EVALUATION OF SOME BREEDING METHODS IN DURUM WHEAT

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Abstract

Four breeding methods representing different cycles of phenotypic selection were evaluated using durum wheat (Triticum durum L.) crosses. This included; 1) pedigree method (PM) with three cycles of selection in F3, F4 and F5, 2) modified bulk1 (MB1) two cycles of selection in F_4 and F_5 , 3) modified bulk₂ (MB₂) where only one cycle of selection in F_3 was exercised, 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 2005/2006 through 2008/2009 to evaluate the efficiency of four different breeding methods in improving grain yield potentiality and some other agronomic traits in six durum wheat crosses. The lines derived from various selection cycles were evaluated in terms of number of spikes/plant, number of kernels/spike, 100-kernel weight and grain yield/plant. Results of analysis of variance for every cross showed significant differences among breeding methods in all crosses. Moreover, the genotypes showed significant differences in number of spikes/plant except crosses No. 1, 2 and 5, number of kernels/spike, except cross No. 1, 100-kernel weight except cross No. 2 and grain yield/plant for all crosses. The interaction between genotypes and methods of breeding was significant in all characteristics studied for all crosses except number of spikes/plant in cross No. 5, number of kernels/spike in cross No. 4, 100-kernel weight in crosses No. 1 and 6 and grain yield/plant for all crosses. Combined analysis for all methods of breeding crosses and genotypes showed significant differences for crosses (C), methods of breeding (M), genotypes (G), (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 2 (MP2) .Results revealed that the six durum wheat crosses differed in all studied characteristics. Cross No. 5 had the highest number of spikes/plant, cross No. 2 had the highest number of kernels/spike, cross No. 3 had the highest 100-kernel weight and cross No. 5 the highest grain yield/plant.

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). The bulk and pedigree methods both have been used extensively in the development of 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 later generations. However, the pedigree method involves phenotypic selection between space-planted individuals within crosses from the F2 through F5 generations before yield tests are conducted (Ortiz Ferrara, 1981), who 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 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 et al. (1997) found that the modified bulk method was as 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 (MB2) followed by (PM), for 100-kernel weight (MB1) followed by (MB2) for grain yield per plant (BM) and (MB2).

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 2005/2006, 2006/2007, 2007/2008 and 2008/009 to compare the efficiency of four breeding methods in six durum wheat crosses (*Triticum turgidum var. durum*), which were chosen from a diallel cross made and evaluated for combining ability for several agronomic traits (El-Sayed,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 between and within families in each cross in F_3 , F_4 and F_5 .
- 2. Modified bulk1 (MB1) was exercised using 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 bulk2 (MB2) was conducted using 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 remaining plants from each cross after mixing the grains and then random samples were taken in the next three generations.

Table 1. The pedigree of the six durum wheat crosses.

| Cross | Name of cross and pedigree |
|-------|--|
| 1 | Bani-swef1 / Bani- swef 3 |
| 2 | Sohag 3 / bani swef 3 |
| 3 | Taler-1 / Tarro-1 // sohag 3 |
| 4 | Taler-1 / Tarro-1 // Bani-swef 1 |
| 5 | Snturk mi 83- 84375/Nigris 5 // Tantol -1 /3/ sohag 1 |
| 6 | Snturk mi 83- 84375/Nigris 5 // Tantol -1 /3/ Taler-1/ Tarro-1 |

In 2005/2006 season, 150 plants from F_2 of each cross were randomly selected and subjected to the four selection methods.

In 2006/2007 season, 50 F_3 families from each cross in addition to the bulk population were sown in one row plot for each family with 3.0 m long, 30 cm apart and 5 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 from 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) in the F_4 generation. Also, grains produced from F_3 bulk were mixed to be tested in F_4 bulk.

In 2007/2008 season, 13 rows (6 F_4 families for PM, 6 families for MB2 and one row for BM), of each cross were grown as the same practice in the F_3 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 the bulk population in the F_5 generation. In addition, seeds of the 10 plants for each 6 families of MB2 were mixed to be 6 lines in F_5 generation in the next season.

In 2008/2009, 18 F_5 lines, (6 lines from each method of PM,MB1 and MB2 for each cross and the population bulk 6 lines) were sown in spilt—spilt plot experiment with four replications. Selection methods were in the main plot, crosses in sub-plots and the lines were in sub-sub plots. Each line was planted in one row with 2.0 m long, 30 cm a part and 5.0 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 durum 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 means.

RESULTS AND DISCUSSION

1- Analysis of variance

Results of this study will be presented with regard to the performance of five F_5 lines derived from each six durum wheat crosses and each breeding method. 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 characteristics.

