

## Efficiency of Pedigree Selection in Bread Wheat under Drought Stress Conditions. I. Morphological traits

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**Abstract:** Pedigree selection was practiced on two bread wheat populations, namely Debeira x Sahel 1 and Sids 6 x Sahel 1 as a first and second population, respectively under drought stress conditions (at 12 % soil moisture content) in order to improve some morphological traits (plant height, spike length, no. of spikelets /spike and days to maturity). The obtained results revealed that all F<sub>3</sub> families in both populations were significantly affected by soil moisture content. Also, significant differences were found among families in F<sub>4</sub> and F<sub>5</sub> generations for both populations, except no. of spikelets / spike in F<sub>4</sub> generation for first population. The results showed that broad sense heritability (B.S.H) estimates were moderately in F<sub>3</sub> generation for both populations. Meanwhile, B.S.H estimates ranged from low to moderate /high for both F<sub>4</sub> and F<sub>5</sub> generations in two populations. Small differences were found between phenotypic and genotypic variability estimates (P.C.V.) and (G.C.V.) for all the three generations in both populations. Estimates of realized gains showed that a notable decrease was found after two cycles of pedigree selection in days to maturity by (-4.86, -9.52 and -6.18 %) and (-11.40, -11.40 and -7.89%) from the best parent, bulk sample and check variety in first and second population, respectively. Moreover, a notable increase was found after two cycles in plant height by (1.85, 8.23 and 6.60%) from the best parent, bulk sample and check variety in second population only. The families no. 29 and 30 gave superiority for spike length, spikelets no. /spike and days to maturity in population I. Concerning population II, families no. 22 and 25 gave superiority for plant height, spike length and days to maturity, while family no. 41 gave superiority for plant height, no. of spikelets / spike and days to maturity. Also, family no. 45 realized enhancement for spike length, no. of spikelets / spike and days to maturity. These families could be considered the best selected families produced from pedigree selection method for studied morphological traits.

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### 1. Introduction

Bread wheat (*Triticum aestivum* L.) is the most important cereal crop not only in Egypt but also all over the world, that play an important role in people's nutrition. The annual consumption of wheat grains in Egypt is about 14 million tons, while the annual local production in 2011 is about 8.5 million tons (Wheat Res. Dept., 2011). Therefore, increasing wheat production is an important goal to reduce the gap between production and consumption. This can be achieved by great continued efforts of wheat breeders and genetics. Effective improving planning depends not only on amount of variability among the diverse genotypes, but also on heritability for the traits under consideration. Breeders can reduce the required time for improving promising genotypes, if they have significant genotypic variability. Development of cultivars tolerant to drought is an objective in many breeding programs in dry and

semi-dry regions. Drought usually is the most important a biotic stress that affects crop production. Agricultural drought as defined by (Van Bavel and Verlinden, 1956) is a condition that exists when there is insufficient water supply to meet crop water requirements. However, the plant breeding for drought tolerance is difficult, long-term project and presents some problems such as complexity and quantitative inheritance of this trait, difficulty of founding some selection indices, and the lack of detailed physiological and genetic knowledge on drought stress (Borojevic, 1990). Breeding wheat cultivars with improved drought tolerance is challenged in adequate screening and tolerance quantification procedures. Successful breeding program will depend on the magnitude of genetic variation in the population (base population). Hence, selection for drought resistance and production of tolerant cultivars with high yield potential is the main

objective of breeding programs. The most efficient breeding methods and expected gain from selection depends not only upon the ratio between genetic variance and phenotypic one (heritability in narrow sense), but also on magnitude and the mode of gene effects i.e., additive, dominance and interactions between them for the studied traits (Alkaddoussi, 1996). Many researchers (Passioura, 1996; Richards, 1996 and Quarrie *et al.*, 1999) believed that tolerance to drought stress must be done via genetic improvement of physiological traits. Heritability in broad sense should be recognized as the first step before starting any breeding program. Ismail *et al.*, (2003) indicated that drought stress resulted in a significant reduction in yield components and vegetative attributes of durum wheat genotypes. Higher heritability was observed for plant height and its components. However, the heritability was in general found to lower under moisture stress conditions (Singh and Chaudhary, 2006). Meanwhile, high heritability (b.s.) for plant height was found under water stress (Abd El-Kareem and El-Saidy, 2011). Hence, the main objective of this study was to assess the response of two bread wheat populations to pedigree selection under water stress conditions.

