

## **SELECTION FOR GRAIN YIELD IN BREAD WHEAT UNDER NORMAL IRRIGATION AND DROUGHT STRESS CONDITIONS.**

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### **ABSTRACT**

To improve grain yield/plant, two cycles of pedigree selection were achieved in a segregating population of wheat (*Triticum aestivum* L.) in the  $F_4$ ,  $F_5$  and  $F_6$  generations under normal and drought stressed environments. Significant differences ( $p < 0.01$ ) among the selected families for the selection criterion; grain yield/plant were observed in all the studied traits under the two environments in  $F_4$  and  $F_6$ -generations. After two cycles of pedigree selection for grain yield/plant the values of gcv and pcv were decreased from  $F_4$  to  $F_6$ -generation in all traits under both environments and were very close to each other, resulted in very high estimates of heritability in broad sense which calculated from the expected mean squares. The average direct gain in grain yield/plant was 90.20, 70.14 and 37.64, 52.46% from the bulk sample and the better parent under normal irrigation and drought stress; respectively. Under irrigation, the best five families, No.127, No.146, No.273, No.377 and No.452 outyielded the better parent Giza 168 by 38.87, 46.57, 42.63, 56.75 and 64.96%; respectively. The family No.452 was like Giza 186 in earliness. Under drought stress, selection for grain yield/plant delayed maturity by 8.59% from the better parent, but, not from the bulk sample. The best families in grain yield; No.202, No.296, No.379, No.389, No.395 and No.397 showed significant delay in maturity than the earlier parent. The best two families No. 92 and No.306 were early as the earlier parent Sisd4 and showed significant ( $p < 0.01$ ) grain yield/plant from the better parent Giza 168 of 26.46 and 59.72%; respectively. In the  $F_6$ -generation under both environments all the traits which showed positive genotypic correlation with grain yield, days to heading, plant height, biological yield/plant and number of spikes/plant showed negative correlations with grain weight/spike, number of grains/spike, and 100-grain weight.

### **INTRODUCTION**

Wheat (*Triticum aestivum* L.) is the strategic cereal crop not only in Egypt, but also all over the world. In Egypt, wheat consumption 17.7 M tons, production about 8.7 M tons and wheat imports about 8.5 M tons (USDA 2014). Increasing wheat production both vertically and horizontally is an important target to meet the gap between production and consumption. These targets could be realized through expanding the wheat cultivated area partially in new reclaimed lands using drought tolerant wheat cultivars in the North Sea coast. Pedigree selection method has become the most popular plant breeding procedure. Most of the Egyptian wheat cultivars were produced through this method. It is preferred by plant breeders because it is versatile, relatively rapid and makes possible conducting of genetic studies

along with the plant breeding work (Mahdy, 2012c). Pedigree selection for grain yield/plant needs to evaluate selections under different environments such as different planting dates and different water stress (Zakaria, 2008; Ali, 2011a and b; Ali and Abo-El-Wafa, 2006; Golabadi *et al.*, 2006 and El-Morshidy *et al.*, 2010). Many workers indicated that pedigree selection was effective in improving grain yield (Eissa, 1996; Ismail *et al.*, 1996; Ismail, 2001; Ahmed, 2006 and Mahdy, 2012b). Abd El-Kader (2011) found that the genotypic coefficient of variability decreased rapidly after two cycles of selection for grain yield/plant from 28.60 to 3.80% in the F<sub>3</sub> and F<sub>5</sub>-generations; respectively. Abdel El-Kareem and El-Saidy (2011) found high estimates of pcv, gcv and broad sense heritability under irrigation and drought stress. Abd El-Shafi (2014) suggested that the directional selection appears to reduce the range and variability in grain yield/plant after selection in the F<sub>4</sub>, and reported high values of broad sense heritability for the two crosses in the F<sub>4</sub> generation. Mahdy *et al.* (2012a) after two cycles of selection for grain yield/plant, found that average grain yield/plant of ten selected families from two populations was significant (P<0.01) outyielded both of the higher yielding parent and the bulk sample. Ali (2011a and b) increased grain yield/plant by 25.00 and 25.54% over the bulk samples for normal and drought stressed environments; respectively after two cycles of pedigree selection. The increase in grain yield/plant was accompanied by late in heading date under both environments. Nouri-Ganbalani *et al.* (2009) estimated the average yield loss of 17 to 70% in grain yield due to drought stress. They observed no significant correlation between grain yield and other morphological characters under normal irrigation, but under the drought stress conditions there were positive highly significant correlations between the grain yield and 1000-grain weight and number of tillers per plant. However, the effect of selection for grain yield/plant on weight and number of grains increased in the negative direction. Ferdous *et al.* (2010) found significant positive correlation between harvest index and grain yield/plant. Otherwise, the genotypic correlation between grain yield/plant and weight and number of grains changed by selection from positive to negative selection. The objectives of this study was aimed to estimate the efficiency of pedigree selection for grain yield in a segregating population (Giza 168 × Sids 4) (*Triticum aestivum* L.) under normal irrigation and drought stressed environments.

## **MATERIALS AND METHODS**

This investigation was carried out during the period of 2011/2012 – 2013/2014 at Fac. Agric. Edu. Farm, Minia University, Egypt. The basic materials consisted of 240 families in the F<sub>4</sub>-generation derived from the segregating population (Giza 168 × Sids 4). The families were planted in two separated experiments under normal irrigation and drought conditions. The recommended cultural practices for wheat production were adopted throughout the growing seasons except irrigation which was applied as follows:

- 1- First experiment (normal irrigation); the experiment was irrigated six times.
- 2- Second experiment (drought); the experiment was irrigated only two times (planting irrigation and another one three weeks later).

**Table1. The pedigree of the parents of the wheat population**

Parental cultivars	Pedigree
Giza 168	MIL/Buc//Seri CM93046-8M-04-0M-2Y-0B
Sids 4	Maya ( S )/Man ( S )//CMH 74A-592/3/Giza 157*2

**In 2011/2012 season:** The 240 F<sub>4</sub>-families were grown in Nov 28<sup>th</sup> in two separated experiments (irrigation and drought conditions) along with the two parents and the unselected bulk sample. The bulk sample consisted of a mixture of equal number of grains from each family. A randomized complete block design of three replications was used. The plot size was one row, 1.5m long, 30cm apart and 5cm between grains within the row. At the end of the season, the highest 20 yielding plants from the highest 20 families were saved.