Signal analysis 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 six durum wheat crosses showed that breeding methods had significant effect for all characteristics in all crosses. The genotypes had significant differences for most characteristics studied except for number of spikes per plant in crosses No. 1,2 and 5, number of kernels/spike for cross No. 1, 100-kernel weight for cross No. 2. On the other hand, the interaction

between genotypes and breeding methods were significant for number of spikes/plant except for cross No. 5, number of kernels/spike except for cross No. 4, 100-kernel weight except for crosses No. 1 and 6 and grain yield/plant for all crosses.

Mean squares of combined analysis for the six lines derived from six durum wheat crosses and four breeding methods are presented in Table (3) through Table (6). Results of analysis showed that highly significant differences were observed among the six crosses, four breeding methods and six lines derived from each cross and method 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) and Falcinelli et al. (1988).

Table 2. Mean squares for the characteristics studied in six durum wheat crosses.

| | | | Cross | | | | | | |
|-----------|------|--------------|------------------|------------|---------------|--|--|--|--|
| SOV | d.f | No. of spike | No. of kernels / | 100 kernel | Grain yield / | | | | |
| | 1 1 | /plant | spike | weight | plant | | | | |
| Reps, | 3 | 1.500 | 39.911** | 0.102 | 4.921 | | | | |
| Methods | 3 | 219.732** | 730.302** | 2.255** | 3802.707** | | | | |
| Genotypes | 5 | 0.973 | 22.270 | 0.656* | 104.280** | | | | |
| MxG | 15 | 3.753** | 68.171* | 0.300 | 57.087** | | | | |
| Error | 69 | 1.453 | 37.775 | 0.313 | 22.621 | | | | |
| | | | Cross | | | | | | |
| Reps. | 3 | 8.280** | 6.976 | 0.089 | 60.497** | | | | |
| Methods | 3 | 55.763** | 1162.381** | 10.778** | 2047.263** | | | | |
| Genotypes | 5 | 3.881 | 145.117** | 0.167 | 406.020** | | | | |
| MxG | 15 | 6.310** | 90.334** | 0.488** | 135.518** | | | | |
| Error | 69 | 2.209 | 17.696 | 0.255 | 18.396 | | | | |
| | | | Cross | No. 3 | | | | | |
| Reps. | 3 | 1.301 | 5.772 | 0.379 | 2.642 | | | | |
| Methods • | 3 | 369.735** | 786.503** | 11.919** | 2778.684** | | | | |
| Genotypes | 5 | 5.429** | 21.951** | 1.584** | 92.434** | | | | |
| MxG | 15 | 4.337** | 18.809** | 1.085** | 51.354* | | | | |
| Error | 69 | 1.150 | 4.037 | 0.205 | 25.271 | | | | |
| 2.10 | _ | Cross No. 4 | | | | | | | |
| Reps. | 3 | 8.282 | 3.561 | 0.089 | 121.551 | | | | |
| Methods | 3 | 173.465** | 227.963** | 6.658** | 2133.371** | | | | |
| Genotypes | 5 | 13.337** | 81.354** | 0.726** | 101.104** | | | | |
| MxG | 15 | 14.314** | 23.817 | 0.586** | 76.618* | | | | |
| Error | 69 | 3.007 | 14.001 | 0.244 | 37.439 | | | | |
| - | | 1 | Cros | s No. 5 | | | | | |
| Reps. | 3 | 0.371 | 0.0634 | 0.076 | 18.290 | | | | |
| Methods | 3 | 162.025** | 743.429** | 3.366** | 1035.744** | | | | |
| Genotypes | 5 | 1.631 | 29.944** | 1.370** | 55.638** | | | | |
| MxG | - 15 | 2.493 | 20.975** | 0.762** | 52.917** | | | | |
| Error | 69 | 2.685 | 6.995 | 0.296 | 8.705 | | | | |
| | | | Cros | s No. 6 | | | | | |
| Reps. | 3 | 4.640 | 9.169 | 0.312 | 31.864 | | | | |
| Methods | 3 | 124.533** | 688.685** | 9.603** | 403.223** | | | | |
| Genotypes | 5 | 8.830** | 17.565** | 0.511* | 34.506* | | | | |
| MxG | 15 | 4,145** | 26.411** | 0.298 | 28.136** | | | | |
| Error | 69 | , 1.514 | 8.543 | 0.247 | 13.324 | | | | |

^{*, **} Significant at probability 5% and 1% respectively

2- Mean performances

2.1:- Number of spikes per plant

Data in Table (3), revealed that average of number of spikes/plant ranged from 17.0 for cross No. 1 to 22.0 for cross No. 5 with an average 19.9 for over all crosses . On the other hand average varied from 13.4 for cross No. 1 to 25.3 for cross No. 3 with an average 21.5 in the pedigree method (PM) , from 19.1 for cross No. 2 to 22.7for cross No. 5 with an average 21.0 of the modified bulk 1(MB1), from 15.7 for cross No. 1 to 23.4 for cross No. 6 with an average 19.9 of the modified bulk 2 (MB2) and varied from 16.7 for cross No. 3 to 18.9 for cross No.1with an average 17.6 for the bulk method (BM) . These results are in line with those obtained by El-Sayed (1996) and Tammam (2004).

