COMPARISON AMONG FOUR BREEDING METHODS IN SOME BREAD WHEAT CROSSES

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ABSTRACT: Four breeding methods representing different cycles of phenotypic selection were evaluated using four bread wheat (Triticum aestivum L.) crosses. These method were ; 1) pedigree method (PM) with three cycles of selection in F_3 , F_4 and F_5 , 2) modified bulk₁ (MB₁) used two cycles of selection in F_4 and F_5 , 3) modified bulk₂ (MB₂) that only one cycle of selection in F₃ was exercised, and 4) bulk method (BM) where only natural breeding or selection was involved. This study was conducted at the farm of El-Giza Agric. Res. Station, ARC, Egypt, during four successive seasons from 2006/2007 to 2009/2010 to evaluate the efficiency of four different breeding methods in improving grain yield potentiality and some other agronomic traits in four bread wheat crosses. The lines derived from various selection cycles were evaluated in for; number of spikes/plant, number of kernels/spike, 100-kernel weight and grain yield/plant. The results of analyes of variance for each cross showed significant differences among breeding methods in all crosses except for, 100 kernel weight in crosses No.1 and No.4. Moreover, the genotypes showed significant differences in all studied traits for all crosses. The interaction between genotypes and breeding methods was significant in all studied characteristics for all crosses. Combined analysis for all methods of breeding crosses and genotypes showed significant differences for crosses (C), except for, 100 kernel weight and grain yield/plant, methods of breeding (M), genotypes (G), except for 100 kernel weight, (C x M), (M x G) and (C x M x G). The best methods of breeding for all studied traits were pedigree method (PM) followed by modified bulk 1 (MP1) .The results revealed that, four bread wheat crosses differed in number of spikes plant and number of kernel spike. Cross No. 4 had the highest number of spikes/plant, number of kernels/spike and grain yield /plant. Cross No. 1 had the highest 100-kernel weight.

key words: wheat, modified bulk Method, pedigree methods, bulk method, analysis of variance.

INTRODUCTION

Plant breeders are searching continuously for more effective and efficient breeding and selection procedure. Numerous methods have been proposed, but only a few valid comparisons have been made among alternative

procedures (Griganc et al., 1978). Both bulk and pedigree methods have been used extensively in the developing small-grain crops. The bulk system involves natural selection operating on solid-seeded segregating populations followed by individual plant selection within the desired crosses in the later generations. However, the pedigree method involves phenotypic selection between individuals space-planted within crosses from the F₂ through F₅ generations before yield tests are conducted (Ortiz Ferrara, 1981) found that, differences in response to phenotypic selection based on the four selection methods were observed depending on the traits and cross involved. In general, superior performance of F₅ selections obtained by the pedigree, modified bulk1 and modified bulk2 methods were achieved when compared to the bulk method. El-Shamy (1987) and Faleinelli et al. (1988) reported that no significant differences among methods of breeding and / or selection for vield and its components were found, Mahdy (1988) revealed that, single trait selection for two cycles was an efficient method in improving selection criterion in bread wheat. Kheiralla (1993) reported that, two cycles of selection for, 100-kernel weight, number of kernels/spike, number of spikes/plant and grain yield were enough to identify the promising genotypes and further selection among and within families will be useless. The results of Knott (1979) and Mohamed (1999) showed that, pedigree selection method proved to be superior in mean values of the selected populations. Meanwhile, Deghais and Auriau (1993); Ismail (1995); Fahim et al. (1996) and Pawar et al. (1997) found that the modified bulk method was an effective as pedigree method. Tammam (2004) showed that (PM) and (MP1) are the best methods for breeding or selection for, number of spikes per plant, (PM) for number of kernels per spike, and kernel weight per spike and pedigree method was the most effective method for improving grain yield. El-Sayed (2006) showed that, the best methods of breeding for number of spikes per plant was (BM) followed by (PM), for number of kernels per spike (MB-2) followed by (PM), for 100-kernel weight (MB-1) followed by (MB-2) for grain yield per plant (BM) and (MB2). El-sayed and Moussa (2010) studied some breeding methods in six durum wheat crosses and they found that, the best method of breading for grain yield no. of spike/plant and for, 100 kernel weight was pedigree method (PM)

The objective of this investigation was to determine the best efficient breeding methods in improving wheat lines with high grain yielding ability.

