Efficiency of Three Breeding Methods on Three Bread Wheat Populations

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Abstract

The present study was carried out at the Experimental Research Station of Moshtohor, Benha University, Qalubia Governorate, Egypt during the three successive seasons of 2015-2016, 2016-2017 and 2017-2018. The present study aimed to evaluate the efficiency of three methods of selection used in the wheat breeding program namely; pedigree method (PM), bulk method (BM) and single seed descent method (SSDM). The final evaluation of the F5 generation of three crosses i.e., Sids 12 × Line 116, Gemmiza 11 × Line 145 and Gemmiza 11 × line 124 was done during 2017/2018 season. The high yielding selected lines were evaluated in nested design with three replications in each cross. The efficiency of the breeding methods was evaluated on the basis of the following parameters: mean performance results in the first cross (Sids 12 × Line 116) indicated that, the differences between breeding methods. The pedigree method gave the highest values for grain yield/plant and number of spikes/plant. While the Bulk method gave the highest values for 1000-kernel weight, however, single seed descent (SSD) method exhibited significantly for number of kernels/spike. Pedigree method is considered the best breeding method for grain yield/ plant, number of spikes/plant and the second for 1000-Kernel weight, than those bulk and SSD method in this cross (Sids 12 × Line 116). The pedigree method produced consistently more superior lines for grain yield/plant compared to the best parent or the average population. The best lines were number No. 7 (67.97 g), No. 5 (66.61 g), No. 9 (64.6 g), No. 19 (63.48 g), No. 8 (60.19 g), No. 20 (59.11 g), No. 4 (58.89 g), No. 2 (57.36 g), No. 3 (56.18 g) No. 18 (55.47 g), No. 13 (55.21 g), No. 17 (54.83 g), No. 16 (54.24 g), No. 15 (54.21 g) and No. 12 (52.51 g) for pedigree method. But in bulk method line No. 19 (57.76 g) was more superior compared to the best parent or the average population. The mean squares for breeding methods in the second cross (Gemmiza 11 × Line 145) were significant for yield and its components. The pedigree method gave the highest values for grain yield/plant, number of kernels / spike, number of spikes / plant and 1000- kernel weight**. Pedigree method is considered the best breeding method for grain yield/ plant, number of spikes / plant, number of kernels / spike and 1000- Kernel weight, than those SSD and bulk methods in this cross (Gemmiza 11 × Line 145). The pedigree method produced consistently more superior lines for grain yield / plant compared to the best parent or the average population. The best lines were number No. 5 (59.01 g), No. 14 (57.44 g), No. 15 (56.29 g) and No. 16 (56.29 g) for pedigree method. There aren't any lines significant higher in bulk method and single seed descent method than the best parent in this cross. The mean squares for breeding methods in the third cross (Gemmiza 11 × line 124) were significant for yield and its components. The pedigree method gave the highest values for grain yield / plant, number of spikes / plant, number of kernels / spike and 1000-Kernel weight**. Pedigree method is considered the best breeding method for grain yield / plant, number of spikes / plant, number of kernels / spike and 1000-Kernel weight, than those SSD and bulk method in this cross (Gemmiza 11 × line 124).

Key words: Breeding methods, Pedigree, modified bulk, single seed descent, wheat.

Introduction

Wheat (*Triticum aestivum* L.) is one of the most staple food crops grown worldwide on more than 17% of the cultivated land and produced in a wide range of climatic environment systems and geographic regions **(Okechukwu, *et.al*., 2016)**. Wheat cultivation area across world is around 222.95 million ha with a production of 730.48 mt (2017-2018) **(FAO, 2018)** and the normal world productivity is 3029 Kg/ha. China is the top most producer of wheat with production reaching 130.18 mt in 2016, although in China, it is the third most cultivated crop after maize and rice. It is estimated that wheat production must increase by 2 per cent annually to meet future food demands. As land is limited; thus, there is need to enhance the wheat

productivity per unit land area already under wheat cultivation. The cultivated area in 2017/2018 season was nearly 3.07 million Fed. (Including bread and durum wheat) produced 9.00 million tons of grain yield, with an average of 2.67 tons per Fed.

Wheat provides 21 % of the food calories and 20 % of the protein for more than 4.5 billion people in 94 countries of the world, it encompass provides 10 to 20 % of the daily caloric requirements to people in more than sixty countries worldwide. A full matured wheat grain has 82.5 per cent endosperm, 15 per cent bran, and 2.5 per cent germ. Bread wheat provides more than 50 % of the total calories and 60 % of the total protein taken by human **(Sial, *et. al*., 2005)**.

In self-pollinating crops, such as bread wheat (T*riticum aestivum* L.), breeding programs must include a three step process for developing germplasm: (1) recombination of genes for enlarging

variation, (2) identification and selection of recombinant genotypes according to their agronomic types and (3) Fixation of genes in homozygous genotypes. Pedigree selection (PS) is the conventional method of accumulating genetic recombination in each generation. The heterozygosity in early generations makes the efficient identification and selection of recombinant genotypes more difficult. Repeated pedigree selection can increase homozygosity, but many generation cycles are required to reach homozygosity in loci associated with agronomic traits. The single-seed descent (SSD) method can be used to obtain homozygous inbreds by accelerating generation cycles, but its application is dependent on growth habit of the plant materials used (**Inagaki, *et al.,* 1998**).

Several methods of selection can be used in segregating generations after crossing in self-pollinated crops. The information for each method of selection as well as the relationship between these methods of selection and yield would help in determining the best method of selection for breeding program to obtain high yielding cultivars of wheat and to apply this method in the following breeding program.