**In 2012/2013 season:** The 20 selected plants (F<sub>5</sub>-generation) along with the two parents and bulk sample were sown on Nov.14<sup>th</sup> in two separate experiments. The experimental design and plot size were as in the previous season except for the distance between plants in a row was 10 cm. The 10 best plants in grain yield from each of the best 10 families were saved.

**In 2013/2014 season:** The 10 selected families (F<sub>6</sub>-generation) were evaluated and sown on Nov.20<sup>th</sup> in two separate experiments as in the previous season. In the F<sub>4</sub>, F<sub>5</sub> and F<sub>6</sub>-generations data were recorded on ten guarded plants from each plot; and the mean of the ten plants was calculated. The studied traits were as follows: days to heading [DH], plant height [PH] in cm, spike length [SL] in cm, number of spikes/plant (NS/P), number of grains/spike (NG/S), weight of grains/spike in g (WG/S), 100-grain weight [100-GW] in g, biological yield/plant [BY/P] in g, grain yield/plant [GY/P] in g, and harvest index% [HI].

Results were subjected to proper statistical analysis of RCBD according to Steel and Torrie (1980) on plot mean basis.

**Table 2. The form of analysis of variance, covariance and their expectations.**

S. O. V.	d.f	M. S.	E. M. S.	
			Variance	Covariance
Replications	r-1	M <sub>3</sub>	$\sigma^2_e + g \sigma^2_r$	
Genotypes	g-1	M <sub>2</sub>	$\sigma^2_e + r \sigma^2_g$	cov.e + r cov.g
Error	(r-1) (g-1)	M <sub>1</sub>	$\sigma^2_e$	cov.e

where: r and g are number of replications and genotypes; respectively,  $\sigma^2_e$  and cov.e are error variance and covariance; respectively, and  $\sigma^2_g$  and cov.g are genetic variance and genetic covariance; respectively. Two analyses of variance were done. The first, was for all entries (selected families + parents + bulk sample), and the second one was for the selected families to calculate heritability, genotypic and phenotypic coefficients of variations.

The phenotypic ( $\sigma^2_p$ ) and genotypic ( $\sigma^2_g$ ) variances were calculated according to the following formula:

$$\sigma^2_g = (M_2 - M_1) / r. \quad \sigma^2_p = \sigma^2_g + \sigma^2_e / r.$$

Heritability in broad sense (H) =  $\sigma^2 g / \sigma^2 p$  according to Walker (1960).

Realized heritability ( $h^2$ ) was calculated as:  $h^2 = R / S$  (Falconer, 1989).

where R = response to selection and S = selection differential.

The phenotypic (pcv %) and genotypic (gcv %) coefficients of variability were calculated as outlined by Burton (1952), as follows:

$$\text{pcv \%} = \sigma p / \bar{x} \cdot 100. \quad \text{gcv \%} = \sigma g / \bar{x} \cdot 100.$$

where:  $\sigma p$  and  $\sigma g$  are the phenotypic and genotypic standard deviation of the families mean; respectively, and  $\bar{x}$  is families mean for a given trait.

The calculation of the phenotypic covariance (cov.p<sub>12</sub>), and genotypic covariance (cov.g<sub>12</sub>) between pairs of traits (1 and 2) followed the same form as variance analysis.

Genotypic correlation coefficient ( $rg_{xy}$ ) was calculated as outlined by Walker (1960), as follows:  $rg_{xy} = \text{cov}g_{xy} / (\sigma g_x \cdot \sigma g_y)$ .

Mean comparisons were calculated by using revised L.S.D where, L.S.D = least significant difference, at 0.05 and 0.01 level of probability, according to El-Rawi and Khalafala (1980) and was calculated as:

**RLSD Family** =  $t^1 \cdot (2\text{MSE}/r)^{1/2}$  to compare families with the better parent and the bulk sample.

**RLSD Average** =  $t^1 \cdot (\text{MSE}/r + \text{MSE}/rf)^{1/2}$  to compare average with the better parent and the bulk sample.

The significance of observed direct and correlated response to selection was measured as deviation percentage of families mean from the bulk or the better parent using L.S.D. where, L.S.D = least significant difference between mean of the selected families and the bulk or the better parent, and was calculated as:

**LSD Family** =  $t \cdot (2\text{MSE}/r)^{1/2}$  to compare families with the better parent and

**LSD Average** =  $t \cdot (\text{MSE}/r + \text{MSE}/rf)^{1/2}$  to compare average with the better parent and the bulk sample.

$$\text{LSD \%} = (\text{LSD value} / \text{the bulk or the better parent}) \cdot 100$$

Where f: number of families, r: number of replicates and  $t^1$  is the t value from "minimum-average-risk t-table" at F-value of treatments, treatment d.f. and experimental error d.f.

## RESULTS AND DISCUSSION

### 1- Description of the base population, season 2011/2012:

Mean squares of all the studied traits in F<sub>4</sub>-generation (Tables 3 and 4) were significant ( $p < 0.01$ ) under two environments indicating the presence of variability in the criteria of selection. Similar results were observed by El-Morshidy *et al.* (2010), Mahdy *et al.* (2012b).

The F<sub>4</sub>-family mean of grain yield / plant ranged from 10.42 to 30.68 with an average of 19.82 g., and from 8.01 to 30.03 with an average of 14.59 g. for irrigated and drought stressed environments; respectively. Mean grain yield/plant significant ( $p < 0.01$ ) outyielded both of the parents and the unselected bulk sample reflecting non-additive effects of heterozygosity and/or transgressive segregation under both environments. The reduction in grain yield/plant caused by drought stress was 26.39%.

