

Genetic Analysis and Selection in Segregating Populations of Three Wheat Crosses for Grain Yield and Some Agronomic Traits

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ABSTRACT

This study was conducted at the Experimental Farm of the Faculty of Agriculture, Ain Shams University, at Shalakan, Kalubia Governorate, Egypt during the three successive growing seasons 2012/2013, 2013/ 2014 and 2014/2015 to study the relative response to selection in three bread wheat crosses for two cycles started in F3 using pedigree selection procedure for improving grain yield and some other agronomic traits, i. e. days to heading, plant height, spike length, number of spikes/ plant, number of spikelets/ spike, number of kernels/ spike and 1000-kernel weight. The results obtained revealed the presence of sufficient genetic variability among selected families or genotypes regarding the studied traits and a great response to selection can be expected from the progenies of these crosses. Genotypic coefficient of variation values were near those of phenotypic coefficient of variation for all traits, indicating minor role for the environment on variation among genotypes. This may interpret the high values of heritability and expected genetic gain of selection. The highest estimates of phenotypic and genotypic coefficient of variation were shown by number of spikes/ plant and grain yield/ plant while, the low estimates were shown by days to heading and no. of spikelets/ spike across the F3, F4 and F5 generations. The heritability estimates in broad sense were; low for number of spikes/ plant, moderate for spike length, number of spikelets/ spike and 1000-kernel weight and high for days to heading, plant height, number of kernels/ spike and grain yield/ plant across the three generations. The promising lines; 7, 8, 10, 19, 24, 27, 30 and 31 exhibited the best performance in F5 –generation and surpassed most check cvs. in grain yield and most yield components. Thus, these promising lines could be used in breeding programs for improving wheat grain yield. Grain yield was positively and significantly correlated with each of spike length, no. of spikelets/ spike, no. of spikes/ plant, no. of kernels/ spike and 1000-kernel weight at phenotypic and genotypic levels and with each of days to heading and plant height at genotypic level only. Thus, these traits could be considered as selection criteria in wheat breeding programs for yield improvement.

Keywords: *Triticum aestivum* L., Selection, Phenotypic and genotypic coefficient of variation, Heritability, Expected genetic gain, Correlation.

INTRODUCTION

Increasing wheat production is considered an important national goal to face the increasing food needs of Egyptian population. This increment could be achieved through maximizing production per unit area (vertical expansion) and /or cultivating more land with wheat (horizontal expansion). However, increasing production per unit area seems to be the most appropriate approach to minimize the gap between total local production and consumption. This can be attained via developing high yielding varieties and simultaneously, implementing suitable cultural practices. The main objective of most wheat breeding programs is to develop high yielding varieties with good qualities. Pedigree selection for yielding potential in wheat assumes selection in the F2 generation of individual plants spaced apart to enable their evaluation then, selection from F3 to F6 generation is practiced among and within families following evaluation in row plots and /or in yield trials (Poehlman and Sleper, 1995). Wheat breeders improve grain yield through selection by using grain yield itself as a selection criterion (Loffler and Busch, 1982). Mahdy (1988), Mahmoud (2007) and Ali (2011) reported that selection could be also based on grain yield as well as increased spike length, number of spikes/ plant and number of kernels/ spike. Information about phenotypic and genotypic coefficients of variation, heritability, expected genetic gain and correlation coefficients among studied traits can help breeders for increasing the selection efficiency. Rady *et al.* (1981), Ehdai and Waines (1989), Belay *et al.* (1993), Moghaddam *et al.* (1997), Menshawy (2007), Abd El-Fattah *et al.* (2009), Khalil *et al.* (2010), El-Ameen (2012), Ahmed *et al.* (2014) and Mohamed (2014) found; significant variation in yield and its components among wheat

genotypes, moderate values of phenotypic and genotypic variation for grain yield, moderate to high values of heritability and expected genetic gain for grain yield and its compounds and significant positive correlation between grain yield and its components. The main objectives of this work were to: (1) Estimate the efficiency of pedigree selection method for improving grain yield by comparing the resultant promising lines with commercial cultivars. (2) Estimate phenotypic and genotypic coefficients of variation, heritability in the broad sense, expected genetic gain upon selection and correlation coefficients among studied traits to formulate appropriate breeding program to improve yield.