Selection for seed yield and production of the cultivars with high yield potential is the main objective of breeding programs. Many researchers (**Quarrie et al., 1999; Richards, 1996**) believed that genetic improvement of grain yield must be done via genetic improvement of physiological traits. In determining the potential of genetically different lines and cultivars, breeders have to observe many different characters that influence yield. Accurate evaluation of these characters is made more difficult by the genotype by environment interaction (**Tadesse and Bekele, 2001).**

Numerous methods have been proposed for wheat selection. Pedigree methods of selection are very common selection techniques in wheat crop. However, pedigree method has drawbacks due to high costs of record keeping, utilization of manpower, genetic drift and loss of desirable genes (Borghi et al., 1998). Results of Verma et al. (1997) and El-Ameen et al. (2013) showed that pedigree method of selection was more effective in improving grain yield and its components.

The main objectives of the present investigation were to evaluate the efficiency of three breeding methods, i. e., pedigree, modified bulk and single seed descent methods on three bread wheat populations by using the lines produced from F_5.

Materials and Methods

The experiment was carried out at the Experiment Research Station of Moshtohor, Benha University, Kalubia Governorate, Egypt during the three successive seasons of 2015-2016, 2016-2017 and 2017-2018.

The present study aimed to evaluate the efficiency of three methods of selection used in the wheat breeding program namely; pedigree method (PM), bulk method (BM) and single seed descent method (SSDM) on three hexaploid bread wheat populations derived from previous work by the other (self) for Muster Degree in 2015. F2 seed from the previous work furnished the source material for subsequent generations. Used in this study, three hexaploid bread wheat (*Triticum aestivum.,* L.) populations (2n = 42 chromosomes) (**Table 1**). The selection intensity of 10 % approximately was used with pedigree method (PM), bulk method (BM) and single seed descent method (SSDM) using yield components of wheat, i.e., number of spikes/plant [S/P], number of kernels/spike [K/S] and 1000-kernel weight [1000-KW] in gm.

Table 1. The pedigree of the parents and general combining ability (GCA) effect for grain yield/plant of the three wheat populations

Parental name	Pedigree	G.C.A effect
	Population 1 (Sids 12× Line 116)	H×H
(P₁) Sids 12	BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/ CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX SD7096-4SD-1SD-1SD 0SD	H
(P₂) Line 116	MILAN \ S7116 \\ Hall //(Ne700011)	H
	Population 2 (Gemmiza 11× Line 145)	L×H
(P₁) Gemmiza 11	BOW"S"/KVZ"S"//7C/SER182/3/GIZA 168/SAKHA61. GM7892-2GM-1GM-2GM-1GM-0GM.	L
(P₂) Line 145	MILAN \ S7145 \\ OAPYMex	H
	Population 3 (Gemmiza 11× Line 124)	L×L
(P₁) Gemmiza 11	BOW"S"/KVZ"S"//7C/SER182/3/GIZA 168/SAKHA61. GM7892-2GM-1GM-2GM-1GM-0GM.	L
(P₂) Line 124	MILAN \ S87124 \\ BABAX	L

In 2014/2015 season, three groups of random plants were taken from each F_2 population; each group consisted of 400 plants. The first group of random plants was handled by taken single seed from

each plant to produce (SSD), and then plants were harvested in mass to produce bulk population. The second group of random plants was threshed each plant separately and recorded the following characters, i.e., no of spike/plant, no of kernels/spike, 1000-kernel weight and grain yield/plant and the highest 10% approximately of each character was determined. While, high 5% approximately of plants for grain yield were used as pedigree method.

Pedigree method (PM): Each selected F_2 plant was taken by main spike and sown in a separate row represented F_3 families on the basis 30 grains per row during 2015/2016 season. Grains were spaced at 10 cm, while row spacing was 30 cm. Selection between and within families was practiced as described earlier, primary selection was practiced at heading stage, and final selection at maturity stage. Forty families were selected from 70 F_3 families from three populations under study and grown in three replications in a randomized complete block design (RCBD).

The pedigree method was practiced on F_4 generation during 2016/2017 season and selection was done between and within growing families. Twenty families were selected from F_4 generation for each population and retained to be raised as F_5 generation in the final evaluation trial during 2017/2018 season.

Modified bulk method (MB): Few grains from each selected plant from each F_2 generation were mixed to form the population seed bulk. The mixed grains were planted in a 20 rows per plot; a row was three meters in length, 30 cm. between rows and 10 cm. between grains, during 2015/2016 growing season as F_3 generation. Selection was practiced on the basis of best plants per each population. Grains of the selected plants were mixed to form grains bulk and grains sample were taken to be raised as F_4 generation during the growing season of 2016/2017. Grains of the F_4 generation were sown in a 20 rows per plot; a row was three meters in length, 30 cm between rows and 10 cm between grains. Similarly, twenty plants per population were selected. Grains from each plant were kept and planted separately as F_5 generation during 2017/2018 growing season.

Single seed descent method (SSD): In this procedure, one grain was taken from 400 plants from

F_2 generation and planted during 2015/2016 season as F_3 generation. One grain was taken from each plant to be grown as F_4 generation during the growing season of 2016/2017. Similarly, twenty plants were selected from each population and harvested individually. Grains from each plant were kept and planted separately as F_5 generation during 2017/2018 season.

In 2018 season, the high yielding selected lines (20) from each methods of breeding (three methods i.e. pedigree, bulk and SSD) of their crosses were represented by one row per plot, a row was three meters in length, 20 cm between rows and 10 cm between grains were evaluated in nested design with three replications in each cross.

Characters studied

The following characteristics were measured on random sample of 10 guarded plants in each plot for each line in F_5 generation of all studied methods as well as selection criteria. The mean of the 10 plants were subjected to the statistical and genetic analysis for: **number of spikes per plant [S/P]**, **number of kernels per spike [K/S]:** average number of kernels per spike (Main spike) counted manually, **1000-kernel weight [1000-KW]** and **Grain yield per plant [GY/P]:** average grain weight of individual guarded plants in grams.