**Table 3. Mean squares of the studied traits for the 240 families in F<sub>4</sub>- generation under normal irrigation, family mean, the parents and the bulk sample, phenotypic(pcv) and genotypic (gcv) coefficients of variability, expected genetic advance ( $\Delta G$ ) and heritability in broad sense (H).**

Items	d.f	DH	PH	SL	NS/P	100-GW	NG/S	WG/S	BY/P	GY/P	HI%
MS Rep	2	2.00	12.42	0.14	2.93	0.70	6.63	2.51	36.93	9.62	8.65
MS Entries	242	102.2**	191.93**	7.15**	2.98**	0.32**	428.71**	1.56**	202.41**	37.64**	49.01**
MS Error	484	1.43	4.93	0.44	0.81	0.24	10.34	0.25	6.76	1.53	6.99
Mean $\pm$ SE		87.30 $\pm$ 0.37	92.07 $\pm$ 0.51	13.75 $\pm$ 0.10	6.67 $\pm$ 0.05	5.50 $\pm$ 0.01	67.92 $\pm$ 0.76	3.77 $\pm$ 0.04	51.13 $\pm$ 0.52	19.82 $\pm$ 0.22	38.91 $\pm$ 0.24
Min		52.67	73.67	10.00	4.48	4.64	44.55	2.47	29.21	10.42	25.78
Max		109.00	117.33	18.00	11.36	6.96	113.74	6.66	74.47	30.68	48.73
g.c.v%		6.42	8.58	10.88	12.30	3.12	17.42	17.56	15.58	17.28	9.69
p.c.v%		6.47	8.69	11.23	14.59	6.03	17.64	19.17	15.85	17.65	10.43
H%		98.49	97.46	93.84	71.05	26.78	97.60	83.91	96.58	95.85	86.17
$\Delta G$		10.23	14.35	2.67	1.27	0.16	21.52	1.12	14.40	6.17	6.44
$\Delta G$ /mean%		11.72	15.59	19.39	19.08	2.97	31.68	29.61	28.17	31.14	16.55
Giza 168		86.00	94.00	15.11	5.06	5.38	59.34	2.97	37.44	13.08	35.25
Sids 4		65.00	79.78	16.00	3.80	5.71	70.75	4.03	35.54	14.03	39.49
Bulk		75.67	86.83	12.92	4.71	5.17	53.57	2.91	36.59	14.07	38.55
RLSD Aver0.05		1.19	2.26	0.70	1.10	0.76	3.20	0.55	2.65	1.26	2.89
RLSD Aver0.01		1.56	2.97	0.92	1.37	1.54	4.19	0.72	3.47	1.65	3.81

\*,\*\* significant at 0.05 and 0.01 levels of probability; respectively.

$\Delta G$  = expected genetic advance from selection the superior 8.33% of the families.

RLSD. Aver. = to compare families mean with the bulk sample or the better parent.

The pcv and gcv estimates were high and reached 17.65 and 17.28% under irrigation and 25.68 and 25.38% under stress environments; respectively. The close estimates of phenotypic and genotypic variability resulted in very high estimates of heritability under irrigation (95.85%) and drought stress (97.61%). Similar results were found by Abdel El-Kareem and El-Saidy (2011). The high estimates of genetic variability coupled with high heritability gave unreliable estimates of expected genetic advance under irrigation (31.14%) and under drought stress (46.14%). Similar results were found by El-Morshidy *et al.* (2010).

#### **Genotypic correlation.**

In the base population (F<sub>4</sub>) grain yield/plant showed weak genotypic correlation with DH (0.02) and negative correlation with the other traits ranged from -0.12 (PH) to -0.81(BY) (Table 5) under normal irrigation. Otherwise, under drought stress it showed weak negative correlation with DH (-0.09) and positive with the other traits ranged from 0.24 (PH) to 0.87 for BY/P indicating different gene associations among traits under both environments. The results are in agreement with Abdel El-Kareem and El-Saidy (2011).



Table 5. Genotypic correlation under irrigation (above diagonal) and drought (below diagonal) among traits in the F<sub>4</sub>-generation.

Trait	DH	PH	SL	NS/P	100GW	NG	WG/S	BY/P	GY/P	HI
DH	-	-0.22	0.14	0.00	0.08	0.18	0.09	-0.01	0.02	0.06
PH	0.00	-	0.04	-0.21	0.06	0.05	0.07	-0.20	-0.12	0.09
SL	-0.06	0.11	-	0.07	-0.32	-0.63	-0.40	-0.37	-0.26	0.10
NS/P	0.03	0.27	0.20	-	-0.11	0.19	0.17	-0.49	-0.57	-0.21
100GW	-0.34	0.30	0.16	0.13	-	-0.23	-0.34	-0.19	-0.17	-0.01
NG	-0.05	0.06	0.66	0.30	-0.03	-	-0.70	-0.26	-0.26	-0.01
WG/S	-0.11	0.12	0.43	0.12	0.41	0.55	-	-0.22	-0.24	-0.01
BY/P	-0.04	0.26	0.37	0.77	0.09	0.44	0.33	-	-0.81	0.14
GY/P	-0.09	0.24	0.39	0.84	0.25	0.48	0.37	0.87	-	-0.44
HI	-0.12	-0.04	0.06	0.18	0.36	0.12	0.12	-0.20	0.29	-

2- Pedigree selection for grain yield/plant.

Variability and heritability estimates.

Mean squares (Table 6) of the selected families for grain yield/plant and correlated traits was significant ( $p < 0.01$ ) under both environments after two cycles of pedigree selection. Similar results are obtained by Mahdy *et al.* (2012a).

Table 6. Mean squares, heritability estimates, genotypic (g.c.v%) and phenotypic (p.c.v%) coefficients of variability of selected families for grain yield/plant under normal and stress conditions in F<sub>6</sub>-generation.

Enviro	S. V.	d.f.	Selection criterion	Correlated traits									
				GY /P; g	DH	PH; cm	SL; cm	NS /P	100GW; g	NG/S	WG /S; g	BY /P; g	HI%
Irrigation	Reps	2	0.07	1.29	1.45	2.58	0.94	0.08	2.25	0.25	8.77	1.91	
	Entries	12	143.68**	270.94**	387.92**	9.65**	11.18**	0.91**	274.5**	1.47**	495.05**	69.15**	
	Error	24	1.89	1.37	9.49	0.42	0.23	0.10	7.76	0.10	6.50	2.12	
	g.c.v %		12.01	10.15	12.66	13.06	19.68	9.93	12.39	15.97	12.12	5.36	
	p.c.v %		12.29	10.18	12.81	13.34	19.99	10.51	12.54	16.57	12.25	5.79	
	H%		95.63	99.31	97.59	95.94	96.93	89.32	97.53	92.87	97.90	85.88	
	h <sup>2</sup>	C1		89.15									
		C2		94.29									
Drought	S. V.	d.f.	GY /P; g	DH	PH; cm	SL; cm	NS /P	100 GW; g	NG /S	WG /S; g	BY /P; g	HI%	
	Reps	2	1.47	6.42	3.76	0.73	0.18	0.01	8.14	0.08	1.31	3.29	
	Entries	12	100.89**	193.22**	367.79**	5.62**	13.99**	1.41**	872.69**	2.93**	362.27**	53.73**	
	Error	24	1.57	0.86	7.81	0.69	0.28	0.07	7.52	0.30	7.60	3.63	
	g.c.v %		16.76	9.94	12.81	8.79	33.52	11.57	23.45	20.64	12.56	6.71	
	p.c.v %		17.05	9.96	12.96	9.39	33.78	11.86	23.54	22.24	12.84	7.31	
	H%		96.60	99.44	97.69	87.64	98.43	95.20	99.27	86.12	95.73	84.24	
	h <sup>2</sup>	C1		57.96									
C2			79.06										