MATERIALS AND METHODS

The field experimental work of the present investigation was carried out at the Experimental Farm of the Faculty of Agriculture, Ain Shams University, at Shalakan, Kalubia Governorate, Egypt during the three successive growing seasons 2012/2013, 2013/ 2014 and 2014/2015 to study the relative response to selection in three bread wheat crosses for three cycles started in F3 using pedigree selection procedure for improving grain yield and its components. Besides estimating phenotypic and genotypic coefficients of variation, heritability in the broad sense, expected genetic gain upon selection through three generations (F3, F4 and F5). The F2 seeds of the three crosses; Giza168 x Cham8 (Cross1), Giza168 x Bohouth6 (Cross 2) and Sakha 94 x Bohouth6 (Cross 3) were obtained from a previous work by Osman *et al.* (2013). While, the six check cultivars; (Sids 1, Sids12, Sakha93, Gemmeiza 9, Gemmeiza 12 and masr2) were obtained from wheat Dept. Agric. Res. Cent., Giza, Egypt.

In 2012/2013 (F3 generation), 150 superior F2 plant were planted on 21th Nov. where the progeny of

each plant was planted in three single rows represent three replication. Single plants were grown in rows 3 m long and spaced 25cm apart and 15 cm between plants within rows. Data were recorded for eight characters; days to heading, plant height (cm), spike length (cm), number of spikelets/ spike, number of spikes/ plant, number of kernels/ spike, 100- kernel weight (g) and grain yield/ plant. The 20 superior families (progenies) were selected using different selection criteria in each cross (60 families) and seeds of the superior plant of each selected families were saved to initiate the first cycle of early pedigree line selection.

In 2013/ 2014 (F4 generation), The progeny of each selected plant from F3 was grown on 25th Nov. in three rows as done in F3. The seeds of best; 15 plants from the first cross, 12 plants from the second cross and 13 plants the third cross were saved to the next season (a total of 40 promising lines).

In 2014/2015 (F5 generation), the 40 superior promising lines, their parents and the six check cultivars; (Sids 1, Sids12, Sakha93, Gemmeiza 9, Gemmeiza 12 and masr2) were sown on 2nd Dec. in a randomized complete block design with three replications; each replicate consisted of 50 plots of wheat entries distributed randomly within the replicate. The plot consisted of three rows. Each row was 3 m. in length and 20 cm apart. Grains were spaced at 10 cm within row and one plant was left per hill. The recommended cultural practices for wheat production were followed during the growing season. Days to heading, was measured as the number of days from sowing till the main stem spikes of about 50% of plants per plot were fully emerged from the flag leaf. At the harvest, plant height (cm), spike length (cm), number of spikes/ plant, number of spikelets/ spike, number of kernels/ spike, 1000-kernel weight (g) and grain yield/ plant (g) were recorded on 10 competitive individual plants for each genotype in each replicate. The analysis of variance for F3, F4 and F5 populations were performed according to Gomez and Gomez (1984). L.S.D was computed to compare differences among means at 5% level. The phenotypic and genotypic coefficients of variability were calculated according to Burton (1952).

Table 1. Analysis of variance for all the traits studied of bread wheat genotypes in the F3, F4 and F5 - generation.

Source of variation	Df	Days to heading	Plant height(cm)	Spike length(cm)	Number of spikelets/spike	Number of spikes/plant	Number of kernels/spike	100-kernel weight (g)	Grain yield/ plant (g)
F3									
Families	59	84.35**	254.07**	5.83**	5.44**	11.34**	340.28**	1.41**	70.08**
Error	118	1.75	4.71	0.76	1.28	6.32	14.78	0.24	4.24
F4									
Families	59	60.39**	578.67**	5.15**	5.52**	47.04**	411.19**	1.04**	70.21**
Error	118	0.39	4.68	0.79	1.04	21.33	8.07	0.21	4.32
F5									
Genotypes	49	38.01**	497.49**	1.86**	3.29**	15.21**	120.94**	74.89**	127.15**
Error	98	1.01	3.39	0.59	0.57	3.25	8.73	3.61	3.89

** = denote significant at 0.01 level of probability.

Genetic parameters

Variance is considered as an important measure for efficiency of selection and breeding methods. The data of phenotypic (P.C.V) and genotypic (G.C.V) coefficient of variations, broad-sense

-Phenotypic (P.C.V) and genotypic (G.C.V) coefficient of variation.

$$P.C.V = \frac{\sigma^P}{\bar{X}} \times 100 \quad G.C.V = \frac{\sigma^G}{\bar{X}} \times 100$$

Where: σ^P , σ^G and \bar{X} are the phenotypic, the genotypic standard deviation and genotypes mean, respectively.

-Broad sense heritability (h^2) was estimated following Walker (1960).

$$h^2 = \frac{\sigma^2g}{\sigma^2P} \times 100$$

Where: σ^2g and σ^2P denote variance of genotypes and phenotypic, respectively.

- The expected genetic gain upon selection (AG):

a-As an amount $\Delta G = (h^2) (\sigma^p) (K)$

Where: h^2 = the broad sense heritability. σ^p = standard deviation of phenotypic variance.