## 2. Materials and Methods

The present study was carried out at The Experimental Farm, Fac. of Agric., Al-Azhar Univ., Assiut, Egypt during four successive winter growing seasons, 2004/05, 2005/06, 2006/07 and 2007/08 in order to estimate the response to pedigree selection under water stress conditions in early segregating generations of two bread wheat populations. The

basic material used consisted of two F<sub>2</sub> populations of crosses established between three varieties, namely, Debeira, Sahel 1 and Sids 6. The first population was derived from the cross (Debeira x Sahel 1) and the second population was derived from the cross (Sids 6 x Sahel 1). The genetic parameters were estimated in F<sub>3</sub>, F<sub>4</sub> and F<sub>5</sub> generations. The pedigree and origin of the three parents and the check variety are presented in Table (1). In the first season (Nov. 15<sup>th</sup>, 2004), 1000 plants from F<sub>2</sub> of each population were grown individual with non-replicated plants. Also, the parents and check variety (Sids 1) were sown in one row for each population; each row was 3 m. long and 0.30 m. wide having 30 plants. Grains were sown in clay loam soil at 10 cm. spacing with one grain per hill. The selection intensity was 10% for grain yield / plant. The 205 highest yielding plants from each population were selected.

Soil samples for moisture determination were taken down to 30 cm soil depth by soil auger. The samples were weighted and then oven dried. Percentage of soil moisture content was calculated on oven dry basis. The experiments were grown and given one surface –irrigation 30 days after planting irrigation (two irrigation were given through the whole season, the soil moisture content reached about 12 % which is considered moisture stress treatment) for all growing seasons. Some soil properties of The Experimental Farm are shown in Table (2). All the agronomic practices were applied as commonly used for growing wheat and carried out according to the recommendations set by the Ministry of Agriculture.

**Table 1.** The pedigree and origin of three parents and local check variety used in the present study.

Parental name		Pedigree	Origin
Population I	Debeira	HYBRID-DELHI-2160/5/TOBARI-66/CIANO-67//BLUEBIRD/3/NAINARI-60*2//TOM-THUMB/SONORA-	(India/Syria)
	Sahel 1	N.S.732 / Plm // veery " S " D 735-4 S d-1Sd-O S d	Egypt
Population II	Sids 6	Maya " S " /Mon " S " //CMH 74 A.592/3 Sakha 8* 2	Sids- Egypt
	Sahel 1	N.S.732 / Plm // veery " S " D 735-4 S d-1Sd-O S d	Egypt
(local check variety)	Sids 1	HD 2172 /Pavon " S " // 1158. 57 /Maya 74 "S"	Sids- Egypt

**Table 2.** Soil properties of the studied area.

Depth (cm)	Percentage (%)			Texture class	Organic Matter (%)	CaCO <sub>3</sub> (%)	pH	EC (dS m <sup>-1</sup> )	Soluble ions (meq L <sup>-1</sup> )						
	Sand	Silt	Clay						CO <sub>3</sub> <sup>-</sup> +HCO <sub>3</sub> <sup>-</sup>	Cl <sup>-</sup>	SO <sub>4</sub> <sup>-</sup>	Ca <sup>++</sup>	Mg <sup>++</sup>	Na <sup>+</sup>	K <sup>+</sup>
0-30	25.00	39.65	35.35	Clay loam	1.20	3.50	7.87	1.05	2.50	1.25	6.15	2.70	1.35	5.74	0.11
30-60	24.65	39.00	36.35	Clay loam	1.10	3.20	7.88	1.00	2.34	1.16	6.00	2.60	1.15	5.53	0.22

