

Efficiency of Pedigree Selection in Bread Wheat under Drought Stress Conditions II – Yield and its component traits

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Abstract: Pedigree selection was practiced on two bread wheat populations, namely i.e. (Debeira x Sahel 1) as considered population I and (Sids 6 x Sahel 1) as considered population II. Experiments were conducted under drought stress conditions (at 12 % soil moisture content) in order to improve yield and its component traits (no. of spikes / plant, biological yield, grain yield / plant and 1000-grain weight). Variance analysis revealed that all F_3 families in both populations were highly significantly affected by soil moisture content. Also, significant or highly significant differences were found among families in both F_4 and F_5 generations for two populations, except no. of spikes/plant in F_4 generation in both populations, also biological yield/plant and grain yield/plant in F_5 generation in population I, and also no. of spikes/plant in F_5 generation in population II. Results showed that broad sense heritability estimates were low to moderately in F_3 generation for both populations. Also, estimates of broad sense heritability (B.S.H) ranged from low to moderate /high for both F_4 and F_5 generations in two populations. Moderately differences were found between phenotypic and genotypic variability estimates (p.c.v.) and (g.c.v.) for all the three generations in both populations. Realized response to selection was found after two cycles of pedigree selection for 1000-grain weight in first population and grain yield/plant in the second population. In the first population after two cycles of the pedigree selection resulted one superiority family no. 16 which exceeded the best parent ,bulk sample and check variety by (18.12, 0.46 and 16.22 %) , (9.10, 3.26 and 28.19 %), (10.47, 29.97 and 2.70 %) and (11.88, 7.91 and 15.40 %), for no. of spikes / plant, biological yield , grain yield / plant and 1000-grain weight, respectively. In this regard, in the second population, the results revealed three families i.e. 21, 26 and 41 were attained the superiority for the studied traits. Concerning family no. 21 was exceeded by (30.51, 23.25 and 14.89%), (62.13 , 24.19 and 51.45 %), (14.43, 51.51 and 70.48 %) and (2.12, 15.31 and 23.29%) for no. of spikes / plant, biological yield , grain yield / plant and 1000-grain weight, respectively. Regarding, families no. 26 and 41 were exceeded by (37.34, 5.20 and 28.29 %) and (48.98, 14.40 and 39.16%), (38.72, 83.68 and 106.67 %) and (11.60, 47.76 and 66.26 %) and (12.46, 26.98 and 35.77 %) and (0.25, 13.20 and 21.03%) for biological yield, grain yield / plant and 1000-grain weight, respectively.

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1. Introduction

Wheat (*Triticum aestivum* L.) is the most important cereal crop in many parts of the world, it is a staple diet for more than one third of the world population, so it is commonly known as king of cereals. In Egypt, the annual consumption of wheat grains in Egypt is about 14 million tons, while the annual local production is about 8.5 million tons in 2011(Wheat Res. Dept., 2011). Drought is one of the prime a biotic stresses in the world. Water deficiency is generally considered as one of the limiting factors for crop productivity, which affects physiological as well as biochemical processes in plants (Osborne *et al.*, 2002). High yield and drought tolerance are the

main objectives of most wheat breeding programs. Thus, successful of breeding program for improving wheat under a biotic stress conditions depends on the magnitude of genetic variation in the population (base population). Moreover, reliable estimates of genetic and environmental variations will be helpful to estimate heritability ratio and consequently predicted genetic advance from selection. These estimates are useful to initiate such breeding program in order to improve wheat productivity. Developing crop cultivars with high grain yield has been the principle aim of wheat breeding programs worldwide (Bhutta, 2006). Considering that yield is polygenic and its heritability is low to achieve high yield,

