EFFECT OF FOUR SELECTION METHODS IN SOME BREAD WHEAT CROSSES

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ABSTRACT

Four methods of breeding or selection representing different cycles phenotypic selection were evaluated in six spring bread wheat *(Triticum aestivum* L.*)* crosses.

The methods were :

1- The pedigree method (PM) with three cycles of breeding selection in F_3, F_4 and F_5.
2- The modified bulk$_1$ (MB$_1$) two the cycles of breeding or selection in F_4 and F_5 were practiced.
3- The modified bulk$_2$ (MB$_2$) where only one cycle of breeding or selection in F_3 was exercised.
4- The bulk method where only natural breeding or selection were involved (BM).

This study was conducted at the farm of El-Giza Agric. Res. Stn., ARC, Egypt, during four successive seasons from 2001/2002 to 2004/2005 to evaluate the efficiency of four different breeding or selection methods in improving grain yield potentiality and some other agronomic traits in six bread wheat crosses. The lines which were produced from various cycles were evaluated in terms of number of spikes/plant, number of kernels/spike, 100 kernel weight, kernel spike weight and grain yield/plant.

Results of single analysis of variance for every cross showed significant differences for selection methods in all crosses. Genotypes showed significant variation in number of spikes/plant except for crosses No. 4 and 5, in number of kernels/spike and 100 kernel weight except for crosses No. 1 and 5, in kernel spike weight and grain yield/plant except for cross No. 1. The interaction between genotypes and methods of selection was significant in all studied characters for all crosses except for number of spikes/plant in crosses No. 4 and 6, number of kernels/spike except for cross No. 6 , 100 kernel weight except for cross No. 1, kernel spike weight and grain yield/plant.

Analysis of variance for methods of selection, crosses and genotypes showed significant differences for crosses (C), methods of selection (M), genotypes (G), and the interactions of (C x M), (C x G), (M x G) and (C x M x G).

The best methods of selection for number of spikes/plant was (BM) followed by (PM), for number of kernels /spike (MB$_2$), followed by (PM), for 100 kernel weight (MB$_1$) followed by (MB$_2$), for kernel spike weight (MB$_2$), followed by (PM) and for grain yield /plant, (MB) followed by (MB$_2$).

Results revealed that six bread wheat crosses differed in all studied characters. Cross No. 6 had the highest number of spikes/plant, cross No. 3 had the highest number of kernels/spike, 100 kernel weight and kernel spike weight, cross No. 5 had the highest grain yield/plant.

INTRODUCTION

The practical value of a plant is usually affected by several traits. Hence, deciding which are the most valuable individuals to select for parents of next generation forces the breeder to consider several different characteristics. These characteristics are not likely of equal importance or to be independent of each other. There are many ways of breeding or selecting for several things which are not often be equally efficient. The most efficient method is that results in the maximum genetic improvement per unit of time and effort expended (Hazel and Lush 1942).

There are no available reliable methods for the plant breeder to predict the hybrid combinations from which the highest proportion of superior segregates will be derived. Consequently, the breeder is forced to evaluate the progeny of many crosses according to his available facilities. Therefore, breeding procedures which utilize the facilities as efficiently as possible must be chosen. To enhance the efficiency, selection should be started as early as possible, preferably in the F2 generation. Although selection based on individual F2 plants is effective for simple characters, it has generally been found to be ineffective for yield (Knott 1972 and Depauw and Shebeski 1973).

Plant breeders are searching continuously for a more effective and efficient selection procedure. Numerous methods have been proposed, but only a few valid comparisons have been made among alternative procedures (Gringnac et al. 1978). Both bulk and pedigree methods both have been used extensively in the development of wheat cultivars. The bulk system involves natural selection operating on solid seeded segregating populations followed by individual plant selection within the desired crosses in later generations. In contrast, the pedigree method involves phenotypic selection between spaced plants individuals 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 the F5 selections obtained by the pedigree, modified bulk1 and modified bulk2 methods were achieved when compared to the bulk method. El-Shamy (1987) and Falcinelli et al. (1988) reported that no significant differences between methods of breeding and or selection for yield 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 1000-kernel weight, number of kernels/spike, number of spikes/plant and grain yield were enough to identify the promising genotypes and further selection between and within families will be useless. 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 (1997) found that the modified bulk method was as effective as pedigree method.

The objective of this investigation was to determine the best efficient selection method in improving wheat lines having high grain yield ability.

