.66	22.93	10.13	8.57	6.97	9.28
34	73.60	9.52	8.03	12.76	10.27	-6.89	-2.47	0.20	10.87	16.51	14.78	17.26
36	70.13	4.36	2.94	7.45	10.73	-2.72	1.90	4.68	10.47	12.22	10.56	12.94
41	74.13	10.31	8.81	13.57	11.87	7.62	12.73	15.80	15.07	61.52	59.13	62.57
108	67.53	0.49	-0.88	3.46	11.33	2.72	7.60	10.54	11.20	20.04	18.27	20.82
141	69.40	3.27	1.86	6.33	11.33	2.72	7.60	10.54	10.60	13.61	11.93	14.35
258	69.00	2.68	1.28	5.71	11.47	3.99	8.93	11.90	10.47	12.22	10.56	12.94
261	69.53	3.47	2.05	6.53	11.87	7.62	12.73	15.80	11.20	20.04	18.27	20.82
289	65.20	-2.98	-4.30	-0.11	10.73	-2.72	1.90	4.68	11.00	17.90	16.16	18.66
291	73.20	8.93	7.44	12.15	11.33	2.72	7.60	10.54	13.53	45.02	42.87	45.95
296	65.73	-2.19	-3.52	0.70	11.33	2.72	7.60	10.54	11.20	20.04	18.27	20.82
313	75.27	12.01	10.48	15.32	11.07	0.36	5.13	8.00	11.67	25.08	23.23	25.89
321	62.67	-6.74	-8.01	-3.98	10.00	-9.34	-5.03	-2.44	10.93	17.15	15.42	17.91
401	74.47	10.82	9.31	14.10	12.00	8.79	13.96	17.07	10.80	15.76	14.04	16.50
441	67.47	0.40	-0.97	3.37	11.67	5.80	10.83	13.85	10.67	14.36	12.67	15.10
460	65.93	-1.89	-3.23	1.01	11.53	4.53	9.50	12.49	11.33	21.44	19.64	22.22
466	67.47	0.40	-0.97	3.37	11.73	6.35	11.40	14.44	10.93	17.15	15.42	17.91
474	67.13	-0.10	-1.47	2.85	10.73	-2.72	1.90	4.68	12.80	37.19	35.16	38.08
518	62.15	-7.51	-8.78	-4.78	10.68	-3.17	1.42	4.20	12.18	30.55	28.62	31.39
536	68.53	1.98	0.59	4.99	12.60	14.23	19.66	22.93	12.20	30.76	28.83	31.61
Average	69.02	2.71	1.31	5.75	11.34	2.81	7.69	10.63	11.46	22.83	21.01	23.62
Bulk	67.20				11.03				9.33			
Debeira	68.13				10.53				9.47			
Sahel	63.40				9.97				9.07			
Mid-parents	65.27				10.25				9.27			
L.S.D. 0.05 Entr.	4.72				1.07				1.97			
L.S.D. 0.05 Fam.	6.29				1.42				2.63			
L.S.D. 0.01	4.68				1.06				2.61			
L.S.D. 0.01	6.28				1.42				3.51			
	Spikelets number/spike				Biological yield/plant, g				Weight of spikes/plant, g			
28	23.67	15.63	17.59	20.95	48.89	32.67	24.66	35.02	27.87	38.52	23.70	41.47
34	20.20	-1.32	0.35	3.22	43.29	17.48	10.38	19.55	24.30	20.78	7.86	23.35
36	20.07	-1.95	-0.30	2.55	42.41	15.09	8.13	17.12	23.84	18.49	5.81	21.02
41	23.07	12.70	14.61	17.88	52.71	43.04	34.40	45.57	28.45	41.40	26.28	44.42
108	20.07	-1.95	-0.30	2.55	42.59	15.58	8.59	17.62	25.49	26.69	13.14	29.39
141	21.00	2.59	4.32	7.31	40.54	10.01	3.37	11.96	23.31	15.85	3.46	18.32
258	20.73	1.27	2.98	5.93	41.06	11.42	4.69	13.39	24.84	23.46	10.25	26.09
261	21.40	4.54	6.31	9.35	47.40	28.63	20.86	30.90	25.28	25.65	12.21	28.32
289	21.13	3.22	4.97	7.97	41.61	12.92	6.09	14.91	23.14	15.01	2.71	17.46
291	22.20	8.45	10.28	13.44	46.44	26.02	18.41	28.25	24.53	21.92	8.88	24.52
296	21.40	4.54	6.31	9.35	46.29	25.62	18.03	27.84	26.47	31.56	17.49	34.37
313	22.40	9.43	11.28	14.46	45.64	23.85	16.37	26.04	23.97	19.14	6.39	21.68
321	21.00	2.59	4.32	7.31	40.16	8.98	2.40	10.91	23.65	17.54	4.97	20.05
401	21.27	3.91	5.66	8.69	49.32	33.84	25.75	36.21	26.95	33.95	19.62	36.80
441	20.87	1.95	3.68	6.64	39.69	7.71	1.20	9.61	24.33	20.92	7.99	23.50
460	21.40	4.54	6.31	9.35	47.86	29.88	22.03	32.17	28.52	41.75	26.59	44.77
466	21.40	4.54	6.31	9.35	44.28	20.16	12.90	22.29	24.69	22.71	9.59	25.33
474	21.67	5.86	7.65	10.73	43.45	17.91	10.79	19.99	24.65	22.51	9.41	25.13
518	19.77	-3.42	-1.79	1.02	46.61	26.49	18.84	28.72	27.20	35.19	20.73	38.07
536	21.53	5.18	6.95	10.02	53.38	44.86	36.10	47.42	29.73	47.76	31.96	50.91
Average	21.31	4.10	5.86	8.89	45.18	22.61	15.20	24.77	25.56	27.04	13.45	29.75
Bulk	20.47				36.85				20.12			
Debeira	20.13				39.22				22.53			
Sahel	19.00				33.20				16.86			
Mid-parents	19.57				36.21				19.70			
L.S.D. 0.05 Entr.	1.16				2.64				2.70			
L.S.D. 0.05 Fam.	1.55				3.51				3.59			
L.S.D. 0.01	1.10				2.68				2.70			
L.S.D. 0.01	1.48				3.60				3.62			