After two cycles of pedigree selection for grain yield / plant the gcv and pcv were 12.01 and 12.27 compared to 17.28 and 17.65% in the F<sub>4</sub>-generation under irrigation, and 16.76 and 17.05 compared to 25.38 and 25.68% in the F<sub>4</sub>-generation under drought stress; respectively. It could be

noticed that the retained genetic variability after two cycles of selection was sufficient for further cycles of selection. In addition, the variability under drought was larger than that under normal irrigation. Abd El-Kader (2011) found that gcv decreased rapidly after two cycles of selection for grain yield/plant from 28.60 to 3.80%.

**Table 7. Mean of the studied traits of the selected families for grain yield after two cycles of selection under normal irrigation.**

Fam. No.	DH	PH; cm	SL; cm	NS/P	100 GW; g	NG/S	WG/S; g	BY/P; g	GY/P; g	HI%
33	76.67	77.17	14.50	6.40	5.63	98.29	4.95	67.42	25.26	37.47
66	74.00	87.00	16.50	5.98	6.82	92.75	6.01	83.23	28.32	34.04
127	90.33	111.00	14.00	8.95	5.93	78.91	4.61	88.21	32.32	36.63
146	92.67	86.67	13.17	6.52	5.60	68.74	3.82	99.50	34.11	34.27
273	82.67	97.50	17.33	7.48	5.97	78.08	4.29	86.07	33.19	38.56
372	94.67	112.33	11.83	8.96	4.67	68.50	3.22	85.78	31.55	36.77
377	83.67	85.50	15.67	9.89	5.95	78.66	4.48	101.39	36.48	35.99
389	79.00	85.17	13.55	8.65	4.97	89.98	4.47	88.25	28.36	32.18
432	96.00	98.00	16.50	6.81	5.82	94.40	5.25	83.27	32.34	38.82
452	99.33	105.67	12.00	10.62	5.34	84.82	4.69	104.79	38.39	36.67
Average	86.90	94.60	14.51	8.02	5.67	83.31	4.58	88.79	32.03	36.14
bulk	83.89	95.12	13.70	4.81	5.38	76.20	4.26	72.74	16.84	23.19
Sids4	72.00	82.59	16.31	4.18	5.94	87.11	4.96	60.72	16.24	26.70
Giza168	99.17	103.84	15.69	6.65	5.11	75.60	3.89	79.23	23.27	29.38
R.L.S.D0.05 Fam	1.71	4.50	0.98	0.69	0.50	4.07	0.48	3.73	2.01	2.13
R.L.S.D0.01 Fam	2.27	5.99	1.30	0.92	0.67	5.41	0.64	4.96	2.67	2.83
R.L.S.D0.05 Aver	1.27	3.34	0.72	0.51	0.37	3.02	0.36	2.76	1.49	1.58
R.L.S.D0.01 Aver	1.68	4.44	0.96	0.68	0.50	4.01	0.48	3.68	1.98	2.10

R.L.S.D (Fam.), to compare families with the better parent and the bulk sample.

R.L.S.D (Aver.), to compare average with the better parent and the bulk sample.

Respect to the pcv and gcv in the correlated traits, harvest index showed low variability under both environments. The variability was moderate for the 100-grain weight under normal irrigation, and days to heading and spike length under drought stress. The other traits showed high genetic variability under both environments. The pcv and gcv in all traits under both environments were very close to each other, resulted in very high estimates of heritability in broad sense which calculated from the expected mean squares. These high estimates of heritability could be attributed to two main causes. First; the evaluation of the selected families at one site for one year inflated the families mean squares by the confound effects of the interactions of families with locations and years in families mean squares. In consequence; large estimates of genotypic variance were obtained. Second; the small error variance (Table 6) caused the phenotypic variance to be very close to genotypic one. The realized heritability estimates were 94.29 and 89.15% under normal irrigation and 79.06 and 57.96% under drought stress in the second compared to the first cycle; respectively.

**Means and direct observed gain for grain yield/plant.**

Mean grain yield/plant after two cycles of selection ranged from 25.26 to 38.39 with an average of 32.03g under normal irrigation, and from 15.76 to 30.63 with an average of 24.12g under drought stress environment (Tables 7 and 10). All the ten selected families under normal irrigation and nine under



drought stress and their average were significant ( $p < 0.01$ ) out yielded the bulk sample and both parents. Mahdy *et al.* (2012a) found similar results.

**Observed direct and correlated responses to pedigree selection for grain yield after two cycle of selection ( $F_6$ ) in percentage bulk sample under normal irrigation conditions; season 2013/2014.**