MATERIALS AND METHODS

The present study was carried out at the farm of El-Giza Agric. Res. Station, ARC, Egypt during four successive growing seasons of 2006/2007, 2007/2008, 2008/2009 and 2009/2010 to compare the efficiency of four breeding methods in six bread wheat crosses (*Triticum aestivumL.*), which chosen from a diallel cross mating and evaluated for combining ability for

four agronomic traits (Sabah H. Abo Elela 2006) on basis of their genetic diversity and performance under field conditions (Table 1). breeding methods were as follows:

- 1. Pedigree method (PM) was conducted using individual plant selection procedure for three cycles from selection among and within families in each cross in F_3 , F_4 and F_5 .
- 2. Modified bulk-1 (MB-1) was exercised using individual plant selection procedure for two cycles from selection among and within families in each cross in F_3 and F_4 generations and sowing as a bulk in F_5 generation.
- 3. Modified bulk-2 (MB-2) was conducted using individual plant selection procedure for one cycle from selection among and within families in each cross in F_3 families and sowing bulk in the F_4 and F_5 generations.
- 4. Bulk method (BM) was conducted by harvesting the remaining plants from each cross after mixing the grains and then random samples were taken and sown in the next three generations.

Cross No.	Cross name and pedigree
1	Sakha93 x Giza168
2	Gemmeiza7 x Sakha 69
3	Sahel x KAUS/ATILA
4	Gemmeiza7 x Giza168

In 2006/2007 season, 150 plants from F_2 of each cross were randomly selected and subjected to the four selection methods.

In 2007/2008 season, $50 \, F_3$ families from each cross in addition to the bulk population were sown in one row for each family with 3.0 m long,and 30 cm apart and 10 cm within rows. At F_3 , 10 guarded plants were selected from each family and bulk population. Data were recorded for four characteristics (number of spikes/plant, number of kernels/spike, 100-kernel weight, and grain yield/plant). Selection intensity was 10% for the best families and plants within families (selection among and within families). Selected plants within each family were subjected to the pedigree method (PM), grains of the remaining plants were mixed for each family to be subjected to the modified bulk2 (MB2) as the F_4 generation. Also, grains produced from F_3 bulk were mixed to be tested as F_4 bulk.

In 2008/2009 season, 13 rows (6 F₄ families for PM, 6 families for MB2 and one row for BM), of each cross were grown as the same practice in the F₃

generation. At maturity, 10 guarded plants from each family were harvested and data were recorded for each plant of the above–mentioned characteristics. The best plant from each 6 F_4 families of the PM was kept to represent PM in the next generation. The remaining grains plants for each 6 families of PM were mixed to represent the modified bulk1 (MB1). Also, seeds of 10 plants of bulk population (BM) were mixed to be sown as a bulk population in the F_5 generation. In addition, seeds of the 10 plants for each 6 families of MB2 were mixed to obtain 6 lines in F_5 generation in the next season.

In 2009/2010, 18 F₅ lines, (6 lines from each method of PM,MB1 and MB2 for each cross and the population bulk, 6 yows) were sown in aspilt–spilt plot experiment with four replications. Selection methods were in the main plot, crosses in sub-plots and the lines in sub-sub plots. Each line was planted in one row with 3.0 m long, 30 cm a part and 10.0 cm within rows. In addition, the population bulk was planted in five rows as the same sowing method in each replicate. At maturity, 10 guarded plants were harvested and data were recorded for the above-mentioned characteristics on each plant and each line. The cultural practices were carried out as recommended for bread wheat production.

Data for mean of ten plants of six lines for each method were subjected to analysis of variance with the design of spilt split plot according to *Snedecor and Cochran (1967)*. Also, six lines for each method were analyzed as RCBD to compute the significance of methods of breeding, genotypes and the interaction between methods and genotypes.