K = selection differential coefficient given the value 2.06 at 5% selection intensity.

b- As percentage of the mean = $\frac{\Delta G}{\bar{X}} \times 100$

Where: \bar{X} = genotypes mean.

4- Phenotypic and genotypic correlation coefficients were calculated between all possible pairs of studied traits according to Singh and Narayanan (2000).

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance for all studied traits are presented in Table (1). The analysis indicates the presence of high significant differences among genotypes for all studied traits across the three generations F3, F4 and F5 for all studied traits. These results reveal presence of sufficient genetic variability among selected families or genotypes regarding the studied traits and a greater response to selection can be expected from the progenies of these crosses. Similar results were found by Tammam (2004), Menshawy (2007) and Abd El-Fattah *et al.* (2009), Khalil *et al.* (2010), El-Ameen (2012), El-Ameen *et al.* (2013), Ahmed *et al.* (2014), Mohamed (2014).

heritability (h^2 b.s) and expected genetic gain are shown in Table (2). For number of days to heading, the genotypic coefficient of variation across the three generations (F3, F4 and F5) gave a value of 5.39, 4.66 and 3.84 % respectively which was approximately equal

to the corresponding phenotypic coefficient of variation 5.56, 4.70 and 3.99 %, through the three generation F3, F4 and F5, respectively, indicating that most variation exists among genotypes is genetic in nature for days to heading. Estimates of the broad sense heritability for this trait gave a value of 94.02, 98.09 and 92.43 % across the three generations F3, F4 and F5, respectively which is considered as a high estimate, indicating that this trait is mainly affected by the genetic factors and partially by the environmental ones. The expected genetic gain upon selecting the earliest 5% of wheat genotypes would be 10.48, 9.12 and 6.96 day or about 10.77, 9.50 and 7.61 % through the three generations F3, F4 and F5, respectively of the population mean. These results suggested that a relative progress can achieved through the selection for early lines.

Concerning plant height, the phenotypic and genotypic coefficient of variation had values of (9.68, 12.64 and 12.67 %) and (9.42, 12.49 and 12.54 %)

across the three generations F3, F4 and F5, respectively. These inclined estimates detected for P.C.V and G.C.V, suggested that the effect of environment on the expression of this is relatively less than the genotypic effect. Thus, selection for this trait may be providing a chance for some genetic improvement. The broad sense heritability for this trait gave an estimate of 94.64, 97.61 and 97.98 % in F3, F4 and F5- generation, respectively which is considered a high percentage, indicating that plant height is mainly determined by the genetic factors with few environmental influences. Thus, selection may lead to progressive genetic improvement for this trait. The expected genetic gain upon selecting the best 5% for plant height in the wheat genotypes would be 18.27, 28.15 and 26.17 cm or about 18.87, 25.42 25.57 % in F3, F4 and F5-generations, respectively of the population mean. This relatively high gain percentage support the conclusion mentioned above for importance of the genetic role in the expression of this trait.

Table 2. Means, phenotypic (P.C.V) and genotypic (G.C.V) coefficients of variation, broad sense heritability (h² b.s) and expected genetic gain for the traits studied of bread wheat genotypes in the F3, F4 and F5 – generation.

Traits	Mean	P.C.V %	G.C.V %	h ² b.s %	Expected genetic gain	
					Amount	% mean
F3 generation						
Days to heading	97.33	5.56	5.39	94.02	10.48	10.77
Plant height (cm)	96.83	9.68	9.42	94.64	18.27	18.87
Spike length (cm)	11.43	13.69	11.37	68.98	2.22	19.46
No. of spikelets/spike	22.09	7.39	5.33	52.00	1.75	7.92
No. of spikes/plant	8.51	33.22	15.20	20.93	1.22	14.33
No. of kernels/spike	73.84	15.04	14.11	88.01	20.13	27.26
100-kernel weight (g)	4.51	17.60	13.85	61.90	1.01	22.44
Grain yield/plant (g)	20.78	24.63	22.54	83.81	8.83	42.52
F4 generation						
Days to heading	96.05	4.70	4.66	98.09	9.12	9.50
Plant height (cm)	110.73	12.64	12.49	97.61	28.15	25.42
Spike length (cm)	13.43	11.15	8.98	64.78	2.00	14.88
No. of spikelets/spike	25.17	6.32	4.86	58.95	1.93	7.68
No. of spikes/plant	18.03	30.33	16.24	28.66	3.23	17.91
No. of kernels/spike	77.68	15.36	14.92	94.33	23.19	29.86
100-kernel weight (g)	3.29	21.20	15.99	56.85	0.82	24.83
Grain yield/plant (g)	30.93	16.58	15.15	83.56	8.83	28.53
F5 generation						
Days to heading	91.45	3.99	3.84	92.43	6.96	7.61
Plant height (cm)	102.33	12.67	12.54	97.98	26.17	25.57
Spike length (cm)	12.24	8.22	5.32	41.78	0.87	7.08
No. of spikelets/spike	22.72	5.35	4.19	61.40	1.54	6.76
No. of spikes/plant	14.89	18.07	13.41	55.09	3.05	20.50
No. of kernels/spike	70.80	9.59	8.64	81.08	11.34	16.02
1000-kernel weight (g)	45.13	11.59	10.80	86.81	9.36	20.73
Grain yield/plant (g)	26.77	25.05	23.94	91.35	12.62	47.14