	Selection criterion	Correlated traits								
	GY/ P; g	DH	PH; cm	SL; cm	NS/ P	100 GW; g	NG/S	WG/ S; g	BY/ P; g	
	49.99**	-8.61**	-18.88**	5.81	33.09**	4.52	28.99**	16.20*	-7.32*	
	68.15**	-11.79**	-8.54**	20.41**	24.36**	26.63**	21.72**	41.11**	14.42**	
	91.90**	7.68**	16.69**	2.16	86.13**	10.22*	3.56	8.38	21.27**	
	102.54**	10.46**	-8.89**	-3.92	35.56**	4.02	-9.79**	-10.34	36.79**	
	97.09**	-1.46	2.5	26.49**	55.68**	10.96*	2.48	0.7	18.33**	
	87.34**	12.85**	18.09**	-13.65**	86.28**	-13.31*	-10.10**	-24.43**	17.94**	
	116.61**	-0.26	-10.12**	14.32**	105.61**	10.59*	3.23	5.17	39.39**	
	68.40**	-5.83**	-10.47**	-1.12	79.84**	-7.74	18.09**	5.09	21.33**	
	92.02**	14.44**	3.03	20.41**	41.68**	8.11	23.89**	23.26**	14.48**	
	127.95**	18.41**	11.09**	-12.43**	120.88**	-0.8	11.31**	10.26	44.07**	
	90.20**	3.59**	-0.55	5.85	66.91**	5.32	9.34**	7.56	22.07**	
am%	13.78	2.35	5.46	8.03	16.64	10.03	6.15	12.22	5.91	
am %	18.65	3.18	7.40	10.87	22.46	13.75	8.35	16.68	8.00	
ver %	10.21	1.74	4.05	5.91	12.27	7.43	4.57	9.16	4.39	
ver %	13.84	2.36	5.49	8.03	16.64	10.22	6.19	12.22	5.94	

n.), to compare families with the better parent and the bulk sample.

er.), to compare average with the better parent and the bulk sample.

ificant at 0.05 and 0.01 level of probability; respectively.

The average direct gain in grain yield/plant after two cycles of selection under normal irrigation was 90.20 and 37.64%, and 70.41 and 52.46% under drought stress from the bulk sample and the better parent; respectively. Ali (2011a) by pedigree selection for the two cycles noted increase in grain yield/plant of 25.00 and 25.54% from the bulk samples under normal and drought stress conditions; respectively.

**The correlated gains under normal irrigation.**

The average correlated gains (Tables 8 and 9) were significant ( $p < 0.01$ ) from the bulk sample for days to heading (3.59%), biological yield/plant (22.07%), harvest index (55.86%), number of spikes/plant (66.91%) and number of grains/spike (9.34%). Likewise, significant ( $p < 0.01$ ) average correlated gain in biological yield/plant, harvest index, number of spikes/plant of 12.07, 23.01 and 20.67% from the better parent were obtained. Otherwise, adverse effects measured from the better parent were significant ( $p < 0.01$ ) for days to heading (20.69%), spike length (-11.07%), grain weight/spike (-7.69%), number of grains/spike (-4.36%) and 100-grain weight (-4.55%). It could be observed that all the selected families were significant delayed in days to heading respect the earlier parent Sids4. These results are in line with Ali (2011a and b). It could be concluded that two cycles of selection for grain yield/plant succeeded to isolate higher yielding families over the better parent Giza 168, but, it failed to isolate high yielding families earlier than or similar the earlier parent Sids4. However, family No. 452 outyielded the better parent Giza 168 by 64.96% and like it in earliness. Also, families No. 377, No. 146, No. 273 and No. 127 outyielded the better parent

by 56.75, 46.57, 42.63 and 38.87%; respectively, and significantly earlier than Giza 168 and later than Sids4. All the above families their grain yield/plant depended on number of spikes/plant. One family No. 66 outyielded the better parent Giza 168 by 21.68%, and its yield depended in its superiority in number of grains/spike, grain weight/spike and 100-grain weight. In other words, this family has long spike of many heavy grains as Sids4. Therefore, multiple trait selection using selection index could be recommended to overcome the drawbacks of single trait selection.

**Table 9. Observed direct and correlated responses to pedigree selection for grain yield after two cycle of selection (F<sub>6</sub>) in percentage of the better-parent under normal irrigation conditions; season 2013/2014.**

Fam. No.	Selection criterion	Correlated traits									
	GY/P; g	DH	PH; cm	SL; cm	NS/P	100GW; g	NG/S	WG/S; g	BY/P; g	HI%	
33	8.54	6.48**	-25.66**	-11.10**	-3.79	-5.27	12.83**	-0.2	-14.91**	27.55**	
66	21.68**	2.78*	-16.22**	1.16	-10.1	14.76**	6.47*	21.10**	5.04	15.86**	
127	38.87**	25.46**	-6.9*	-14.16**	34.56**	-0.11	-9.41**	-6.99	11.33**	24.69**	
146	46.57**	28.70**	-16.54**	-19.27**	-1.99	-5.72	-21.09**	-23.05**	25.58**	16.64**	
273	42.63**	14.81**	-6.1	6.27	12.55*	0.56	-10.36**	-13.58*	8.63**	31.24**	
372	35.57**	31.48**	8.18*	-27.45**	34.67**	-21.44**	-21.36**	-35.15**	8.27**	25.14**	
377	56.75**	16.20**	-17.66**	-3.94	48.65**	0.22	-9.70**	-9.74	27.96**	22.49**	
389	21.87**	9.72**	-17.98**	-16.92**	30.01**	-16.39**	3.3	-9.81	11.38**	9.52*	
432	38.96**	33.33**	-5.62	1.16	2.42	-2.02	8.37**	5.78	5.1	32.14**	
452	64.96**	37.96**	1.76	-26.43**	59.68**	-10.10*	-2.63	-5.38	32.26**	24.80**	
Average	37.64**	20.69**	-8.9**	-11.07**	20.67**	-4.55**	-4.36**	-7.69**	12.07**	23.01**	
L.S.D0.05 Fam%	9.97	2.74	6.28	6.74	12.03	9.09	5.38	10.48	5.43	8.34	
L.S.D0.01 Fam %	13.49	3.71	8.52	9.14	16.24	12.46	7.30	14.31	7.35	11.30	
L.S.D0.05 Aver %	7.39	2.03	4.66	4.97	8.87	6.73	3.99	7.86	4.03	6.19	
L.S.D0.01 Aver %	10.01	2.75	6.32	6.74	12.03	9.26	5.42	10.48	5.45	8.37	

L.S.D (Fam.), to compare families with the better parent and the bulk sample.

L.S.D (Aver.), to compare average with the better parent and the bulk sample.

\*, \*\*, significant at 0.05 and 0.01 level of probability; respectively.