In the second season (Nov. 25<sup>th</sup>, 2005), the best 205 F<sub>3</sub> families were tolerant to water stress conditions for each population including the parents, F<sub>3</sub> bulked random sample (a mixture of equal number of grains from each plant to represent the generation mean) and the check variety (Sids 1) were sown in two separated experiments using a randomized complete block design of three replications under water stress conditions. Each family, bulk sample, parents and check variety for both populations were represented by one row, 3 meter long and 30 cm. apart and 10 cm. between plants in each replicate. The data were recorded and measured on random sample of 7 guarded plants for each family and the means of the 7 plants were subjected to the statistical and genetic analysis. Selection between and within families was practiced. Data were recorded on individual guarded plants on basis as plant height, spike length, no. of spikelets / spike and days to maturity. The best 66 F<sub>4</sub> plants from the best 66 families of each population were saved to give the F<sub>4</sub> families.

In the third season (Nov. 19<sup>th</sup>, 2006), the 66 F<sub>4</sub> families from each population with the parents, F<sub>4</sub> bulk sample and the check variety Sids1 were sown in two separated experiments in a randomized complete block design of three replications. The best 19 plants from the best 19 families of both populations were saved to give the F<sub>5</sub> families. Again data were taken as in the previous season.

In the fourth season (Nov. 30<sup>th</sup>, 2007), the 19 F<sub>5</sub> families from each population with the parents, F<sub>5</sub> bulk sample and the check variety Sids1 were sown in two separated experiments in a randomized complete block design of three replications. The data were recorded and measured as in the previous seasons.

#### Statistical analysis:

Analysis of mean squares with randomized complete block design (RCBD) to compute the significance for genotypes made according to Snedecor and Cochran (1980). The least significant difference (LSD) test at 0.05 % and 0.01% levels of probability, according to Steel and Torrie (1980) was used to compare among means. Estimates of phenotypic and genotypic variance ( $\delta^2g + \delta^2ph$ ) and heritability estimates were calculated from the partitioning mean squares expectation (EMS) of variance components of the selected families according to Al-jiburi et al., (1958), Table (3).

Broad sense heritability ( $H^2b$ ) was calculated as the ratio of genotypic ( $\delta^2g$ ) to the phenotypic ( $\delta^2g$ )

+  $\delta^2e$ ) variance according to Fehr (1987). The genotypic (G.C.V %) and phenotypic (P.C.V %) coefficients of variability were estimated using the formulae developed by Burton (1952).

Genotypic coefficient variability:

$$G.C.V. \% = (\delta g / x) \times 100.$$

Phenotypic coefficient variability:

$$P.C.V. \% = (\delta p_h / x) \times 100.$$

**Table 3.** Analysis of variance and mean square expectations.

Source of variance	d.f	M.S	Expected mean square
Replications	r-1	m <sub>3</sub>	$\delta^2e + g\delta^2r$
Genotypes	g-1	m <sub>2</sub>	$\delta^2e + r\delta^2g$
Error	(r-1)(g-1)	m <sub>1</sub>	$\delta^2e$

where :  $\delta g$  and  $\delta p$  are the genotypic and phenotypic standard deviations of the family mean, and x is the family mean for a given trait.  $\delta^2g = m_2 - m_1/r$ ;  $\delta^2ph = \delta^2g + \delta^2e$  and  $\delta^2e = m_1$

#### Response to selection:

The realized response to selection was estimated as the difference between the mean of the selected families and the mean of the best parent, bulk population and check variety, Falconer (1989).