MATERIALS AND METHODS

The present study was carried out at the farm of El-Giza Agric. Res. Stn. ARC. Egypt, during the four successive growing seasons of 2001/2002, to 2004/005, to compare the efficiency of four selection methods in six bread wheat crosses, which were chosen from wheat breeding program at El-Giza Agric. Res. Stn., on basis of their genetic diversity and performance under field conditions. However, the name and pedigree of theses crosses are presented in Table 1. Selection methods were as follows:

1- Pedigree method (PM): was conducted by individual plant selection procedure for three cycles from selection between and within families in each cross.

2- Modified bulk$_1$ (MB$_1$): was exercised by individual plant selection procedure for two cycles from selection between and within families in each cross in F$_3$ and F$_4$ generations and sowing bulk in F$_5$ generation.

3- Modified bulk$_2$ (MB$_2$): was conducted by individual plant selection procedure for one cycle from selection between 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 all plants from each cross and mixing grains and random sample were used in the next three generations.

Table (1): The pedigree of the six bread wheat crosses.

Cross No.	Crosses name and pedigree
1	Giza 168 / Irena
2	Sids 1/ Giza 170
3	Bow "s"/ crow "s"// Gemmeiza 3/3/ cettia
4	Gemmeiza 7 /3/ kauz // altra 84/ Aos.
5	Sakha 93/5/ Maya "s" Mono "S" /CMH 74A.529/3/Sakha 8*2.
6	Sakha 69 /3/ vee / MJI // 2 *TUI.

In 2001/2002 season, 150 plants from F$_2$ of each cross were randomly selected and subjected to the four selection methods. Selection was practiced twice in each season at maturity stage for all studied characters.

In 2002/2003 season, 50 F$_3$ families from each cross in addition the bulk population were sown in one row/plot for each family with 3.0 m. long, 30 cm. apart and 10 cm. within row. At maturity, 10 guarded plants were selected from each family and other plants wear taken as a bulk population. Data were recorded for five characters (number of spikes/plant, number of kernels/spike, 100 - kernel weight, spike kernel weight and grain yield/plant). Selection intensity was 10 % for the best families and plants within family (selection among and within families). Selected plants from each family were

subjected to the pedigree method (PM) method grains of the remaining plants were mixed for each family to be subjected to (MB$_2$) method in the F$_4$ generation. Also, grains produced from F$_3$ bulk was mixed to will be in F$_4$ bulk.

In 2003/2004 season, 11 rows (5 F$_4$ families for PM, 5 families for MB$_2$ and one row for BM), of each cross were grown. At maturity, 10 guarded plants from each family were harvested and data were recorded for the five mentioned above characters. The best plant from each 5 F$_4$ families of the PM was kept to the PM in the next generation. The remain plants for each 5 families of PM were mixed to be (MB$_1$) method. Also, grains of 10 plants of (BM) method were mixed to be the bulk population in the F$_5$ generation. As well as kernels of the 10 plants for each 5 families of (MB$_2$) were mixed to be 5 lines in F$_5$ generation in the next season.

In 2004/2005, 15 F$_5$ lines for each cross and the population bulk were sown in a split-split plot experiment with four replications. Crosses were allocated to the main plot, selection methods to sub plots and the lines to sub-sub plots. Each line was planted in one row with 2.0 m. long, 30 cm. apart and 10.0 cm. between plants. In addition, the population bulk was planted in five rows in each replicate. At maturity, 10 guarded plants were harvested and data were recorded for the five previous characters on each plant. The cultural practices were carried out as recommended for wheat production.

Data for mean of ten plants of five lines for each method were subjected to analysis of mean squares with the design of split split-plot according to Snedecor and Cochran (1967). Also, single analyses for five genotypes or lines for each method were made as RCBD to compute the significance for genotypes, methods of selection and their interaction.

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

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 six bread wheat crosses and each selection 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 five agronomic characters.

Single analysis for every cross (methods of selection, genotypes and their interactions), are presented in Table (2). Mean squares for selection methods were significant for all characters in all crosses. The differences among genotypes for most studied characters were significant except for number of spikes/plant in crosses No. 4 and No. 5, 100 kernel weight in crosses No. 1 and No. 5 and grain yield/plant for cross No. 1. On the other hand, the interactions between genotypes and methods of selection were significant for number of spikes/plant except in cross No. 4, number of kernels/spike except in cross No. 6, 100 kernel weight except in cross No. 1, as well as kernel spike weight and grain yield/plant for all crosses.

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Table (2): Mean squares for the studied characters in six bread wheat crosses using four breeding or selection methods.