Meanwhile the mean of lines or genotypes ranged from 19.8 for genotypes No. 4 to 20.3 for genotype No. 6 in the overall mean . The best genotype with pedigree method (PM) No. 5 (21.9) , genotype No. 5 (21.5) in the modified bulk 1 (MB1) genotype No. (20.4) in the modified bulk 2(MB2) and genotype or line No. 6 (18.01) 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), modified bulk1 (MB1) and modified bulk 2 (MB2) varied significant differences than bulk method (BM).

Table 3. Mean performance for number of spikes / plant in six durum wheat crosses using four breeding methods .

| | | Genotype | | | | | | |
|--------------|-------|----------|-------|-------|-------|-------|-------|-------|
| Method Cross | Cross | 1 | 2 | 3 | 4 | 5 | 6 | Mean |
| | 1 | 12.21 | 14.75 | 13.25 | 11.75 | 14.75 | 13.70 | 13.40 |
| | 2 | 18.25 | 20.65 | 17.73 | 19.85 | 20.45 | 21.60 | 19.75 |
| | 3 | 25.75 | 25.50 | 26.75 | 24.50 | 25.05 | 24.45 | 25.33 |
| PM | 4 | 25.30 | 24.40 | 22.90 | 22.63 | 22.63 | 22.75 | 23.44 |
| | 5 | 23.90 | 24.75 | 23.60 | 22.75 | 25.35 | 22.70 | 23.84 |
| | 6 | 22.73 | 22.60 | 23.09 | 23.75 | 23.05 | 23.65 | 23.15 |
| Mea | | 21.36 | 22.11 | 21.20 | 20.87 | 21.88 | 21.48 | 21.48 |
| | 1 | 20.50 | 19.48 | 20.61 | 19.20 | 20.38 | 20.04 | 20.03 |
| | 2 | 20.45 | 19.65 | 18.40 | 18.13 | 18.15 | 19.50 | 19.05 |
| | 3 | 21.95 | 22.10 | 21.20 | 22.45 | 20.90 | 21.85 | 21.74 |
| MP1 | 4 | 16.30 | 22.58 | 20.40 | 22.65 | 23.35 | 20.35 | 20.94 |
| | 5 | 22.05 | 23.60 | 22.45 | 22.00 | 23.25 | 22.60 | 22.66 |
| | 6 | 20.60 | 21.30 | 19.60 | 22.45 | 23.15 | 23.78 | 21.82 |
| Mean | | 20.31 | 21.45 | 20.45 | 21.15 | 21.53 | 21.35 | 21.04 |
| | 1 | 16.12 | 16.39 | 15.09 | 16.26 | 15.13 | 15.25 | 15.71 |
| | 2 | 21.90 | 18.85 | 19.40 | 18.13 | 18.20 | 19.73 | 19.37 |
| | 3 | 18.38 | 16.95 | 19.55 | 17.90 | 19.30 | 21.20 | 18.88 |
| MP2 | 4 | 20.60 | 19.73 | 18.08 | 18.08 | 16.93 | 18.43 | 18.64 |
| | 5 | 23.20 | 22.65 | 24.10 | 23.45 | 23.20 | 23.30 | 23.32 |
| | 6 | 22.15 | 23.65 | 23.03 | 23.35 | 24.55 | 23.75 | 23.41 |
| Me | an | 20.39 | 19.70 | 19.87 | 19.53 | 19.55 | 20.28 | 19.89 |
| | 1 | 18.68 | 18.21 | 18.46 | 19.89 | 18.59 | 20.15 | 18.91 |
| | 2 | 16.10 | 16.35 | 17.90 | 16.45 | 15.73 | 15.85 | 16.40 |
| | 3 | 15.45 | 15.85 | 16.70 | 15.15 | 15.50 | 18.30 | 16.16 |
| BM | .4 | 19.67 | 20.25 | 16.25 | 16.50 | 15.50 | 15.75 | 17.32 |
| | 5 | 19.30 | 18.10 | 18.05 | 17.60 | 17.33 | 18.63 | 18.17 |
| | 6 | 17.60 | 17.93 | 18.95 | 20.40 | 16.48 | 19.38 | 18.45 |
| Me | an | 17.71 | 17.78 | 17.72 | 17.66 | 16.52 | 18.01 | 17.57 |
| | 1 | 16.75 | 17.21 | 16.85 | 16.77 | 17.21 | 17.29 | 17.01 |
| | 2 | 19.18 | 18.88 | 18.36 | 18.14 | 18.13 | 19.17 | 18.64 |
| Over all | 3 | 20.38 | 20.10 | 21.03 | 20.00 | 20.19 | 21.45 | 20.52 |
| mean | 4 | 20.47 | 21.74 | 19.41 | 19.96 | 19.60 | 19.32 | 20.08 |
| | 5 | 22.11 | 22.28 | 22.05 | 21.45 | 22.28 | 21.81 | 22.00 |
| | 6 | 20.77 | 21.37 | 21.18 | 22.49 | 21.81 | 22.64 | 21.71 |
| Mo | an | 19.94 | 20.26 | 19.81 | 19.80 | 19.87 | 20.28 | 19.99 |