The least significant difference (L.S.D) test at 5% level of probability, according to *Steel and Torrie* (1980) was used to compare values among mean traits.

RESULTS AND DISCUSSION

1- Analysis of variance:

The results of this study will be presented with regard to the performance of five F_5 lines derived from each four bread wheat crosses and four breeding methods The performance of the F_5 lines was evaluated in terms of the effectiveness of zero, one, two and three cycles of phenotypic or visual selection for fur agronomic characteristics.

Analysis of variance for each cross (methods of selection, genotypes and the interaction between methods of selection and genotypes), are presented in Table (2). Mean squares for the studied characteristics in four bread wheat crosses showed that, breading methods had significant effect for all characteristics in all crosses, except for, 100 kernel weight in crosses 1 and 4 in cross No.2. The interaction between genotypes and breeding methods were significant differences for all characteristics studied in all crosses.

Table (2): Mean squares for the characteristics studied in four bread wheat crosses

Crosses	S.afv.	d.f	Gy	Nos/P	Nok/S	100 Kwt
	Rep (R)	3	7.22t	4.35	3.0	0.257
1	Methods (M)	3	306.55*	23.55*	1156.49*	0.058
	Genotype (G)	5	216.75*	98.43*	434.01*	2.323*
	MXG	15	107.70*	22.33*	99.61*	1.279*
	Error	69	11.77	3.14	6.44	0.158
	Rep (R)	3	17.591	13.057	2.962	0.012
2	Methods (M)	3	979.846*	141.093*	184.943*	5.502*
	Genotype (G)	5	275.12*	31.117*	43.065*	2.157*
	MXG	15	202.797*	65.051*	130.292*	2.507*
	Error	69	14.915	5.263	5.717	0.148
	Rep (R)	3	13.041	7.684	8.345	0.065
3	Methods (M)	3	532.45*	92.003*	1208.437*	8.924*
	Genotype (G)	5	188.102*	55.658*	153.583*	0.931*
	MXG	15	129.124*	37.162*	173.289*	1.335*
	Error	69	16.255	1.997	4.398	0.114
	Rep (R)	3	12.294	7.900	4.136	0.143
4	Methods (M)	3	285.455*	108.368*	3683.612*	0.058
	Genotype (G)	5	193.961*	22.084*	259.798*	1.339*
	MXG	15	285.282*	55.123*	421.606*	2.945*
	Error	69	22.427	3.515	7.036	0.055

Gy= Grain yield

Noslp= no.op spike lplant

Nokls= number of kernels per References

100 Kwt= 100 Kernel weight

Mean performance of combined analysis for the six lines derived from four bread wheat crosses and four breading methods are presented in Table (3) through Table (6). Results of analysis showed that, highly significant differences were observed among the four crosses, except for, 100 kernel weight and grin yield per plant, four breeding methods and six lines derived from each cross and methods except 100 kernel weight for all studied characteristics. Also, high significance interaction of crosses and methods, crosses and lines, methods and lines and the interaction of crosses and methods and lines indicating that response to selection methods were different according to crosses and methods. These results are in agreement

with those obtained by Ortiz Ferrara (1981), El-Shamy (1987) Falcinelli *et al.* (1988). and El-Sayed (2006)

Table (3) :- Mean performance for number of spikes /plant in four bread wheat

crosses using four breeding methods.