**Table 7. Continued.**

Fam. No.	Grains yield/plant, g				Harvest index, %				Threshing index, %			
	Mean	Bulk	Better parent	M.-parents	Mean	Bulk	Better parent	M.-parents	Mean	Bulk	Better parent	M.-parents
28	18.26	36.47	15.35	31.56	37.25	2.59	-7.71	-2.38	65.44	-4.80	-7.60	-7.12
34	17.18	28.40	8.53	23.78	39.42	8.57	-2.33	3.30	70.56	2.65	-0.37	0.14
36	16.96	26.76	7.14	22.19	40.20	10.71	-0.40	5.35	71.60	4.16	1.10	1.62
41	18.88	41.11	19.27	36.02	36.28	-0.08	-10.11	-4.93	66.34	-3.49	-6.33	-5.85
108	18.20	36.02	14.97	31.12	42.64	17.43	5.65	11.74	71.34	3.78	0.73	1.25
141	16.53	23.54	4.42	19.09	40.83	12.45	1.16	7.00	70.84	3.05	0.03	0.54
258	17.53	31.02	10.74	26.30	42.74	17.71	5.90	12.00	70.70	2.85	-0.17	0.34
261	17.74	32.59	12.07	27.81	37.64	3.66	-6.74	-1.36	70.99	3.27	0.24	0.75
289	16.39	22.50	3.54	18.08	38.79	6.83	-3.89	1.65	70.95	3.22	0.18	0.70
291	17.06	27.50	7.77	22.91	36.52	0.58	-9.51	-4.30	69.41	0.97	-1.99	-1.49
296	19.31	44.32	21.98	39.12	41.62	14.62	3.12	9.07	73.42	6.81	3.67	4.20
313	17.40	30.04	9.92	25.36	38.05	4.79	-5.72	-0.29	72.64	5.67	2.57	3.09
321	17.55	31.17	10.87	26.44	43.40	19.53	7.53	13.73	74.03	7.70	4.53	5.07
401	18.06	34.98	14.09	30.12	36.53	0.61	-9.49	-4.27	66.84	-2.76	-5.62	-5.14
441	16.86	26.01	6.51	21.47	42.35	16.63	4.93	10.98	69.33	0.86	-2.10	-1.60
460	19.32	44.39	22.05	39.19	39.36	8.40	-2.48	3.14	66.40	-3.40	-6.24	-5.76
466	16.42	22.72	3.73	18.30	37.18	2.40	-7.88	-2.57	66.31	-3.54	-6.37	-5.89
474	17.10	27.80	8.02	23.20	39.87	9.80	-1.21	4.48	69.44	1.02	-1.95	-1.45
518	19.65	46.86	24.13	41.57	43.49	19.77	7.76	13.97	73.11	6.36	3.23	3.76
536	19.92	48.88	25.84	43.52	37.59	3.53	-6.86	-1.49	67.11	-2.37	-5.24	-4.75
Average	17.82	33.18	12.57	28.39	39.59	9.03	-1.91	3.75	69.84	1.60	-1.38	-0.88
Bulk	13.38				36.31				68.74			
Debeira	15.83				40.36				70.26			
Sahel	11.94				35.96				70.82			
Mid-parents	13.88				38.16				70.46			
L.S.D. 0.05	2.25				5.13				5.07			
Entr. 0.01	3.00				6.84				6.75			
L.S.D. 0.05	2.40				5.05				4.71			
Fam. 0.01	3.21				6.77				6.32			

