

Selection for Yield and some Quality Traits in Durum Wheat (*Triticum tuargidum* L. var. durum)

I- Yield

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Abstract

The breeding materials used in this study were the F₃, F₄ and F₅ generations of two durum wheat crosses, to improve grain yield using four selection criteria with pedigree selection. Differences between F₃ families were highly significant in both populations and satisfactory genotypic coefficients of variation were detected for the selection criteria i.e., grain yield, no. of spikes/plant, no. of kernels/spike and 1000-kernel weight. The results indicated that selection for no. of spikes/plant improved it by 13.33 and 12.09% from the bulk sample and the check cultivar after two cycles of selection in population I, respectively. Such increase was accompanied with increasing no. of kernels/spike (5.29%), 1000-kernel weight (4.88%), grain yield/plant (12.08%) and biological yield/plant (19.45%), and decreasing heading date (1.56%) and plant height (2.13%) from the bulk sample. Selection for no. of kernels/spike after two cycles of pedigree selection increased the criterion of selection by 11.63 and 17.86% for pop. I

and 4.37 and 14.49 for pop. II from the bulk sample and the check cultivar, respectively. Such increase in no. of kernels/spike caused decrease in grain yield/plant (-4.35 and -14.45%) and 1000-kernel weight (-0.68 and -7.21%) in population I but increase for the same traits in population II.

Respect to pedigree selection for grain yield/plant, the resulting families showed realized response to selection accounted 17.39% from the bulk sample after two cycles of selection. Such increase accompanied with increase in biological yield/plant (26.36%), 1000-kernel weight (6.1%). No. of kernels/spike (6.65%) and no. of spikes/plant (8.89%) and decrease in heading date (-1.78%) and plant height (-3.68%), in population I. The results in population II behaved the same results as in population I. In population I, family No. 5 was higher in grain yield/plant by 35.26 and 61.84%, no. of spikes/plant (27.77 and 26.37%) and no. of kernels/spike (18.7 and 25.51%) than the bulk sample and check cultivar, respectively. But in population II, family

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No. 4 was higher in grain yield/plant by 42.56 and 60.69%), no. of spikes/plant (35.1 and 39.56%) and 1000-kernel weight (16.81 and 19.53%) than the bulk and check cultivar, respectively.

Key words: durum wheat, pedigree selection, selection criterion.

Introduction

Wheat is the world's most important and most widely grown cereal crop. Its importance is derived from many properties and uses of its grains, which makes it a staple food for more than one third of the world population (Poehlman, 1979).

When breeding for high productivity the breeder is faced with three major decisions. The first is to identify germplasm which have the desired attributes. Secondly, it is necessary to decide in what combinations the prospective parents should be used for hybridization. Finally, the breeder must determine which method could be adopted in handling the resulting segregating populations. The pedigree method involves the waste of considerable effort spent in propagating poor yielding strains (Allard and Harding, 1963).

McNeal *et al.* (1978) reported that grain weight and number of kernels/spike were good traits for indirect selection for yield improvement. Hauerud and Cantrell (1984) and Kheiralla (1993) showed that direct selection for grain weight, grains/spike and spikes/plant was accompanied by an increase in

grain yield which accounted 5.63, 5.90, 6.93 and 7.50%, respectively, after two cycles of selection calculated as a deviation from the best parent mean. Moreover, Tammam (1995) reported from selection in two wheat populations that response to selection and the genetic gain varied according to the initial genetic variability and the relationships among the parents. Verma *et al.* (1998), evaluated three populations of durum wheat crosses and reported that the F_5 population had a higher number of stable genotypes for 1000-grain weight and number of spikes/plant.

Direct selection for grain yield was effective for increasing grain yield (Tammam, 2004; Zakaria, 2004; Mohamed, 2006; Talaat, 1996; Ghoname, 2007 and Sharma and Sharma, 2007) where method of pedigree selection was reported to be the best in improving grain yield of wheat. The objective of this study was to determine the relative response to selection in two wheat populations for two cycles started in the F_3 using the pedigree selection procedure in improving no. of spikes/plant, no. of kernels/spike, grain weight and grain yield/plant.

Materials and Methods

The present study was carried out at El-Mattana, Agric. Res. Center, Ministry of Agric, Egypt, during the period from 2005 to 2008 growing seasons.