#### The correlated gain under drought stress.

The average correlated gain (Tables 11 and 12) as measured from the bulk sample was significant ( $p < 0.01$ ) for spike length (11.58%), biological yield/plant (30.42%), harvest index (29.99%), number of spikes/plant (59.70%), grain weight/spike (36.63%), number of grains/spike (23.49%) and 100-grain weight (14.87%). The average correlated gains as measured from the better parent were positive and significant, and ranged from 8.59 for days to heading to 25.85% for grain weight/spike. It could be noticed that selection for grain yield/plant delayed maturity by 8.59% from the better parent, but, not from the bulk sample. The only family; No. 74 which showed significant ( $p < 0.01$ ) negative (earlier) days to heading from the earlier parent Sids4 was lower in grain yield/plant, biological yield/plant and number of spikes/plant. The best families in grain yield; No. 202, No.296, No. 379, No. 389, No. 395 and No. 397 showed significant delay in maturity than the earlier parent. The best two families which were early as the earlier parent Sisd4 and showed significant ( $p < 0.01$ ) grain yield/plant from the better parent Giza 168 of 26.46 and 59.72% were family No. 92 and No. 306; respectively. The first family

(No. 92) its grain yield/plant depended mainly upon its superiority in grain weight/spike, number of grains/spike and 100-grain weight over the better parent by 55.71, 44.56 and 11.75%; respectively. The second family (No. 306) its grain yield/plant depended mainly upon number of spikes/plant.

**Table 10. Means of the studied traits of the selected families for grain yield after two cycles of selection under drought conditions.**

Fam. No.	DH	PH; cm	SL; cm	NS/P	100 GW; g	NG/S	WG/S; g	BY/P; g	GY/P; g	HI%
13	75.00	85.50	17.17	5.05	5.31	119.81	6.18	66.58	24.74	37.20
74	68.67	89.33	17.33	2.74	6.83	87.04	5.45	50.16	15.76	31.39
92	72.67	77.67	16.67	3.98	5.61	100.37	5.45	60.26	20.01	33.16
202	78.33	108.33	15.50	6.10	6.13	67.05	4.74	69.17	24.25	35.08
296	92.67	114.17	14.17	9.39	4.77	64.62	3.76	75.15	26.42	35.16
306	71.67	91.50	13.50	6.59	5.46	71.26	3.94	66.90	25.27	37.85
379	85.33	78.00	14.33	9.20	4.54	77.32	3.67	77.98	30.63	39.28
389	77.33	88.83	15.50	5.65	5.98	68.48	3.70	64.44	22.10	34.34
395	74.00	91.50	17.17	7.68	5.50	75.68	3.83	76.35	27.58	36.11
397	88.00	85.50	14.17	7.92	5.35	59.07	3.33	76.89	24.44	31.81
Average	78.37	91.03	15.55	6.43	5.55	79.07	4.40	68.39	24.12	35.14
bulk	79.22	91.83	13.94	4.03	4.83	64.03	3.22	52.44	14.15	27.03
Sids4	72.17	81.72	16.39	3.23	5.02	69.43	3.07	47.18	11.64	24.66
Giza168	92.17	102.53	15.25	5.59	4.37	66.37	3.50	51.87	15.82	30.49
R.L.S.D05 Fam%	1.36	4.08	1.35	0.77	0.41	4.01	0.86	4.03	1.83	2.97
R.L.S.D01 Fam%	1.81	5.43	1.73	1.02	0.54	5.33	1.15	5.36	2.43	3.97
R.L.S.D05 Aver %	1.01	3.03	1.00	0.57	0.30	2.97	0.64	2.99	1.36	2.20
R.L.S.D01 Aver %	1.34	4.03	1.28	0.76	0.40	3.95	0.85	3.97	1.80	2.94

R.L.S.D.(Fam.), to compare families with the better parent and the bulk sample.

R.L.S.D.(Fam.), to compare average with the better parent and the bulk sample.

\*\*\*. Significant at 0.05 and 0.01 level of probability; respectively.

**The effect of selection for grain yield/plant on genotypic correlation.**

Under normal irrigation in the F<sub>4</sub> (base population), the correlation between grain yield and other traits were negative except with days to heading which was weak and positive. Therefore, it is expected that selection for high yielding families could cause lateness flowering, in other words increase vegetative period, and plant height under favorable environment, which affect biological yield and harvest index. So, the correlation between grain yield (Table13) and the other traits changed from 0.02 to 0.71 for days to heading, -0.12 to 0.48 for plant height, -0.57 to 0.67 for number of spikes/plant, -0.81 to 0.91 for biological yield/plant and from -0.46 to 0.17 for harvest index, from F<sub>4</sub> to F<sub>6</sub>-generation; respectively. Nouri-Ganbalani *et al.* (2009) observed no significant correlation between the grain yield and other morphological characters under normal irrigation, but under the drought stress conditions there were positive highly significant correlations between the grain yield and the 1000-grain weight and number of tillers per plant.



However, the effect of selection for grain yield/plant on weight and number of grains increased in the negative direction. These results indicate

that the most effective component in grain yield would be number of spikes/plant. This was confirmed by the obtained results of selection.

Under drought stress, the genetic correlation between grain yield/plant and the other traits before selection was positive except for days to heading which was negative and weak (-0.09). Selection for grain yield/plant under drought stress, the genotypic correlations with grain yield increased from 0.84 to 0.90 for number of spikes/plant, from 0.87 to 0.94 for biological yield/plant, from 0.29 to 0.82 for harvest index and from -0.09 to 0.58 for days to heading from the F<sub>4</sub> to the F<sub>6</sub>-generation; respectively. Otherwise, the genotypic correlation between grain yield/plant and weight and number of grains changed by selection from positive to negative selection. Ferdous *et al.* (2010) observed harvest index showed significant and positive correlation with grain yield/plant.

In the F<sub>6</sub>-generation under both environments all the traits which showed positive genotypic correlation with grain yield, days to heading, plant height, biological yield/plant and number of spikes/plant showed negative correlations with grain weight, number of grains/spike, and 100-grain weight. Similar results are obtained by Ferdous *et al.* (2010).