selection is done using yield components (Khayatnejad *et al.*, 2010). On the other hand, Richards (1996) stated that heritability of this trait has been low because of genotype $\times$ environment interaction; hence, selection based on yield would not be profitable for its improvement. Sadiq *et al.*, (1994) found high grain yield proved to be the best indicator of drought tolerance. Saxen and Bahatia (1970) pointed that high heritability is not always associated with high genetic advance, but in order to make effective selection, high heritability should be associated with high genetic gain. Selection for yield is one of the most important and difficult challenge of plant breeding. The efficiency of a breeding program for drought tolerance depends largely on the selection criteria and selection method used to achieve genetic improvement through selection. In addition to the complexity of drought itself (Passioura, 2007). Growth of wheat grain is reduced depending upon degree of water stress and on the rate of stress development, thereby limiting final wheat yield (Plaut *et al.*, 2004). Breeding for drought tolerance by selecting solely for grain yield is difficult, because the heritability of yield under drought conditions is low, due to small genotypic variance or to large genotype-environment interaction variances (Blum, 1988). Broad sense heritability should be determined as the first step before starting any breeding program. Heritability measures are the portion of the total genetic variance that are due to heritability factors. Genetic variance and heritability estimates were higher in the irrigated environment than in the drought-stressed environment (Nasir ud- Din 1992). The ideal genotype for moisture stress conditions must combine a reasonably high yield potential with specific plant characters which could buffer yield against severe moisture stress (Blum, 1983). The difficulty in breeding for moisture stress is the use of yield as principal selection index because the variability as well as heritability is reduced under drought stress conditions (Roy and Murthy, 1969; Turner, 1986). This causes slow progress in selection under drought stress conditions as compared to environment with optimal rainfall. Phenotypic and genotypic variance, heritability and genetic advance have been used to assess the magnitude of variance in wheat breeding material (Jhonson *et al.*, 1956; Zaheer *et al.*, 1987; Khan, 1990). The heritability was in general found to lower under moisture stress conditions Singh and Chaudhary (2006). Rab *et al.* (1984) reported that water deficit at tillering stage caused reduction in grain yield. Kobata *et al.*, (1992) summarized that grain yield and 1000-grain weight was reduced under drought stress. Grain yield increased with the increase in soil moisture content

(Dawood *et al.*, 1988). Hassan *et al.*, (1998) reported significant variation in grain yield of wheat genotypes grown under different management practices. Crop yield losses due to drought stress are considerable (Ashraf, 2010). Ismail *et al.*, (2003) indicated that drought stress resulted in a significant reduction in yield components and vegetative attributes of durum wheat genotypes. Using yield components and selection criterion should be superior to improve yield under drought condition. Relative yield performance of genotypes in drought stressed and more favorable environments seems to be a common starting point in identification of traits related to drought tolerance and selection of genotypes for use in breeding for dry environment (Clarke *et al.*, 1984). The main objective of this study was to assess response of two bread wheat populations to pedigree selection under moisture stress conditions.

2. Materials And Methods

The present study was carried out at the Experimental Farm of the Faculty of Agriculture, Al-Azhar University, Assiut, Egypt. During four successive winter growing seasons, 2004 / 2005, 2005 / 2006, 2006 / 2007 and 2007 / 2008. The objective of this study was to estimate the response to pedigree selection under water stress conditions in early segregating generations of two bread wheat populations. The basic material used in this study consisted of two F_2 populations of crosses established between three varieties, namely, Debeira, Sahel 1 and Sids6. The first population was derived from the cross (Debeira $\times$ Sahel 1) and the second population was derived from the cross (Sids 6 $\times$ Sahel 1). The genetic parameters were estimated in F_3 , F_4 and F_5 generations. The pedigree and origin of the three parents and the check variety are presented in Table (1). In the first season, (Nov.15th, 2004), 1000 plants from F_2 of each of the two populations were grown individual with non-replicated plants. Also, the parents and check variety (Sids 1) were sown in one row for each population, the single row was three meter long, 30 cm. wide and contained 30 plants. Grains were sown at 10 cm. , spacing with one grain per hill. Grains were sown in clay loam soil at 10 cm. spacing with one grain per hill.

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 / PIm // 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 / PIm // 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 ₃ (%)	pH	EC (dS m ⁻¹)	Soluble ions (meq L ⁻¹)						
	Sand	Silt	Clay						CO ₃ ²⁻ +HCO ₃ ⁻	Cl ⁻	SO ₄ ²⁻	Ca ⁺⁺	Mg ⁺⁺	Na ⁺	K ⁺
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.25th,2005), The best 100 and 99 F₃ families for highest grain yield / plant were selected to water stress conditions from population I and population II, respectively . Parents, F₃ bulked random sample of each population (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. 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 no. of spikes / plant, biological yield , grain yield / plant and 1000-grain weight. The best 66 and 68 F₄ families for grain yield / plant were selected and saved to give the F₄ families from population I and II, respectively .

In the third season (Nov.19th,2006), the best 66 and 68 F₄ families for grain yield / plant were selected from population I and population II, respectively with the parents, F₄ bulk sample of each population 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 F₅ families. Again data were taken in the previous season.

