

## Estimation of Genetic Variability, Heritability and Genetic Advance in Grain Sorghum Population

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**Abstract:** The present study was carried out at Shandaweel Agricultural Research Station, Sohag, Egypt during 2009, 2010 and 2011 summer seasons to evaluate grain yield/plant of sorghum population and select the elite pure lines for using as parents for production of commercial hybrids. The breeding materials used in this study were F5, F6 and F7 generations of grain sorghum (*Sorghum bicolor* (L.) Moench) traced back to a single cross between (R Line-92003 x ICSV-273). After two cycles of pedigree selection, the F7 generation showed 15.98%, 18.12% and 24.66% increasing in grain yield/plant over bulk sample, better parent and the check cultivar, respectively. The selection for grain yield/plant was accompanied by decreasing in days to flowering by -6.81%, -7.21% and -2.91%. The observed gain reached to 10.33% and 1.11% the bulk sample and check cultivar for 1000-grain weight. This increasing was also accompanied by increasing in panicle length and width. Sufficient genotypic coefficient of variability for grain yield / plant and other studied traits was observed. Phenotypic and genotypic variances are expressed as PCV% and GCV% were slightly decreased after the second cycle of selection for 1000-grain weight and days to flowering compared to the first cycle. Family No. 9 could be considered the best selected family since it showed 48.06 % increase in yield over the bulk sample and was earlier than the bulk sample by -7.70%. These results indicated that the direct selection for grain yield/plant was effective in improving the sorghum population.

**Key words:** Phenotypic and genotypic variances • Selection • Sorghum population • Grain yield

### INTRODUCTION

Sorghum is the fifth most important crop and is the dietary staple of more than 500 million people in more than 30 countries. It is grown on 42 m ha in 98 countries of Africa, Asia Oceania and America. The success in a crop improvement program depends on the amount of genetic variability available and its utilization. Although many Sorghum breeders have used traditional breeding methods successfully, genetic potentials have not been fully utilized. The reason is the limited amount of genetic variability capitalized upon by traditional breeding methods [1]. Selection for yield is one of the most important and difficult challenge of plant breeding. Grafius *et al.* [2] indicated that individual yield components might contribute valuable information in breeding for yield. Johnson *et al.* [3] emphasized that increase in yield levels are progressively more difficult to be obtained and that evaluation of individual yield components might provide a better basis for progeny evaluation than yield it self. Grain yield in sorghum showed significant genotypic and

phenotypic correlations either with grain weight [4] or plant height and days to flowering [5-7]. Ali *et al.* [8] showed that selection for grain yield/ plant was accompanied by decrease in days to flowering of -7.43, -6.66% and 7.03% and increase in grain weight of 4.27, 5.70 and 4.89% over the bulk sample at Sohag, Qena and across locations, respectively. Menkir *et al.* [9] and Igaruta *et al.* [10] reported that selection was effective in improving grain yield, but it was associated with undesired increase in plant height and late flowering.

The present study aims to evaluate grain yield of sorghum population and select elite pure lines for using as parents for production of commercial hybrids.

### MATERIALS AND METHODS

This study was conducted at the Experimental Farm of Shandaweel Agricultural Research Station, Sohag, Egypt, during 2009, 2010 and 2011 summer growing season. The breeding materials used in this study were F4 generations from cross (R-Line 92003 \*ICSV-273) were

Table 1: Description of the main characters of the parental genotypes.

Parents	Origin	Characters					
		Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/ plant (g)	1000 grains weight (g)
R-Line 92003	ICRISAT (India)	70	185	30	6	87	30
ICSV-273	ICRISAT (India)	73	240	26	9	69	27

developed by sorghum department at Shandaweel Agricultural Research Station. In 2009 growing season, F4-generation was cultivated in unreplicated experiment (150-rows, 4 m long, 60 cm apart and 20 cm between grains within a row). After full emergence, seedlings were thinned to two plants per hill. At anthesis, 500 plants were tagged for pedigree selection for grain yield/plant. At harvest, 50 heads were selected based on grain yield /plant. The main characters of parents are presented in Table 1.