With respect to spike length, the phenotypic coefficient of variation across the three generations F3, F4 and F5 gave a value of 13.69, 11.15 and 8.22 %, respectively whereas the genotypic one gave a value of 11.37 8.98 and 5.32 % in F3, F4 and F5-generations, respectively, indicating that this trait is affected by both genetic and environmental factors. The broad sense heritability for this trait had an estimate of 68.98, 64.78 and 41.78 % for F3, F4 and F5- generation, respectively, which is considered a moderate percentage, indicating that this trait is mainly determined by genetic factors and partially by environmental ones. The expected genetic gain upon selecting the best 5% of the genotypes for spike length would be 2.22, 2.00 and 0.87 cm or about 19.49, 14.88 and 7.08 % in F3, F4 and F5-generations, respectively of the population mean.

Concerning number of spikelets/ spike, the phenotypic and genotypic coefficients of variation across the three generations F3, F4 and F5 had values of (7.39, 6.32 and 5.35 %) and (5.33, 4.86 and 4.19 %), respectively. The inclined estimates detected for the P.C.V and the G.C.V., suggesting that the effect of environment on the expression of this trait is relatively less than the genotypic effects. Thus selection for this trait may provide a chance for some genetic improvement. Estimation of the broad sense heritability for this trait gave a value of 52.00, 58.95 and 61.40 % for F3, F4 and F5- generation, respectively, which is considered a moderate percentage, indicating that this trait is mainly determined by genetic factors and partially by environmental ones. The expected genetic gain upon selecting the best 5% of wheat populations would be 1.75, 1.93 and 1.54 spikelet or about 7.92,

7.68 and 6.76 % in F3, F4 and F5-generations of populations mean.

For number of spikes/ plant the phenotypic coefficient of variation across the three generations F3, F4 and F5 gave a value of 33.22, 30.33 and 18.07%, whereas the genotypic one gave a value of 15.20, 16.24 and 13.41 %, indicating that this trait is affected by both genetic and environmental factors. The broad sense heritability for no. of spikes/ plant had an estimate of 20.93, 28.66 and 55.09 %, which is considered a low percentage for F3 and F4 generation meantime moderate for F5 generation, indicating that no. of spikes/ plant is determined by the genetic factors with great environmental influences. Thus, selection may lead to progressive genetic improvement for this trait. The expected genetic gain upon selecting the best 5% of the genotypes for no. of spikes/ plant would be 1.22, 3.23 and 3.05 spike or about 14.33, 17.91 and 20.50 % in F3, F4 and F5-generations of the population mean.

Regarding number of kernels/ spike, the phenotypic and genotypic coefficient of variation had values of (15.04, 15.36 and 9.59 %) and (14.11, 14.92 and 8.64 %) across the three generations F3, F4 and F5, respectively. These inclined estimates detected for P.C.V and G.C.V, suggested that the effect of environment on the expression of this is relatively less than the genotypic effect. Thus, selection for this trait may be providing a chance for some genetic improvement. The broad sense heritability for this trait gave an estimate of 88.01, 94.33 and 81.08 % in F3, F4 and F5- generation, respectively which is considered a high percentage, indicating that no. of kernels/ spike is mainly determined by the genetic factors with few environmental influences. Thus, selection may lead to progressive genetic improvement for this trait. The expected genetic gain upon selecting the best 5% for number of kernels/ spike in the wheat genotypes would be 20.13, 23.19 and 11.34 spikes or about 27.26, 29.86 and 16.02 % in F3, F4 and F5-generations, respectively of the population mean. This relatively high gain percentage support the conclusion mentioned above for importance of the genetic role in the expression of this trait.