C.V % 7.13 L.S.D 5 % Methods "M" 0.33

 List.D
 3 70

 Methods "M"
 0.33

 Crosses "C"
 0.45

 Genotypes "G"
 0.41

 Cx G
 1.00

M x C x G 2.00

2.2- Number of kernels per spike

Data for number of kernels per spike (Table 4), exhibited that average of number of kernels per spike varied from 41.6 for cross No. 4 to 57.1 for cross No. 2 with an average 47.4 for PM, from 35.2 for cross No. 4 to 49.6 for cross No. 2 with an average 40.4 for MB1, from 35.4 for cross No. 6 to 45.2 for cross No.1 with an average 39.4 for MB2 and ranged from 33.2 for cross No. 5 to 54.2 for cross No. 1 with an average 39.6 for BM. This results indicated that PM was superior in improving number of kernels per spike and response to selection using PM was 7.8 kernels per spike 19.6%, when compared to bulk method in over all crosses .

Also, cross No. 2 had the highest number of kernels per spike (48.2) followed by cross No. 1 (46.3) and varied significantly with other four crosses in the over all crosses. On the other hand, genotypes or lines No. 3 and 5 for PM, 3 and 4 for MB1,1 and 6 for MB2, 1 and 2 for BM and 1 and 3 for overall genotypes or lines gave the highest number of kernels per spike. These results are in agreement with those reported by Kherialla (1983), Deghais and Auriau (1993), Ismail (1995), Fahim et al. (1996), Pawar et al. (1997), Tammam (2004) and El-Sayed (2006) who reported that using pedigree method was more effective than other methods in improving number of kernels per spike.

Table 4. Mean performance for number of kernels/spike in six durum wheat crosses using four breeding methods.