L.S.D. Entr.: to compare families with parents and bulk sample.

L.S.D. Fam.: to compare families with each other.

0.05 & 0.01, significant at 0.05 and 0.01 levels of probability, respectively.

**Table 8. Observed direct and correlated responses in cycle two (F<sub>6</sub>) of pedigree line selection for grain yield/plant in percentage of the better parent, mid parents and bulk sample in population II.**

Fam. No.	Plant height, cm				Spike length, cm				Spikes number/plant			
	Mean	Bulk	Better parent	M.-parents	Mean	Bulk	Better parent	M.-parents	Mean	Bulk	Better parent	M.-parents
1	70.80	-0.59	-3.90	-0.04	11.87	12.73	19.54	20.26	11.80	28.54	20.53	21.90
59	78.13	9.70	6.05	10.31	11.87	12.73	19.54	20.26	12.40	35.08	26.66	28.10
70	89.40	25.53	21.35	26.22	11.20	6.36	12.79	13.48	10.50	14.38	7.25	8.47
154	74.00	3.90	0.45	4.48	10.53	0.00	6.04	6.69	12.60	37.25	28.70	30.17
192	77.40	8.68	5.06	9.28	10.27	-2.47	3.42	4.05	15.40	67.76	57.30	59.09
226	79.67	11.86	8.14	12.48	10.60	0.66	6.75	7.40	11.87	29.30	21.25	22.62
236	73.20	2.78	-0.64	3.35	10.27	-2.47	3.42	4.05	13.07	42.37	33.50	35.02
249	82.27	15.52	11.67	16.15	12.20	15.86	22.86	23.61	14.53	58.28	48.42	50.10
279	75.93	6.61	3.07	7.20	11.87	12.73	19.54	20.26	10.80	17.65	10.32	11.57
289	79.20	11.20	7.51	11.82	11.73	11.40	18.13	18.84	13.27	44.55	35.55	37.09
Average	78.00	9.52	5.88	10.12	11.24	6.74	13.19	13.88	12.62	37.47	28.91	30.37
Bulk	71.22				10.53				9.18			
Giza 165	68.00				9.80				9.56			
Sakha 93	73.67				9.93				9.79			
Mid-parents	70.83				9.87				9.68			
L.S.D. 0.05	2.69				1.18				2.07			
Entr. 0.01	3.65				1.60				2.81			
L.S.D. 0.05	2.31				1.22				2.11			
Fam. 0.01	3.16				1.68				2.89			