Method	cross	Genotype						Mean
		1	2	3	4	5	6	
	1	24.66	22.63	24.79	21.19	19.35	20.51	22.19
PM	2	23.70	22.60	25.55	28.95	30.65	18.80	25.04
	3	19.75	16.75	20.75	21.20	23.10	23.45	20.83
	4	21.90	31.30	24.0	25.65	23.6	25.25	25.28
Mean		22.50	23.32	23.77	24.25	24.18	22.0	23.34
	1	29.16	22.55	27.10	15.35	19.65	23.50	22.88
MP-1	2	30.85	26.43	24.75	18.90	24.10	20.85	24.31
	3	19.70	26.05	26.55	24.100	26.10	26.10	24.77
	4	23.75	19.50	26.75	15.75	22.0	17.25	20.83
Mean		25.86	23.63	26.28	18.53	22.96	21.93	23.20
	1	25.27	19.18	19.81	17.29	19.59	22.40	20.59
MP-2	2	17.200	22.35	17.65	26.30	21.35	19.20	20.68
	3	25.85	16.00	18.90	16.60	19.55	27.95	20.81
	4	28.45	23.70	28.75	27.25	20.46	21.18	24.96
Mean		24.19	20.31	21.28	21.86	20.22	22.68	21.76
	1	23.58	22.60	24.19	23.56	19.38	20.91	22.37
ВМ	2	21.15	17.80	16.50	21.15	20.75	24.75	20.35
	3	23.05	25.50	21.30	21.40	22.60	26.30	23.36
	4	22.10	20.70	21.25	20.10	23.75	26.50	22.4
Mean		22.47	21.65	20.81	21.55	21.62	24.61	22.12
	1	25.67	21.74	23.97	19.35	19.49	21.83	22.01
	2	23.23	22.30	21.10	23.83	24.21	20.9	22.59
Mean	3	22.09	21.08	21.88	20.83	22.84	25.95	22.44
	4	24.05	23.80	25.19	22.19	22.44	22.54	23.37
		23.76	22.23	23.03	21.55	22.25	22.81	22.60

L.S.D 5 % Methods "M" 0.49

0.70

Crosses "C"

M x C 1.41 M x G 1.25 M x C x G 2.5

Genotypes "G" 0.63

C x G 0.125

2- Mean performances:-

2.1:- Number of spikes per plant :-

Data in Table (3), revealed that, average of number of spikes/plant ranged from 23.37for cross no. 4 to 22.01 for cross no. 1 with an average 22.6 for overall crosses. On the other hand, average varied from 20.83 for cross no. 3 to 25.28 for cross no. 4 with an average 23.34 in the pedigree method (PM), from 20.83 for cross no. 4 to 24.77 for cross no. 3 with an average 23.20 of the modified bulk 1(MB1), from 20.59 for cross no. 1 to 24.96 for cross No. 3 with an average 21.76 of the modified bulk 2 (MB2) and varied from 20.35 for cross no. 2 to 23.36 for cross no.3 with an average 22.12 for the bulk method (BM). These results are in line with those obtained by El-Sayed (1996), Tammam (2004), And El-sayed and Moussa (2010).

Meanwhile the mean of lines or genotypes ranged from 21.55 for genotypes no. 4 to 23.76 for genotype no. 1 in the overall mean. The best genotype with pedigree method (PM) no. 4(24.25), genotype no. 3 (26.28) in the modified bulk-1 (MB-1) genotype no. 1 (24.19) in the modified bulk- 2 (MB-2) and genotype or line no. 6 (24.61) in bulk method (BM).

On the other hand, average of number of spikes per plant showed significant differences among breeding methods (M), crosses (C) and lines or genotypes (G) and the first and second order of interaction (MxC), (MxG), (CxG) and (MxCxG). Also, in the selection methods, pedigree method (PM) and modified bul-k1 (MB-1) varied significant differences than bulk method (BM).

2.2- Number of kernels per spike:-

The data for number of kernels per spike (Table 4), exhibited that average of number of kernels per spike varied from 50.67 for cross no. 4 to 37.48 for cross no. 2 with an average 44.10 for PM, from 50.66 for cross no. 4 to 33.64 for cross no. 1 with an average 40.74 for MB1, from 44.68 for cross no. 3 to 30.88 for cross no.4 with an average 38.00 for MB2 and ranged from 36.24 for cross no. 1to 27.58 for cross no. 3 with an average 31.67 for BM. These results indicated that, PM was superior in improving number of kernels per spike and response to selection using PM was 12.43 kernels per spike 39.25 %, when compared to bulk method in overall crosses .