**Table 13. Genotypic correlation for selected families for grain yield under irrigation (above diagonal) and drought (below diagonal) in F<sub>6</sub>-generation.**

Trait	DH	PH	SL	NS/P	100GW	NG/S	WG/S	BY/P	GY/P	HI
DH	-	0.72	-0.51	0.46	-0.46	-0.47	-0.47	0.52	0.71	0.39
PH	0.36	-	-0.38	0.50	-0.31	-0.47	-0.38	0.28	0.48	0.42
SL	-0.67	-0.25	-	-0.54	0.83	0.41	0.63	-0.33	-0.20	0.31
NS/P	0.83	0.30	-0.72	-	-0.50	-0.34	-0.40	0.65	0.67	0.01
100GW	-0.72	0.05	0.58	-0.85	-	0.36	0.84	-0.11	-0.07	0.08
NG/S	-0.52	-0.47	0.71	-0.58	0.08	-	0.85	-0.58	-0.56	0.06
WG/S	-0.64	-0.21	0.77	-0.82	0.42	0.96	-	-0.32	-0.31	-0.01
BY/P	0.76	0.17	-0.57	0.96	-0.84	-0.46	-0.71	-	0.91	-0.26
GY/P	0.58	0.09	-0.54	0.90	-0.90	-0.27	-0.58	0.94	-	0.17
HI	0.11	-0.05	-0.37	0.52	-0.73	0.14	-0.19	0.57	0.82	-

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**الانتخاب لمحصول الحبوب في قمح الخبز تحت ظروف الري العادي وإجهاد الجفاف**  
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أجريت دورتين من الانتخاب المنسب خلال الموسم الزراعيه من ٢٠١٢/٢٠١١ الى ٢٠١٤/٢٠١٣ لتحسين محصول الحبوب/نبات في عشيره انعزاليه من قمح الخبز في الجيل الرابع والخامس والسادس تحت ظروف الري العادي والجفاف ، حيث وجدت اختلافات عالية المعنوية في كل الصفات تحت الدراسة بين العائلات المنتخبة لصفة محصول الحبوب/نبات في الجيل الرابع والسادس في كلا البيئتين ، وبعد دورتين من الانتخاب المنسب لمحصول الحبوب/نبات إنخفضت قيم معامل الاختلاف الوراثي ومعامل الاختلاف المظهري لكل صفات الدراسة من الجيل الرابع الى الجيل السادس تحت كلا البيئتين ، كما إقتربت هذه القيم من بعضها مما أدى الى تقديرات عالية لدرجة التوريث بالمعنى العام المحسوبه من متوسط التباين المتوقع ، وكانت قيم التقدم المباشر في محصول الحبوب/نبات ٩٠.٢٠ ، ٧٠.١٤ و ٣٧.٦٤ ، ٥٢.٤٦ % بالنسبه الى العينه المجمعه الغير منتخبه والاب الافضل تحت ظروف الري والجفاف على التوالي ، وتحت ظروف الري العادي نتجت خمسة عائلات هي أرقام ١٢٧ ، ١٤٦ ، ٢٧٣ ، ٣٧٧ ، ٤٥٢ زاد محصولها عن الاب الافضل جيزة ١٦٨ بمقدار ٣٨.٨٧ ، ٤٦.٥٧ ، ٤٢.٦٣ ، ٥٦.٧٥ ، ٦٤.٩٦ على التوالي ، وكانت العائله رقم ٤٥٢ مساويه له في التكيير ، بينما تحت ظروف الجفاف فإن الانتخاب لمحصول الحبوب/نبات أدى الى تأخير النضج بمقدار ٨.٥٩ % عن الاب الافضل ولم يتأخر عن العينه المجمعه الغير منتخبه وكانت أفضل العائلات في محصول الحبوب هي أرقام ٢٠٢ ، ٢٩٦ ، ٣٧٩ ، ٣٨٩ ، ٣٩٥ ، ٣٩٧ وهي تأخرت معنوياً عن الاب المبكر ، وكانت العائلتين أرقام ٩٢ ، ٣٠٦ مبكرة مثل الاب المبكر سدس٤ وارتفع محصولها بصورة عالية المعنويه عن الاب الافضل جيزة ١٦٨ بمقدار ٢٦.٤٦ ، ٥٩.٧٢ على التوالي ، وفي الجيل السادس تحت كلا البيئتين فإن الصفات الى أظهرت ارتباط وراثي موجب مع صفات محصول الحبوب وعدد أيام طرد السنابل وطول النبات والمحصول البيولوجي/نبات قد أظهرت ارتباط وراثي سالب مع صفات وزن حبوب السنبله وعدد حبوب السنبله ووزن ١٠٠ حبه.





Table 4. Mean squares of the studied traits for the 240 families in F<sub>4</sub>-generation under drought stress, family mean, the parents and the bulk sample, phenotypic(pcv) and genotypic (gcv) coefficients of variability, expected genetic advance ( $\Delta G$ ) and heritability in broad sense (H). where,

Items	d.f	DH	PH; cm	SL; cm	NS/P	100GW; g	NG/S	WG/S; g	BY/P; g	GY/P; g	HI%
MS Rep	2	1.35	42.60	12.20	0.73	0.84	52.88	1.47	63.68	20.90	20.57
MS Entries	242	81.42**	152.11**	7.27**	3.73**	0.36**	340.96**	0.70**	264.90**	42.97**	60.40**
MS Error	484	1.42	5.26	0.51	0.74	0.22	9.56	0.23	6.34	1.01	8.62
Mean $\pm$ SE		86.94 $\pm$ 0.33	83.17 $\pm$ 0.45	12.20 $\pm$ 0.10	5.50 $\pm$ 0.06	5.11 $\pm$ 0.01	60.17 $\pm$ 0.67	2.87 $\pm$ 0.03	38.01 $\pm$ 0.60	14.59 $\pm$ 0.24	38.69 $\pm$ 0.27
Reduction%		0.41	9.67	11.27	17.54	7.09	11.41	23.87	25.66	26.39	0.56
Min		66.00	64.67	8.00	3.44	3.69	34.12	2.15	22.30	8.01	18.73
Max		107.00	107.67	16.33	9.50	5.95	88.79	5.30	73.20	30.03	48.71
gcv		5.63	8.44	12.28	17.99	4.16	17.43	13.86	24.23	25.38	10.74
pcv		5.69	8.59	12.74	20.15	6.76	17.68	16.90	24.53	25.68	11.60
Hb%		98.06	96.56	92.98	79.70	37.80	97.21	67.26	97.55	97.61	85.75
$\Delta G$		8.93	12.69	2.66	1.62	0.24	19.04	0.60	16.74	6.73	7.08
$\Delta G$ /mean%		10.27	15.26	21.80	29.55	4.70	31.64	20.92	44.05	46.14	18.31
Giza 168		83.33	81.89	14.22	3.89	4.48	42.20	2.34	24.47	7.60	31.13
Reduction%		3.10	12.88	5.88	23.04	16.63	28.89	20.97	34.64	41.96	11.69
Sids 4		63.00	79.89	14.44	3.58	5.31	53.96	3.06	24.95	9.59	38.41
Reduction%		3.08	-0.14	9.72	5.69	6.85	23.73	24.24	29.80	31.64	2.74
Bulk		75.00	75.08	11.83	3.95	4.74	50.64	2.38	22.66	8.58	37.67
RLSD Aver 0.05		1.19	2.34	0.75	0.94	0.73	3.08	0.58	2.51	1.00	3.21
RLSD Aver 0.01		1.55	3.07	0.98	1.31	1.48	4.03	0.69	3.37	1.34	4.23

\*, \*\* significant at 0.05 and 0.01 levels of probability; respectively.

