COMPARISON OF THREE SELECTION METHODS TO IMPROVE YIELD AND ITS COMPONENTS IN TWO BREAD WHEAT POPULATIONS

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ABSTRACT

This study was carried out at the field of Shandaweel Agric. Res. Station, ARC, Egypt, during three successive seasons from (2007/08 to 2009/10), to compare the efficiency of the three selection methods, i.e., Pedigree methods (PM), Modified bulk method (MB) and Bulk method (BM) to improve yield and its components in two bread wheat populations (*Triticum aestivum* L.).

Results of analysis of variance and combined analysis showed that significant and highly significant differences were observed between lines derived from each population and method for all studied characters and also between the three selection methods except for number of spikes/plant in population II. Also, the results exhibited that the interaction between lines and methods was highly significant for all studied characters.

The Bulk method (BM) had the lowest values for plant height, while the pedigree method (PM) had the highest values in both populations. The PM and MB methods were significantly superior to BM method of selection for number of spikes/plant in the population I, while in population II the differences between these methods were insignificant. PM and BM were superior to MB in improving kernels/spikes in the two populations. PM and BM were superior to MB in improving 100-kernel weight in the population I, while MB and BM were superior to PM in improving 100-kernel weight in the population II. The pedigree method (PM) was more effective than MB and BM of selection in improving grain yield/plant in the two populations. Broad sense heritability estimates ranged from low to high according to selection method and population in all studied characters.

INRRODUCTION

Wheat crop is considered as one of the essential strategic cereal crops not only in Egypt but also all over the world since it is a staple food for humans. Breeding methods play major role in developing high yielding cultivars, resistant to disease with better quality. Yield is a complex character controlled by a large number of genes because it is affected by several yield components i.e. number of spikes/plant, number of kernels/spike, 100-kernel weight. Therefore, wheat breeders have been concerned with the simultaneous improvement of more than one of these components. Plant breeders are searching continuously for more effective and efficient selection procedure. Numerous methods have been proposed but only a few

valid comparisons have been made among alternative procedures. **Ortiz-Ferrara (1981), Tammam (2004) and EL-Sayed (2006)** 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 F_5 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 selection for yield and its components were found. Results of **Knott and Kumar (1975), Knott (1979), Pawar *et al.* (1986) and Mohamed (1999)** showed that pedigree selection method proved to be superior in mean values of the selected populations. Meanwhile, **Salmeron (1985), Fahime *et al.* (1996) and Pawar (1997)** found that modified bulk method was as effective as pedigree method. **Grignac *et al.* (1978) and Srivastave *et al.* (19^^)** reported that pedigree method was as effective as bulk method for tillers/plant, kernels/ear and grain yield/plant. **Tammam (1995) and Verma *et al.* (1997)** showed that pedigree method of selection was more effective in improving plant height and yield and its components. **EL-Karamity *et al.* (2007)** reported that pedigree and modified bulk methods were effective in improving number of kernels/spike, plant height and 100-kernel weight. **Ehdaie and Waines (1989)** observed high values of phenotypic and genotypic variances for number of kernels/spike, 100-kernel weight and grain yield/plant. **Tammam and Abd EL-Rady (2010)** found that Broad sense heritability values varied from intermediate to high for plant height and yield and its components.

MATERIALS AND METHODS

The present study was carried out at the experimental field of Shandaweel Agric. Res. Station, Agric. Res. Center, Ministry of Agric., Egypt. During the three growing seasons 2007/08, 2008/09 and 2009/10.The objective of this study was to compare the efficiency of three selection methods, i.e., Pedigree methods (PM), Modified bulk method (MB) and Bulk method (BM) in two bread wheat populations (*Triticum aestivum* L.), which were chosen from wheat breeding program at Shandaweel Agric. Res. Station, based on their genetic diversity and performance under field conditions (Table 1).

Table (1): the pedigree and origin of the two wheat populations.