In general, cross no.4 had the highest number of kernels per spike (39.99) followed by cross no. 1 (39.84) and varied significantly with other four crosses in the overall crosses. On the other hand, genotypes or lines no. 1 and 2 for PM, 5 and 6 for MB-1, 1and 2 for MB-2, 2 and 3 for BM and 1 and 2 for overall genotypes or lines gave the highest number of kernels per spike. These results are in agreement with those reported by Kherialla (1993), Deghais and Auriau (1993), Ismail (1995), Fahim et al. (1996), Pawar et al.

(1997) ,Tammam (2004) and El-Sayed (2006) who reported that, pedigree method was more effective than other selection methods in improving number of kernels per spike.

Table (4):- Mean performance for number of kernels/spike in four bread wheat crosses using four breeding methods.

Crosses	Genotype						
	1	2	3	4	5	6	
1	50.19	55.30	45.3	41.15	55.26	49.8	49.49
2	34.20	43.45	34.60	35.25	39.45	37.9	37.48
3	44.60	44.50	39.95	31.10	31.7	40.85	38.78
4	59.00	46.25	46.75	62.00	43.75	46.25	50.67
	47.00	47.38	41.65	42.38	42.53	43.7	44.10
1	39.54	40.60	23.95	27.30	33.36	37.10	33.64
2	35.45	37.30	52.75	39.35	41.60	42.8	41.54
3	26.00	37.80	45.60	35.2	32.6	45.6	37.13
4	43.25	32.90	41.30	58.5	73.50	54.5	50.66
	36.06	37.15	40.9	40.08	45.26	45.00	40.74
1	47.01	46.46	34.58	36.31	33.19	42.33	39.98
2	41.60	33.00	41.00	31.10	36.45	35.55	36.45
3	33.20	45.30	43.45	45.45	57.45	43.25	44.68
4	46.15	41.05	26.65	24.75	26.00	20.7	30.88
	41.99	41.45	36.42	34.40	38.27	35.46	38.00
1	35.68	46.30	44.11	24.93	28.91	37.49	36.24
2	34.20	35.50	34.35	47.05	30.60	28.9	35.10
3	26.30	22.9	27.9	25.7	28.70	33.95	27.58
4	31.70	24.40	28.10	26.00	28.10	28.23	27.75
	31.97	32.28	33.62	30.92	29.08	32.14	31.67
1	43.10	47.17	36.98	32.42	37.66	41.68	39.84
2	36.36	37.31	40.68	38.19	37.03	36.29	37.64
3	32.53	37.63	39.23	34.36	37.61	40.91	37.04
4	45.03	36.15	35.60	42.81	42.84	37.42	39.99
	39.25	39.56	38.15	36.95	38.79	39.07	38.63
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L.S.D 5 %

Methods "M" 0.73 Crosses "C" 0.85 M x C 1.16 M x G 1.7

M x C x G 3.4

Genotypes "G" 1.10

C x G 1.7

2.3- 100-kernel wheat:-

Average of 100-kernel weight (Table 5) ranged from 5.69 g for cross no. 1 to 6.56 g for cross no. 3 with an average 6.01 g for pedigree method (PM), from 5.31g for cross no. 3 to 5.75 g for cross no. 4 with an average 5.54 g for modified bulk-1 (MB-1), from 5.24 g for cross no. 3 to 5.75 g for cross no. 1 with an average 5.53g for modified bulk-2 (MB-2) and from 5.66 g for cross no. 4 to 5.90 g for cross no. 2 with an average 5.79 g for bulk method (BM). The results showed significant differences between the four breeding methods. Meanwhile, pedigree method (PM) had the highest value of 100kernel weight followed by bulk method (BM), modified bulk-2 (MB-2), and modified bulk-1 (MB-1). Also crosses no. 2and 3 in PM, crosses no. 4 and 1 in MB1, crosses 1 and 4 in MB2, crosses no. 2 and 3 in BM and crosses no. 1 and 3 in the overall crosses gave the highest values of 100-kernel weight in overall means of genotypes or lines. Generally, these results indicated that, breeding methods for developing kernel weight in wheat varied according to the crosses and methods . Similar results were obtained by Ortiz Ferrare (1981), El-Shamy (1987), Falcinelli et al. (1988), Tammam (2004), El-Sayed (2006) and El-Sayed and Mousa (2010).