| | | · · | | Geno | type | | | |
|----------|-------|-------|-------|-------|-------|-------|-------|-------|
| Method | Cross | 1 | . 2 | 3 | 4 | 5 | 6 | Mean |
| | 1 | 44.06 | 42.45 | 46.51 | 41.68 | 54.06 | 36.37 | 44.19 |
| | 2 | 48.65 | 57.98 | 57.23 | 64.10 | 58.25 | 56.53 | 57.12 |
| | 3 | 46.90 | 44.90 | 54.50 | 46.45 | 49.40 | 43.95 | 47.68 |
| PM | 4 | 38.25 | 39.30 | 41.90 | 39.90 | 40.30 | 50.13 | 41.63 |
| 3.9 | 5 | 51.88 | 46.26 | 44.10 | 45.48 | 46.54 | 44.23 | 46.42 |
| | 6 | 51.05 | 49.75 | 50.60 | 44.20 | 44.60 | 43.40 | 47.27 |
| Mea | an | 46.80 | 46.77 | 49.14 | 46.97 | 48.86 | 45.77 | 47.38 |
| | 1 | 42.18 | 39.25 | 41.75 | 42.50 | 38.00 | 45.75 | 41.57 |
| 100 | 2 | 55.15 | 49.50 | 55.20 | 52.20 | 35.70 | 46.88 | 49.11 |
| · . | 3 | 36.75 | 35.28 | 36.30 | 37.25 | 39.60 | 37.40 | 37.10 |
| MP1 | 4 | 35.45 | 37.60 | 36.20 | 32.85 | 33.65 | 35.45 | 35.20 |
| 41 | 5 | 33.90 | 38.50 | 35.50 | 41.10 | 34.85 | 34.05 | 36.32 |
| | 6 | 42.25 | 43.70 | 46.65 | 43.75 | 41.90 | 44.03 | 43.71 |
| Mean | | 40.95 | 40.64 | 41.93 | 41.61 | 36.83 | 40.59 | 40.43 |
| | 1 | 45.00 | 48.50 | 42.75 | 44.25 | 45.25 | 45.25 | 45.17 |
| | 2 | 49.55 | 41.98 | 47.37 | 47.20 | 47.70 | 42.18 | 46.00 |
| · | 3 | 36.05 | 37.85 | 38.63 | 38.18 | 39.78 | 40.56 | 38.51 |
| MP2 | 4 | 38.15 | 33.63 | 36.25 | 31.55 | 35.30 | 36.90 | 35.30 |
| | 5 | 37.75 | 36.83 | 35.80 | 35.65 | 35.35 | 35.20 | 36.10 |
| | 6 | 34.75 | 34.55 | 33.15 | 39.90 | 32.55 | 37.43 | 35.39 |
| Me | an | 40.21 | 38.90 | 39.05 | 39.45 | 39.49 | 39.59 | 39.45 |
| | 1 | 58.50 | 57.25 | 49.50 | 52.00 | 53.50 | 54.75 | 54.25 |
| | 2 | 39.68 | 39.85 | 46.35 | 43.40 | 37.40 | 35.73 | 40.40 |
| | 3 | 35.25 | 33.35 | 33.75 | 35.45 | 36.98 | 33.93 | 34.79 |
| BM | 4 | 34.20 | 37.08 | 34.55 | 32.40 | 36.08 | 41.88 | 36.03 |
| | _ 5 | 37.45 | 35.35 | 35.20 | 31.38 | 31.95 | 32.20 | 33.92 |
| | 6 | 37.75 | 37.35 | 39.60 | 38.30 | 38.90 | 36.70 | 38.10 |
| Me | an | 40.47 | 40.10 | 39.86 | 38.82 | 39.13 | 39.20 | 39.60 |
| | 1 | 47.43 | 46.86 | 45.13 | 45.11 | 47.70 | 45.53 | 46.29 |
| | 2 | 48.26 | 47.33 | 53.68 | 51.73 | 44.76 | 45.33 | 48.52 |
| Over all | 3 | 38.74 | 37.84 | 40.79 | 39.33 | 40.76 | 38.96 | 39.40 |
| mean | 4 | 36.51 | 36.91 | 37.23 | 34.18 | 36.33 | 41.09 | 37.04 |
| | 5 | 40.24 | 39.23 | 37.65 | 38.40 | 37.42 | 36.42 | 38.23 |
| | 6 | 41.45 | 41.44 | 42.50 | 41.54 | 39.49 | 40.39 | 41.14 |
| Me | an | 42.11 | 41.60 | 42.50 | 41.71 | 41.08 | 41.28 | 41.71 |

C.V % 9.26 L.S.D 5 % Methods "M" 0.53 M x C 2.16 M x C x G 5.41 Crosses "C" 1.09 M x G 2.21 Genotypes "G" 1.10 C x G 2.71

2.3- 100-kernel wheat

Average of 100-kernel weight (Table 5) ranged from 4.492 g for cross No. 1 to 6.395 g for cross No. 3 with an average 5.40 g for pedigree method (PM), from 4.729 g for cross No. 1 to 5.977 g for cross No. 2 with an average 5.329 g for modified bulk 1(MB1), from 4.458 g for cross No. 5 to 5.209 g for cross No. 3 with an average 4.819 g for modified bulk 2 (MB2) and from 4.147 g for cross No. 1 to 4.716 g for cross No. 3 with an average 4.413 g for bulk method (BM). Results showed significant differences between the four breeding methods. Meanwhile, pedigree method (PM) had the highest value of 100-kernel weight followed by modified bulk 1 (MB1), modified bulk 2 (MB2), and bulk method. Also crosses No. 3,2 and 6 in PM, crosses No. 2.6 and 3 in MB1, crosses 3,1 and 2 in MB2, crosses No. 3,4 and 5 in BM and crosses No. 3,6 and 2 in the overall crosses gave the highest values of 100-kernel weight in over all 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) and El-Sayed (2006).