Results and Discussion

1. First cross Sids 12 × Line 116 (F_5 generation):
Mean squares due to breeding methods were significant for yield and its components **(Table 2).** This result indicated the differences between breeding methods.

Mean squares due to lines were highly significant, indicating the presence of high degree of genetic variability between them **(Table 2).**

Table 2. Mean squares of the breeding methods of the F_5 lines for the four studied traits in the first cross (Sids 12 × Line 116).

Source of variation	Degrees of freedom	No. of spikes/plant	No. of kernels/spike	1000- kernel weight (g)	Grain yield/plant (g)
Replications	2	114.61**	227.64**	10.45	23.34
Lines (L)	59	46.24**	485.54**	66.63**	242.69**
Methods(M)	2	506.89**	2220.76**	78.62**	4383.92**
L/M	57	30.08**	424.65**	66.21**	97.38**
Error	118	8.68	16.30	8.98	10.74

*, ** Highly significant at 0.05 and 0.01 respectively.

The pedigree method gave the highest values for grain yield/plant and number of spikes / plant. While the Bulk method gave the highest values for 1000-kernel weight, however, single seed descent (SSD) method exhibited significantly for number of kernels / spike **(Table 3)**. It could be concluded pedigree method is considered the best breeding method for grain yield/ plant , number of spikes / plant and the second for 1000- Kernel weight, than those bulk and SSD method in this cross. This result is logic expected where the two parents were high of GCA effects for grain yield/plant.

The pedigree and single seed descent methods proved to be more efficient than the modified bulk method for selection based on grain yield **(Deghais and Auriau 1993)**. Pedigree method of individual selection was very efficient in breeding for increased values of some grain yield components **(Perovic 1997)**.The pedigree method produced more superior lines compared to the overall mean **(El-Hosary and El-Badawy 2003)**. Pedigree method possessed higher values of phenotypic and genotypic coefficients of variability and broad sense heritability for number of spikes per plant, number of kernels per spike, 1000-kernel weight, and grain yield per plant in the two populations **(Mobarek 2007)**. The pedigree method expressed significant desirable values for number of spikes per plant, 1000-kernel weight, number of kernels/spike and grain yield/plant than those bulk and SSD method **(El-Hosary et al. 2011 and El-Hosary et al., 2014)**.

Table 3. Mean performance of the breeding methods of the F5 lines for the four studied traits in the first cross (Sids 12 × Line 116).

Breeding methodology	No. of spikes/plant	No. of kernels/spike	1000- kernel weight (g)	Grain yield/plant (g)
Pedigree	22.19	55.68	49.16	56.73
Bulk	18.53	47.94	49.61	40.67
Single seed	16.45	59.94	47.44	43.63
L.S.D $_{0.05}$	1.07	1.46	1.08	1.19
L.S.D $_{0.01}$	1.41	1.94	1.44	1.57

Mean squares due to genotypes (lines of breeding methods as well as two parents) were significant for the four traits under study **(Table 4)**.

Also, the efficiency of the breeding methods in the present study was evaluated based on the number of superior lines having higher values of grain yield / plant than the best parent.

Table 4. Mean squares of the breeding methods and both parents of the F_5 lines for the four studied traits in the first cross (Sids 12 × Line 116).

Source of variation	Degrees of freedom	No. of spikes/plant	No. of kernels/spike	1000- kernel weight (g)	Grain yield/plant (g)
Replications	2	87.15*	185.02**	7.67	24.81
Lines (L)	61	49.68**	489.89**	65.11**	236.74**
Error	122	9.67	19.371	8.88	11.01

*, ** Significant and highly significant at 0.05 and 0.01 respectively.

For number of spikes / plant, one line No. 4 (29.53) in pedigree method had the highest number of spikes / plant compared with best parent. There aren't any lines significant higher in bulk method and single seed descent method than the best parent in this cross.

For number of kernels / spike the results indicated the single seed descent method produced more superior lines followed by pedigree method and then by bulk method compared to the best parent or average over lines with twelve, eleven and three lines, respectively. The best lines were No. 20 (94.26), No. 8 (74.61), No. 11 (72.25), No. 9 (69.70), No. 12 (69.49), No. 4 (65.57), No. 10 (64.28), No. 5 (62.88), No. 7 (60.52), No. 6 (59.08), No. 16 (58.40) and No. 14 (57.33) in single seed descent method, No. 5 (82.63), No. 8 (77.97), No. 20 (64.61), No. 19 (60.46), No. 18 (60.28), No. 15 (59.98), No. 16

(58.76), No. 6 (58.07), No. 14 (57.31), No. 17 (56.97) and No. 2 (56.57) in pedigree method and No. 19 (92.94) and No. 17 (61.08) in bulk method.

Results of the present study indicate that visual selection for yield by pedigree method or early generation testing in wheat can lead to produce lines with higher yield, which the parents in the cross were high good combiner for grain yield/plant.

Regarding to 1000-kernels weight, thirteen, twelve and eleven lines showed, significant higher than the best parent and average over lines for pedigree, bulk and SSD methods, respectively. The heavier lines were No. 10 (55.82 g), No. 11 (55.35 g), No. 9 (55.11 g), No. 12 (53.39 g), No. 1 (52.92 g), No. 7 (52.91 g), No. 13 (52.19 g), No. 14 (51.92 g), No. 6 (51.66 g), No. 2 (51.08 g), No. 15 (51.07 g), No. 20 (50.49 g) and No. 3(50.01 g) in pedigree method, followed by lines No. 6 (53.15 g), No. 20