In 2010 growing season, the 50 selected families along with the bulk random sample (a mixture of equal number of grains from each of the 500 heads to represent the generation mean), the parents and the check cultivar were sown on 20<sup>th</sup> January at Shandaweel Agricultural Research Station, Sohag, Egypt. The experiment was arrangement in randomize complete block design with three replications. Each plot consisted of one row 4 m long, 60 cm apart and 20 cm between hills within a row. After full emergence. Seedlings were thinned to two plants per hill. The cultural practices were carried out as recommended for sorghum production. At harvest time, data were collected on ten random guarded plants in each plot. Measurement were recorded on each plant for the following traits: days to flowering, was recorded on plot mean basis as days from sowing to flowering, plant height (cm), panicle length (cm), panicle width (cm), grain yield /plant (g) and 1000-grain weight(g). The highest plant in grain yield was selected from each of the fifty families and saved for using in the next season. In 2011 growing season, the 50 families for selection were saved and evaluated in the F6-generation.

**Statistical Analysis:** The analysis of variance and covariance were performed as outlined by Federer [11]. The phenotypic (PCV %) and genotypic (GCV %) coefficients of variability were estimated using the formula developed by Burton [12]. Phenotypic and genotypic correlations and heritability in broad sense were calculated as outlined by Walker [13].

The observed gain as the difference between the mean of selected families and random bulk sample value was tested using revised LSD method.

## RESULTS AND DISCUSSION

**Base Population:** Means and ranges of all studied characters were calculated from 500 fertile plants (Table 2). The Results showed wide ranges of these characters, indicating genetic gain from selection that cold be expected from these parents.

### The First Cycle of Selection

**Means and Variance:** Mean of grain yield/plant, correlated traits and days to 50% flowering were calculated on 500 plants in 2009 season. The best 50 heads in grain yield were reserved in 2009season. In 2010 season the 50 selected families along with the bulk sample and the parents were grown in randomized complete block design of three replications. The first analysis of variance included the selected families to estimate heritability, genotypic (GCV %) and phenotypic (PCV %) coefficients of variability. The second analysis of variance included the selected families along with the bulk sample, the parents and the check cultivar to estimate the phenotypic and genotypic correlations and correlated response to selection for grain yield/plant. The analysis of variance for the F6 generation in 2010 season is presented in Table 3. Families mean squares were highly significant after the first cycle of selection for grain yield/plant and its correlated traits, indicating the presence of genetic variability among families in grain yield and the correlated traits. Means of the selected families and bulk sample are presented in Table 4.

Means of the 50 families based upon grain yield/plant in this population (Table 4) indicated that the best family in grain yield/plant number (9) which was out yielded, earlier and heavier in grains than the bulk sample by 43.93, -6.97 and 27.83%, respectively. Most of mean grain yield/plant for 50 families significantly exceeded the random bulk sample. It should be recalled that selection

Table 2: Mean and range for the selected characters of F4 population in 2009 growing season

Traits	Mean	Range
Days to 50% flowering	72.00	68.00-76.67
Plant height (cm)	204.25	171.67-225.00
Panicle length(cm)	29.75	25.67-33.33
Panicle width (cm)	5.25	3.67-6.00
Grain yield/plant (g)	72.93	55.08-90.78
1000-grain weight (g)	24.07	18.00-31.00

Table 3: Mean squares of the 50 selected families in 2010 season

Source of variation	d.f	Mean squares					
		Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (g)	1000-grain weight (g)
Reps	2	1.14	144.01**	1.45	1.49	24.18	6.66**
Families	49	9.05**	897.33**	15.60**	3.25**	498.61**	39.79**
Error	98	1.64	21.53	1.33	0.75	7.10	0.93

\* and\*\*, significant at 0.005 and 0.01 probability levels, respectively.