 $\begin{tabular}{ll} \begin{tabular}{ll} Table 5. Mean performance for 100-kernel weight in six durum wheat crosses using four breeding methods . \end{tabular}$

| | | | | Geno | type | | | Monn |
|----------|-------|-------|-------|-------|-------|-------|-------|-------|
| Method | Cross | 1 | . 2 | 3 | 4 | 5 . | 6 | Mean |
| | 1 | 3.933 | 4.634 | 4.376 | 4.956 | 4.543 | 4.512 | 4.492 |
| | 2 | 5.137 | 4.991 | 5.093 | 5.609 | 5.165 | 5.669 | 5.277 |
| | 3 | 5.848 | 5.913 | 5.970 | 6.322 | 6.741 | 7.574 | 6.395 |
| PM | 4 | 5.236 | 4.910 | 6.314 | 5.999 | 5.988 | 5.768 | 5.703 |
| | 5 | 5.069 | 4.825 | 4.803 | 5.315 | 4.484 | 4.749 | 4.874 |
| _ | 6 | 5.450 | 5.916 | 5.659 | 5.539 | 5.705 | 5.693 | 5.660 |
| Mea | an | 5.112 | 5.198 | 5.369 | 5.623 | 5.438 | 5.661 | 5.400 |
| | 1 | 4.492 | 4.669 | 5.142 | 4.726 | 4.785 | 4.559 | 4.729 |
| | 2 | 6.352 | 6.088 | 5.683 | 5.369 | 6.158 | 6.209 | 5.977 |
| | 3 | 5.252 | 6.414 | 4.960 | 5.702 | 4.761 | 5.647 | 5.456 |
| MP1 | 4 | 5.268 | 4.716 | 5.092 | 5.339 | 4.958 | 4.505 | 4.980 |
| | 5 | 4.814 | 5.956 | 5.714 | 5.085 | 4.586 | 4.520 | 5.113 |
| | 6 | 5.410 | 5.789 | 5.377 | 6.016 | 5.988 | 5.753 | 5.722 |
| Me | an | 5.264 | 5.605 | 5.328 | 5.373 | 5.206 | 5.199 | 5.329 |
| | 1 | 4.692 | 4.795 | 4.630 | 5.509 | 4.584 | 4.830 | 4.840 |
| | 2 | 5.123 | 4.782 | 4.901 | 4.372 | 5.169 | 4.505 | 4.809 |
| | 3 | 5.397 | 5.590 | 5.276 | 5.449 | 4.738 | 4.802 | 5.209 |
| MP2 | 4 | 4.359 | 4.506 | 4.595 | 5.050 | 5.396 | 4.835 | 4.790 |
| | 5 | 5.331 | 4.880 | 3.824 | 4.610 | 4.272 | 3.834 | 4.459 |
| | 6 | 4.891 | 4.697 | 4.913 | 5.003 | 4.900 | 4.433 | 4.806 |
| Me | an | 4.965 | 4.875 | 4.690 | 4.999 | 4.843 | 4.450 | 4.819 |
| | 1 | 3.777 | 3.731 | 4.290 | 4.154 | 4.523 | 4.405 | 4.147 |
| | 2 | 3.863 | 4.434 | 4.691 | 4.531 | 4.523 | 4.471 | 4.419 |
| | 3 | 4.405 | 5.552 | 4.427 | 5.204 | 4.245 | 4.462 | 4.716 |
| BM | 4 | 4.985 | 4.263 | 4.197 | 4.288 | 4.368 | 4.634 | 4.456 |
| | 5 | 4.152 | 4.446 | 3.805 | 4.774 | 4.489 | 4.113 | 4.297 |
| | 6 | 3.832 | 4.732 | 4.574 | 5.093 | 4.083 | 4.365 | 4.447 |
| Me | an | 4.169 | 4.527 | 4.331 | 4.674 | 4.372 | 4.408 | 4.413 |
| | 1 | 4.224 | 4.457 | 4.609 | 4.837 | 4.609 | 4.576 | 4.552 |
| | 2 | 5.112 | 5.074 | 5.092 | 4.970 | 5.254 | 5.214 | 5.119 |
| Over all | . 3 | 5.225 | 5.867 | 5.158 | 5.669 | 5.121 | 5.621 | 5.444 |
| mean | 4 | 4.962 | 4.599 | 5.050 | 5.169 | 5.178 | 4.936 | 4.982 |
| | 5 | 4.841 | 5.026 | 4.536 | 4.946 | 4.458 | 4.304 | 4.685 |
| | 6 | 4.896 | 5.284 | 5.131 | 5.413 | 5.169 | 5.061 | 5.159 |
| Me | ean | 4.878 | 5.051 | 4.929 | 5.167 | 4.965 | 4.952 | 4.990 |