Parental name	Pedigree	Origin
Population I		
Giza 168	MRL / BUC // SERI.	Egypt
Sakha 93	SAKHA 92 / TR 810328	Egypt
Population II		
Sids 1	HD21 / PAVON "S" // 1158.57 / MAYA74"S"	Egypt
Sakha 93	SAKHA 92 / TR 810328	Egypt

Experiments layout.
1- 2007/08 season:
1500 plants of each F_3 population were grown in non replicated plots. Each plot consists of 15 rows, 10 cm. long, 30 cm. apart and 10 cm. between plants within rows. Lodged, unprotected and bird damaged plants were discarded. At maturity, plants were individually harvested and threshed. Data were collected on 450 harvested plants of each population. Data were recorded for five characters (plant height, number of spikes/plant, number of kernels/spike, 100-kernel weight and grain yield/plant). The selection intensity was 10% for yield and its components. Sixty plants from each population were selected and were subjected to the three breeding methods.
2- 2008/09 season:
In pedigree method, each of 60 plants for each population was sown in a separate row as F_4 families during 2008/09 season in Randomized complete design with three replications. Selection between and within families was practiced. 10 families and the best plant within each selected family were selected from each population to be raised as F_5 families in the final evaluation trial during 2009/10.

In the Modified bulk method, one spike from each selected F_3 plant from each population was bulk harvested and threshed to form the population seed bulk. A random sample of bulked seed of each population was space-planted as F_4 generation during 2008/09 season. Selection was practiced on the basis of 60 plants per each population. 10 plants from each population were selected. Grains of each selected plant were kept separately to be raised as F_5 generation in the final evaluated trail during 2009/10.

In the Bulk method, the remaining unselected F_3 plants, plus the remaining grains from the selected F_3 plants were mixed to form the population seed bulk for each population. A random sample of mixed grains was space-planted as F_4 generation during 2008/09 season. Selection was practiced on the basis of 60 plants per each population. Ten plants from each population were selected. Grains of

each selected plant were kept separately to be raised as F_5 generation in the final evaluated trail during 2009/10.

3- 2009/10 season:

Ten F_5 lines for each population and each selection method were sown in a randomized complete block design with three replications. Each plot was represented by one row; a row was 2.5 m long, 30 cm apart and 10 cm between grains within row. At maturity, 10 guarded plants were harvested and data were recorded for the five previous characters on each plant and each line. The cultural practices were carried out as recommended for wheat production.

Data for mean of ten plants of ten lines for each population and each method were subjected to analysis of variance by MSTATC computer program in randomized complete blocks design (RCBD) to compute the genetic parameters and variability in each method according to **Snedecor and Cochran (1967).** The combined analysis was performed between methods and the least significant difference (L.S.D) test at 5% level of probability was used to compare among means.

Heritability in the broad sense was estimated from the analysis of variance.

Table (2) the analysis of variance and expected mean squares.

Source of variance	D.F	M. S	E. M. S
Replication	$r-1$	M_3	$\sigma^2 e + g\,\sigma^2 r$
Genotypes	$g-1$	M_2	$\sigma^2 e + r\,\sigma^2 g$
Error	$(r-1)(g-1)$	M_1	$\sigma^2 e$

The phenotypic variance $\sigma^2 p = \sigma^2 g + \sigma^2 e$
The genotypic variance $\sigma^2 g = M_2 - M_1 / r$
The phenotypic (PCV %) and genotypic (GCV %) coefficient of variability were

calculated as $\sigma p / \overline{X} \times 100$ and $\sigma g / \overline{X} \times 100$, respectively.
Heritability in broad sense (H) = $\sigma^2 g / \sigma^2 p$

RESULTS AND DISCUSSION

The results of this study will be presented with regard to the performance of ten F_5 lines derived from each population and each selection method. The analysis of variance and combined analysis for the ten F_5 lines derived from the two populations and the three selection methods is presented in Table 3, Data showed that significant and highly significant differences were observed among the three selection methods, lines derived from each population and method for all studied characters except for number of spikes/plant in population II. Also, the results exhibited that the interaction between lines / methods was highly significant for all studied characters, indicating that response to selection was different according to

method of selection. Similar results were found by **Ortiz- Ferrara (1981), Falcinelli et al. (1988) and Tammam (2004).**

Table (3): Mean squares of the combined analysis of variance for the studied characters over all methods in 2009/10 growing season.

Ent.No.	S.O.V	D.F	Mean Squares				
			Plant height	Number of spikes / plant	Number of kernels / spike	100-kernel weight	Grain yield / plant
population I	Methods (M)	2	266.14*	34.93*	246.70*	0.779*	8.72*
	Error	6	27.05	3.73	27.12	0.086	16.66
	Genotypes (G)	9	53.37**	10.47**	64.05**	0.241**	54.32**
	M × G	18	140.86**	6.53**	48.59**	0.196**	46.17**
	Error	54	6.01	1.52	8.57	0.037	3.92
population II	Methods (M)	2	309.32**	14.53ns	82.49*	0.463**	86.45*
	Error	6	10.36	6.15	13.54	0.036	16.69
	Genotypes (G)	9	212.34**	9.98**	51.43**	0.781**	67.65
	M × G	18	212.10**	4.87**	126.85**	0.40**	30.79**
	Error	54	4.72	1.06	4.89	0.033	2.89

* and **: Significant at 5 % and 1 % level of probability, respectively.