Table 4: mean trait values of some characters for the selected families of the first cycle of pedigree selection in growing season 2010

Family No.	Traits					
	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (g)	1000-grain weight (g)
1	70.67**	215*	28.67**	5.67	72.70	22.0
2	71.00**	195**	28.33*	6.00*	69.00	19.0
3	68.67**	200**	30.33**	5.55	77.30*	27.0**
4	73.00**	202**	28.67**	6.00*	73.30	26.0**
5	72.33**	195**	29.67**	4.00	98.30**	19.0
6	70.67**	196**	27.00	5.00	88.20**	30.0**
7	71.33**	215*	28.00*	6.67**	92.70**	21.0
8	69.67**	195**	29.67**	5.00	83.00**	30.0**
9	71.33**	185**	28.67**	6.00*	103.20**	29.4**
10	71.67**	195**	27.33	6.00*	93.70**	20.0
11	70.00**	230	32.33**	5.00	84.00**	20.0
12	71.33**	225	28.67**	5.00	80.30**	23.0
13	70.33**	212**	25.67	5.67	93.00**	23.0
14	73.33*	190**	31.00**	5.00	80.30**	19.0
15	72.00**	180**	26.00	6.00*	87.70**	21.3
16	72.67**	215*	28.33*	6.00*	77.90**	24.0
17	70.33**	207**	29.33**	5.67	81.30**	28.0**
18	70.33**	195**	29.67**	6.33	72.30	18.0
19	69.00**	212**	31.67**	4.67	88.00**	22.0
20	73.33*	215*	31.33**	6.00	81.70**	17.3
21	69.67**	225	28.67**	4.33	78.00**	22.0
22	73.33*	185**	30.00**	4.67	85.30**	28.0**
23	70.33**	212**	29.00**	6.00*	77.3*	22.0
24	69.00**	205**	29.00**	5.00	76.80*	23.3
25	71.67**	225	26.00	5.00	86.00**	28.3**
26	72.33*	205**	28.67**	6.00*	77.60**	26.0**
27	67.33**	235*	29.00**	5.00	79.60**	31.0**
28	71.00**	195**	27.00	5.33	85.00**	32.0**
29	69.00**	212**	30.33**	4.33	73.65	21.7

Table 4: Continued

Family No.	Traits					
	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (g)	1000-grain weight (g)
30	72.00**	175**	28.67**	5.33	77.00*	25.0*
31	70.67**	252**	26.33	5.33	77.30*	26.0**
32	66.67**	215*	31.00**	5.00	66.00	30.0**
33	70.67**	220**	28.00**	4.67	64.10	26.0**
34	72.67*	205**	31.33**	5.00	70.10	25.0*
35	69.6**7	212**	31.00**	6.33**	62.30	18.7
36	71.67**	205**	30.00**	5.33	67.00	23.3
37	70.00**	185**	29.00**	6.00*	70.00	29.3**
38	68.67**	205**	31.33**	6.00*	78.00**	23.3
39	68.00**	180**	28.00*	6.00*	74.30	23.0
40	69.33**	225	28.33**	4.00	71.30	20.3
41	70.0**	205**	29.67**	5.00	85.30**	24.0
42	70.67**	212**	28.33**	6.00*	72.30	29.0**
43	70.33**	212**	30.33**	7.00**	68.70	28.7**
44	73.33*	225	33.33**	6.00*	73.00	19.0
45	71.00**	225	28.33**	5.00	79.00**	23.0
46	73.00*	190**	29.33**	4.30	80.30**	24.0
47	71.00**	185**	29.67**	6.00*	80.30**	23.0
48	71.67**	205**	30.67**	6.33**	80.20**	27.0**
49	70.67**	185**	25.67	6.00*	78.00**	26.0**
50	70.33**	195**	29.33**	4.67	67.00	25.0*
Mean	70.77	206	27.3	5.43	78.8	24.2
Bulk	76.67	225.00	25.67	4.33	71.70	23.0
Check	73.00	145.00	24.67	5.25	66.43	26.74
R-lin92003	72.34	185.00	26.88	5.18	70.33	28.00
R-line-273	74.45	235	25.67	6.45	69.45	26.84
LSD0.05*	2.43	8.11	2.20	0.40	3.41	1.57
LSD0.01*	3.18	10.88	2.88	0.52	4.47	2.06