In the fourth season (Nov.30th,2007), the 19 F₅ families from each population with the parents , F₅ 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 to compute the significance for genotypes made according to Snedecor and Cochran (1980). The least significant difference (L.S.D) 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 ($\delta^2_g + \delta^2_{ph}$) 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^2_b) was calculated as the ratio of genotypic (δ^2_g) to the phenotypic ($\delta^2_g + \delta^2_e$) 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:

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

Phenotypic coefficient variability:

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

Table 3: The analysis of variance and mean square expectations

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

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

3. Results And Discussion

I-Analysis of variance and mean performance of the base population (F₃ families) :

Analysis of variance for F₃ and their parents for no. of spikes / plant, biological yield , grain yield / plant and 1000-grain weight of the two populations are presented in Table (4). Mean squares were highly significant differences among families in F₃ (base population) families in both populations for all studied traits, indicating the presence of genetic variability among selected families under drought stress conditions. Similar results were obtained by Subhani and Chowdhry (2000), Asif *et al.*, (2003) and Sadeghzadeh and Alizadeh (2005), Ali (2011) and El-Sayed, (2012).

The obtained results in Table (4), showed the no. of spikes/plant ranged from 4.0 to 7.17 spikes with an average of 5.52 spikes and 4.34 to 8.67 spikes with an average of 6.24 spikes in population I and population II, respectively. The minimum biological yield/plant was 11.08 and 12.03 gm. to 23.97 and 38.64 gm. with an average of 16.06 and 23.54 gm. in first and second population, respectively. The least no. of grain yield/plant ranged from 2.70 and 2.24 gm. to 11.40 and 13.04 gm. with an average of 6.45 and 6.12 gm. in population I and populations II, respectively. The 1000-grain weight ranged from 22.50 and 21.50 gm. to 32.0 and 50.88 gm. with an average of 27.96 and 40.98 gm. in population I and population II, respectively.

Phenotypic and genotypic coefficients of variability and broad sense heritability of F₃ plants (base population) for all studied traits are presented in Table (4). The values of phenotypic coefficients of variability (p.c.v.) were (16.80 and 20.08 %), (21.78 and 25.85%), (29.25 and 39.96%) and (9.41 and 13.32%) for no. of spikes / plant, biological yield , grain yield / plant and 1000-grain weight in first and

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).

second population, respectively. Also, the values of genotypic coefficients of variability (g.c.v.) were (9.24 and 11.22%), (13.68 and 15.99%), (20.33 and 29.0%) and (5.49 and 9.01%) in the same both traits and conditions in population I and population II, respectively. These results showed sufficient of phenotypic and genotypic coefficients of variability according to pedigree selection which increases of homogeneity of plants. Moderately differences were observed between (p.c.v.) and (g.c.v.) in the F₃ generation, indicating the importance of the genetic effects in the inheritance of all studied traits.

Heritability estimate consider one of the most important parameters to selection response in early generations. From Table (4) results showed clearly that the broad sense heritability for the studied traits ranged from low 30.23 and 31.21 (no. of spikes/plant) for both populations to moderate 48.31 and 52.68 (grain yield/plant) for first and second population, respectively. Similar results were in line with those obtained by Dawood *et al.*, (1988), 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.

II -Analysis of variance and performance of pedigree selection cycles (F₄ and F₅ families):

The analysis of variance for no. of spikes / plant, biological yield , grain yield / plant and 1000-grain weight of the two populations are presented in Table (5). Results revealed significant or highly significant among families in both F₄ and F₅ generations for all studied traits, except no. of spikes/plant in F₄ generation in both populations, and also biological yield/plant and grain yield/plant in F₅

generation in population I, also no. of spikes/plant in

F₅ generation in population II.

Table 4: Analysis of variance, means, range, phenotypic and genotypic coefficients of variability and broad sense heritability for all studied traits of F₃ selected families (base population) in two populations of bread wheat under drought stress conditions in 2005 / 2006 seas