Performance:

Data for plant height (Table 4) showed significant differences among selection methods in the two populations. The Bulk method (BM) had the lowest values (87.77 and 108.10), while the pedigree method (PM) had the highest values (93.67 and 113.92) in the population I and II, respectively. Results indicated a significantly higher mean of the PM over the (MB) and BM methods and insignificant differences between MB and BM in the population I. These results indicated that the three selection methods had differential impact on changing the mean of the population as earlier observed by **Pawar et al. (1986).** A significantly higher mean of the PM and MB than BM and insignificant differences between the PM and MB were found in the population II. Similar results were reported by **Salmeron (1985) and Fahim et al. (1996)** who found that modified bulk method was as effective as pedigree method.

The results of number of spikes/plant (Table 4) revealed that the PM and MB were superior to the BM in the population I. These results are in line with those reported by **Ortiz-Ferrara (1981), Salmeron (1985), Srivastva et al. (1989) and Tammam (2004)** who showed____ that superior performance of the F_5 lines selections were obtained by pedigree and modified bulk method were achieved when compared to the bulk method. On the other hand, there were no significant differences between methods for number of spike/plant in

the population II. Similar results were obtained by **El-Shamy (1987) and Falcinelli** *et al.* **(1988)** who reported that no significant differences were found between methods of selection for yield and its components.

Average number of kernels/spike (Table 4) showed that the PM and BM were superior to MB in the population I. Meanwhile PM was superior to MB and BM in improving number of kernels/spike in population II. These results are in agreement with those reported by **knott and kumar (1975), Verma** *et al.* **(1997), Mohammed (1999) and Tammam (1995 and 2004).** who reported that using pedigree selection method was more effective than other methods in improving number of kernels/spike.

The results of 100-kernel weight (Table 4) exhibited significant differences between the three methods of selection. Lines developed by the BM and PM were significantly superior than the MB method in the population I. Meanwhile BM Lines developed by the MB and BM were significantly superior than the PM in the population II. These results indicated that selection for developing kernel weight was different according to crosses and methods. These results are in line with those obtained by **Ortiz-Ferrara (1981) and Tammam (2004).**

Regarding to grain yield/plant (Table 4), average of grain yield/plant was (27.74, 23.94 and 24.80) for PM, MB and BM, respectively in the population I and (28.35, 25.09 and 25.89) for PM, MB and BM, respectively in the population II. The pedigree method (PM) showed a significantly higher mean over the modified bulk (MB) and bulk method (BM) for grain yield/plant in the two populations. These results indicated that using pedigree selection method was the most effective method for improving wheat grain yield and it possess a significant effect compared with the remaining methods. Similar results were reported by **Srivastava** *et al.* **(1989) and Tammam (1995 and 2004).** Insignificant differences were found between the MB and BM for grain yield/plant in the two populations. Similar results were found by **El-Shamy (1987) and Falcinelli** *et al.* **(1988)** who reported that no significant differences were found between methods of selection for yield and its components.

Variability:

Variance is considered one of the most important factors for efficiency of breeding methods. Data for plant height (Table 5) showed different values of phenotypic, genotypic variances and variability of (PCV & GCV) according to crosses and selection methods. These results are in agreement with those obtained by **Ortiz-Ferrara (1981), Tammam (2004) and El-Karamity et al. (2007).** The pedigree selection method had the highest values of phenotypic, genotypic variances and variability of (PCV & GCV) as compared to the other methods in the two populations except for the MB in the population II. The small differences between PCV and GCV over all selection

methods, confirming the importantce of genetic components of variability controlling plant height rather than the environmental effects. These results are in line with those obtained by **Ehdaie and Wainnes (1989) and Tammam (2004).** Broad sense heritability estimates for plant height (Table 5) were (85.25, 83.95 and 87.56) and (89.91, 96.77 and 95.05) for PM, MB and BM in the population I and II, respectively. these results indicate that plant height was less affected by environmental factors. Similar results were obtained by **Tammam (2004).**

Table (4): Mean performance of the ten F_5 lines obtained from three selection methods (pedigree (PM), modified bulk (MB) and bulk method (BM)) in the two bread wheat populations for five studied characters.