With respect to 1000-kernel weight, the phenotypic coefficient of variation across the three generations F3, F4 and F5 gave a value of 17.60, 21.20 and 11.59 %, respectively whereas the genotypic one gave a value of 13.85, 15.99 and 10.80 % in F3, F4 and F5-generations, respectively, indicating that this trait is affected by both genetic and environmental factors. The broad sense heritability for this trait had an estimate of 61.90, 56.85 and 86.81 % for F3, F4 and F5- generation, respectively, which is considered a moderate percentage for F3 and F4 generation meantime high for F5 generation, indicating that this trait is mainly determined by genetic factors and partially by environmental ones. The expected genetic gain upon selecting the best 5% of the genotypes for 1000-kernel weight would be 1.01, 0.82 and 9.36 g or about 22.44, 24.83 and 20.73 % in F3, F4 and F5-generations, respectively of the population mean.

Regarding grain yield/ plant, the phenotypic coefficient of variation across the three generations F3, F4 and F5 gave a value of 24.63, 16.58 and 25.05 %, respectively which is somewhat near the value of the genotypic one (22.54, 15.15 and 23.94 %) in F3, F4 and F5-generations, respectively, indicating that, this trait is determined by both genetic and environmental factors with predominance of the genetic ones. The broad sense heritability for grain yield/plant gave an estimate of 83.81, 83.56 and 91.36 % for F3, F4 and F5- generation, respectively which is considered a relatively high estimate, indicating that this trait is mainly determined by the genetic factors and partially by the environmental ones. The expected genetic gain upon selecting the best 5% of the wheat genotypes would be 8.83, 8.83 and 12.62 g or about 42.52, 28.53 and 47.14 % of the population mean. This result suggested that a relatively high progress can be achieved through the selection for this trait in such population.

From the above mentioned results, it is noticed that the values of G.C.V. and P.C.V. decreased from cycle one to cycle two of direct pedigree selection under different selection criteria and the late pedigree single trait selection was more effective than early selection in wheat.

Results in the same direction were obtained by Rady *et al.* (1981), Mahdy (1988), Ehdaie and Waines (1989), Belay *et al.*(1993), Moghaddam *et al.* (1997), Tammam (2004), Mahmoud (2007), Menshawy (2007) and Abd El-Fattah *et al.* (2009), Khalil *et al.* (2010), Ali (2011), El-Ameen (2012), El-Ameen *et al.* (2013), Ahmed *et al.* (2014) and Mohamed (2014) who reported that the phenotypic and genotypic coefficient of variation, heritability and expected genetic gain for grain yield and its components were moderate to high.

Performance of wheat genotypes

The mean values of the studied genotypes for grain yield/ plant and its related agronomic traits in F5-generation are shown in Table (3). The results reveal that wheat genotypes greatly differed in their response in F5- generation for the studied traits. Number of days to heading ranged from 85 days (line 37) to 99.33 days (Bouhoth 6 (P4)) with an average of 91.45 days. Table (3) shows that some lines; 2, 4, 8, 15, 32 and 37 were earlier than the earliest check varieties and parents (Sakha 93 which gave a value of 88 days). With respect to plant height, it ranged from 84.25 cm (line 20) to 142.00 cm (line 25) with an average of 102.33 cm. The two lines 22 and 25 were the tallest and surpassed all the check varieties and parents. Concerning spike length, it ranged from 10.00 cm (line 37) to 13.58 cm (line 14) with an average of 12.24 cm. The lines; 14, 24 and 31 showed the highest values of spike length without differ significantly from the best check variety (Sids 1 which gave a value of 13.54 cm). With respect to number of spikes/ plant, it ranged from 11.17 (line 17) to 19.92 (the cv. Sids 1) with an average of 14.89 spikes . Meantime, the lines; 8, 27, 30 and the cv. Gemmeiza 12 gave the highest values for no. of spikes/ plant without differ significantly from the best check variety (Sids 1 which gave a value of 19.92 spikes). Number of spikelets/ spike, ranged from 19.92 (line 34)

to 24.25 (the cv. Sids 1) with an average of 22.72 spikelets. Table (3) shows that some lines were superior to some the check varieties in no. of spikelets/ spike meantime, the lines; 7, 13, 17, 19, 24, 27, 30, 31 and the cvs. Sakha 94, Sids 12 and Gemmeiza 9 recorded the highest values for no. of spikelets/ spike without differ significantly from the best check variety (Sids 1 which gave a value of 24.25 spikelets). Concerning number of kernels/ spike, it ranged from 56.75 (line 25) to 82.42 (line 19) with an average of 70.80 kernels. The lines; 18, 19 and 31 and the cvs. Sakha 94 and Gemmeiza 9 showed the highest values of no. of kernels/ spike without differ significantly from the best check variety (Sids 1 which gave a value of 81.67 kernels). For 1000-kernel weight, it ranged from 32.06 g (line 16) to 53.57

g (the cv. Gemmeiza 9) with an average of 45.13 g. Some lines were superior to some the check varieties in 1000-kernel weight meantime, the lines; 10, 14, 22, 24, 26 and 27 and the cv. Gemmeiza 12 recorded the highest values for 1000-kernel weight without differ significantly from the best check variety (Gemmeiza 9 which gave a value of 53.57 g). Grain yield/ plant, ranged from 13.50 g (line 23) to 38.58 g (line 24) with an average of 26.77 g. Table (3) shows that some lines were superior to the most check varieties and their parents in grain yield/ plant in the F5- generation meantime, the lines; 7, 24, 27, 30 and 31 showed the highest values of grain yield/ plant without differ significantly from the best check variety (Sids 1 which gave a value of 37.67 g).