(52.92 g), No. 3 (52.81 g), No. 7 (52.61 g), No. 18 (52.16 g), No. 5 (52.13 g), No. 1 (51.67 g), No. 12 (51.30 g), No. 19 (51.13 g), No. 2 (50.90 g), No. 16 (50.81 g) and No. 8 (50.30 g) in bulk method and No. 1 (53.07 g), No. 2 (52.39 g), No. 3 (52.17 g), No. 18 (51.91 g), No. 15 (51.81 g), No. 13 (51.78 g), No. 6 (51.51 g), No. 19 (51.46 g), No. 10 (50.63 g), No. 17 (50.55 g) and No. 8 (50.48 g) in SSD method **(Table 5).**

Data presented in **(Table 5)** show that the pedigree method produced consistently more superior lines for grain yield / plant compared to the best parent or the average population. The best lines were number No. 7 (67.97 g), No. 5 (66.61 g), No. 9 (64.6 g), No. 19 (63.48 g), No. 8 (60.19 g), No. 20 (59.11 g), No. 4 (58.89 g), No. 2 (57.36 g), No. 3 (56.18 g) No. 18 (55.47 g), No. 13 (55.21 g), No. 17 (54.83 g), No. 16 (54.24 g), No. 15 (54.21 g) and No. 12 (52.51 g) for pedigree method. But bulk method No. 19 (57.76 g) produced consistently more superior lines compared to the best parent or the average population.

Table 5. Mean performance of the selected F_5 lines of breeding methods and two parents in the first cross (Sids 12 × Line 116).

Breeding method	No. of line	No. of spikes/plant	No. of kernels/ Spike	1000-kernel weight (g)	Grain yield/plant (g)
	1	21.93	43.10	52.92	49.45
	2	22.27	56.57	51.08	57.36
	3	23.73	48.05	50.01	56.18
	4	29.53	48.91	41.39	58.89
	5	20.73	82.63	40.86	66.61
	6	17.27	58.07	51.66	50.19
	7	26.80	48.99	52.91	67.97
	8	18.93	77.97	44.34	60.19
	9	25.00	46.80	55.11	64.60
pedigree	10	24.20	40.52	55.82	53.50
	11	22.20	43.29	55.35	50.14
	12	21.13	49.34	53.39	52.51
	13	22.92	50.96	52.19	55.21
	14	17.07	57.31	51.92	50.39
	15	17.87	59.98	51.07	54.21
	16	21.07	58.76	46.23	54.24
	17	25.67	56.97	39.73	54.83
	18	22.60	60.28	41.31	55.47
	19	24.47	60.46	45.36	63.48
	20	18.44	64.61	50.49	59.11
	1	17.22	44.37	51.67	37.89
	2	25.33	33.25	50.90	40.01
	3	21.00	42.70	52.81	45.07
	4	22.33	35.00	49.62	38.80
	5	17.13	43.02	52.13	37.80
	6	16.58	45.24	53.15	38.32
	7	16.75	49.87	52.61	38.67
	8	15.92	44.78	50.30	34.50
	9	21.22	35.91	46.80	33.88
	10	15.27	49.68	49.55	36.55
	11	20.83	46.78	48.40	47.51
	12	21.22	43.29	51.30	45.11
Bulk	13	19.50	45.79	41.43	33.85
	14	15.58	54.28	47.49	37.00
	15	18.92	53.14	46.33	39.43
	16	15.13	45.59	50.81	34.25
	17	18.11	61.08	40.64	44.02
	18	22.22	39.20	52.16	44.56
	19	12.50	92.94	51.13	57.76
	20	17.83	52.86	52.92	48.34

Table 5 Cont.

Breeding method	No. of line	No. of spikes/plant	No. of kernels/ Spike	1000-kernel weight (g)	Grain yield/plant (g)
	1	17.53	47.76	53.07	40.89
	2	17.80	49.30	52.39	44.60
	3	17.67	49.27	52.17	43.82
	4	15.17	65.57	39.19	38.59
	5	15.89	62.88	48.72	51.21
	6	14.08	59.08	51.51	42.35
	7	19.67	60.52	44.24	49.84
	8	12.75	74.61	50.48	46.63
	9	17.07	69.70	41.85	49.46
Single seed descent	10	13.75	64.28	50.63	42.31
	11	16.25	72.25	41.62	48.01
	12	16.93	69.49	42.13	48.29
	13	19.33	46.27	51.78	45.11
	14	16.93	57.33	40.98	37.29
	15	18.92	48.46	51.81	46.45
	16	19.27	58.40	40.25	43.69
	17	21.83	46.96	50.55	47.32
	18	14.73	54.37	51.91	40.55
	19	15.93	48.04	51.46	38.44
	20	7.50	94.26	42.05	27.69
Parent 1 (Sids 12)		23.17	54.91	45.05	51.59
Parent 2 (Line 116)		28.37	34.06	48.12	42.54
Over mean		19.27	54.73	48.67	47.01
L.S.D 0.05		4.72	7.04	4.80	5.24
L.S.D 0.01		6.20	9.26	6.30	6.89

2. Second cross Gemmiza 11 × Line 145 (F₅ generation):

Mean squares due to breeding methods were significant for yield and its components (**Table 6**).

This result indicated the differences between breeding methods.

Mean squares due to lines were highly significant, indicating the presence of high degree of genetic variability between them (**Table 6**).

Table 6. Mean squares of the breeding methods of the F_5 lines for the four studied traits in the second cross (Gemmiza 11 × Line 145).

Source of variation	Degrees of freedom	No. of spikes/plant	No. of kernels/spike	1000-kernel weight (g)	Grain yield/plant (g)
Replications	2	72.54**	52.26	1.99	13.15
Lines (L)	59	15.13**	162.16**	74.47**	158.29**
Methods(M)	2	82.04**	1364.81**	31.81**	3488.13**
L/M	57	12.78*	119.96**	75.97**	41.45**
Error	118	7.91	25.21	5.72	13.64

*, ** Significant and highly significant at 0.05 and 0.01 respectively.