### 3. Results and Discussion

A successful breeding program is largely dependent on the magnitude of genetic variation in the base population as well as the efficiency of selection method used. So two cycles of pedigree selection were made to improve some morphological traits in two bread wheat segregating crosses.

#### I-Analysis of variance and mean performance of the base population (F<sub>3</sub> families):

Analysis of variance for F<sub>3</sub> and their parents for plant height, spike length, no. of spikelets /spike and days to maturity of the two populations are presented in Table (4). Mean squares realized highly significant differences among families in F<sub>3</sub> (base population) families in both populations for all studied traits, indicating the presence of genetic variability among selected families.

The obtained results in Table (4), showed the plant height ranged from 69.17 to 105.0 cm. with an average of 86.96 cm. and 80.83 to 115.84 cm. with an average of 99.46 cm. in population I and II, respectively. The minimum spike length was 9.34 and 10.5 cm. to 13.67 and 15.0 cm. with an average of 11.65 and 12.37 cm. in first and second population, respectively. The least no. of spikelets /spike ranged from 16.5 and 17.0 spikelets /spike to 24.5 and 26.0 spikelets /spike with an average of 21.18 and 21.11 spikelets/spike in population I and II, respectively. The days no. to maturity ranged from

122.0 and 91.0 days to 137.0 and 101.0 days with an average of 127.29 and 92.19 days in population I and II, respectively.

Phenotypic and genotypic coefficients of variability and broad sense heritability of  $F_3$  plants are presented in Table (4). The values of phenotypic coefficients of variability in the first population were 9.93, 9.56, 9.36 and 2.79 % for plant height, spike length, no. of spikelets /spike and days to maturity, respectively. The corresponding values were 8.92, 9.22, 11.32 and 3.36% in the second population. Also, the values of genotypic coefficients of variability in the first population were 7.73, 6.13, 6.51 and 1.71 % while the values in the second population were 6.49, 6.47, 8.71 and 2.08 % for the corresponding traits. These results showed sufficient phenotypic and genotypic coefficients of variability according to pedigree selection which increases the homozygosity of plants. Small differences were

observed between (P.C.V.) and (G.C.V.) in the  $F_3$  generation, indicating the importance of the genetic effects in the inheritance of all studied traits.

Heritability estimate is considered one of the most important parameters for selection response in early generations. The results clearly showed that the broad sense heritability for the previous studied traits ranged from low 37.49 and 38.16 (days to maturity) for first and second populations to moderate 60.48 and 59.19 for (plant height and no. of spikelets / spike) of first and second population, respectively. Similar results were in line with those obtained by Tammam (1989), Nasir ud- Din (1992), Abdel – Haleem (2003), El-Sayed (2006), Memon *et al.*, (2007), Abdel-Moneam and Sultan (2009) and El-Sayed (2012). They reported that decreasing in genetic variance magnitude and heritability under stress conditions.

**Table 4.** Analysis of variance, means, range, phenotypic and genotypic coefficients of variability and broad sense heritability for all studied traits of  $F_3$  selected families (base population) in two populations of bread wheat under drought stress conditions in 2005 / 2006 season.