2.4 - Grain yield per plant :-

Regarding grain yield per plant (Table 6), average of grain yield per plant (gm) varied from 56.09 g in cross no. 1 to 52.01 g in cross no. 3 with an average 54.05 g when using pedigree method (PM), varied from 46.92 g. in cross no.3 to 57.23 g in cross no.2 with an average 52.33g when using modified bulk-1 (MB-1), from 48.16 g in cross no. 2 to 54.97g. in cross no. 3 with an average 50.90 g when using modified bulk-2 (MB-2) and ranged from 43.33 g in cross no. 2 to 49.46 g in cross no. 3 with an average 46.79 g when using bulk method (BM). These results indicated that using pedigree method was the most effective method for improving wheat grain yield significantly comparing to the other studied methods.

On the other hand, crosses no. 4 (51.54 g) and cross no. 2 (50.95 g), had the highest value of grain yield per plant. Lines no. 1 and no. 2 in the pedigree method (PM), lines no. 5 and 6 in the modified bulk 1(MB1), lines no. 4 and 6 in the modified bulk 2 (MB2) lines no.1 and 6 in bulk method (BM), and lines no. 4 and 6 in the overall means were the highest value of grain yield per plant. These results are in line with those reported by Knott (1972), Depauw and Shebeski (1973), Ortiz Ferrara (1981), El-Shamy (1987), Falcinelli et al. (1988) Tammam (2004) and El-Sayed and Moussa (2010).

Table (5) :- Mean performance for 100-kernel weight in four bread wheat crosses using four breeding methods .

Method	cross	3 using	Mean					
		1	2	3	4	5	6	
	1	5.86	5.26	5.89	6.73	5.19	5.19	5.69
PM	2	4.31	6.89	6.79	5.87	6.77	5.58	6.04
PIVI	3	6.49	6.99	7.53	6.39	6.40	5.57	6.56
	4	5.38	5.74	5.12	6.29	5.41	6.64	5.76
Mean		5.51	6.22	6.33	6.23	5.94	5.74	6.01
	1	5.68	5.90	5.03	6.59	6.72	4.44	5.73
MB-1	2	5.63	5.84	5.16	4.67	5.25	5.76	5.38
IVID-I	3	4.90	4.54	5.09	6.33	5.34	5.64	5.31
	4	5.40	5.42	5.84	5.70	5.57	6.59	5.75
Mean		5.40	5.42	5.28	5.82	5.72	5.61	5.54
	1	5.77	5.56	5.61	5.31	6.56	5.70	5.75
MB-2	2	6.02	6.37	4.53	4.36	5.11	6.35	5.46
IVID-Z	3	5.41	4.39	5.22	5.47	5.57	5.36	5.24
	4	5.46	7.15	6.15	5.62	5.13	4.64	5.69
Mean		5.66	5.89	5.37	5.19	5.59	5.51	5.53
	1	5.39	5.43	5.48	6.02	6.57	5.94	5.80
ВМ	2	7.04	5.75	5.48	5.71	5.32	6.11	5.90
DIVI	3	5.77	6.11	6.61	5.52	5.36	5.51	5.81
	4	7.64	5.41	6.13	4.65	4.70	5.46	5.66
Mean	Mean		5.67	5.92	5.47	5.49	5.75	5.79
	1	5.68	5.54	5.50	6.16	6.26	5.32	5.74
	2	5.75	6.21	5.49	5.16	5.61	5.95	5.69
Mean	3	5.64	5.51	6.11	5.93	5.66	5.52	5.73
	4	5.97	5.93	5.81	5.56	5.20	5.83	5.72
		5.76	5.80	5.73	5.70	5.68	5.65	5.72
160	5.0	١,,						

L.S.D 5 % Methods "M" 0.10 Crosses "C" Genotypes "G"

M x C 0.18 M x G 0.24 C x G 0.24

M x C x G 0.48

Table (6) :- Mean performance for grain yield per plant in four bread wheat crosses using four breeding methods .