Table 3. Mean performance of; promising lines from three crosses, parents and six check varieties for studied traits.

Genotypes	Days to heading	Plant height(cm)	Spike length(cm)	Number of spikelets/spike	Number of spikes/ plant	Number of kernels/spike	1000-kernel weight (g)	Grain yield/ plant (g)
Cross I								
Line 1	91.67	116.83	11.75	21.50	15.33	66.67	43.93	21.58
2	86.33	103.50	12.08	22.17	15.17	70.67	34.07	26.38
3	87.00	101.42	11.67	22.33	13.75	67.00	40.57	14.88
4	86.00	98.92	12.58	23.17	16.14	74.33	38.50	31.08
5	93.00	99.17	12.25	22.33	11.25	63.25	44.07	24.25
6	95.00	95.00	12.33	23.00	14.00	69.17	44.76	22.50
7	93.00	103.08	12.42	23.50	16.58	75.50	47.33	35.92
8	86.00	102.67	12.50	23.33	18.33	68.92	47.94	34.00
9	90.00	103.67	12.75	22.83	12.42	77.00	40.75	27.42
10	87.00	106.58	13.00	25.00	17.33	76.42	51.62	33.17
11	87.33	104.00	11.83	22.50	13.75	66.92	43.41	21.83
12	91.33	98.92	12.25	23.00	12.58	74.17	45.01	24.00
13	91.00	102.25	11.75	23.67	13.25	66.50	44.01	29.58
14	91.33	104.00	13.58	23.17	15.65	59.08	50.51	29.25
15	86.67	101.00	11.17	22.83	12.92	64.00	44.23	25.50
Cross II Line 16	90.67	132.08	12.42	23.33	12.50	73.08	32.06	27.50
17	88.67	85.92	12.83	24.00	11.17	70.17	36.85	15.42
18	87.33	109.25	11.75	22.17	14.33	80.42	41.85	27.42
19	95.33	94.92	12.67	23.83	16.58	82.42	36.20	34.75
20	91.00	84.25	11.83	22.25	14.17	64.25	46.26	20.75
21	92.33	100.25	11.83	22.50	14.25	66.33	40.10	19.17
22	91.00	139.00	12.00	22.33	12.83	73.17	51.82	22.25
23	91.67	93.50	11.17	21.83	12.25	73.50	41.15	13.50
24	88.00	123.67	13.00	23.50	14.58	64.25	52.10	38.58
25	89.67	142.00	12.33	23.17	14.83	56.75	46.43	24.25
26	90.00	97.06	12.50	23.33	11.25	67.42	51.43	24.83
27	91.67	125.25	11.83	23.83	18.33	70.00	51.33	35.67
Cross III Line 28	96.00	86.25	12.58	22.50	13.67	69.42	47.75	25.25
29	94.00	95.33	12.00	22.50	12.92	68.17	43.44	19.08
30	97.00	101.42	12.50	23.67	18.42	74.42	46.94	37.08
31	94.00	100.42	13.56	23.67	16.83	79.00	49.71	34.04
32	86.00	93.42	12.25	21.75	14.58	65.50	45.10	24.75
33	89.67	96.83	11.42	22.17	13.83	74.75	37.72	18.42
34	91.00	94.08	11.17	19.92	15.42	65.50	42.59	19.17
35	95.00	92.92	11.25	20.25	13.58	60.58	49.88	26.25
36	91.00	84.58	10.58	20.75	13.92	63.92	41.12	23.08
37	85.00	112.17	10.00	23.08	13.42	72.17	47.81	20.83
Table 3. Cont. 38	94.67	103.75	12.17	22.00	13.77	72.17	46.28	26.92
39	89.00	91.83	10.75	21.83	13.25	66.17	47.07	26.17
40	93.00	115.42	12.50	22.33	13.08	61.00	47.67	22.08
Parents Giza 168 (P1)	97.00	94.50	12.17	21.33	12.85	81.25	46.55	17.33
Sakha 94 (P2)	95.33	101.75	13.50	23.50	18.93	73.42	43.28	32.17
cham 8 (P3)	96.00	89.92	12.17	22.50	17.30	68.92	43.39	31.75
Bouhoth 6 (P4)	99.33	86.83	13.08	20.17	17.92	74.33	45.68	34.75
Check varieties Sids 1	94.00	112.92	13.54	24.25	19.92	81.67	52.18	37.67
Sid12	90.33	103.25	13.42	24.00	16.78	81.17	46.33	29.75
Sakha 93	88.00	84.28	12.25	23.33	14.75	72.00	41.17	24.42
Gemmiza 9	96.00	103.25	12.50	23.50	18.33	81.58	53.57	33.33
Gemmiza 12	94.00	97.58	13.08	23.00	18.92	72.00	51.67	32.58
Masr 2	97.00	105.83	13.25	23.67	16.67	79.50	51.27	36.08
Mean	91.45	102.33	12.24	22.72	14.89	70.80	45.13	26.77
L.S.D. 0.05	1.63	2.98	1.24	1.22	2.92	4.79	3.08	3.20