C.V % 10.28 L.S.D 5 % Methods "M" 0.163

 Methods "M"
 0.163
 M x C
 0.261

 Crosses "C"
 0.130
 M x G
 0.293

 Genotypes "G"
 0.147
 C x G
 0.359

M x C x G 0.718

2.4 - Grain yield per plant

Regarding grain yield per plant (Table 6) , average of grain yield per plant varied from 37.74 g in cross No. 1 to 67.57 g in cross No. 4 with an average 58.17 g when using pedigree method (PM), varied from 49.01 g. in cross No. 6 to 57.39 g in cross No.3 with an average 52.94 g when using modified bulk 1 (MB1) , from 45.33 g in cross No. 2 to 56.14 g. in cross No. 1 with an average 49.47 g when using modified bulk 2 (MB2) and ranged from 38.15 g in cross No. 2 to 68.05 g in cross No. 1 with an average 48.02 g when using bulk method (BM) . These results indicated that using pedigree method was the most effective method for improving wheat grain yield significantly compared to the other methods.

On the other hand, crosses No. 5 (54.79 g) cross No. 4 (54.33 g) , cross No. 3 (53.82 g) and cross No. 1 (53.11 g) , had the highest value of grain yield per plant and differed significantly when compared to cross No. 2 (48.44 g) , and cross No. 6 (48.41 g) . Also crosses No.5,4 and 3 were significantly differed with overall mean crosses (52.15 g) . Lines No. 1 and No. 5 in the pedigree method (PM), lines No. 2 and 6 in the modified bulk 1(MB1) , lines No. 5 and 6 in the modified bulk 2 (MB2) lines No.1 and 6 in bulk method (BM) , and lines No. 5 and 6 in the over all 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) and Tammam (2004) .

 $\label{thm:constraint} \mbox{Table 6. Mean performance for grain yield per plant \ in six durum wheat crosses using four breeding methods .}$

| Method | Cross | Genotype | | | | | | |
|----------|-------|----------|-------|-------|-------|-------|-------|-------|
| | | 1 | 2 | 3 | 4 | 5 | 6 | Mean |
| | 1 | 38.31 | 39.47 | 37.14 | 39.31 | 36.03 | 36.18 | 37.74 |
| | 2 | 71.03 | 49.04 | 46.74 | 57.49 | 69.26 | 67.46 | 60.17 |
| DM | 3 | 65.69 | 71.57 | 64.65 | 65.22 | 66.01 | 68.86 | 67.00 |
| PM | 4 | 75.62 | 56.46 | 62.23 | 66.99 | 74.21 | 69.90 | 67.57 |
| | 5 | 56.05 | 60.30 | 64.54 | 64.36 | 60.52 | 74.10 | 63.31 |
| | 6 | 48.71 | 58.07 | 51.57 | 51.88 | 54.12 | 55.12 | 53.25 |
| Mea | an | 59.24 | 55.82 | 54.48 | 57.54 | 60.02 | 61.94 | 58.17 |
| | 1 | 48.81 | 47.75 | 50.17 | 50.05 | 52.80 | 53.42 | 50.50 |
| | 2 | 46.38 | 57.18 | 45.68 | 46.29 | 48.88 | 56.38 | 50.13 |
| MP1 | 3 | 54.21 | 54.86 | 57.00 | 64.68 | 54.61 | 59.01 | 57.39 |
| MPI | 4 | 53.71 | 52.16 | 57.46 | 51.85 | 56.19 | 55.83 | 54.53 |
| | 5 | 57.24 | 54.16 | 56.44 | 55.45 | 55.57 | 57.65 | 56.09 |
| | 6 | 48.30 | 50.96 | 50.33 | 48.30 | 46.55 | 49.65 | 49.01 |
| Mean | | 51.44 | 52.84 | 52.85 | 52.77 | 52.43 | 55.32 | 52.94 |
| 1 | 1 | 52.74 | 44.48 | 53.83 | 61.62 | 66.53 | 57.67 | 56.15 |
| | 2 | 56.28 | 47.10 | 35.41 | 39.35 | 45.96 | 47.87 | 45.33 |
| MP2 | 3 | 46.63 | 48.23 | 53.05 | 48.02 | 46.19 | 49.91 | 48.67 |
| MPZ | 4 | 40.90 | 48.68 | 42.56 | 47.00 | 52.41 | 49.37 | 46.82 |
| | 5 | 49.68 | 51.54 | 47.02 | 52.62 | 56.75 | 52.95 | 51.76 |
| | 6 | 49.80 | 51.99 | 49.89 | 46.13 | 47.95 | 42.96 | 48.12 |
| Mea | in | 49.34 | 48.67 | 46.96 | 49.12 | 52.63 | 50.12 | 49.47 |
| | 1 | 66.27 | 65.87 | 67.58 | 69.38 | 70.05 | 69.14 | 68.05 |
| | 2 | 39.35 | 40.86 | 35.63 | 33.11 | 39.74 | 40.25 | 38.16 |
| ВМ | 3 | 42.15 | 37.66 | 47.56 | 42.23 | 34.43 | 49.34 | 42.23 |
| Diri | 4 | 49.13 | 47.48 | 50.96 | 45.20 | 50.80 | 46.94 | 48.42 |
| | 5 | 49.00 | 48.61 | 50.23 | 45.30 | 46.21 | 48.71 | 48.01 |
| | 6 | 44.86 | 44.35 | 38.29 | 43.95 | 44.80 | 43.28 | 43.25 |
| Mea | n | 44.46 | 47.47 | 48.37 | 46.53 | 47.67 | 49.61 | 48.02 |
| | 1 | 51.53 | 49.39 | 52.18 | 55.09 | 56.35 | 54.10 | 53.11 |
| | 2 | 53.26 | 48.54 | 40.86 | 44.06 | 50.96 | 52.99 | 48.45 |
| Over all | 3 | 52.17 | 53.08 | 55.57 | 55.04 | 50.31 | 56.78 | 53.83 |
| mean | 4 | 54.84 | 51.19 | 53.30 | 52.76 | 58.40 | 55.51 | 54.33 |
| | 5 | 52.99 | 53.65 | 54.56 | 54.43 | 54.76 | 58.35 | 54.79 |
| | 6 | 47.92 | 51.34 | 47.52 | 47.56 | 48.35 | 47.75 | 48.41 |
| Mea | n | 52.12 | 51.20 | 50.66 | 51.49 | 53.19 | 54.25 | 52.15 |