\*, \*\*: Significant at 0.005 and 0.01 probability levels, respectively comparing with the bulk

Table 5: Mean of the 50 selected families, P.C.V, G.C.V and broad sense heritability after the first cycle

Genetic parameters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (g)	1000-grain weight (g)
Bulk mean	76.67	225.00	25.67	4.33	71.70	23.00
Mean	70.77	206.00	27.30	5.43	78.80	24.20
PCV %	2.46	8.40	8.35	19.17	16.36	15.05
GCV %	2.22	8.29	7.99	16.81	16.24	14.87
Hb %	81.79	97.60	91.54	76.92	98.58	97.66

was practiced depending on grain yield/plant. The overall mean of others traits were significantly higher than those of the bulk sample. Therefore, the selection for grain yield/plant which include such families my affect on the initial genotypic correlations among these traits. The overall mean 1000-grain weight was insignificant heavier grains than the bulk sample, but the individual family means showed that 3, 4, 6, 8, 9, 17, 22, 25, 26, 27, 28, 37, 38, 42, 43, 48 and 49 families were heavier grains than the bulk sample. The overall mean of days to 50% to flowering and plant height were highly significant earlier and shorter than the bulk sample.

#### Phenotypic and Genotypic Coefficient of Variability:

The overall family mean, phenotypic and genotypic coefficient of variability and heritability estimates in broad sense of the 50 selected families are presented in Table 5. After the first cycle of selection for grain yield/plant, the retained variability in the selection criterion was high and accounted 16.36 and 16.24 % for Phenotypic and genotypic coefficient of variability, respectively. Therefore, further cycles of pedigree selection could be practiced for grain yield in this population. The genetic variability of the correlated traits, days to 50% flowering, plant height, panicle length, panicle width

Table 6: The observed gain from the pedigree selection measured in percentage comparing with the bulk sample, better parent and check cultivar after the first cycle

Pedigree Population	Item	Characters of selected population					
		Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (g)	1000-grain weight (g)
R-02003 x ICSV-273	F5-Bulk	-7.70**	-8.44**	6.35**	25.40**	9.90**	5.22
	F5-BP	-2.17	11.35**	1.56	4.83	12.04**	-13.57**
	F5-check	-3.6	42.07**	10.66*	18.00	17.42**	-9.50**

\*and\*\* significant and highly significant at 0. 05 and 0. 01 levels of probability, respectively.

Table 7: Phenotypic and genotypic correlation between grain yield/plant and the other traits of the selected families after the first cycle in season 2010

Character	Correlations	
	Rg	Rp
Days to 50% flowering	-0.13	-0.10
Plant height (cm)	0.10	0.09
Panicle length (cm)	0.13	-0.09
Panicle width (cm)	0.14	0.12
1000-grain weight (g)	0.30*	0.29*

Table 8: Mean squares of the 50 selected families during season 2011

Source of variation		Mean squares					
		Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (g)	1000-Grain weight (g)
Reps	2	0.73	38.73	0.62	0.47	69.55**	1.39
families	49	8.64**	428.87**	10.86**	1.49*	345.52**	29.21**
Error	98	1.67	27.20	1.17	0.87	4.49	1.23

\*and\*\*, significant at 0. 005and0. 01 probability levels, respectively

and 100-grain weight were also sufficient and equaled 2.22, 8.29, 7.99, 16.81 and 14.87% as measured by G. C. V% in this population, respectively. High estimates of heritability in broad sense were obtained for all traits. These results are in line with those obtained by Ali *et al.* [8], Kumer and Singh [14] and Mahdy *et al.* [15].