S.O.V	D.F	Population I				D.F	Population II			
		Plant height (cm.)	Spike length (cm.)	No. of spikelets (no.)	Maturity (day)		Plant height (cm.)	Spike length (cm.)	No. of spikelets (no.)	Maturity (day)
Replications	2	115.89	5.11**	58.41**	2410.78**	2	1106.38**	22.41**	38.42**	85.01**
Genotypes	204	171.35**	2.26**	8.28**	22.06**	204	160.06**	2.59**	12.25**	17.17**
Error	408	40.95	0.72	1.98	7.74	408	36.71	0.67	2.33	6.34
Mean $\pm$ S.E ( $F_3$ selected families)		86.96 $\pm$ 3.14	11.65 $\pm$ 0.49	21.18 $\pm$ 0.82	127.29 $\pm$ 1.62		99.46 $\pm$ 3.52	12.37 $\pm$ 0.47	21.11 $\pm$ 0.88	92.19 $\pm$ 1.41
Best parent		97.5	12.0	17.17	124.5		106.67	11.33	20.67	96.0
Bulk sample		90.0	10.17	17.34	124.5		100.84	11.17	21.5	96.0
Check variety (Sids1)		89.17	11.17	19.67	124.5		95.0	12.5	20.67	93.5
Range		69.2- 105.	9.4 – 13.7	16.5 – 24.5	122 - 137		80.9 – 116	10.5 – 15.0	17.0 – 26.0	91 – 101
P.C.V %		9.93%	9.56%	9.36%	2.79%		8.92%	9.22%	11.32%	3.36%
G.C.V %		7.73%	6.13%	6.51%	1.71%		6.49%	6.47%	8.71%	2.08%
B.S.H %		60.48%	41.13%	48.35%	37.49%		52.84%	49.23%	59.19%	38.16%

## II -Analysis of variance and performance of pedigree selection cycles ( $F_4$ and $F_5$ families):

Results in Table (5) presented the analysis of variance of plant height, spike length, no. of spikelets / spike and days to maturity for the two populations. The results realized significant differences among families in both  $F_4$  and  $F_5$  generations for all studied traits, except no. of spikelets / spike in  $F_4$  generation in first population. These results refer to the sufficient of genetic variability among selected families in these traits.

Table (5) showed the mean, range, phenotypic and genotypic coefficients of variability and broad sense heritability for all studied traits. The obtained results of plant height ranged from 80.78 to 108.89 cm. with an average of 95.67 cm. and from 73.43 to 99.80 cm. with an average of 83.24 cm. for first

population in the  $F_4$  and  $F_5$  generations, respectively. For second population, plant height ranged from 81.11 to 131.69 cm. with an average of 112.75 and from 80.73 to 110.6 cm. with an average of 97.08 cm. in the  $F_4$  and  $F_5$  generations, respectively. The least spike length varied between 9.14 and 12.28 cm. with an average of 10.74 cm. and from 7.35 to 11.83 cm. with an average of 9.79 cm. for population I in the  $F_4$  and  $F_5$  generations, respectively. Meanwhile, for population II, spike length ranged from 10.97 to 17.05 cm. with an average of 14.15 cm. and ranged from 11.78 to 17.03 cm. with an average of 13.85 cm. in both  $F_4$  and  $F_5$  generations, respectively. For first population, the minimum no. of spikelets /spike was 16.68 while the maximum one was 22.89 spikelets with an average of 19.86 spikelets. The corresponding values of minimum and maximum

were 18.25 was 23.25 with an average of 20.43 spikelets in the F<sub>4</sub> and F<sub>5</sub> generations, respectively. For population II, no. of spikelets /spike ranged from 17.93 to 27.0 with an average of 22.63 and ranged from 21.96 to 26.27 with an average of 24.39 in both F<sub>4</sub> and F<sub>5</sub> generations, respectively. The no. of days to maturity ranged from 129.0 to 144.0 with an average of 137.09 and from 130.33 to 146.0 with an average of 135.73 in population I in the F<sub>4</sub> and F<sub>5</sub> generations, respectively. For second population the no. of days to maturity ranged from 128.67 to 163.0 with an average of 145.14 and from 121.33 to 145.0 with an average of 132.02 in both F<sub>4</sub> and F<sub>5</sub> generations, respectively.