The pedigree method gave the highest values for grain yield/plant, number of kernels / spike, number of spikes / plant and 1000- kernel weight **(Table 7).** It could be concluded pedigree method is considered the best breeding method for grain yield/ plant, number of spikes / plant, number of kernels / spike and 1000- Kernel weight, than those SSD and bulk method in this cross. The obtained results were logic which the one parent was

higher of GCA effects for grain yield/plant in the cross.

Mean squares due to genotypes (lines of breeding methods as well as two parents) were significant for the four traits under study **(Table 8).**

Also, the efficiency of the breeding methods in the present study was evaluated based on the number of superior lines having higher values of grain yield / plant than the best parent.

Table 7. Mean performance of the breeding methods of the F5 lines for the four studied traits in the second cross (Gemmiza 11 × Line 145).

Breeding methodology	No. of spikes/plant	No. of kernels/spike	1000- kernel weight (g)	Grain yield/plant (g)
Pedigree	18.48	56.41	53.09	52.63
Bulk	16.20	47.66	52.65	38.28
Single seed descent	16.90	48.76	51.67	40.99
L.S.D $_{0.05}$	1.02	1.82	0.87	1.34
L.S.D $_{0.01}$	1.35	2.41	1.15	1.77

Table 8. Mean squares of the breeding methods and both parents of the F_5 lines for the four studied traits in the second cross (Gemmiza 11 × Line 145).

Source of variation	Degrees of freedom	No. of spikes/plant	No. of kernels/spike	1000- kernel weight (g)	Grain yield/plant (g)
Replications	2	73.30**	41.58	1.78	8.63
Lines (L)	61	24.96**	174.35**	72.70**	160.02**
Error	122	7.71	24.90	5.98	14.03

*, ** Significant and highly significant at 0.05 and 0.01 respectively.

For number of spikes / plant the results indicated that the pedigree method produced more superior lines followed by single seed descent method and then by bulk method compared to the average over lines (grand mean) with eleven, four and three lines, respectively. The best lines were No. 5 (23.20), No. 12 (21.80), No. 14 (21.67), No. 15 (20.93), No. 11 (19.33), No. 13 (19.27), No. 4 (19.07), No. 17 (19.07), No. 7 (18.47), No. 6 (18.33) and No. 18 (18.07) in pedigree method, No. 12 (20.17), No. 13 (19.78), No. 9 (19.13) and No. 2 (18.08) in single seed descent method and No. 9 (21.75), No. 12 (19.13) and No. 11 (18.67) in bulk method.

For number of kernels / spike the results indicated that, the pedigree method produced more superior lines followed by single seed descent method and then by bulk method compared to the best parent or average over lines with twenty, twenty and eighteen lines, respectively. The best lines were No. 15, 11, 3, 20, 9, 2, 10, 19, 4, 16, 6, 8, 1, 17, 18, 14, 7, 5, 13 and No. 12 in pedigree method; No. 4, 11, 9, 5, 16, 18, 15, 20, 8, 13, 17, 14, 6, 7, 19, 1, 10,

2, 12 and No. 3 in single seed descent method and No. 2, 6, 19, 15, 5, 16, 4, 3, 18, 17, 7, 9, 1, 13, 11, 20, 12 and No. 14 in bulk method.

Regarding to 1000-kernel weight, thirteen, thirteen and nine lines showed, significant higher than the best parent and average over lines for pedigree, bulk and SSD methods, respectively. The heavier lines were No. 13 (66.69 g), No. 16 (57.48 g), No. 20 (57.41 g), No. 12 (56.85 g), No. 9 (56.81 g), No. 7 (56.41 g), No. 17 (55.97 g), No. 5 (55.28 g), No. 14 (54.53 g), No. 18 (54.35 g), No. 10 (53.90 g), No. 3 (53.85 g) and No. 1 (53.61 g) in pedigree method, followed by lines No. 14 (57.93 g), No. 20 (57.17 g), No. 12 (56.90 g), No. 8 (56.88 g), No. 10 (56.77 g), No. 11 (56.05 g), No. 5 (55.74 g), No. 4 (54.78 g), No. 18 (54.41 g), No. 6 (54.26 g), No. 16 (53.28 g), No. 15 (53.15 g) and No. 13 (52.62 g) in bulk method and No. 1 (53.07 g), No. 2 (52.39 g), No. 3 (52.17 g), No. 18 (51.91 g), No. 15 (51.81 g), No. 13 (51.78 g), No. 6 (51.51 g), No. 19 (51.46 g), No. 10 (50.63 g), No. 17 (50.55 g), and No. 8 (50.48 g) in single seed descent method **(Table 9).**

Table 9. Mean performance of the selected F$_5$ lines of breeding methods and two parents in the second cross (Gemmiza 11 × Line 145).