**The Observed Gain after the First Cycle:** The observed gains from the first cycle of selection for grain yield/plant and correlated traits in percentage comparing with the random bulk sample are presented in Table 6. The direct selection increased grain yield/plant by 9.90%, 12.04% and 17.42% comparing with the bulk sample, better parents and check cultivar, respectively. This increasing was accompanied by increasing in panicle length (6.35%, 1.56% and 10.66%), panicle width (25.40%, 4.83% and 18.00%) comparing with the bulk sample, better parent and check cultivar, respectively. Also, the 1000-grain weight (5.22% comparing with the bulk sample), favorable decrease in days to 50% flowering (-7.70%) and plant height (-8.44%) comparing with the sample was found. The observed gains from one cycle of selection are very high, it could be due to heterozygosis in the early

generations and the breeder have to follow the superior families through pedigree selection till homozygosis. These results are in agreement with those obtained by Ali *et al.* [8], Mahdy *et al.* [16], Jinks and Connolly [17] and Chigwe [18].

**Phenotypic and Genotypic Correlation after One Cycle of Selection:** Slight differences between the phenotypic and genotypic correlation were observed. Genotypic correlation between grain yield/plant and days to 50% flowering was negative and weak (-0.13). While it was positive with plant height (0.10) and significant positive with 1000-grain weight (0.30). Johnson *et al.* [19] estimated the genotypic and phenotypic correlation among traits are useful in planning, evaluating breeding programs and facilitate the interpretation of results already obtained. Menkir *et al.* [9] showed that significant positive correlation between grain yield/plant and panicle length, panicle weight and 1000-grain weight. Who also reported that, weak correlations between grains yield/plant and plant height, days to 50% flowering. These results are in agreement with those obtained by Ali *et al.* [8] and Potdukhe *et al.* [20].

Table 9: Means of the selected families for six traits after the second cycle of pedigree selection during season 2011

Characters						
Family No.	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (gm)	1000-grain weight (g)
1	70.7**	205.0**	29.0**	6.3*	82.7	21.0
2	69.0**	190.0**	27.0	6.3*	79.0	26.0*
3	69.7**	195.0**	30.0**	6.3*	87.3**	26.0*
4	69.0**	190.0**	30.3**	5.3	73.3	24.7
5	70.0**	205.0**	28.0**	6.3*	98.3**	28.3**
6	70.0**	190.0**	29.7**	5.3	105.0**	20.7
7	69.3**	205.0**	29.0**	5.3	92.7**	29.0**
8	71.3**	185.0**	29.7**	6.0*	83.0	24.0
9	69.3**	210.0*	28.0**	7.9**	118.0**	30.3**
10	72.0**	185.0**	28.0**	6.3*	93.7**	21.0
11	69.7**	220.0	31.0**	5.3	84.0*	25.0
12	70.0**	210.0*	30.0**	5.3	101.3**	25.3
13	69.7**	200.0**	27.0	5.3	93.0**	21.0
14	70.7**	185.0**	28.3**	6.3*	74.0	21.3
15	71.3**	180.0**	29.3**	6.3*	87.7**	25.0
16	70.0**	215.0	27.0	5.3	97.3**	30.0**
17	70.7**	195.0**	30.3**	7.3**	101.3**	20.0
18	68.0**	185.0**	29.3**	5.3	72.3	23.0
19	67.0**	205.0**	29.7**	5.3	88.0**	28.0**
20	69.0**	196.7**	31.0**	5.3	81.7	25.0
21	71.0**	210.0*	29.7**	7.3**	78.0	29.0**
22	72.0**	175.0**	29.3**	5.9*	105.0**	25.0
23	72.7**	200.0**	28.3**	7.3**	81.3	23.0
24	71.0**	190.0**	28.0**	5.7	89.7**	28.3**
25	70.0	210.0*	27.0	5.3	102.3**	27.0**
26	69.0	190.0**	29.0**	5.3	87.3**	30.0**
27	70.0	210.0*	28.0**	6.3*	89.7**	32.0**
28	69.3	185.0**	28.3**	7.3**	95.7**	25.0
29	70.7	195.0**	31.3**	5.3	73.0	25.0
30	69.7**	180.0**	29.7**	7.6**	81.7	26.3
31	70.3**	225.0	29.0**	5.9	115.0**	30.0**
32	68.0**	215.0	32.0**	6.0*	81.7	27.0**
33	71.0**	210.0*	30.0**	6.3*	75.3	25.0
34	70.3**	200.0**	31.0**	5.3	71.3	21.3
35	69.0**	190.0**	26.3	5.6	62.3	23.3
36	68.0**	190.0**	31.0**	5.3	87.0**	29.0**
37	69.0**	200.0**	29.3**	6.3*	105.0**	28.3**
38	69.0**	208.3**	32.3**	6.3*	85.3**	23.0
39	70.0**	181.0**	28.3**	5.3	74.3	23.0
40	70.0**	225.0	29.3**	5.3	71.3	26.0*
41	68.0**	200.0**	27.7**	5.6	85.3**	29.7**
42	70.0**	205.0**	28.7**	5.3	102.3**	30.0**
43	69.0**	201.7**	32.0**	6.3*	111.7**	27.0**
44	68.7**	206.7**	28.0**	6.3*	73.0	24.0
45	72.0**	185.0**	28.7**	5.3	80.0	26.0*
46	70.0**	195.0**	29.7**	5.7	83.7	23.3
47	69.3**	195.0**	30.3**	7.3**	80.3	28.3**
48	70.7**	195.0**	29.7**	7.6**	102.7**	27.0**
49	69.7**	195.0**	27.3	7.0**	88.3**	26.0*
50	69.0**	205.0**	27.0	6.3*	73.0	24.0
Mean	69.9	198.5	29.3	6.1	87.8	25.4
Bulk	75.02	220.00	25.02	4.71	75.7	23.03
Check	72.00	140.00	24.67	5.25	70.43	25.14
R-lin92003	75.34	190.00	27.33	5.76	74.33	27.00
R-line-273	74.45	240.00	26.13	6.45	65.45	25.00
LSDO. 05*	2.02	8.29	2.05	1.49	3.85	1.75
LSDO. 01*	2.61	10.83	2.68	1.94	5.05	2.29