S. of V.	d. f	Cr₁	Cr₂	Cr₃	Cr₄	Cr₅	Cr₆
		No. of spikes /plant					
Replications	3	4.50	0.81	5.25*	13.85*	5.68*	0.98
Methods "M"	3	86.91*	159.05*	23.95*	63.55*	25.68*	171.88*
Genotypes "G"	4	5.84*	2.64*	5.83*	5.16	2.91	1.83*
M x G	12	6.61*	1.63*	5.87*	4.39	3.11*	1.21
Error	57	2.08	0.62	1.85	2.35	1.46	0.66
		No. of Kernels /spike					
Replications	3	2.056	17.78*	8.60	11.56*	11.51	33.30
Methods "M"	3	1319.84*	1564.69*	3218.72*	2723.82*	2232.57*	1392.25*
Genotypes "G"	4	45.67*	15.14*	43.20*	23.84*	57.92*	75.30*
M x G	12	71.32*	15.50*	47.32*	6.64*	59.44*	34.63
Error	57	4.11*	4.51	13.76	2.53	11.160	19.65
		100 kernel weight					
Replications	3	0.07	0.12*	0.20*	0.50*	.067	0.066
Methods "M"	3	4.01*	3.75*	0.861*	4.226*	0.415*	8.381*
Genotypes "G"	4	0.07	0.09*	0.610*	0.293*	0.065	0.162*
M x G	12	0.05	0.08*	0.279*	0.155*	0.160*	0.155*
Error	57	0.03	0.03	0.071	0.058*	0.033	0.058
		kernels spike weight					
Replications	3	0.01	0.02*	0.03	0.004	0.030	0.013
Methods "M"	3	3.85*	5.984*	10.473*	13.151*	4.259*	5.807*
Genotypes "G"	4	0.15*	0.041*	0.102*	0.134*	0.111*	0.128*
M x G	12	0.11*	0.015*	0.076*	0.033*	0.049*	0.195*
Error	57	0.01	0.006	0.020	0.005	0.018	0.029
		Grain yield /plant					
Replications	3	72.63*	126.54*	152.53*	111.54*	84.24*	91.65*
Methods "M"	3	2350.85*	6429.83*	3611.19*	6274.87*	7877.30*	6372.54*
Genotypes "G"	4	37.12	90.54*	295.24*	212.95*	111.45*	211.89*
M x G	12	47.73*	70.97*	146.25*	120.56*	66.48*	51.69*
Error	57	22.99	14.66	18.84	22.66	15.74	17.03

*, Significant at 5% probability

Mean squares of over all analysis for five lines derived from six bread wheat crosses and four selection methods is presented in Table (3). Results of the analysis showed that highly significant differences were observed among

six crosses, four selection methods and five lines derived from each cross and method for all studied characters. Also, exhibited highly significance for interactions 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 was different according to the cross and the method. These results are in agreement with those obtained by Ortiz Ferrara (1981), El-Shamy (1987). And Faleinelli *et al.*(1988).

2- Mean performances:

Data in Table (3), revealed that the average number of spikes/plant ranged from 13.84 in Cr_1 to 17.70 in Cr_6 with an average of 16.11 in the pedigree method (PM), varied from 11.97 in Cr_1 to 17.75 in Cr_6 with an average of 16.01 in the modified bulk 1 (BM_1), from 11.50 of Cr_2 to 17.50 in Cr_3 with an average 13.79 of the modified bulk 2 (MB_2) and varied from 14.85 in Cr_3 to 18.35 in Cr_6 with an average of 16.57 in bulk method (BM). Data revealed that significant differences observed between BM and PM, MB_1, MB_2 and overall mean bulk method (BM), existed in three crosses Cr_1, Cr_5 and Cr_6 in number of spikes/plant and it was the best one, meanwhile MB_2 had the lowest number of spikes/plant. These results are in line with those obtained by El-Sayed (1996) and Tammam (2004).

Data for number of kernels/spike (Table 3), exhibited that average number of kernels/spike varied from 39.14 for Cr_2 to 45.29 for Cr_3. The average of pedigree method (PM), ranged from 39.28 for Cr_2 to 56.18 for Cr_3 with an average 47.87, modified bulk$_1$ (MB_1) varied from 32.12 for Cr_4 to 36.38 for Cr_1 with an average 34.13, modified bulk 2 (MB_2) varied from 48.77 for Cr_6 to 57.32 for Cr_4 with an average 53.28 and bulk method (BM), different from 33.03 for Cr_2 to 41.26 for Cr_1 with an average 35.51 These results indicated that modified bulk 2 (MB_2) was superior in improving number of kernels/spike and response to selection using modified bulk 2 (MB_2) was 5.4 and 10.58 (11.3 and 24.78 %) when compared to pedigree method (PM) in overall crosses and overall mean, respectively. These results are in agreement with those reported by Kherialla (1993), Deghais and Auriau (1993), Ismail (1995), Fahim *et al.*(1996) and Pawar *et al.*(1997).