S.O.V	D.F	Population I				D.F	Population II			
		No. of spikes/plant	Biological yield	Grain yield/plant	1000-grain weight		No. of spikes/plant	Biological yield	Grain yield/plant	1000-grain weight
Replications	2	16.42**	1190.66**	122.45**	69.36**	2	9.71**	88.76*	0.48	9373.40**
Genotypes	99	1.36**	21.55**	7.13**	11.39**	98	2.53**	64.04**	11.86**	54.87**
Error	198	0.61	7.98	2.81	4.63	196	1.05	22.39	2.81	15.54
Mean ± S.E (F ₃ selected families)		5.52±0.45	16.06±1.57	6.45±0.78	27.96±1.23		6.24±0.60	23.54±2.76	6.12±0.97	40.98±2.32
Best parent		5.83	13.15	9.77	30.0		6.17	21.51	6.02	41.75
Bulk sample		4.67	12.37	5.53	28.5		5.5	19.26	4.61	43.18
Check variety (Sids1)		5.34	14.48	5.45	29.75		6.5	19.85	6.2	40.92
Range		4.0-7.17	11.08-23.97	2.7-11.4	22.5-32.0		4.34-8.67	12.03-38.64	2.24-13.04	21.5-50.88
P.C.V %		16.80 %	21.78 %	29.25 %	9.41%		20.08%	25.85%	39.96%	13.32%
G.C.V %		9.24 %	13.68%	20.33	5.49%		11.22%	15.99%	29.0%	9.01%
B.S.H %		30.23%	39.49%	48.31%	34.10%		31.21%	38.27%	52.68%	45.77%

Results presented in Table (5) showed that mean, range, phenotypic and genotypic coefficients of variability and broad sense heritability for all studied traits. From obtained results, no. of spikes/plant ranged from 4.19 to 5.80 spikes with an average 4.99 spikes/plant and from 4.74 to 6.52 spikes with an average 5.68 spikes/plant for first population in the F₄ and F₅ generations, respectively. For second population, no. of spikes/plant ranged from 4.09 to 6.33 spikes with an average 5.30 spikes/plant and from 5.59 to 8.64 spikes with an average 7.09 spikes/plant in the F₄ and F₅ generations, respectively. The least biological yield/plant was 23.29 to 45.45 gm. with an average 35.27 gm. and from 17.89 to 27.82 gm. with an average 21.43 gm. for population I in the F₄ and F₅ generations, respectively. Meanwhile, for population II, biological yield/plant ranged from 23.22 to 48.55 gm. with an average 36.07 gm. and ranged from 20.94 to 42.77 gm. with an average of 34.77 gm. in both F₄ and F₅ generations, respectively. For first population, the minimum of grain yield/plant was 9.44 and the maximum was 18.47 gm. with an average 14.17 gm. while, the minimum was 6.86 and the maximum was 9.31 gm. with an average 7.73 gm. in the F₄ and F₅ generations, respectively. For population II, grain yield/plant ranged from 4.96 to 16.89 gm. with an average 9.93 gm. and ranged from 7.30 to 15.19 gm. with an average 10.25 gm. in both F₄ and F₅ generations, respectively. The weight of 1000-grain ranged from 37.41 to 54.83 gm. with an average of 45.21 gm. and from 35.06 to 44.60 gm. with an average 39.97 in population I in the F₄ and F₅ generations, respectively. For second population the 1000-grain weight ranged from 37.0 to 61.38 gm. with an average of 46.29 gm. and from 28.72 to 46.6

gm. with an average of 37.18 gm. in both F₄ and F₅ 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). The values of phenotypic coefficient variability (p.c.v.) of no. of spikes / plant, biological yield, grain yield / plant and 1000-grain weight were (11.16 and 11.68 %), (22.62 and 17.54 %), (31.34 and 16.21%) and (10.64 and 8.60 %) in population I for both F₄ and F₅ generations, respectively. In addition, for population II, the values of phenotypic coefficients of variability (p.c.v.) for the same traits were (14.74 and 17.62 %), (19.45 and 21.70 %), (36.04 and 31.60 %) and (12.96 and 15.09 %) for both F₄ and F₅ generations, respectively. Also, the values of genetic coefficients of variability (g.c.v.) of the same traits were (3.47 and 5.28 %) , (6.97 and 7.96 %), (8.32 and 1.83 %) and (8.75 and 6.36 %) in first population for both F₄ and F₅ generations, respectively. In this regard, for the second population, the values of genotypic coefficients of variability for the same traits were (8.85 and 9.36 %), (10.39 and 14.34 %), (20.56 and 18.97 %) and (10.95 and 12.65 %) for both F₄ and F₅ generations, respectively.