\*and\*\* significant and highly significant at 0. 05 and 0. 01 levels of probability, respectively. Comparing with the bulk

Table 10: Mean of the 50 selected families, PCV, GCV and broad sense heritability after the second cycle

Genetic parameters	Days to 50% Flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (g)	1000- Grain weight (g)
Bulk Mean	75.02	220.00	25.02	4.71	75.7	23.03
Mean	69.91	198.53	29.31	6.12	87.8	25.42
PCV %	2.43	6.02	6.49	11.55	12.22	12.29
GCV %	2.18	5.83	6.13	7.45	12.14	12.02
Hb %	80.67	93.66	92.27	41.59	98.70	95.80

### The Second Cycle of Selection

**Means and Variances:** The fifty selected families for grain yield/plant were evaluated after the second cycle of selection. Families mean squares (Table 8) were highly significant for grain yield/plant and the correlated traits except panicle width were significant. This indicates existence of sufficient variability for further improvement. Secrist and Atkins [21] reported that estimate of genetic variance among families was significantly greater for seeds/panicle and days to mid flowering but it was not significantly different from IAPI (M) random mating-grain sorghum population C3 (cycle 3) for grain yield, panicles/plant and plant height. Means of the selected families and bulk sample are presented in Table 9. After second cycle of selection for grain yield/plant, the family (No. 9) was highly significant yielding than the bulk sample. The increasing was 48.06%, 26.25% and 11.91% for grain yield/plant, 1000-grain weight and panicle length, respectively. While respective decreasing in days to 50% flowering reached to -7.63%.

### Phenotypic and Genotypic Coefficient of Variability:

The overall family mean, phenotypic and genotypic coefficient of variability and heritability estimates in broad sense for the 50 selected families are presented in Table 10. The genotypic coefficient of variability among the fifty selected families after second cycle of selection for grain yield/plant was 12.14%, while it gave 12.02%,