Average of 100 kernel weight (Table 3), ranged from 4.298 g. in Cr_6 to 4.801 g in Cr_3 with an average 4.562 for pedigree method (PM), from 4.583 in Cr_5 to 5.689 in Cr_3 with an average 5.164 for modified bulk 1 (MB_1), from 4.709 in Cr_6 to 5.356 in Cr_3 with an average 5.072 for modified bulk 2 (MB_2), and from 3.301 for Cr_6 to 4.517 for Cr_1 with average 4.253 for bulk method (BM). Results showed significant difference between four methods of selection. Meanwhile modified bulk 1(MB_1) had the highest value of 100 kernel weight followed by modified bulk 2 (MB_2). Also Cr_1, Cr_3 and Cr_4 were the highest values of 100 kernel weight with modified bulk 1 (MB_1) and Cr_2, Cr_3 and Cr_4 were the highest values of 100 kernel weight with modified bulk 2 (MB_2). Generally, these results indicated that selection methods for developing kernel weight in wheat was different according to crosses and methods. Similar results were obtained by Oritz Ferrare (1981), El-Sahmy (1987), Faleinelli *et al.*(1988) and Tammam (2004).

Table (3): Mean performance for the studied characters in six bread wheat crosses using four breeding methods.

Characters	Breeding methods	Crosses						Overall mean
		Cr_1	Cr_2	Cr_3	Cr_4	Cr_5	Cr_6	
No. of spikes/ plant	PM	13.84	17.45	15.95	16.10	15.60	17.70	16.11
	MB 1	11.97	17.45	15.85	17.25	15.80	17.75	16.01
	MB 2	14.04	11.50	17.50	13.05	14.55	12.10	13.79
	BM	17.02	16.05	14.85	15.85	17.30	18.35	16.57
	Mean	14.22	15.61	16.04	15.56	15.81	16.48	15.62
No. of kernels /spike	PM	40.44	39.28	56.18	46.50	54.75	50.10	47.87
	MB 1	36.38	32.64	35.08	32.12	33.82	34.75	34.13
	MB 2	55.04	51.60	56.35	57.32	50.63	48.77	53.28
	BM	41.26	33.03	33.55	34.42	35.50	35.28	35.51
	Mean	43.28	39.14	45.29	42.59	43.68	42.22	42.70
100 kernel weight	PM	4.634	4.525	4.801	4.647	4.465	4.298	4.562
	MB 1	5.476	5.136	5.689	5.473	4.583	4.629	5.164
	MB 2	5.144	5.273	5.356	5.200	4.747	4.709	5.072
	BM	4.517	4.409	4.368	4.495	4.427	3.301	4.253
	Mean	4.943	4.836	5.054	4.954	4.556	4.234	4.763
Kernel spike weight	PM	1.981	1.760	2.412	2.107	2.268	2.068	2.098
	MB 1	1.974	1.627	1.767	1.752	1.608	1.654	1.730
	MB 2	2.798	2.699	2.992	2.965	2.394	2.306	2.692
	BM	1.837	1.493	1.345	1.012	1.471	1.076	1.372
	Mean	2.147	1.895	2.129	1.959	1.935	1.776	1.973
Grain yield /plant	PM	43.09	42.29	44.01	41.05	38.65	37.97	41.18
	MB 1	46.54	44.00	46.65	46.92	48.85	46.83	46.63
	MB 2	58.13	56.70	50.27	54.91	54.60	49.12	53.95
	BM	66.71	81.14	73.13	81.18	84.80	79.02	77.70
	Mean	53.62	56.03	53.57	56.02	56.73	53.23	54.87

L. S. D. 5%	No. of spikes/plant	No. of kernels /spike	100 kernel weight	Kernel spike weight	Grain yield /plant
Crosses "C"	0.55	1.02	0.115	0.040	2.10
Methods "M"	0.32	0.77	0.055	0.030	1.09
Genotypes "G"	0.36	0.86	0.061	0.033	1.22
C x M	0.78	1.89	0.134	0.073	2.67
C x G	0.87	2.11	0.150	0.082	2.99
M x G	0.71	1.72	0.127	0.067	2.44
C x M x G	1.75	4.22	0.300	0.164	5.99

Average of spike kernel weight (Table 3), showed significant differences among methods of selection in all studied crosses and varied from 1.372 for bulk method (BM), to 2.692 for modified bulk 2 (MB_2). Also modified bulk 2 (MB_2) existed in all crosses in kernel spike weight it was the best one, meanwhile bulk method (BM) had lowest of kernel spike weight in overall crosses. Crosses No. 1 and 3 were heavy in kernel spike weight.