Generally, the promising lines; 7, 8, 10, 19, 24, 27, 30 and 31 exhibited the best performance in F5-generation and surpassed the most check cvs. for grain yield and most yield components. Thus, these promising lines could be used in breeding programs for improving wheat grain yield.

Phenotypic and genotypic correlation coefficients

Phenotypic and genotypic correlation coefficients among the various studied characters for 50 genotypes of bread wheat are presented in Table (4). Generally, phenotypic and genotypic correlation coefficients were similar in signs in all cases except correlation between days to heading and no. of spikelets/ spike. Also, genotypic correlation coefficients were comparatively higher in magnitudes than the corresponding phenotypic one. These findings reflect that, the significant correlation detected herein in most cases were mainly due to genetic effect. Grain yield/ plant showed significant relationship under phenotypic and genotypic

levels with all studied traits except days to heading and plant height under phenotypic level; whereas, grain yield/ plant was positively associated and significant with spike length, no. of spikelets/ spike, no. of spikes/ plant, no. of kernels/ spike and 1000-kernel weight for the two types of correlations and days to heading and plant height only at genotypic level. These results indicated that, the breeder can utilize such correlated response to obtain high grain yield genotypes through selection for one or more of these traits. These results are in agreement with the results that obtained by Salem and El-Banna (1982); Belay *et al.* (1993); Moghaddam *et al.* (1997); Tammam *et al.* (2005); Abd El-Fattah *et al.* (2009), Khalil *et al.* (2010), Saleh (2011), El-Ameen (2012) who found positive and significant correlation coefficient between grain yield/ plant and each of spike length, no. of spikelets/ spike, no. of spikes/ plant, no. of kernels/ spike and 1000-kernel weight.

Table 4. Phenotypic (r_{ph}) and genotypic (r_g) correlation coefficients between all pairs of eight traits recorded for bread wheat genotypes in the F5- generation.

		1	2	3	4	5	6	7	8
1- Grain yield/plant	r _{ph}	0	0.24	0.17	0.55**	0.44**	0.73**	0.31*	0.39**
	r _g	0	0.25*	0.18*	0.69**	0.51**	0.84**	0.33**	0.41**
2- Days to heading	r _{ph}		0	-0.18	0.34*	-0.14	0.29*	0.25	0.25
	r _g		0	-0.19*	0.42**	0.16*	0.35**	0.26*	0.26*
3- Plant height	r _{ph}			0	0.10	0.29*	0.05	-0.05	0.20
	r _g			0	0.12	0.32**	0.07	-0.05	0.21*
4- Spike length	r _{ph}				0	0.53**	0.47**	0.35*	0.25
	r _g				0	0.61**	0.62**	0.46**	0.30*
5- No.of spikelets/spike	r _{ph}					0	0.29*	0.35*	0.18
	r _g					0	0.36**	0.39**	0.20*
6- No.of spikes/plant	r _{ph}						0	0.36**	0.33*
	r _g						0	0.41**	0.37**
7- No.of kernels/spike	r _{ph}							0	-0.01
	r _g							0	0.02
8- 1000-kernel weight	r _{ph}								0
	r _g								0

*and** denote significant differences at 0.05 and 0.01of probability levels, respectively.

Other inter-traits correlations revealed that days to heading was significantly and positively correlated with spike length and no. of spikes/ plant at the two levels of correlation and no. of spikelets/ spike, no. of kernels/ spike and 1000-kernel weight only at genotypic level, while it gave negative and significant correlation with plant height only at genotypic level.