The breeding materials used in this study were 400 F_3 - fami-

lies traced back to random F₂-plants from two crosses i.e. (Kucuk x Rascon/Kitti) in population I and (Sohag 2 x Sohag 3) in population II.

In 2005/2006 season, the 400 F₃- families from each population with the original parents, and F₃ bulked random sample (a mixture of equal number of seeds from each plant to represent the generation mean) were sown on 27th of November in separate experiments in a randomized complete block design with three replications. Each family was represented by one row 3 m long and 20 cm apart and 10 cm between plants. Parents and bulk populations were also grown in each replicate.

The following traits were measured on random sample of 10 guarded plants for each family and the means of the 10 plants were subjected to the statistical and genetic analysis.

- 1- Days to heading (DH): Number of days from planting to days when the tip of the upper most spikelets appeared above the flag leaf of the main culm.
- 2- Plant height (PH) in cm: The distance from the base of the culm to the tip of the spike of the main Culm excluding awns.
- 3- Number of spikes/plant (No. of S/PL).
- 4- Number of kernels/spike (No. of K/S).
- 5- 1000-kernel weight in grams (1000-KW).
- 6- Grain yield/plant in grams

(GY/PL).

- 7- Biological yield/plant in grams (BY/PL): Which is the total biomass produced by the plant during the season (excluding the roots).

The best 40 plants from the best 40 families of both populations for each of the selection criteria i.e. grain yield/plant, number of spikes/plant, 1000-kernel weight, and number of kernels/spike were saved to give the F₄ families.

In 2006/2007 season, the 40-F₄- families selected from each of selection criterion with the parents and F₄ bulk sample were sown on 23th November in a separate experiments in a randomized complete block design of three replications. Each family was a single row 3m long, 20 cm between plants. Data were recorded as previously mentioned. Each group of families (40 families) for each selection criterion was analyzed separately. The best 20 families for each selection criterion were saved to give the F₅ families.

In 2007/2008 season, the 20-F₅ families for each selection criterion the parents, check cultivar and F₅ bulk sample of both populations were sown in a separate experiments. Again data were taken as in the previous experiments.

Statistical analysis:

For each season, estimates of phenotypic and genotypic variance and covariance, as well as heritability estimates were calculated from EMS of variance and

covariance components of the selected families

The phenotypic (δ^2_p) and genotypic (δ^2_g) variances were calculated as given by Al-Jiburi et al (1958).

The calculation of the genetic covariance (cov.g₁₂) and phenotypic covariance (cov.p₁₂) between pairs of traits (1 and 2) followed the same form as variance analysis by Steel and Torrie (1980). Genotypic and phenotypic correlation coefficients were calculated as described by Johanson et al. (1955) as following:-

The phenotypic (Pcv%) and genotypic (Gcv %) coefficients of variability were estimated using the formula developed by Burton (1952).

Realized heritability was calculated according to Falconer (1989), from the equation of response, $R=Sh^2$ which was discussed earlier from the point of view of predicting the response to selection, the heritability being estimated as the ratio of the $h^2 = R/S$.

Heritability in the narrow sense was estimated using the correlation and parent-offspring regression according to Smith and Kinman (1965)

The realized gains from each selection criterion and correlated traits as a deviation percentage of the mean of selected families were calculated from the bulk sample, the best parent and check cultivar means for the selection criteria.

Results and Discussion

The analysis of variance of the base population (F_3 families) of the two studied populations indicated highly significant differences among families for all the studied traits. The genetic variability measured as a genotypic coefficient of variability (Table 1) in both populations was sufficient for selection in the base population for the four selection criteria i.e., grain yield/plant, no. of spikes/plant, no. of kernels/spike and 1000-kernel weight. However, it decreased rapidly in the first and second cycles of selection for both of no. of spikes/plant and grain yield/plant. On the other hand, the genotypic coefficient of variability (GCV) among the selected families for no. of kernels/spike and 1000-kernel weight were sufficient for further improvement after the second cycle and accounted 8.1 and 7.2% for population I, respectively. In consequence, rapid decrease in variability was obtained for both traits. Falconer (1989) stated that selection reduces the variance. The findings of the heritability in broad sense confirmed these results, in which high estimates of heritability were found for all traits in both populations. In general heritability estimates decreased from the F_3 to F_5 generation (cycle 2) in both populations. This could be due to the increase in the experimental error, on the other hand, the environmental variance as the homozygosity of the lines increased, which maximized the phenotypic

relative to the genotypic variance. These results are in line with those reported by Ismail (1995).