The values of broad sense heritability (B.S.H.) of no. of spikes / plant, biological yield, grain yield / plant and 1000-grain weight Table (5), were (9.68 and 20.46%), (9.51 and 20.59 %), (7.05 and 1.27 %) and (67.59 and 54.70 %) in population I for both F₄ and F₅ generations, respectively. Meanwhile, for population II it was (36.07 and 28.21 %), (28.55 and 43.66 %), (32.55 and 36.03 %) and (71.36 and 70.28 %) of the same traits for the F₄ and F₅ 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 F4 and F5 generations 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			
			No. of spikes/plant	Biological yield (g.)	Grain yield/plant (g.)	1000-grain weight (g.)		No. of spikes/plant	Biological yield (g.)	Grain yield/plant (g.)	1000-grain weight (g.)
F4	Replications	2	0.29	1136.83**	111.11**	10.75	2	5.56	862.77**	63.73**	62.41**
	Families	65	0.34	102.98*	23.61*	52.62**	67	6.15	91.01**	23.71**	89.68**
	Error	130	0.27	66.33	19.96	7.28	134	5.19	35.59	8.74	10.0
F5	Replications	2	0.80	91.35**	6.91	4.97	2	10.10**	332.49**	3.69	6.28
	Families	18	0.63*	18.36	1.73	24.4**	18	2.10	113.13**	16.86**	64.71**
	Error	36	0.33	11.97	2.31	5.01	36	1.15	33.23	5.81	9.25
F4	Mean $\pm$ S.E (F ₄ selected families)		4.99 $\pm$ 0.3	35.27 $\pm$ 4.38	14.17 $\pm$ 2.65	45.21 $\pm$ 1.58		5.30 $\pm$ 0.36	36.07 $\pm$ 3.42	9.93 $\pm$ 1.70	46.29 $\pm$ 1.85
	Best parent		4.95	33.92	10.17	46.08		4.94	24.17	6.13	38.5
	Bulk sample		5.16	30.77	7.94	50.38		4.46	27.51	4.68	51.67
	Check variety (Sids1)		5.01	38.20	11.61	44.0		4.94	29.33	4.84	42.84
	Range		4.19 – 5.80	23.3-45.45	9.44-18.47	37.5-54.9		4.09-6.33	23.22-48.55	4.96-16.89	37.0-61.38
	P.C.V %		11.16%	22.62%	31.34%	10.64%		14.74%	19.45%	36.04%	12.96%
	G.C.V %		3.47%	6.97%	8.32%	8.75%		8.85%	10.39%	20.56%	10.95%
	B.S.H %		9.68%	9.51%	7.05%	67.59%		36.07%	28.55%	32.55%	71.36%
F5	Mean $\pm$ S.E (F ₅ selected families)		5.68 $\pm$ 0.35	21.43 $\pm$ 1.93	7.73 $\pm$ 0.72	39.97 $\pm$ 1.33		7.09 $\pm$ 0.61	34.77 $\pm$ 3.27	10.25 $\pm$ 1.50	37.18 $\pm$ 1.77
	Best parent		5.52	23.51	7.93	38.04		6.62	26.38	10.95	40.13
	Bulk sample		6.49	24.84	6.74	39.44		7.01	34.44	8.27	35.54
	Check variety (Sids1)		5.61	20.01	8.53	36.88		7.52	28.24	7.35	33.24
	Range		4.74-6.52	17.9-27.82	6.86-9.31	35.06-44.6		5.59-8.64	20.9-42.8	7.3-15.19	28.7- 46.6
	P.C.V %		11.68%	17.54%	16.21%	8.60%		17.62%	21.70%	31.60%	15.09%
	G.C.V %		5.28%	7.96%	1.83%	6.36%		9.36%	14.34%	18.97%	12.65%
	B.S.H %		20.46%	20.59%	1.27%	54.70%		28.21%	43.66%	36.03%	70.28%

III- Realized gains to pedigree selection:

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 (6). In first population, the results indicated that selection after two cycles of pedigree selection led to a desirable increase in 1000-grain weight by (5.07, 1.34 and 8.38 %) from the best parent, bulk sample and check variety ,respectively. Meanwhile, in the second population, realized response to selection was obtained for grain yield/plant by (31.80, 0.96 and 23.12 %) from the best parent ,bulk sample and check variety, respectively. In this present study, realized response to selection was found for 1000-grain weight in first population and grain yield/plant in the second population, 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.