Breeding method	No. of line	No. of spikes/plant	No. of kernels/ Spike	1000-kernel weight (g)	Grain yield/plant (g)
pedigree	1	17.87	53.87	53.61	50.45
	2	17.40	60.55	49.15	50.55
	3	15.07	63.82	53.85	50.91
	4	19.07	57.49	46.49	48.82
	5	23.20	48.91	55.28	59.01
	6	18.33	55.78	51.05	51.63
	7	18.47	49.62	56.41	48.09
	8	17.80	54.69	51.63	48.84
	9	14.93	60.76	56.81	49.81
	10	17.33	60.26	53.90	55.19
	11	19.33	64.65	40.54	48.72
	12	21.80	44.18	56.85	54.66
	13	19.27	44.58	66.69	55.11
	14	21.67	52.59	54.53	57.44
	15	20.93	74.30	37.89	56.29
	16	17.80	55.90	57.48	56.29
	17	19.07	53.04	55.97	55.24
	18	18.07	53.02	54.35	51.24
	19	17.60	58.47	51.87	52.55
	20	14.67	61.75	57.41	51.77
Bulk	1	17.33	45.13	50.07	38.04
	2	15.50	54.04	46.40	37.48
	3	17.25	49.85	47.65	38.41
	4	14.58	50.27	54.78	39.24
	5	12.78	51.65	55.74	35.00
	6	13.78	70.47	54.26	37.66
	7	14.33	47.02	51.97	34.98
	8	17.67	37.81	56.88	36.68
	9	21.75	45.20	43.02	40.95
	10	15.83	38.05	56.77	33.60
	11	18.67	44.77	56.05	46.32
	12	19.13	41.47	56.90	42.92
	13	16.25	44.81	52.62	37.62
	14	17.87	41.24	57.93	41.15
	15	15.00	51.93	53.15	41.29
	16	14.58	50.40	53.28	39.00
	17	16.07	46.06	49.98	37.16
	18	16.83	47.00	54.41	40.12
	19	16.27	52.07	44.03	37.08
	20	12.53	43.85	57.17	30.93

Table (9): Cont.

Breeding method	No. of line	No. of spikes/plant	No. of kernels/ Spike	1000-kernel weight (g)	Grain yield/plant (g)
	1	16.56	46.49	57.84	43.53
	2	18.08	43.57	57.33	42.42
	3	15.75	39.53	52.39	32.52
	4	16.07	57.60	47.13	43.63
	5	17.73	53.92	49.47	44.53
	6	14.50	47.42	54.91	37.50
	7	16.83	47.26	51.03	38.30
	8	16.00	49.29	51.11	38.69
	9	19.13	54.73	39.19	40.71
Single seed descent	10	16.53	44.89	51.47	37.21
	11	13.67	55.37	54.71	41.18
	12	20.17	43.38	52.50	44.71
	13	19.78	48.68	57.88	53.54
	14	17.33	47.73	51.41	41.46
	15	16.53	49.88	48.53	38.07
	16	16.60	50.84	52.64	43.11
	17	15.17	48.29	52.86	37.70
	18	15.73	50.20	50.00	38.37
	19	17.42	46.81	50.31	37.85
	20	18.47	49.33	50.64	44.74
Parent 1(Gemmiza 11)		28.33	38.12	51.68	55.44
Parent 2 (Line 145)		26.83	36.69	48.82	47.55
Over mean		17.53	50.24	52.40	44.21
L.S.D $_{5\%}$		4.50	7.99	3.83	5.91
L.S.D $_{1\%}$		5.91	10.49	5.03	7.77

Data presented in **(Table 9)** show that the pedigree method produced consistently more superior lines for grain yield / plant compared to the best parent or the average population. The best lines were number No. 5 (59.01 g), No. 14 (57.44 g), No. 15 (56.29 g) and No. 16 (56.29 g) for pedigree method. There aren't any lines significant higher in bulk method and single seed descent method than the best parent in this cross.

Results of the present study indicate that visual selection for yield by pedigree method or early generation testing in wheat can lead to lines with increased yield.

3. Third cross Gemmiza 11 × line 124 (F$_5$ generation):

Mean squares due to breeding methods were significant for yield and its components **(Tables 10).** This result indicated the great differences between breeding methods.

Mean squares due to lines were highly significant, indicating the presence of high degree of genetic variability between them **(Table 10).**

Table 10. Mean squares of the breeding methods of the F$_5$ lines for the four studied traits in the third cross (Gemmiza 11 × line 124).

Source of variation	Degrees of freedom	No. of spikes/plant	No. of kernels/spike	1000-kernel weight (g)	Grain yield/plant (g)
Replications	2	142.55**	22.29	30.76*	15.16
Lines (L)	59	20.69**	168.02**	16.98**	125.07**
Methods(M)	2	15.96	1036.59**	30.88*	1367.55**
L/M	57	20.85**	137.54**	16.50**	81.47**
Error	118	6.12	13.12	8.62	10.21

*, ** Significant and highly significant at 0.05 and 0.01 respectively.

The pedigree method gave the highest values for grain yield / plant, number of spikes / plant, number of kernels / spike and 1000-Kernel weight **(Table 11).** Therefore, pedigree method is considered the best breeding method for grain yield / plant, number of spikes / plant, number of kernels / spike and 1000-Kernel weight, than those SSD and bulk method in this cross.

Table 11. Mean performance of the breeding methods of the F5 lines for the four studied traits in the third cross (Gemmiza 11 × line 124).

Breeding methodology	No. of spikes/plant	No. of kernels/spike	1000- kernel weight (g)	Grain yield/plant (g)
Pedigree	18.02	60.16	48.65	50.46
Bulk	17.90	51.85	47.39	41.37
Single seed descent	17.07	55.71	47.43	43.38
L.S.D $_{0.05}$	0.90	1.31	1.06	1.16
L.S.D $_{0.01}$	1.19	1.74	1.41	1.53

Mean squares due to genotypes (lines of breeding methods as well as two parents) were significant for the four traits under study **(Table 12).**

Table 12. Mean squares of the breeding methods and both parents of the F_5 lines for the four studied traits in the third cross (Gemmiza 11 × line 124).

Source of variation	Degrees of freedom	No. of spikes/plant	No. of kernels/spike	1000- kernel weight (g)	Grain yield/plant (g)
Replications	2	137.35**	18.12	26.85*	11.27
Lines (L)	61	31.91**	190.65**	19.16**	141.00**
Error	122	6.05	13.02	8.54	10.89

*, ** Significant and highly significant at 0.05 and 0.01 respectively.

Also, the efficiency of the breeding methods in the present study was evaluated based on the number of superior lines having higher values of grain yield / plant than the best parent.