**Table 8. Continued.**

Fam. No.	Spikelets number/spike				Biological yield/plant, g				Weight of spikes/plant, g			
	Mean	Bulk	Better parent	M.-parents	Mean	Bulk	Better parent	M.-parents	Mean	Bulk	Better parent	M.-parents
1	22.47	10.85	12.74	13.09	54.78	57.59	48.90	60.98	30.88	53.02	49.90	61.76
59	21.33	5.23	7.02	7.35	44.15	27.01	20.01	29.74	25.67	27.21	24.61	34.47
70	20.60	1.63	3.36	3.67	46.58	34.00	26.61	36.88	27.36	35.58	32.82	43.32
154	20.60	1.63	3.36	3.67	41.19	18.50	11.96	21.04	24.25	20.17	17.72	27.03
192	20.60	1.63	3.36	3.67	51.53	48.25	40.07	51.43	27.62	36.87	34.08	44.68
226	21.27	4.93	6.72	7.05	46.59	34.03	26.64	36.91	26.27	30.18	27.52	37.61
236	20.60	1.63	3.36	3.67	45.06	29.63	22.48	32.41	25.21	24.93	22.38	32.06
249	22.87	12.83	14.75	15.10	56.05	61.25	52.35	64.71	32.51	61.10	57.82	70.30
279	21.33	5.23	7.02	7.35	40.26	15.82	9.43	18.31	23.73	17.59	15.19	24.31
289	20.80	2.61	4.37	4.68	48.34	39.07	31.39	42.05	27.78	37.66	34.85	45.52
Average	21.25	4.83	6.62	6.95	47.45	36.51	28.98	39.44	27.13	34.44	31.70	42.12
Bulk	20.27				34.76				20.18			
Giza 165	19.80				31.32				17.58			
Sakha 93	19.93				36.79				20.60			
Mid-parents	19.87				34.03				19.09			
L.S.D. 0.05	1.31				2.49				3.18			
Entr. 0.01	1.78				3.38				4.33			
L.S.D. 0.05	1.43				2.57				3.29			
Fam. 0.01	1.97				2.52				4.52			
Fam. No.	Grains yield/plant, g				Harvest index, %				Threshing index, %			
	Mean	Bulk	Better parent	M.-parents	Mean	Bulk	Better parent	M.-parents	Mean	Bulk	Better parent	M.-parents
1	20.06	41.37	32.94	45.89	36.74	-10.0	-10.54	-8.92	65.09	-7.44	-11.13	-9.50
59	16.85	18.75	11.66	22.55	38.36	-6.03	-6.60	-4.91	65.60	-6.71	-10.43	-8.79
70	20.01	41.01	32.60	45.53	42.88	5.05	4.41	6.30	73.05	3.88	-0.26	1.57
154	17.51	23.40	16.04	27.35	42.75	4.73	4.09	5.97	72.47	3.06	-1.05	0.76
192	18.57	30.87	23.06	35.05	35.89	-12.08	-12.61	-11.03	67.00	-4.72	-8.52	-6.84
226	18.33	29.18	21.47	33.31	39.39	-3.50	-4.09	-2.35	69.92	-0.57	-4.53	-2.78
236	18.16	27.98	20.34	32.07	40.40	-1.03	-1.63	0.15	71.99	2.37	-1.71	0.10
249	22.03	55.25	45.99	60.22	39.69	-2.77	-3.36	-1.61	67.93	-3.40	-7.25	-5.55
279	16.66	17.41	10.40	21.16	41.66	2.06	1.44	3.27	70.48	0.23	-3.77	-2.00
289	19.60	38.13	29.89	42.55	40.58	-0.59	-1.19	0.59	70.82	0.71	-3.30	-1.53
Average	18.78	32.35	24.45	36.58	39.83	-2.43	-3.02	-1.26	69.44	-1.25	-5.19	-3.45
Bulk	14.19				40.82				70.32			
Giza 165	12.41				39.62				70.60			
Sakha 93	15.09				41.07				73.24			
Mid-parents	13.75				40.34				71.92			
L.S.D. 0.05	2.33				2.24				2.37			
Entr. 0.01	3.17				3.05				3.22			
L.S.D. 0.05	2.45				2.06				2.21			
Fam. 0.01	3.36				2.83				3.03			

L.S.D. Entr.: to compare families with parents and bulk sample.  
 L.S.D. Fam.: to compare families with each other.  
 0.05 & 0.01, significant at 0.05 and 0.01 levels of probability, respectively.