Estimates of phenotypic (P.C.V.) and genotypic (G.C.V.) coefficients of variation and broad sense heritability (B.S.H.) of all studied traits are presented in Table (5). Phenotypic coefficient variability (P.C.V.) values of plant height, spike length, no. of spikelets / spike and days to maturity were (9.32 and 11.62 %), (11.02 and 19.22 %), (10.37 and 10.55%) and (3.12 and 3.92 %) in population I for both F<sub>4</sub> and F<sub>5</sub> generations, respectively. In addition, for population II, P.C.V. values for the same traits were (12.76 and 13.40 %),

(13.43 and 13.25 %), (14.91 and 6.4 %) and (4.78 and 5.16 %) for both F<sub>4</sub> and F<sub>5</sub> generations, respectively. Also, genetic coefficients variability (G.C.V.) values of the same traits were (4.58 and 7.52 %), (3.95 and 15.12%), (3.02 and 6.73%) and (2.17 and 2.69%) in first population for both F<sub>4</sub> and F<sub>5</sub> generations, respectively. Meanwhile, for the second population, the G.C.V. values for the same traits were (11.27 and 12.07%), (6.28 and 11.0%), (7.37 and 2.75%) and (4.41 and 4.12%) for both F<sub>4</sub> and F<sub>5</sub> generations, respectively.

Broad sense heritability (B.S.H.) values of plant height, spike length, spikelets no. /spike and days to maturity (Table 5) were (24.14 and 41.93%), (12.86 and 61.86%), (8.49 and 40.65%) and (48.66 and 47.13%) in population I for both F<sub>4</sub> and F<sub>5</sub> generations, respectively. In this regard, for population II they were (78.02 and 81.16%), (21.88 and 68.48%), (24.41 and 18.15%) and (85.24 and 63.98%) of the same traits for the F<sub>4</sub> and F<sub>5</sub> generations, respectively. These results indicated that drought stress conditions resulted in lower broad sense heritability. Similar results were in agreement with those obtained by Stuber *et al.*, (1962), Johanson *et al.*, (1966) and Asay and Johanson (1990).

**Table 5.** Mean squares, means, range, phenotypic and genotypic coefficients of variability and broad sense heritability for all studied traits of both F<sub>4</sub> generation and F<sub>5</sub> generation in two populations of bread wheat under drought stress conditions in both 2006/2007 and 2007/2008 seasons.

Generations	S.O.V	D.F	Population I				D.F	Population II			
			Plant height (cm.)	Spike length (cm.)	No. of spikelets / Spike (no.)	Date to maturity (d.)		Plant height (cm.)	Spike length (cm.)	No. of spikelets / Spike (no.)	Days to maturity (d.)
F <sub>4</sub>	Replications	2	60.04	8.73**	10.46	1716.10**	2	182.63*	8.81*	2.76	91.37**
	Families	65	152.48**	1.77*	4.84	34.75**	65	500.14**	5.25**	16.42**	141.37**
	Error	130	63.87	1.17	3.75	9.68	130	50.67	2.75	8.83	7.08
F <sub>5</sub>	Replications	2	241.89**	33.86**	17.95**	39.28	2	25.04	4.73*	1.23	119.49**
	Families	18	301.22**	3.37**	6.93*	62.31**	18	373.29**	10.63**	5.40**	213.63**
	Error	36	52.87	1.42	3.13	14.65	36	32.88	1.12	2.07	17.21
F <sub>4</sub>	Mean ± S.E (F <sub>4</sub> selected families)		95.67±4.48	10.74±0.64	19.86±1.14	137.09±1.80		112.75±3.89	14.15±0.97	22.63±1.7	145.14±1.54
	Best parent		115.92	11.24	19.79	133.67		113.0	13.16	21.77	155.0
	Bulk sample		102.67	11.48	19.03	137.67		119.56	13.64	20.78	156.33
	Check variety (Sids1)		104.92	12.08	21.56	136.67		108.0	13.61	20.49	155.0
	Range		80.8-108.9	9.14-12.28	16.7-22.89	129.0-144.0		81.1 - 131.7	10.9-17.05	17.93-27.0	128.7-163.0
	P.C.V %		9.32%	11.02%	10.37%	3.12%		12.76%	13.43%	14.91%	4.78%
	G.C.V %		4.58%	3.95%	3.02%	2.17%		11.27%	6.28%	7.37%	4.41%
	B.S.H %		24.14%	12.86%	8.49%	48.66%		78.02%	21.88%	24.41%	85.24%
F <sub>5</sub>	Mean ± S.E (F <sub>5</sub> selected families)		83.24±4.25	9.79±0.67	20.43±0.96	135.73±2.23		97.08±3.26	13.85±0.59	24.39±0.8	132.02±2.36
	Best parent		115.41	10.92	21.49	142.67		95.34	11.30	23.10	149.0
	Bulk sample		88.27	10.91	20.89	150.0		89.70	15.03	25.10	149.0
	Check variety (Sids1)		85.0	8.73	19.59	144.67		91.07	9.97	21.99	143.33
	Range		73.5-99.80	7.35-11.83	18.3 - 23.3	130.3-146.0		80.73-110.6	11.8-17.03	21.9-26.3	121.3-145.0
	P.C.V %		11.62%	19.22%	10.55%	3.92%		13.40%	13.25%	6.46%	5.16%
	G.C.V %		7.52%	15.12%	6.73%	2.69%		12.07%	11.0%	2.75%	4.12%
	B.S.H %		41.93%	61.86%	40.65%	47.13%		81.16%	68.84%	18.15%	63.98%