For number of spikes / plant the results indicated the pedigree method produced more superior lines followed by bulk method and then by single seed descent method rather than the average over lines (grand mean) with eight, eight and four lines, respectively. The best lines were No. 17 (22.07), No. 11 (21.13), No. 6 (21.07), No. 3 (20.40), No. 4 (18.73), No. 16 (18.73), No. 20 (18.47) and No. 13 (18.13) in pedigree method, No. 14 (26.83), No. 9 (21.83), No. 12 (21.58), No. 17 (21.47), No. 3 (19.92), No. 16 (19.92), No. 18 (19.58) and No. 6 (18.78) in bulk method and No. 14 (21.67), No. 11 (21.08), No. 7 (19.44) and No. 13 (18.20) in single seed descent method.

For number of kernels / spike, the results indicated that, the pedigree method gave more superior lines followed by single seed descent method and then by bulk method compared to the best parent or average over lines with twenty, twenty and nineteen lines, respectively . The best lines were No. 14, 10, 15, 19, 7, 9, 3, 12, 4, 13, 18, 5, 1, 2, 8, 20, 11, 16 and No. 17 in pedigree method; No. 3, 18, 7, 12, 15, 9, 6, 4, 16, 13, 20, 17, 2, 19, 14, 5, 8, 1, 11 and No. 10 in single seed descent method and No. 20, 19, 6, 1, 8, 11, 18, 7, 4, 13, 16, 10, 15, 3, 5, 2, 17, 9 and No. 12 in bulk method.

Regarding to 1000-kernels weight, ten, nine and seven lines showed, significant higher than the average over lines for pedigree, bulk and SSD methods, respectively. The heavier lines were No. 11 (52.45 g), No. 6 (51.49 g), No. 18 (51.33 g), No. 2 (51.27 g), No. 9 (51.25 g), No. 10 (50.55 g), No. 4 (50.15 g), No. 13 (49.67 g), No. 14 (49.64 g) and No. 7 (48.07 g) in pedigree method, followed by lines No. 3 (49.82 g), No. 8 (49.5 g), No. 11 (49.04 g), No. 13 (48.97 g), No. 15 (48.83 g), No. 9 (48.78 g), No. 10 (48.63 g), No. 16 (48.20 g) and No. 4 (48.04 g) in bulk method and No. 17 (52.40 g), No. 9 (51.63 g), No. 8 (50.83 g), No. 19 (50.49 g), No. 20 (50.45 g), No. 12 (48.93 g) and No. 14 (48.77 g) in SSD method **(Table 13).**

Table 13. Mean performance of the selected F_5 lines of breeding methods and two parents in the third cross (Gemmiza 11 × line 124).

Breeding method	No. of line	No. of spikes/plant	No. of kernels/ Spike	1000-kernel weight (g)	Grain yield/plant (g)
pedigree	1	17.87	58.29	47.89	45.83
	2	17.20	58.09	51.27	50.26
	3	20.40	61.68	46.79	55.89
	4	18.73	60.28	50.15	54.22
	5	17.87	58.74	47.29	48.18
	6	21.07	54.08	51.49	55.75
	7	17.80	64.90	48.07	53.42
	8	17.40	56.54	47.13	45.02
	9	15.87	64.48	51.25	52.51
	10	16.07	71.50	50.55	56.83
	11	21.13	52.93	52.45	56.66
	12	16.47	61.02	45.51	44.76
	13	18.13	60.15	49.67	53.38
	14	14.13	74.06	49.64	51.28
	15	15.73	66.95	45.26	47.59
	16	18.73	52.40	47.44	44.78
	17	22.07	46.40	46.60	46.06
	18	17.60	59.30	51.33	51.20
	19	17.67	65.55	45.38	49.99
	20	18.47	55.83	47.88	45.62
Bulk	1	15.33	58.76	44.44	39.99
	2	16.08	47.89	45.68	34.65
	3	19.92	48.39	49.82	46.43
	4	17.75	51.25	48.04	42.01
	5	15.67	48.30	41.48	30.25
	6	18.78	62.92	47.43	51.43
	7	15.92	52.87	47.58	38.23
	8	13.58	54.91	49.52	35.92
	9	21.83	42.45	48.78	44.01
	10	17.58	49.22	48.63	38.75
	11	13.50	53.73	49.04	31.68
	12	21.58	42.25	46.68	41.71
	13	17.93	50.80	48.97	43.01
	14	26.83	36.51	47.49	46.16
	15	17.08	48.44	48.83	40.68
	16	19.92	50.70	48.20	47.31
	17	21.47	45.60	46.85	45.04
	18	19.58	52.98	47.43	46.63
	19	11.78	68.21	46.46	34.65
	20	15.89	70.87	46.47	48.94

Table 13. Cont.

Breeding method	No. of line	No. of spikes/plant	No. of kernels/ spike	1000-kernel weight (g)	Grain yield/plant (g)
	1	12.00	52.38	45.11	28.22
	2	15.58	54.22	46.23	38.12
	3	13.42	73.77	44.61	42.61
	4	17.56	55.01	44.97	39.64
	5	16.93	53.63	47.64	40.24
	6	17.75	55.90	46.40	46.02
	7	19.44	58.52	42.02	47.32
	8	16.93	53.54	50.83	46.78
	9	17.17	56.75	51.63	49.87
Single seed descent	**10**	16.17	49.88	46.96	37.49
	11	21.08	50.39	43.88	45.18
	12	17.07	57.12	48.93	44.80
	13	18.20	54.44	45.98	43.47
	14	21.67	54.02	48.77	55.60
	15	16.47	56.80	46.69	42.88
	16	17.22	54.59	47.97	43.92
	17	16.22	54.24	52.40	43.34
	18	16.42	60.59	46.65	44.95
	19	16.67	54.11	50.49	42.69
	20	17.50	54.31	50.45	44.48
Parent 1 (Gemmiza 11)		28.33	38.12	51.68	55.44
Parent 2 (line 124)		29.33	39.33	54.33	62.75
Over mean		18.02	55.35	47.99	45.52
L.S.D $_{0.05}$		3.96	5.77	4.70	5.11
L.S.D $_{0.01}$		5.20	7.59	6.17	6.72