### 2.2.6-Family score for selection response (FSSR) in cycle two ( $F_6$ ) of pedigree line selection

The family score for selection response (FSSR) was calculated as a mean of selection responses for each selected  $F_6$  family in different models which included mainly grain yield/plant beside other different traits in both populations (Tables 9). Also, the FSSR was accounted for each  $F_6$  family in relative to better parent, mid parents and unselected bulk sample for each model (Tables 9). The results revealed that the mean of family score for selection response (FSSR) over all selected  $F_6$  family of Model 1 recorded the highest value (34.57 and 36.19%), followed by Model 2 (31.50 and 33.12%) and Model 7 (29.52 and 31.12%) in population I and II, respectively. This results may be due to those models were including traits possessed high selection response such as grain yield/plant, biological yield/plant and weight of spikes/plant. Moreover, means of FSSR over all selected  $F_6$  families in relative to bulk sample were high in rank for model 4 (30.11) and model 6 (35.19%); followed by model 3 (28.01) and model 3 (34.91%); and model 2 (27.89) and model 8 (34.57%) for population I and II, respectively. These models had traits accounted high selection response such as grain yield/plant, biological yield, number and weight of spikes/plant. Meanwhile, the respective rank for FSSR in comparing to the better parent exhibited that the model 3 (16.79) and model 6 (28.51%) were the first order, followed by model 8 (15.68) and model 7 (28.38%) in the second rank and

then model 6 (15.56) and model 8 (28.35%) in population I and II, respectively. Same previous traits in different combinations were belonged to these models. These results revealed that the genes controlled these traits expressed high genetic direct (GY/P) and indirect (BY/P, NS/P and WS/P) responses to pedigree selection in wheat.

The FSSR for individual selected  $F_6$  families scaled that the family no. 536 in population I ranked the highest order in four models (nos. 2, 4, 5 and 7) and second order in four models (nos. 1, 3, 6 and 8) as a mean and also in relative to bulk sample, better parent and mid parents. Its FSSR ranged from 21.65 (mod. 1) to 48.32% (mod. 4), from 15.31 (mod. 1) to 31.30% (mod. 7) and from 22.79 (mod. 1) to 47.28% (mod. 7) in relative to bulk sample, better parent and mid parent, respectively. Also, the family no. 41 in population I arranged to be the first order in four models (nos. 1, 3, 6 and 8), second order in two models (nos. 2 and 7) and the third one in two models (nos. 4 and 5). Its FSSR varied from 23.79 (mod. 1) to 51.31% (mod. 3) from 16.00 (mod. 5) to 39.20% (mod. 3) and from 25.01 (mod. 1) to 49.30% (mod. 3) comparing to the bulk sample, better parent and mid parents, respectively.

It is remark result that both families nos. 41 and 536 were in successes order through the first and second order. Also, the first rank for family no. 536 was correlated with the models having GW/P, BY/P and WS/P and the second order connected with models which had NS/P and *vice versa* for family no. 41. In general,

the lowest FSSR yielded from the model no. 1 which had all studied traits, this due to some traits possessed less selection response such as plant height and other revealed negative values such as harvest index and threshing index (Table 9).

Also, in population II, the FSSR for individual selected  $F_6$  families (cycle two) graded that the family no. 249 ranked to be in the first order in all models for mean of FSSR and relative to the bulk, better parent and mid parents. Its FSSR ranged from 30.43 (mod. 1) to 59.20% (mod. 7), from 27.03 (mod. 1) to 52.05% (mod. 7) and from 32.56 (mod. 1) to 65.26% (mod. 4) comparing to unselected bulk, better parent and mid parents, respectively. Moreover, the family no. 1 exerted to be in the second order for FSSR in five models (nos. 1, 2, 4, 5 and 7) and third order in two models (nos. 6 and 8). Its FSSR varied from 20.68 (mod. 1) to 50.66% (mod. 7), from 17.66 (mod.