$\Delta G$  = expected genetic advance from selection the superior 8.33% of the families.

RLSD. Aver. = to compare families mean with the bulk sample or with the better parent.

$$\text{Reduction\%} = (\bar{X}_i - \bar{X}_s) / \bar{X}_i * 100$$

where,  $\bar{X}_i$  = mean under normal irrigation and  $\bar{X}_s$  = mean under drought stress.

**Table 11. Observed direct and correlated responses to pedigree selection for grain in yield after two cycle of selection (F<sub>6</sub>) percentage of bulk sample under drought conditions; season 2013/2014.**

Fam. No.	Selection criterion	Correlated traits								
	GY/P; g	DH	PH; cm	SL; cm	NS/P	100 GW; g	NG/S	WG/S; g	BY/P; g	HI%
13	74.83**	-5.33**	-6.89*	23.18**	25.45*	10.01*	87.11**	91.80**	26.97**	37.63**
74	11.36	-13.32**	-2.72	24.37**	-32.01**	41.34**	35.94**	69.17**	-4.34	16.13**
92	41.35**	-8.27**	-15.42**	19.59**	-1.11	16.15**	56.75**	69.06**	14.92**	22.67**
202	71.34**	-1.12	17.97**	11.22*	51.62**	26.98**	4.72	47.09**	31.91**	29.77**
296	86.66**	16.97**	24.33**	1.65	133.22**	-1.24	0.92	16.73**	43.31**	30.07**
306	78.53**	-9.54**	-0.36	-3.13	63.72**	13.11**	11.29**	22.08	27.58**	40.02**
379	116.39**	7.71**	-15.06**	2.85	128.41**	-6	20.76**	13.75	48.72**	45.30**
389	56.15**	-2.38*	-3.26	11.22*	40.33**	23.81**	6.95	14.64	22.89**	27.03**
395	94.84**	-6.59**	-0.36	23.18**	90.77**	13.87**	18.19**	18.65	45.60**	33.58**
397	72.67**	11.08**	-6.89**	1.65	96.63**	10.70*	-7.75*	3.36	46.64**	17.67**
Average	70.41**	-1.08	-0.87	11.58**	59.70**	14.87**	23.49**	36.63**	30.42**	29.99**
L.S.D0.05 Fam %	14.91	1.98	5.13	10.05	22.11	9.52	7.22	28.85	8.85	11.88
L.S.D0.01 Fam %	20.21	2.68	6.95	13.56	29.80	12.84	9.78	39.08	12.00	16.09
L.S.D0.05 Aver %	11.02	1.46	3.80	7.46	16.39	7.04	5.36	21.40	6.56	8.80
L.S.D0.01 Aver %	14.98	1.98	5.15	10.05	22.11	9.52	7.25	28.85	8.91	11.95

L.S.D.(Fam.), to compare families with the better parent and the bulk sample.

L.S.D.(Fam.), to compare average with the better parent and the bulk sample.

\*.\*\*. Significant at 0.05 and 0.01 level of probability; respectively.

Table 12. Observed direct and correlated responses to pedigree selection for grain yield after two cycle of selection (F<sub>6</sub>) in percentage of the better-parent under drought conditions; season 2013/2014.

Fam. No.	Selection criterion	Correlated traits								
	GY/P; g	DH	PH; cm	SL; cm	NS/P	100GW; g	NG/S	WG/S; g	BY/P; g	HI%
13	56.41**	3.92**	-16.61**	4.74	-9.64	5.84	72.56**	76.67**	28.36**	22.02**
74	-0.38	-4.85**	-12.87**	5.76	-51.03**	35.99**	25.37**	55.82**	-3.3	2.96
92	26.46**	0.69	-24.25**	1.69	-28.77**	11.75*	44.56**	55.71**	16.18**	8.75
202	53.28**	8.54**	5.66**	-5.43	9.21	22.18**	-3.43	35.49**	33.35**	15.05**
296	66.99**	28.40**	11.35**	-13.57**	67.98**	-4.98	-6.93*	7.51	44.88**	15.31**
306	59.72**	-0.7	-10.76**	-17.63**	17.92**	8.83	2.63	12.45	28.97**	24.14**
379	93.59**	18.24**	-23.92**	-12.55**	64.51**	-9.56*	11.37**	4.77	50.35**	28.82**
389	39.70**	7.15**	-13.36**	-5.43	1.07	19.12**	-1.37	5.59	24.23**	12.62*

395	74.31**	2.54*	-10.76**	4.74	37.40**	9.56*	9.00*	9.29	47.19**	18.43**
397	54.48**	21.93**	-16.61**	-13.57**	41.62**	6.51	-14.92**	-4.8	48.24**	4.33
Average	52.46**	8.59**	-11.21**	-5.13	15.03*	10.52**	13.88**	25.85*	31.85**	15.24**
L.S.D0.05 Fam %	13.34	2.18	5.76	8.54	15.92	9.16	6.65	26.57	8.95	10.53
L.S.D0.01 Fam %	18.08	2.94	7.81	11.53	21.47	12.35	9.02	36.00	12.13	14.27
L.S.D0.05 Aver %	9.86	1.61	4.27	6.35	11.81	6.77	4.94	19.71	6.63	7.81
L.S.D0.01 Aver %	13.40	2.18	5.79	8.54	15.92	9.16	6.68	26.57	9.00	10.59

L.S.D.(Fam.), to compare families with the better parent and the bulk sample.

L.S.D.(Fam.), to compare average with the better parent and the bulk sample.

\*\*. Significant at 0.05 and 0.01 level of probability; respectively.