Mean no. of spikes/plant, no. of kernels/spike, 1000-kernel weight and grain yield/plant over the selected families in C₁ and C₂ for both populations are presented in Table 2. The response to selection was coined by Falconer (1989) as the difference between mean phenotypic value of the offspring of the selected parents and the generation mean of these parents. The bulk sample mean could be considered the parental generation mean before selection. As well as, in the additive genetic model, the parental mean equals the generation mean before selection. The realized response to selection measured as a deviation percentage of the overall cycle means from the bulk sample and the check cultivar are shown in Tables 3 and 4. The results indicated that selection for no. of spikes/plant improved it by 13.33 and 12.09% from the bulk sample and the check cultivar after two cycles of selection in population I, respectively (Table 3). Such increase was accompanied with increasing no. of kernels/spike (5.29%), 1000-kernel weight (4.88%), grain yield/plant (12.08%) and biological yield/plant (19.45%), and decreasing heading date by 1.56% and plant height by 2.13% from the bulk sample. Likewise, selection toward increasing no. of spikes/plant after the two cycles of selection in

population II was accompanied with different effects on the other studied traits (Table 4).

Selection for no. of kernels/spike after two cycles of pedigree selection increased the criterion of selection by 11.63 and 17.86% (pop. I) and 4.37 and 14.19% (pop. II) from the bulk sample and the check cultivar, respectively, (Table 4).

Such increase in no. of kernels/spike caused a decrease in 1000-kernel weight by 0.68 and -7.21% and grain yield/plant by 4.35 and -14.45% in population I after two cycles of pedigree selection but increase for the same traits in population II.

A significant increase in 1000-kernel weight was achieved by direct selection for this trait accompanied with a significant favorable increase by 11.95 and 6.74% from the bulk sample and the check cultivar, respectively, after two cycles of selection in population I. such increase accompanied by increase in grain yield/plant (1.45 and 21.39%), no. of kernels/spike (3.32 and 9.9%) and biological yield/plant (8.0 and 35.62%) and decreased in heading days by 1.56 and 3.71%.

The results in population II showed on increase in 1000-kernel weight (13.86 and 16.51%), grain yield/plant (1.03 and 13.87%) and no. of spikes/plant (14.89 and 18.68%) and a decrease in days to heading by -1.02 and -4.47% from the bulk sample and the check cultivar, respectively. These results

were in accordance with Kheiralla (1993) and Tammam (1995).

Respect to pedigree selection for grain yield/plant, the resulting families showed realized response to selection accounted 17.39% from the bulk sample after two cycles of selection. Such increase was accompanied with an increase in biological yield/plant (26.36%), 1000-kernel weight (6.1%), no. of kernels/spike (6.65%) and no. of spikes/plant (8.89%) and a decrease in heading date (1.78%) and plant height (3.68%), in population I. The results in population II behaved the same as in population I. Similar results were found by Islam *et al.* (1985a), Wells and Kofoid (1986) and Kheiralla (1989).

In the direct selection, the breeder is concerned with the performance of individual selected families. This is because the overall mean might mask the individual family mean.

Means of the selected families after two cycles of pedigree selection for no. of spikes/plant as a selection criterion are presented in Table 5. In population I, family No. 5 was higher in grain yield/plant (35.26 and 61.84%), no. of spikes/plant (27.77 and 26.37%) and no. of kernels/spike (18.7 and 25.51%) than the bulk and check, respectively. Also in population II, family No. 4 was higher in grain yield/plant by 42.56 and 60.69%), no. of spikes/plant (35.1 and 39.56%) and 1000-

kernel weight (16.81 and 19.53%) than the bulk sample and check cultivar, respectively (Table 5).