1) to 43.91% (mod. 7) and from 22.82 (mod. 1) to 56.21% (mod. 7) in relative to bulk sample, better parent and mid parents, respectively. Also, family no. 192 ranked in second order in two models (nos. 3 and 8) and third order in two models (nos. 2 and 7). In general, it is clear that the highest response was exerted from model 7 which includes grain yield/plant, biological yield/plant and weight of spikes/plant (Table 9). These traits had the highest correlation coefficient between each other in base population.

The lowest FSSR accounted from model 1, as revealed in population I and connected to the same conclusion.

The superior families of 41 and 536 in population I and 1 and 249 in population II and others in both populations appear to be in grate order evaluation as a new genotypes exerted from this study.

**Table 9. Family score for selection response (FSSR) in cycle two (F<sub>6</sub>) of pedigree line selection for grain yield/plant in population I and II.**

	Fam. No.	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8
	<b>Population I</b>	28	35.11	33.58	14.20	23.07	15.43	26.29	31.67
34		34.41	30.24	14.03	20.74	13.73	23.91	28.26	17.45
36		34.05	29.69	13.72	20.40	13.85	23.42	27.74	17.09
41		36.31	35.80	16.98	23.67	15.38	28.78	33.35	20.80
108		34.49	30.40	14.70	21.85	14.77	24.37	28.76	18.30
141		33.82	28.54	13.57	19.92	13.93	22.75	26.79	16.81
258		34.28	29.30	14.00	21.19	14.50	23.48	27.81	17.61
261		34.78	32.57	14.47	21.51	14.81	25.41	30.14	18.07
289		33.22	29.00	13.70	19.77	13.56	23.04	27.05	10.84
291		34.91	31.75	15.30	20.80	14.20	25.39	29.34	18.37
296		35.20	32.80	15.26	22.89	15.32	25.82	30.69	18.99
313		35.35	31.52	14.54	20.69	14.24	24.67	29.00	17.68
321		33.71	28.86	14.24	20.60	13.78	23.07	27.12	17.38
401		35.14	33.69	14.43	22.51	15.03	26.28	31.44	18.60
441		33.69	28.28	13.77	20.60	14.27	22.89	20.06	17.29
460		34.63	33.59	15.33	23.92	15.43	26.76	31.90	10.72
466		33.38	30.35	13.68	20.56	14.08	24.08	28.46	17.35
474	34.09	30.28	14.95	20.88	13.92	24.50	28.40	18.18	
518	34.98	33.13	15.92	23.43	15.17	26.41	31.15	19.68	
536	35.84	36.65	16.06	24.83	16.26	28.81	34.34	20.62	
<b>Average</b>	<b>34.57</b>	<b>31.50</b>	<b>14.64</b>	<b>21.69</b>	<b>14.58</b>	<b>25.01</b>	<b>29.52</b>	<b>18.28</b>	
<b>Population II</b>	Fam. No.	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6	Model 7	Model 8
	1	36.05	37.42	15.03	25.47	15.97	29.38	35.24	20.91
	59	34.93	30.50	14.63	21.26	14.36	24.77	28.89	18.31
	70	37.95	33.30	15.26	23.69	15.61	26.11	31.32	19.29
	154	35.10	29.35	15.06	20.88	14.02	23.89	27.65	18.12
	192	36.03	35.05	16.98	23.10	14.42	28.28	32.57	20.53
	226	35.99	32.46	15.10	22.30	14.47	25.77	30.40	18.82
	236	35.33	31.61	15.62	21.69	14.22	25.38	29.48	18.81
	249	38.90	39.04	18.28	27.27	17.12	31.28	36.86	23.02
	279	34.75	28.46	13.73	20.20	14.27	22.86	26.88	17.06
	289	36.90	33.97	16.44	23.69	15.67	27.25	31.91	20.22
<b>Average</b>	<b>36.19</b>	<b>33.12</b>	<b>15.70</b>	<b>22.96</b>	<b>15.01</b>	<b>26.50</b>	<b>31.12</b>	<b>19.51</b>	