Regarding plant height, positive and significant correlation coefficient was obtained with each of no. of spikelets/ spike under both types of correlations and 1000-kernel weight only at genotypic level. Spike length gave positive and significant correlation coefficient with no. of spikelets/ spike, no. of spikes/ plant, no. of kernels/ spike at phenotypic and genotypic levels and 1000-kernel weight only at genotypic levels. Number of spikelets/ spike exhibited positive and significant correlation coefficient with no. of spikes/ plant and no. of kernels/ spike under both phenotypic and genotypic correlations and 1000-kernel weight only at genotypic level. Number of spikes/ plant showed positive and significant correlation with no. of kernels/ spike and 1000-kernel weight at phenotypic and genotypic levels. However, number of kernels/ spike showed insignificant correlation coefficient with 1000-kernel weight under both types of correlations. Similar

results were obtained by Belay *et al.* (1993), Hassan *et al.* (1995), Iskandar (2000), Seleem and Hendawy (2007), Abd El-Moneam and Sultan (2009), Khalil *et al.* (2010), Saleh (2011) and El-Ameen (2012) who found significant and positive correlation between different pairs of studied traits. The rest cases of correlations were insignificant.

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التحليل الوراثي والانتخاب في العشائر الانعزالية ثلاث هجن من قمح الخبز لمحصول الحبوب وبعض الصفات المحصولية سمير حسن صالح

قسم المحاصيل- كلية الزراعة- جامعة عين شمس- شبرا الخيمة- القاهرة- مصر

أجريت هذه الدراسة في المزرعة التجريبية لكلية الزراعة- جامعة عين شمس بشلفان- محافظة القليوبية خلال ثلاث مواسم زراعية ٢٠١٥/٢٠١٤- ٢٠١٤/٢٠١٣- ٢٠١٣/٢٠١٢، وذلك بهدف دراسة الاستجابة النسبية للانتخاب في ثلاثة هجن من قمح الخبز لدورتين انتخابيتين تبدأ من الجيل الثالث باستخدام طريقة الانتخاب بالنسب بهدف تحسين محصول الحبوب وبعض الصفات المحصولية الأخرى مثل عدد الأيام حتى طرد ٥٠% من السنابل، ارتفاع النبات، طول السنبل، عدد السنابل/ نبات، عدد السنابل/ سنبل، عدد الحبوب/ سنبله ووزن الألف حبه. وقد أظهرت نتائج الدراسة المتحصل عليها مايلي:- وجود تباين وراثي كافي بين العائلات المنتخبة أو التراكيب الوراثية للصفات المتعلقة بالدراسة مما يجعل هناك استجابة عالية ومتوقعة للانتخاب من تلك الهجن. - اقتربت قيم معاملي التباين المظهري والوراثي من بعضها البعض بالنسبة للصفات المدروسة مما يدل على ان البيئة ليس لها دور رئيسي في التأثير على التباين بين التراكيب الوراثية وهذا يفسر ارتفاع قيم درجة التوريث لهذه الصفات وفاعلية التحسين الوراثي المتوقع نتيجة الانتخاب. - سجلت صفتي عدد السنابل/ نبات ومحصول الحبوب للنبات الفردي أعلى قيم لمعاملي التباين المظهري والوراثي عبر الثلاث اجيال (الجيل الثالث والرابع والخامس) في حين سجلت صفتي عدد الأيام من الزراعة حتى طرد ٥٠% من السنابل وعدد السنابل/ سنبله أقل قيم لمعاملي التباين المظهري والوراثي عبر الثلاث اجيال. كذلك كانت قيم كفاءة التوريث المقدرة على المستوى الواسع منخفضة لعدد السنابل/ نبات ومتوسطة لصفات طول السنبل، عدد السنابل/ سنبله ووزن الألف حبه وعالية لصفات عدد الأيام حتى طرد ٥٠% من السنابل، ارتفاع النبات، عدد الحبوب/ سنبله ومحصول الحبوب للنبات الفردي عبر الثلاث اجيال. - أظهرت السلالات المبشرة أرقام ١٩، ٢٤، ٢٧، ٣٠، ٣١ أفضل أداء في الجيل الخامس متفوقة على معظم أصناف المقارنة في محصول الحبوب ومعظم مكوناته، لذلك يمكن استخدام هذه السلالات المبشرة في برامج تحسين محصول الحبوب بالقمح. - وجد تلازم موجب ومعنوي بين محصول الحبوب الفردي وكل من طول السنبل، عدد السنابل/ سنبله، عدد السنابل/ نبات، عدد الحبوب/ سنبله ووزن الألف حبه تحت معاملي الارتباط المظهري والوراثي وعدد الأيام حتى طرد ٥٠% من السنابل وارتفاع النبات تحت معامل الارتباط الوراثي فقط وبالتالي فالانتخاب لصفة أو أكثر من تلك الصفات سوف يكون مجديا في برامج تحسين محصول القمح.