Means of the selected families after two cycles of pedigree selection for no. of kernels/spike as a selection criterion are presented in Table (5). In population I, family No. 10 was higher in grain yield/plant by 4.83 and 25.43%, no. of kernels/spike (24.92 and 31.89%) and biological yield/plant (12.00 and 40.63%) than the bulk sample and the check cultivar, respectively (Table 5). For population II, family No. 13 was higher in grain yield/plant by 7.17 and 20.8%), no. of kernels/spike (16.32 and 27.27%) and biological yield/plant (5.88 and 41.55%) than the bulk sample and the check cultivar, respectively (Table 5). Similar results were obtained by Pawar *et al.* (1986) and Tammam (1995) where the pedigree selection method was found to be the best effective in improving no. of kernels/spike.

Means of the selected families after two cycles of pedigree selection for heavier kernel weight are presented in Table 5. In population I, family No. 10 was higher than the bulk sample and the check cultivar in 1000-kernel weight by 35.36 and 29.07%, grain yield/plant by 24.63 and 49.13%, biological yield/plant by 24.72 and 56.62% and no. of spikes/plant by 13.33 and 12.08% and earlier in heading date (-1.56 and -3.7%), than bulk and check, respectively. For

population II, pedigree selection for heavier kernel weight resulted in family No. 6 which was heavier than the bulk sample by 27.05% and it was higher in no., of spikes/plant by 12.77% and earlier by -2.6%, (Table 5).

With respect to grain yield/plant, in the two populations after two cycles of selection (Table 5), all selected families were higher than the bulk sample, and the check cultivar. In

population I family No. 7 yielded 36.71 and 63.58% more than the bulk sample and the check cultivar, respectively. In population II the direct selection for grain yield/plant gave family No. 2 which outyielded the bulk sample and check cultivar by 49.74 and 68.78%, respectively. In addition, all selected families in the two populations significantly outyielded the check cultivar.

Table (1): Genotypic (GCV) and phenotypic (PCV) coefficients of variability and heritability in broad sense (H) of the studied selection criteria for the two cycles of selection for both populations

Selection criterion	Item	Pop. I			Pop. II		
		GCV (%)	PCV (%)	H (%)	GCV (%)	PCV (%)	H (%)
No. of spikes/plant	Base pop. (F ₃)	26.2	27.8	88.9	27.3	29.1	88.4
	C ₁	5.66	8.11	48.65	10.7	12.8	69.4
	C ₂	4.7	6.4	52.6	7.7	8.4	83.9
No. of kernels/spike	Base pop. (F ₃)	13.66	14.26	91.7	17.39	18.1	92.8
	C ₁	7.0	7.9	78.2	5.1	6.0	72.5
	C ₂	8.1	8.4	94.1	5.1	7.3	49.5
1000-kernel weight	Base pop. (F ₃)	10.9	12.6	74.8	13.6	14.4	89.4
	C ₁	6.5	7.6	72.3	5.4	6.0	80.1
	C ₂	7.2	9.0	64.8	5.8	7.4	60.3
Grain yield/plant	Base pop. (F ₃)	28.6	31.1	84.7	31.3	33.2	88.9
	C ₁	11.43	13.59	70.66	7.9	9.0	78.1
	C ₂	3.8	5.5	47.0	3.8	5.1	54.4

Table (2): Mean No. of spikes/plant, No. of kernels/spike, 1000-kernel weight and grain yield/plant over all selected families in the C₁ and C₂ of pedigree selection.

Item	Pop. I				Pop. II			
	No. of spikes/plant	No. of kernels/spike	1000-kernel weight	grain yield/ plant	No. of spikes/plant	No. of kernels/spike	1000-kernel weight	grain yield/ plant
C ₁	9.7	70.6	43.9	23.19	11.2	67.4	50.1	25.2
Bulk	9.3	68.0	40.4	16.2	9.0	68.7	43.4	20.9
Parent 1 (P ₁)	9.5	67.7	38.1	18.0	8.3	65.3	40.2	16.6
Parent (P ₂)	8.0	66.7	39.0	13.3	8.9	60.7	42.7	17.5
LSD 5%	2.75	7.34	5.0	4.8	2.25	6.2	3.8	2.99
C ₂	10.2	73.9	45.9	24.3	11.2	71.6	50.1	26.6
Bulk	9.0	66.2	41.0	20.7	9.4	68.6	44.0	19.5
Parent 1 (P ₁)	8.7	65.7	35.3	19.6	8.5	67.2	41.0	15.3
Parent (P ₂)	8.5	62.3	42.7	15.5	9.1	62.7	43.0	17.3
LSD 5%	4.9	4.35	7.05	2.82	4.41	10.73	6.78	2.67

Table (3): Direct and correlated gains from pedigree selection for the studied selection criteria in the two cycles of selection in population I in percentages from the bulk sample and the check cultivar.