Regarding to grain yield /plant (Table 3), average of grain yield /plant varied from 37.97 g. in Cr_6 to 44.01 g in Cr_3 with an agerage 41.14g. when using pedigree method (PM), varied from 44.00 g in Cr_2 to 48.85 g in Cr_5 with an average 46.63 when using modified bulk 1 (MB_1), from 49.12 g for Cr_6 to 58.13 g for Cr_1 with an average 53.93 for modified bulk 2 (MB_2) and ranged from 66.71 g in Cr_1 to 84.8 g in Cr_5 with an average 77.70 when using bulk method (PM).

These results indicated that using bulk method was the most effective method for improving wheat grain yield and it possess significant effect compared with remaining methods. The Cr_5 had highest value of grain yield/plant (56.73 g.) followed by Cr_2 (56.03 g.) and Cr_4 (56.02 g). These results are in line with those reported by Knott (1972), Depauw and Shebeski (1973), Ortiz Ferrara (1981), El-Shamy (1987) and Falcinelli *et al.*(1988).

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تأثير أربع طرق للتربية في بعض هجن القمح

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أجريت هذه الدراسة في المزرعة البحثية لمحطة البحوث الزراعية بالجيزة في الفترة من ٢٠٠١/٢٠٠٢ حتى ٢٠٠٤/ ٢٠٠٥

استخدم في هذا البحث أربعة طرق للانتخاب هي:

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 ستة هجن من قمح الخبز .

وكانت الصفات محل الدراسة هي عدد السنابل في النبات – عدد حبوب السنبلة - وزن ١٠٠ حبة – وزن حبوب السنبلة و وزن حبوب النبات .

وأظهرت نتائج التحليل الفردي لكل هجين وجود فروق معوية لطرق التربية أو الانتخاب في كل الهجن وأظهرت السلالات المنتخبة من كل هجين فروقاً معنوية في عدد السنابل /نبات فيما عدا الهجين الرابع والخامس وعدد حبوب السنبلة ووزن ١٠٠ حبة فيما عدا الهجين الأول والخامس ، ووزن حبوب السنبلة ومحصول الحبوب في النبات ما عدا الهجين الأول . وأوضح التفاعل بين السلالات المنتخبة وطرق التربية أو الانتخاب فروقاً معنوية في عدد السنابل في النبات ما عدا الهجينين الرابع والسادس وعدد حبوب السنبلة ما عدا الهجين السادس ووزن ١٠٠ حبة ما عدا الهجين الأول ووزن حبوب السنبلة ووزن حبوب النبات .

وأوضح التحليل التجميعي للهجن وطرق التربية أو الانتخاب والسلالات المنتخبة وجود فروق معنوية وفي الهجن وطرق التربية أو الانتخاب والسلالات المنتخبة وكذلك جميع التفاعلات الزوجية أو الثلاثية فيما بينها .

وأظهرت نتائج التهجين ان أفضل طريقة للتربية أو الانتخاب لعدد السنابل/النبات هي التحليل التجميعي ثم طريقة سجل النسب ، وأفضل طريقة لعدد حبوب السنبلة هي طريقة التجميع المحورة ٢ ثم طريقة سجل النسب ، وأفضل طريقة لوزن ١٠٠ حبة هي طريقة التجميع المحورة ١ ثم التجميع المحورة ٢، وأفضل طريقة لوزن حبوب السنبلة هي طريقة التجميع المحورة ٢ ثم سجلات النسب ، وأفضل طريقة لمحصول الحبوب بالنبات هي طريقة التجميع العادية ثم التجميع المحورة ٢ .

وأوضحت النتائج أن الهجن الستة اختلفت فيما بينها في متوسطات الصفات المدروسة وكان الهجين رقم ٦ هو أفضل الهجن في عدد السنابل للنبات والهجين رقم ٣ في عدد حبوب السنبلة ووزن ١٠٠ حبة ووزن حبوب السنبلة وأظهر الهجين رقم ٥ أعلى إنتاجية لوزن حبوب النبات .