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## كفاءة دورتين من الإنبات المنسب في قمح الخبز خلال الزراعة المتأخرة

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### الملخص

تهدف هذه الدراسة إلى تقدير كفاءة دورتين من الإنبات المنسب في قمح الخبز عند الزراعة المتأخرة خلال ثلاث مواسم ٢٠١٢/٢٠١٣ و ٢٠١٣/٢٠١٤ و ٢٠١٤/٢٠١٥ بمزرعة كلية الزراعة بجامعة أسيوط. وإستخدمت لذلك عشيرتين إنعزليتين من قمح الخبز هما ديبيرا \* ساحل و جيزة ١٦٥ \* سخا ٩٣.

أنخفض معامل الإختلاف الوراثي والمظهري لمحصول حبوب النبات من ١٤,٩٠ و ١٧,١٢ في العشيرة الأساسية (الجيل الرابع) إلى ٣,٩٨ و ٦,١٦% بعد دورتين من الإنبات (الجيل السادس) في العشيرة الأولى. كما أنخفضت القيم من ٢١,٩٣ و ٢٢,٦٥ (الجيل الرابع) إلى ٢,٦٨ و ٨,٨٥% (الجيل السادس) في العشيرة الثانية على الترتيب. وقد وجد نفس الإتجاه في الصفات المرتبطة في كلا العشيرتين. وقد أتضح أن درجة التوريث قد أنخفضت لصفتي محصول حبوب النبات وعدد سنابل النبات في العشيرتين بعد دورتي الإنبات مقارنة بالعشيرة الأساسية.

بعد دورتي الإنبات المنسب لصفة محصول حبوب النبات فإن متوسط المنتخبات في الجيل السادس سجل قيمة قدرها ١٧,٨٢ جم في العشيرة الأولى مقارنة بالأباء ديبيرا (١٥,٨٣) و ساحل (١١,٩٤) وكذلك عينة البلك (١٣,٣٨ جم). كما سجلت منتخبات العشيرة الثانية متوسط قدره ١٨,٧٨ جم مقارنة بالقيم المنخفضة ١٢,٤١ و ١٥,٠٩ و ١٤,١٩ جم الناتجة من الأباء جيزة ١٦٥ و سخا ٩٣ وعينة البلك على الترتيب. ومن الواضح أن المنتخبات في كلا العشيرتين زادت عن آبائهم وعينة البلك في الدورة الثانية من الإنبات المنسب (الجيل السادس) لصفة محصول حبوب النبات. أيضا زادت منتخبات الجيل السادس عن أفضل الأباء وعينة البلك لصفات عدد سنابل النبات والوزن البيولوجي للنبات ووزن سنابل النبات وطول النبات وطول السنبل و عدد سنبلات السنبل.

الإستجابة المباشرة للإنبات المنسب لصفة محصول حبوب النبات (الصفة الإنتخابية) سجلت ٣٣,١٨ و ٣٢,٣٥ وكذلك ١٢,٥٧ و ٢٤,٤٥ وأيضا ٣٦,٥٨ و ٢٨,٣٩% لدورتى الأنبات المنسب مقارنة بعينة البلك وأفضل الأباء ومتوسط الأبوين في العشيرة الأولى والثانية على الترتيب. كما أشارت النتائج أن متوسط إستجابة الإنبات لجميع العائلات (FSSR) في الجيل السادس أن الموديل الأول سجل أعلى إستجابة بـ ٣٤,٥٧ و ٣٦,١٩% ثم الموديل الثاني بـ ٣١,٥٠ و ٣٣,١٢% ثم الموديل السابع بـ ٢٩,٥٢ و ٣١,١٢% في العشيرة الأولى والثانية على الترتيب.

وعموما أوضحت النتائج أن الإنبات المنسب المباشر لمحصول حبوب النبات في قمح الخبز في الزراعات المتأخرة يكون أداة فعالة لتحسين محصول الحبوب وللحصول على سلالات عالية المحصول.