Selection criterion	Item	Heading date	Plant height	No. of spikes/ plant	No. of kernels/ spike	1000-kw	Grain yield/ plant	Biological yield/ plant	
No. of spikes/ plant	C ₁	Bulk	-4.64	-8.77	4.3	1.62	5.94	25.82	37.16
		check	-6.65	2.6	8.99	13.84	0.23	30.36	57.93
	C ₂	Bulk	-1.56	-2.13	13.33	5.29	4.88	12.08	19.45
		check	-3.71	5.09	12.09	11.16	0.00	34.1	50.0
No. of kernels/ spike	C ₁	Bulk	-4.42	-11.45	-3.23	3.82	1.73	8.79	20.67
		check	-6.44	-0.42	1.12	16.31	-3.75	13.14	38.94
	C ₂	Bulk	-1.0	-6.1	1.11	11.63	-0.68	-4.35	5.45
		check	-3.16	3.83	0.0	17.86	-7.21	-14.45	32.42
1000-kernel weight	C ₁	Bulk	-4.53	-10.34	-2.15	-0.88	8.66	9.34	21.09
		check	-6.55	0.83	2.25	11.04	2.81	13.71	39.42
	C ₂	Bulk	-1.56	-4.16	2.22	3.32	11.95	1.45	8.00
		check	-3.71	2.91	1.1	9.09	6.74	21.39	35.62
Grain yield/ plant	C ₁	Bulk	-4.5	-8.4	4.3	2.35	7.43	27.47	38.0
		Check (So-hag 3)	-6.55	3.1	8.99	14.66	1.64	32.57	58.89
	C ₂	Bulk	-1.78	-3.68	8.89	6.65	6.1	17.39	26.36
		Check (So-hag 3)	-3.93	3.43	7.69	12.6	1.16	40.46	58.68

Table (4): Direct and correlated gains from pedigree selection for the studied selection criteria in the two cycles of selection in population II in percentages from the bulk sample and the check cultivar.

Selection criterion	Item	Heading date	Plant height	No. of spikes/ plant	No. of kernels/ spike	1000-kw	Grain yield/ plant	Biological yield/ plant	
No. of spikes/ plant	C ₁	Bulk	-1.9	-2.8	24.44	0.73	9.45	6.7	8.29
		check	-7.07	0.93	25.84	14.0	11.24	27.43	56.97
	C ₂	Bulk	0.56	-2.11	19.15	2.92	8.41	23.59	18.80
		check	-2.94	1.04	23.08	12.6	10.93	39.31	58.68
No. of kernels/ spike	C ₁	Bulk	-2.79	-4.6	8.89	-1.89	7.14	-7.18	-5.47
		check	-7.92	-0.93	10.11	11.04	8.9	10.86	37.02
	C ₂	Bulk	-0.56	-2.52	13.83	4.37	7.5	4.62	2.91
		check	-4.03	0.62	17.58	14.19	10.0	17.92	37.44
1000-kernel weight	C ₁	Bulk	-2.56	-4.20	8.89	-0.44	15.44	-5.56	-5.47
		check	-7.71	-0.52	10.11	12.69	17.33	13.14	37.02
	C ₂	Bulk	-1.02	-3.42	14.89	0.15	13.86	1.03	-3.76
		check	-4.47	-0.31	18.68	9.57	16.51	13.87	28.54
Grain yield/ plant	C ₁	Bulk	-1.45	-3.1	21.11	2.77	9.45	20.57	23.38
		Check (Sohag 3)	-6.65	0.6	22.47	16.3	11.24	44.0	78.85
	C ₂	Bulk	-0.56	-2.52	18.09	3.64	8.64	36.41	27.52
		Check (Sohag 3)	-4.03	0.62	21.98	13.4	11.16	53.76	70.32

Table (5): Means of the best families for the four selection criteria after two cycles of pedigree selection in the two populations.