Data presented in **(Table 13)** show that the pedigree method produced consistently more superior lines for grain yield / plant compared to the average population (grand mean). The best lines were number No. 10 (56.83 g), No. 11 (56.66 g), No. 3 (55.89 g), No. 6 (55.75 g), No. 4 (54.22 g), No. 7 (53.42 g), No. 13 (53.28 g), No. 9 (52.51 g), No. 14 (51.28 g), No. 18 (51.20 g), No. 2 (50.26 g), No. 19 (49.99), No. 5 (48.18 g), No. 15 (47.59 g), No. 17 (46.06 g), No. 1 (45.83 g) and No. 20 (45.62 g) for pedigree method. While in bulk method No. 6 (51.43 g), No. 20 (48.94 g), No. 16 (47.31 g), No. 18 (46.63 g), No. 3 (46.43 g) and No. 14 (46.16 g) produced consistently more superior lines compared to the average population. While, for single seed descent method lines No. 14 (55.60 g), No. 9 (49.78 g), No. 7 (47.32 g), No. 8 (46.78 g) and No. 6 (46.02 g) produced consistently more superior lines compared to the average population.

Results of the present study indicate that visual selection for yield by pedigree method or early generation testing in wheat can lead to lines with higher productivity. Also, there aren˙t any lines significant high in the three methods breeding than the best parent in the cross. This result is logic expected which the two parents have the poor GCA effect for grain yield/plant.

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كفاءة ثلاثة طرق تربية علي ثلاثة عشائر من قمح الخبز

علي عبد المقصود الحصري[1] ، سيدهم أسعد سيدهم[1] ، محمد قاسم خليفه[1] ، أحمد علي الحصري[1] ، خالد عبد الواحد بيومي[1]

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أجريت هذه الدراسة في محطة بحوث التجارب في كلية زراعة مشتهر جامعة بنها – محافظة القليوبية ،خلال المواسم الثلاث المتتالية 2015/2016 , 2016/2017 و 2017/2018 . تهدف هذه الدراسة إلي قياس كفاءة ثلاث طرق تربية وهي : طريقة تسجيل النسب , طريقة التجميع المحورة وطريقة الانحدار من حبة واحدة. وقد تم استخدام ثلاثة عشائر في الجيل الثاني . تم تقييم كفاءة طرق التربية في الدراسة استناداً إلي عدد التراكيب الوراثية المتفوقة ذات المحصول العالي مقارنة بالأب الأعلي. **بالنسبة للعشيرة الأولي:**أشارت المتوسطات الى أن هناك معنوية لكل طرق التربية بالنسبة لصفات المحصول ومكوناته والنتائج توضح الفروق بين طرق التربية المختلفة. كانت طريقة النسب هي أفضل طرق التربية المستخدمة بالنسبة لصفات محصول الحبوب وعدد السنابل للنبات ،بينما طريقة التجميع المحورة هي أفضل بالنسبة لصفة وزن ال 1000 حبة ، وطريقة الانتخاب للحبة الواحدة هي أفضل بالنسبة لصفة عدد حبوب السنبلة. كانت أفضل السلالات لصفة محصول الحبوب للنبات هي السلالة رقم 7 (67.97 جم) والسلالة رقم 5 (66.61 جم) والسلالة رقم 9 (64.60 جم) والسلالة رقم 19 (63.48جم) والسلالة رقم 8 (60.19جم) والسلالة رقم 20 (59.11 جم) والسلالة رقم 4 (58.89جم) والسلالة رقم 2 (57.36جم) والسلالة رقم 3 (56.18جم) والسلالة رقم 18 (55.47جم) والسلالة رقم 13 (55.21جم) والسلالة رقم 17 (54.83جم) والسلالة رقم 16 (54.24جم) والسلالة رقم 15 (54.21جم) والسلالة رقم 12 (52.51جم) وذلك في طريقة النسب والسلالة رقم 19 (57.76جم) وذلك في طريقة التجميع المحورة.**وبالنسبة للعشيرة الثانية:**أشارت المتوسطات الى أن هناك معنوية لكل طرق التربية بالنسبة لصفات المحصول ومكوناته والنتائج توضح الفروق بين طرق التربية المختلفة.كانت طريقة النسب هي أفضل طرق التربية المستخدمة بالنسبة لصفات محصول الحبوب للنبات وعدد السنابل فى النبات ,ثم بعد ذلك طريقة انتخاب حبة واحدة ثم طريقة التجميع المحورة.كانت أفضل السلالات لصفة محصول الحبوب للنبات هي السلالة رقم 5 (59.01جم) والسلالة رقم 14 (57.44جم) والسلالة رقم 15 (56.29جم) والسلالة رقم 16 (56.29جم) وذلك في طريقة النسب . **أما بالنسبة للعشيرة الثالثة:**أشارت المتوسطات الى أن هناك معنوية لكل طرق التربية بالنسبة لصفات المحصول ومكوناته والنتائج توضح الفروق بين طرق التربية المختلفة. كانت طريقة النسب هي أفضل طرق التربية المستخدمة بالنسبة لصفات محصول الحبوب للنبات وعدد السنابل فى النبات وعدد حبوب السنبلة، ووزن الـ 1000 حبة ,ثم بعد ذلك طريقة انتخاب حبة واحدة ثم طريقة التجميع المحورة. لم تتفوق التراكيب الوراثية الناتجة في المحصول العالي علي الأب الأعلي ولكن أظهرت عدة تراكيب تفوقها مقارنة بمتوسط العشيرة.

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