Ent. No.	Methods	Plant height	Number of spikes / plant	Number of kernels / spike	100 kernel weight	Grain yield / plant
population I	PM	93.67	13.50	51.03	4.03	27.74
	MB	90.00	13.57	47.14	3.77	23.94
	BM	87.77	11.67	52.73	4.06	24.80
	Mean	90.48	12.91	50.30	3.95	25.49
	LSD 0.05	3.29	1.22	3.29	0.19	2.58
population II	PM	113.92	13.98	47.75	4.27	28.35
	MB	113.37	12.67	44.63	4.51	25.09
	BM	108.10	12.93	45.20	4.46	25.89
	Mean	111.79	13.19	45.86	4.41	26.44
	LSD 0.05	2.03	N.S	2.33	0.12	2.58

Results of variances and variability for number of spikes/plant in (Table 5), show that less variable values were detected according to crosses and selection methods. These results indicate the narrow values of phenotypic and genotypic variances in these lines for this trait. Similar trends for PCV and GCV were observed in this trait. These results proved that number of spikes/plant was affected mainly by non additive gene effects. Similar results were obtained by **Tammam (2004).** Estimates of broad sense heritability for number of spikes/plant varied from low percentage 11.74% in population II with PM to high 92.97% in population II with BM.

The components of variance (phenotypic and genotypic variances), phenotypic (PCV), genotypic (GCV) coefficient of variability and broad sense heritability for number of kernels/spike are presented in (Table 5). Data show different values according to crosses and selection methods. The highest values were in population II with BM (48.93 & 47.47) for phenotypic and genotypic variance, respectively, while the lowest values were in population I with PM (22.82 and 16.63, respectively). These results indicate that lines were produced by applying BM have high of variability and different in number of kernels/spike. In most cases, Broad sense heritability estimates for number of kernels/spike were high. These results indicate that number of kernels/spike was less affected by environmental factors and is controlled mainly by genetic system. Similar observations were found by **Tammam (2oo4) and Tammam and Abd EL-Rady (2010).**

Results of 100-kernel weight (Table 5) show low values of phenotypic, genotypic variances and coefficient of variability for PCV & GCV in the two populations for the three selection methods. These results are expected with applying selection for two segregating generations and with homogeneity of plants (F_5 lines). Similar results were reported by **Tammam (2004).** Broad sense heritability estimates for 100-kernel weight varied from medium percentage 49.63 in population I with BM to high 92.49 in population II with BM.which is results indicate that 100-kernel weight was less affected by environmental factors. These results are in line with findings of **Tammam (2004), EL-Karamity et al. (2007) and Tammam and Abd EL-Rady (2010).**

Data of grain yield/plant (Table 5), revealed that the magnitude of phenotypic and genotypic variances were (21.86 and 13.54) in population I and (11.71 and 4.91) in population II for pedigree method (PM), (9.09 and 7.23) in population I and (10.26 and 8.55) in population II for modified bulk (MB) and (25.78 and 24.20) population I and (27.08 and 26.63) in population II for bulk method (BM). These results indicate that lines produced by PM and BM have high variability and are different in grain yield/plant. Similar results were reported by **Ortiz- Ferrara (1981) and Tammam (2004).** The variability of PCV and GCV have low percentages with PM and MB, indicating decrease of variability in F_5 generation when applying PM and MB as comparing with BM but, the mean performance of the F_5 PM population was superior to BM for grain yield/plant. These results suggested that the directional selection appears to reduce the range and variability for grain yield/plant in the F_5 PM populations without affecting the mean. Narrow of difference between phenotypic, genotypic variances indicate that grain yield/plant were less affected by environmental factors and this is clearing in the high values of broad sense heritability for the two populations for the three selection

method except in population II for pedigree selection method. These results are in agreement with those reported by **Ortiz Ferrara (1981), Tammam (1995 and 2004) and Mohammed (1999)**. Broad sense heritability estimate for grain yield/plant (Table 5) varied from medium of 41.08% in population II with PM to high 98.31% in population II with BM. These results indicated that grain yield/plant was less affected by environmental factors. These results are in agreement with those reported by **Tammam (1995 and 2004), Mohammed (1999) and Tammam and Abd EL-Rady (2010)**.

Tabel (5): phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV) and broad sense heritability (H) for ten F_5 lines in two bread wheat populations produced from using the three selection methods.