Means of the selected families after two cycles of pedigree selection of no. of spikes / plant, biological yield, grain yield / plant and 1000-grain weight for both populations are presented in Table (7). In the first population after two cycles, the pedigree selection resulted one superior family no. 16 which exceeded the best parent ,bulk sample and check variety by (18.12, 0.46 and 16.22 %) , (9.10, 3.26 and 28.19 %), (10.47, 29.97 and 2.70 %) and (11.88, 7.91 and 15.40 %), for the previous studied traits, respectively. Regarding, in the second population, the results Table (7) revealed three families no. 21, 26 and 41 were attained the superiority for the studied traits. Concerning family no. 21 was exceeded by (30.51, 23.25 and 14.89%), (62.13, 24.19 and 51.45 %), (14.43, 51.51 and 70.48 %) and (2.12, 15.31 and 23.29%) for no. of spikes / plant, biological yield, grain yield / plant and 1000-grain weight, respectively. Meanwhile, families no. 26 and 41 were exceeded by (37.34, 5.20 and 28.29 %) and (48.98, 14.40 and 39.16%), (38.72, 83.68 and

106.67 %) and (11.60, 47.76 and 66.26 %) and (12.46, 26.98 and 35.77 %) and (0.25, 13.20 and 21.03%) for biological yield, grain yield / plant and 1000-grain weight, respectively. These results concluded that applying of pedigree selection to

improve **yield** and its component traits after two cycles were effective to isolate high yielding genotypes in both populations under drought stress condition. Similar results were in line with obtained by Ali (2011) and El-Sayed, (2012).

Table 6: 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			
		No. of spikes/plant	Biological yield	Grain yield/plant	1000-grain weight	No. of spikes/plant	Grain yield/plant	Biological yield	1000-grain weight
C1	Best parent	0.81	3.98	39.33	-1.89	7.29	49.23	61.99	20.23
	Bulk sample	-3.29	14.62	78.46	-10.26	18.83	31.12	112.18	-10.41
	Check variety (Sids1)	-0.40	-7.67	22.05	2.75	7.29	22.98	105.17	8.05
C2	Best parent	2.90	-8.85	-2.52	5.07	7.10	31.80	-6.39	-7.35
	Bulk sample	-12.48	-13.73	14.69	1.34	1.14	0.96	23.94	4.61
	Check variety (Sids1)	1.25	7.10	-9.38	8.38	-5.72	23.12	39.46	11.85

Table 7: 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			
	No. of spikes/plant	Biological yield (g.)	Grain yield/plant (g.)	1000 - grain weight (g.)		No. of spikes/plant	Biological yield (g.)	Grain yield/plant (g.)	1000-grain weight (g.)
Best parent	5.52	23.51	7.93	38.04	Best parent	6.62	26.38	10.95	40.13
Bulk Sample	6.49	24.84	6.74	39.44	Bulk Sample	7.01	34.44	8.27	35.54
Check variety (Sids 1)	5.61	20.01	8.53	36.88	Check variety (Sids 1)	7.52	28.24	7.35	33.24
8	5.25	17.89	7.30	41.48	10	7.11	20.94	7.93	46.60
14	5.72	19.29	6.86	40.34	12	6.96	31.06	10.23	36.28
16	6.52	25.65	8.76	42.56	15	7.32	30.29	12.52	34.70
17	5.95	21.43	8.08	39.84	19	6.00	40.48	7.56	36.53
18	5.68	20.40	8.60	43.96	21	8.64	42.77	12.53	40.98
20	5.42	20.19	7.69	35.06	22	6.74	39.15	8.47	28.72
21	5.88	20.27	7.97	39.91	25	5.82	41.64	7.30	35.32
23	5.32	21.46	9.31	43.29	26	7.45	36.23	15.19	45.13
24	5.87	21.21	7.07	38.81	34	7.60	36.18	8.20	33.38
29	6.50	27.82	7.12	39.37	36	7.15	25.99	7.63	32.01
30	5.86	24.28	7.43	35.61	41	7.21	39.30	12.22	40.23
39	5.61	21.18	6.89	39.87	45	5.59	34.81	12.21	36.47
40	4.74	19.9	8.16	37.41	49	8.42	32.12	12.45	36.40
41	5.41	20.2	7.51	37.43	51	8.06	34.29	10.25	32.35
47	5.54	20.28	7.17	44.60	57	6.35	35.56	9.12	42.65
Average	5.68	21.43	7.73	39.97	Average	7.09	34.77	10.25	37.18
LSD 0.05	0.95	5.73	2.52	3.71	LSD 0.05	1.78	9.55	3.99	5.04
0.01	1.28	7.68	3.38	4.97	0.01	2.39	12.80	5.35	6.75

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