Moderal		Genotype						
Method	Crosses	1	2	3	4	5	6	Mean
044	1	68.20	53.73	57.71	56.73	55.02	45.15	56.09
	2	63.92	59.53	47.71	54.49	56.72	48.23	55.10
РМ	3	48.76	71.82	50.57	45.64	40.27	55.02	52.01
	4	46.47	44.04	59.37	54.88	55.96	57.32	53.00
Mean		56.84	57.28	53.84	52.93	51.99	51.13	54.05
	1	49.25	45.43	56.44	41.53	44.09	55.79	48.75
MP-1	2	51.01	57.55	50.05	69.40	59.72	55.64	57.23
IVIF-1	3	51.13	49.51	38.33	43.28	50.67	48.62	46.92
	4	59.79	46.12	59.50	56.47	58.86	57.72	56.41
Mean		52.79	49.65	51.08	52.67	53.33	54.44	52.33
	1	50.69	48.29	49.66	48.52	43.92	52.29	48.89
MP-2	2	34.72	41.44	41.35	52.03	62.07	57.35	48.16
IVIP-2	3	43.19	45.11	60.43	65.86	56.28	58.94	54.97
	4	49.34	56.47	48.65	51.66	47.49	55.99	51.59
Mean		44.48	47.83	50.02	54.52	52.44	56.14	50.90
	1	53.19	49.47	53.59	39.55	45.53	53.95	49.21
ВМ	2	45.60	47.72	36.35	43.78	40.39	46.15	43.33
DIVI	3	36.96	52.80	51.33	51.55	51.63	52.49	49.46
	4	57.55	34.29	48.69	40.26	43.05	47.13	45.16
Mean		48.32	46.07	47.49	43.78	45.15	49.93	46.79
	1	55.33	49.23	54.35	46.58	47.14	51.79	50.74
	2	48.81	51.56	43.86	54.92	54.73	51.84	50.95
Mean	3	45.01	54.81	50.17	51.58	49.71	53.77	50.84
	4	53.29	45.23	54.05	50.79	51.34	54.54	51.54
	F 04	50.61	50.21	50.61	50.97	50.73	52.98	51.02

L.S.D

5 % 0.99

Methods "M" Crosses "C" Genotypes "G" 1.39 M x C 2.28 M x G 2.78 C x G 2.78

M x C x G 5.55

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مقارنة بين أربعة طرق للتربية على بعض هجن قمح الخبز

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الملخص العربي

أجريت هذه الدراسة في المزرعة البحثية لمحطة البحوث الزراعية بالجيزة في أربعة مواسم متتابعة خلال الفترة من ٢٠٠٧/٢٠٠٦ حتى ٢٠١٠/٢٠٠٩. وقد استخدم في هذا البحث أربعة طرق للتربية وهي:-

- ١. طريقة سجل النسب بإجراء ثلاث دورات للانتخاب في الجيل الثالث والرابع والخامس.
 - ٢. طريقة التجميع المحورة ١ بإجراء دورتين للانتخاب في الجيل الثالث والرابع.
 - ٣. طريقة التجميع المحورة ٢ بإجراء دورة واحدة للانتخاب في الجيل الثالث.
 - ٤. طريقة التجميع العادية.