### III- Mean value and realized gains to pedigree selection:

Means of the selected families after two cycles of pedigree selection for all studied traits for both populations under drought stress condition are presented in Table (6). In the first population after two cycles, the pedigree selection for spike length, no. of spikelets /spike and days to maturity resulted two superior families (no. 29 and 30) which exceeded the best parent ,bulk sample and check variety. Concerning family no. 29 exceeded by (5.59, 5.68 and 32.07%), (8.19, 11.30 and 18.86 %) and (-3.74, -8.45 and -5.07 %), for the previous studied traits, respectively. Moreover, family no. 30 exceeded by (8.33, 8.43 and 35.51 %), (7.49, 10.58 and 17.92 %) and (-0.7, -5.55 and -2.07 %) for the same traits, respectively. Regarding after two cycles in the second population, the results in Table (6) revealed four families i.e. 22, 25, 41 and 45 were attained the superiority for the studied traits. Concerning families no. 22 and 25 were exceeded by (1.92, 8.33 and 6.70%) and (10.37, 17.31 and 15.55%), (43.98, 8.25 and 63.19%) and (38.50, 4.13 and 56.97%) and (-11.41, -7.90 and -11.41 %) and (-7.83, -4.19 and -7.83%) for plant height, spike length and days to maturity, respectively. While, family no.41 achieved superiority by (13.59, 20.74 and 18.92 %), (10.91, 2.07 and 16.51 %) and (-15.21, -11.86 and -15.21 %) for plant height, spike length and days to maturity, respectively. While, the last family no. 45 exceeded by (33.63, 0.47 and 51.45 %), (9.52, 0.80 and 15.05 %) and (-6.26, -2.55 and -6.26 %) for spike length,

no. of spikelets / spike and days to maturity, respectively. Previous results summarized that applying of pedigree selection to improve morphological traits after two cycles were effective to isolate promising genotypes in both bread wheat populations under drought stress conditions.

The realized response to selection according Falconer (1989), measured as the deviation percentage of the overall cycle mean from the best parent, bulk sample and the check variety are shown in Table (7). In first population, the results indicated that selection after two cycles of pedigree selection led to a desirable decrease in days to maturity by (-4.86, -9.52 and -6.18%) from the best parent, bulk sample and check variety, respectively. Meanwhile, in the second population, realized response to selection was obtained for plant height by (1.83, 8.23 and 6.60%) from the best parent, bulk sample and check variety, respectively. Moreover, realized response to pedigree selection was found for days to maturity by (-11.40, -11.40 and -7.89%) from the best parent, bulk sample and check variety, respectively. The current study, realized response to selection was found for days to maturity in both populations and plant height in the second population only, suggesting that the pedigree selection practice is high scope for improvement of these traits under drought stress conditions, indicating the role of additive gene action for inheritance of these traits. Similar results were in line with those obtained by Ali (2011) and El-Sayed (2012).