C.V % 9.63
L.S.D 5 %

Methods "M" 1.88 M x C 2.91 M x C x G 6.83

Crosses "C" 1.45 M x G 2.79

Genotypes "G" 1.40 C x G 3.44

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تقييم بعض طرق التربية في قمح الديورم

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أجريت هذه الدراسة في المزرعة البحثية لمحطة البحوث الزراعية بالجيزة في أربعة مواسم متتابعة خلال الفترة من 2006/2005 حتى 2009/2008.وقد استخدم في هذا البحث أربعة طرق للتربية وهي :-

- 1. طريقة سجل النسب بإجراء ثلاث دورات للانتخاب في الجيل الثالث والرابع والخامس .
 - 2. طريقة التجميع المحورة 1 بإجراء دورتين للانتخاب في الجيل الثالث والرابع.
 - طريقة التجميع المحورة 2 بإجراء دورة واحدة للانتخاب في الجيل الثالث.
 - 4. طريقة التجميع العادية .

واستخدم في هذه الدراسة ستة هجن من قمح الديورم وكانت الصفات محل الدراسة هي عدد السنابل في النبات – عدد حيوب السنبلة – وزن 100 حبة و وزن حبوب النبات . وأظهرت نتاتج التحليل الفردي لكل هجين وجود فروق معنوية لطرق الانتخاب في كل الهجن وأظهرت السلالات المنتخبة من كل هجين فروقاً معنوية لكل صفات الدراسة مثل عدد السنابل /النبات فيما عدا الهجين الأول والثاني والخامس وعدد حبوب السنبلة فيما عدا الهجين الأول ، ووزن 100 حبة ومحصول الحبوب في كل الهجن فيما عدا الهجين الثفاعل بين السلالات المنتخبة وطرق الانتخاب فروقاً معنوية في عدد السنابل في النبات ما عدا الهجين الخامس وعدد حبوب السنبلة ما عدا الهجين الرابع ووزن 100 حبة ما عدا الهجين الأول والسادس ووزن حبوب النبات في كل الهجن وأوضح التحليل التجميعي للهجن وطرق التربية والسلالات المنتخبة وجود فروق معنوية في الهجن وطرق التربية أو الانتخاب والسلالات المنتخبة وكذلك جميع التفاعلات الزوجية أو الثلاثية فيما بينها وطرق التربية أو الانتخاب والسلالات المنتخبة وكذلك جميع التفاعلات الزوجية أو الثلاثية فيما بينها وطرق التربية أو الألاثية فيما بينها موضلت المدروسة هي طريقة سجلات النسب والمهات المدروسة وكان الهجين رقم 5 هو أفضل الهجن في عدد السنابل النبات والهجين رقم 5 هو أفضل الهجن في عدد السنابل النبات والهجين رقم 5 أعلى إنتاجية الدون عدوب السنبلة والهجين رقم 5 أعلى إنتاجية الدون