واستخدم في هذه الدراسة أربعة هجن من قمح الخبز وهي : سخا ٩٣ ×جيزه ١٦٨ ، جميزه ٧×سخا ٩٣ ، ساحل ١ (كاوز ×أ ت ي لا) ، جميزه ٧×جيزه ١٦٨ وكانت الصفات محل الدراسة هي عدد السنابل في النبات – عدد حبوب السنبلة – وزن ١٠٠ حبة و وزن حبوب النبات. وأظهرت نتائج التحليل الفردي لكل هجين وجود فروق معنوية لطرق الانتخاب في كل الهجن ماعدا وزن ١٠٠ حبة في الهجين الأول والرابع وأظهرت السلالات المنتخبة من كل هجين فروقاً معنوية لكل صفات الدراسة. أوضح التفاعل بين السلالات المنتخبة وطرق الانتخاب فروقاً معنوية في كل صفات الدراسة. وأوضح التحليل التجميعي للهجن وطرق التربية والسلالات المنتخبة وجود فروق معنوية في الهجن وطرق التربية أو الانتخاب والسلالات المنتخبة ماعدا وزن ١٠٠ حبة بالنسبة للهجين والسلالات المنتخبة وكذلك وزن حبوب النبات بالنسبة للهجن محل الدراسة وكذلك وزن جبوب النبات بالنسبة

وأظهرت نتائج التحليل أن أفضل طريقة للتربية لكل الصفات المدروسة هي طريقة سجلات النسب تتبعها طريقة التجميع المحورة ١. وأوضحت النتائج أن الهجن الأربعة اختلفت فيما بينها في متوسطات الصفات وكان الهجين الرابع هو أحسن الهجن بالنسبة لعدد السنابل في النبات وعدد حبوب السنبلة ومحصول الحبوب للنبات والهجين رقم (١) كان أحسن المتوسطات في وزن ١٠٠٠جم .

مقاربة بين أربعة طرق للتربية على بعض هجن قمح الخبز

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الملخص العربي

أجريت هذه الدراسة في المزرعة البحثية لمحطة البحوث الزراعية بالجيزة في أربعة مواسم متتابعة خلال الفترة من ٢٠٠٧/٢٠٠٦ حتى ٢٠٠٧/٢٠٠٩. وقد استخدم في هذا البحث أربعة طرق للتربية وهي:-

- ٥. طريقة سجل النسب بإجراء ثلاث دورات للانتخاب في الجيل الثالث والرابع والخامس.
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 - ٧. طريقة التجميع المحورة ٢ بإجراء دورة واحدة للانتخاب في الجيل الثالث.
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واستخدم في هذه الدراسة أربعة هجن من قمح الخبز وهي : سخا ٩٣ ×جيزه ١٦٨ ، جميزه ٧×سخا ٩٣ ، ساحل ١ (كاوز ×أ ت ي لا) ، جميزه ٧٠ جبيزه ١٦٨ وكانت الصفات محل الدراسة هي عدد السنابل في النبات – عدد حبوب السنبلة – وزن ١٠٠ حبة و وزن حبوب النبات. وأظهرت نتائج التحليل الفردي لكل هجين وجود فروق معنوية لطرق الانتخاب في كل الهجن ماعدا وزن ١٠٠ حبة في الهجين الأول والرابع وأظهرت السلالات المنتخبة من كل هجين فروقاً معنوية لكل صفات الدراسة. أوضح التفاعل بين السلالات المنتخبة وطرق الانتخاب فروقاً معنوية في كل صفات الدراسة. وأوضح التحليل التجميعي للهجن وطرق التربية والسلالات المنتخبة وجود فروق معنوية في الهجن وطرق التربية أو الانتخاب والسلالات المنتخبة ماعدا وزن حبوب النبات بالنسبة المنتخبة ماعدا وزن حبوب النبات بالنسبة المهجن محل الدراسة وكذلك وزن جبوب النبات بالنسبة المهجن محل الدراسة وكذلك جميع التفاعلات الزوجية أو الثلاثية كان بينها كان بينهما فروقا معنوية.

وأظهرت نتائج التحليل أن أفضل طريقة للتربية لكل الصفات المدروسة هي طريقة سجلات النسب تتبعها طريقة التجميع المحورة ١. وأوضحت النتائج أن الهجن الأربعة اختلفت فيما بينها في متوسطات الصفات وكان الهجين الرابع هو أحسن الهجن بالنسبة لعدد السنابل في النبات وعدد حبوب السنبلة ومحصول الحبوب للنبات والهجين رقم (١) كان أحسن المتوسطات في وزن ١٠٠٠جم .