**Table 6.** Means of the fifteen F5 families (selected under drought stress conditions), best parent, bulk sample and check variety after the second cycle of the pedigree selection in both populations.

No. of selected family	Population I				No. of selected family	Population II			
	Traits					Traits			
	Plant height (cm.)	Spike length (cm.)	No. of spikelets / Spike (no.)	Days to maturity (d.)		Plant height (cm.)	Spike length (cm.)	No. of spikelets / Spike (no.)	Days to maturity (d.)
Best parent	115.41	10.92	21.49	142.67	Best parent	95.34	11.30	23.10	149.0
Bulk Sample	88.27	10.91	20.89	150.0	Bulk Sample	89.70	15.03	25.10	143.33
Check variety (Sids 1)	85.0	8.73	19.59	144.67	Check variety (Sids 1)	91.07	9.97	21.99	149.0
8	76.33	7.35	18.25	130.33	10	80.73	11.78	24.03	121.33
14	76.11	9.45	18.72	135.33	12	88.9	14.03	26.27	130.33
16	78.45	9.43	20.03	138.0	15	84.1	12.38	24.93	133.0
17	77.45	8.81	18.56	141.67	19	82.67	17.03	25.07	133.0
18	78.17	9.56	18.88	143.0	21	108.57	14.1	23.9	130.33
20	80.80	9.60	19.95	137.33	22	97.17	16.27	25.03	132.0
21	86.46	10.39	19.41	141.0	25	105.23	15.65	24.60	137.33
23	90.67	10.86	22.19	140.33	26	109.63	13.53	23.6	133.67
24	73.43	9.87	20.34	137.0	34	88.71	13.53	23.47	136.0
29	99.80	11.53	23.25	137.33	36	90.52	12.01	24.0	126.67
30	90.46	11.83	23.1	141.67	41	108.3	12.23	25.62	126.33
39	94.17	9.91	21.04	144.0	45	81.5	15.1	25.30	139.67
40	82.44	9.76	22.39	145.33	49	109.7	12.07	21.96	128.67
41	83.27	9.15	19.22	146.0	51	110.53	13.40	24.8	127.0
47	80.56	9.39	21.09	144.33	57	110.6	14.56	25.30	145.0
Average	83.24	9.79	20.43	135.73	Average	97.08	13.85	24.39	132.02
LSD <sub>0.05</sub>	12.04	1.84	2.93	6.34	LSD <sub>0.05</sub>	9.49	1.75	2.38	6.87
0.01	16.14	2.47	3.93	8.50	0.01	12.73	2.35	3.19	9.21

**Table 7.** Realized gains in the two cycles of pedigree selection for both populations in percentages from the best parent, bulk sample and the check variety for all studied traits under drought stress conditions.

Item	Population I				Population II				
	Plant height	Spike length	No. of spikelets / Spike	Days to maturity	Plant height	Spike length	No. of spikelets / Spike	Days to maturity	
C1	Best parent	-17.47	-4.45	0.35	2.49	-0.22	7.52	3.95	-6.36
	Bulk sample	-6.82	-6.45	4.36	-0.49	-5.70	3.74	8.90	-7.16
	Check variety (Sids1)	-8.82	-11.09	-7.88	0.24	4.40	3.97	10.44	-6.36
C2	Best parent	-27.87	-10.35	-4.93	-4.86	1.83	22.57	5.58	-11.40
	Bulk sample	-5.70	-10.27	-2.20	-9.52	8.23	-7.85	-2.83	-11.40
	Check variety (Sids1)	-2.07	12.14	4.29	-6.18	6.60	38.92	10.91	-7.89

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