Methods	Ent. no.	Parameters	Plant height	Number of spikes / plant	Number of kernels / spike	100-kernel weight	Grain yield / plant
PM	population I	σ^2p	59.51	3.01	22.82	0.10	21.86
		σ^2g	50.73	1.65	16.63	0.06	13.54
		PCV	8.24	12.86	9.36	7.85	16.85
		GCV	7.60	9.52	7.99	6.08	13.26
		H	85.25	54.82	72.87	60.00	61.93
	population II	σ^2p	91.40	2.24	22.13	0.14	11.71
		σ^2g	82.18	0.26	14.44	0.11	4.91
		PCV	8.39	10.71	9.85	8.85	12.07
		GCV	7.96	3.67	7.96	7.72	7.82
		H	89.91	11.74	65.25	76.17	41.95
MBM	population I	σ^2p	34.70	2.52	23.98	0.09	9.09
		σ^2g	29.13	0.80	8.31	0.07	7.23
		PCV	6.55	44.69	10.39	8.11	12.60
		GCV	6.00	6.58	6.11	6.99	11.23
		H	83.95	31.66	34.64	74.19	79.55
	population II	σ^2p	88.00	3.61	41.77	0.16	10.26
		σ^2g	85.16	2.60	36.70	0.12	8.55
		PCV	8.28	15.09	14.48	8.75	12.77
		GCV	8.14	12.81	13.57	7.57	11.66
		H	96.77	72.05	87.86	74.84	83.34
BM	population I	σ^2p	29.51	5.34	24.08	0.09	25.78
		σ^2g	25.84	3.88	20.23	0.04	24.20
		PCV	6.19	19.82	9.31	7.38	20.47
		GCV	5.79	16.90	8.53	5.20	19.84
		H	87.56	72.68	84.01	49.63	93.87
	population II	σ^2p	42.21	2.84	48.93	0.29	27.08
		σ^2g	40.12	2.64	47.47	0.27	26.63
		PCV	6.49	13.04	15.50	12.10	20.11
		GCV	6.33	12.57	15.26	11.63	19.94
		H	95.05	92.97	97.02	92.44	98.31

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الملخص العربى

مقارنة ثلاث طرق انتخاب فى تحسين المحصول ومكوناته فى عشيرتين من قمح الخبز

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أجريت هذه الدراسة فى المزرعة البحثية لمحطة بحوث شندويل فى الفترة من ٢٠٠٨/٢٠٠٧ – ٢٠١٠/٢٠٠٩ لمقارنة ثلاث طرق انتخاب وهى طريقة سجل النسب و طريقة التجميع المحورة وطريقة التجميع فى تحسين المحصول ومكوناته فى عشيرتين من قمح الخبز .

• أظهرت نتائج تحليل التباين والتحليل التجميعى وجود اختلافات معنوية بين السلالات المنتخبة لكل عشيرة فى كل طريقة لكل الصفات تحت الدراسة. كما كانت الاختلافات بين طرق الانتخاب الثلاثة معنوية لكل الصفات فيما عدا عدد السنابل/ نبات فى العشيرة الثانية. أيضاً أظهرت النتائج أن التداخل بين الطرق والسلالات لكل الصفات تحت الدراسة كان عالى المعنوية.

• أعطت طريقة التجميع اقل قيمة لصفة طول النبات، بينما أعطت طريقة تسجيل النسب أعلى قيمة، وذلك فى العشيرتين.

- كانت طريقتي سجل النسب و التجميع المحورة أفضل من طريقة التجميع لصفة عدد السنابل/ نبات في العشيرة الأولى بينما لم يظهر أي فروق معنوية بين الطرق في العشيرة الثانية.

- تفوقت طريقتي سجل النسب والتجميع المحورة على طريقة التجميع في تحسين عدد الحبوب/ سنبلة، وذلك في العشيرتين.

- كانت طريقة سجل النسب وطريقة التجميع أكثر فاعلية في تحسين وزن ال١٠٠ حبة في العشيرة الأولى بينما كانت طريقة التجميع والتجميع المحورة أفضل من طريقة سجل النسب في العشيرة الثانية.

- كانت طريقة سجل النسب أفضل الطرق وأكثرها فاعلية في تحسين محصول الحبوب / نبات، وذلك في العشيرتين.

- تباينت تقديرات درجة التوريث في المدى الواسع من المنخفضة إلى العالية تبعا لطرق الانتخاب والعشائر.