Selection criterion	Family No.	DHD	PH	No. S/P	No. K/S	1000-kw	GY	BY
Population I								
No. S/P	5	88.0	97.5	11.5	78.7	43.3	28.0	77.6
No. K/S	10	89.0	104.9	9.1	82.7	43.0	21.7	61.6
1000-kw	10	88.3	99.2	10.2	65.6	55.5	25.8	68.6
GY	7	88.0	99.2	10.5	67.9	49.8	28.3	78.6
Bulk	-	89.7	103.3	9.0	66.2	41.0	20.7	55.0
Check	-	91.7	96.2	9.1	62.7	43.0	17.3	43.8
Population II								
No. S/P	4	87.2	102.6	12.7	67.8	51.4	27.8	81.7
No. K/S	13	92.2	109.0	11.7	79.8	50.5	20.9	62.0
1000-kw	6	86.2	94.0	10.6	72.7	55.9	19.5	54.6
GY	2	90.2	106.0	12.0	73.9	49.4	29.2	83.6
Bulk	-	88.5	99.3	9.4	68.6	44.0	19.5	58.5
Check	-	91.7	96.2	9.1	62.7	43.0	17.3	43.8

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الانتخاب للمحصول وبعض صفات الجودة في قمح الديورم

1 - المحصول

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استخدم في هذا البحث الجيل الثالث والرابع والخامس لعشيرتين من قسح المكرونة بهدف تحسين محصول الحبوب باستخدام 4 صفات انتخابية مع طريقة الانتخاب المناسب. كانت الاختلافات بين عائلات الجيل الثالث عالية المعنوية في العشيرتين مع وجود تباين وراثي كاف للصفات المختلفة (محصول الحبوب وعدد السنابل/ نبات وعدد الحبوب في السنبل ووزن الألف حبة). أشارت النتائج إلى أن الانتخاب لصفة عدد السنابل / نبات بعد دورتين انتخابيتين في العشيرة الأولى أدى إلى زيادة مقدارها (13.33 و 12.09%) مقارنة بالعينة العشوائية والصفة المقارنة (سوهاج 3) علي التوالي. كذلك وجدت زيادة في عدد حبوب السنبل قدرها (5.29%) ووزن الألف حبة (4.88%) ومحصول الحبوب (12.08%) والمحصول البيولوجي/ نبات (19.45%) مع التباين (-1.56%) ونقص في طول النبات (-2.13%) مقارنة بالعينة العشوائية.

أدى الانتخاب لصفة عدد الحبوب/سنبل بعد دورتين انتخابيتين إلى زيادة الصفة (11.63% و 17.86%) للعشيرة الأولى و (4.37% و 14.49%) للعشيرة الثانية مقارنة بالعينة العشوائية والصفة المقارنة علي التوالي. كذلك أدت الزيادة في عدد الحبوب / سنبل سببت نقصاً في محصول الحبوب (-4.35 و -14.49%) ووزن 1000 حبة (-0.68% و -7.21%) في العشيرة الأولى بينما زادت هذه الصفات في العشيرة الثانية.

بعد دورتين من الانتخاب زاد محصول الحبوب للنبات من خلال الانتخاب المباشر لهذه الصفة (17.39%) مقارنة بالعينة العشوائية كذلك أدت الزيادة في محصول الحبوب إلى زيادة في المحصول البيولوجي (26.36%) ووزن 1000 حبة (6.1%) وعدد الحبوب / سنبل (6.65%) وعدد السنابل/نبات (8.89%) مع التباين (-1.78%) ونقص في طول النبات (-3.68%) في العشيرة الأولى. سلكت النتائج في العشيرة الثانية نفس سلوك النتائج في العشيرة الأولى.

في العشيرة الأولى تميزت العائلة رقم 5 بالزيادة في محصول الحبوب/نبات (35.26 و 61.84%) وعدد السنابل/نبات (27.77 و 26.37%) وعدد الحبوب/سنبل (18.7 و 25.51%) وبالنسبة للعشيرة الثانية كانت العائلة رقم 4 أعلى في محصول الحبوب/ نبات (42.56 و 60.69%) وعدد السنابل/نبات (35.1 و 39.56%) ووزن الـ 1000 حبة (16.81 و 19.53%) عن العينة العشوائية والصفة المقارنة علي التوالي.