5.83%, 6.13 % and 2.18% for 1000-grain weight, plant height, panicle length and days to 50% flowering, respectively. The comparison between the PCV and GCV after the first and second cycle of selection, revealed slight decreasing in 1000-grain weight and days to 50 % flowering. Falconer [22] reported that the loss of genetic variance should lead to a reduction in genotypic variance, however, is seldom declined by selection as expected, often it increase. Estimates of broad sense heritability after the second cycle of selection were high in all studied traits except panicle width (41.49%) and days to 50% flowering (80.67%). These results are in agreement with those obtained by Maves and Atkins [23] who showed that heritability estimates for grain yield increased from C0 (cycle 0) to C4 (cycle 4). Ecke bil *et al.* [24] indicated that broad sense heritability for blooming date, yield and grain weight was high in all populations. Falconer [22] reported that the loss of genetic variance should lead to a reduction in genotypic variance, however, is seldom declined by selection as expected, often it increase. Estimates of broad sense heritability after the second cycle of selection were high in all studied traits except days to 50% flowering (74.93%) and panicle length (81.06%). Maves and Atkins [23] showed that heritability estimates for grain yield increased from C0 to C4. Also, Ecke bil *et al.* [24] indicated that broad sense heritability for blooming date, yield and grain weight were high in all populations.

Table 11: The observed gain from pedigree selection measured in percentage comparing with the bulk sample, better parent and check cultivar after the second cycle

		Characters					
Pedigree population	Item	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle width (cm)	Grain yield/plant (g)	1000-grain weight (g)
R-02003 x ICSV-273	F6-Bulk	-6.81**	-9.76**	17.15**	29.94*	15.98**	10.33**
	F6-BP	-7.21*	4.49*	7.25	7.94	18.12**	-5.85
	F6-check	-2.90*	41.81**	18.81**	16.57	24.66**	1.11

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

Table 12: Phenotypic and genotypic correlation between grain yield/plant and other traits of the selected families after the second cycle during season 2011

Traits	Correlations	
	Rg	rp
Days to 50% flowering	-0.16	-0.11
Plant height (cm)	0.27	0.26
Panicle length (cm)	0.02	0.02
Panicle width (cm)	0.31	0.09
1000-grain weight (g)	0.37**	0.30*

**The Observed Gain after the Second Cycle of Selection:**

The observed gains for grain yield/plant (Table 11) was increased by 15.98%, 18.12% and 24.66% comparing with the bulk sample, better parent and check cultivar also panicle length and 1000-grain weight were increased, while decreasing was observed for days to 50% flowering reached -6.80% comparing with the bulk sample. It could be concluded that pedigree selection for grain yield /plant was accompanied with favorable effects on the correlated traits, days to 50% flowering, panicle length, panicle width and 1000-grain weight. Dogget [25] found 25% increase in grain yield over the base population after three cycles of selection. Mahdy *et al.* [15] indicated that grain yield was increased in two sorghum populations by 27.46 and 14.09% after two years of selection. Similar results were reported by Maves and Atkins [23].

**Phenotypic and Genotypic Correlation after the Second Cycle of Selection:**

Selection for a trait might increase or decrease of the intensity of a collateral characters. Causes of the genetic correlations are pleiotropy, linkage and or developmental relationships between components that are indirectly the consequence of gene action [26]. Both phenotypic and genetic correlation among the grain yield/plant and others characters are shown in Table 12. In most cases, the phenotypic and genetic correlation agreed in sign. In those cases where the magnitude of the phenotypic and genetic correlation coefficient was nearly the same, the environmental variance and covariance had been reduced to zero or to a negligible level i.e the influence of environment on these relationships was minimal [27]. After the second cycle for grain yield /plant the genotypic correlations between grain yield /plant and each traits was days to 50% flowering (-0.16), plant height (0.27), panicle length (0.02), panicle width (0.31) and 1000-grain weight (0.31). Saad-Alla [28] found that there were positive and significant correlations between grain yield and 1000-grain weight and between plant height with panicle width. Mahdy *et al.* [15] reported that grain yield /plant showed significant positive phenotypic and genotypic correlation with each of 1000-grain weight, number of kernels/plant and plant height, while it was

negative with days to flowering in the two years. These findings are in agreement with those reported by Ali *et al.* [7] and Menkir *et al.* [9].

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