

Pedigree selection for number of bolls/plant in two segregating populations of Egyptian cotton (*Gossypium barbadense* L.)

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Abstract

This work aimed to study the efficiency of pedigree selection for number of bolls/plant to isolate superior families in two segregating population of Egyptian cotton (Giza-90 × Giza-86) and (Giza-95 × Giza-80) in the F₂ - F₄-generations. The experiments were conducted at South Valley University Experimental Farm, Qena, Egypt during summer seasons 2018 to 2020. Differences among the F₄-selected families were highly significant for the selection criterion; number of bolls/plant and all correlated traits after two cycles of selection in both populations. The genetic variability retained after two cycles of selection was greater and sufficient for further cycles of selection of the selection criterion; number of bolls/plant in both populations. However, all studied correlated traits showed greater genotypic variability in both populations after two cycles of selection. After two cycles of selection, number of bolls/plant increased by 10.67 and 12.41% in population I and 10.58 and 17.26% in population II from the better parent and the bulk sample, respectively. Selection for number of bolls/plant was accompanied by favourable decrease in days to first flower in both populations. However, desirable increase for most correlated traits i.e., boll weight, seed cotton yield/plant, lint yield/plant and lint percentage in both populations. Two families; No. 96 and 178 in population I and family No. 60 in population II could be considered the best selected families resulted from selection for number of bolls/plant. Pedigree selection for number of bolls/plant was effective in isolating genotypes for high number of bolls.

Keywords: Pedigree selection, Egyptian cotton, genetic variability and number of bolls.

1. Introduction

Egyptian cotton (*G.barbadense* L.) is considered the best fiber crop not only in Egypt but also all over the world. The principal objectives to all cotton breeders around the world are improvement of early mature, high yielding and high quality cotton varieties. Therefore, plant breeders are continuously searching for a more effective and efficient selection method. Effective breeding program depends upon the

variation present in the gene pool for the yield enhancing traits. Selection is effective when magnitude of variability in the breeding although several selection methods were used for improving several traits in cotton, pedigree selection method has become the most popular of plant breeding procedures. Most of Egyptian cotton varieties were produced through this method. According to FAOSTAT (2019), the total area for cotton cultivation was 100000 hectare, while the production was estimated at 305000 tonnes and yield per ha 3.5 metric tonnes in Egypt. Therefore, the new trend in Egypt is to increase the cultivated area of the cotton in newly reclaimed lands by developing new varieties that tolerate to harsh conditions such as drought, heat, salinity and low soil


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fertility. The coefficient of variation indicates only the extent of variability existing for various traits but does not give any information about the heritable portion of it. Therefore, heritability accompanied by estimates of genetic advance and genetic advance as percent mean were also estimated. Heritability provides no indication about the genetic progress that would result from selection. However, at a fixed selection pressure, the amount of advance varies with magnitude of heritability. Genetic advance in a population cannot be predicted from heritability alone, the genetic gain for specific selection pressure has to be worked out (Basbag and Oktay, 2004 and Alkuddsi *et al.*, 2013). Highly significant differences among selected families for number of bolls/plant and correlated traits i.e., seed cotton yield/plant, lint yield/plant, boll weight and seed index were reported in previous studies (Khan *et al.*, 2009; Soomro *et al.*, 2010; Mahdy *et al.*, 2013 and Ahsan *et al.*, 2015). Several studies indicated that pedigree method succeeded in improving number of bolls/plant in cotton (Ahuja *et al.*, 2004; Khan *et al.*, 2009; Soomro *et al.*, 2010; El-Zanaty *et al.*, 2011; Mahdy *et al.*, 2013b and Ahsan *et al.*, 2015). Ahuja *et al.* (2004), Mahrous (2008), Khan *et al.* (2009), Soomro *et al.* (2010), Mahdy *et al.* (2013b), Ahsan *et al.* (2015), Mahrous and Soliman (2017), Okaz *et al.* (2017), Mahrous (2018) and Abd-El-Sameea *et al.* (2020) reported that high estimates of genetic coefficient of variation, heritability and genetic advance were observed for seed cotton yield per plant, number of bolls per plant, ball weight and plant height. On the other hand, the broad sense heritability, genetic advance as percent of mean were low for number of bolls/plant (3.01 and 3.68%, respectively). In addition, the phenotypic variance was 31.38, genotypic variance was 4.53 and the GCV and PCV values for number of bolls/plant were low to moderate (Alkuddsi *et al.*, 2013). The present work aimed to study the efficiency of pedigree selection in

improving number of bolls/plant to isolate superior families and consequently improving seed cotton in yield.

2. Materials and Methods

2.1. Experimental site

Two experiments were conducted at Experimental Farm of Faculty Agricultural of South Valley University, Qena, Egypt during 2018, 2019 and 2020 summer seasons. Table 1 shows some physical and chemical characteristics of a representative soil sample from the field experimental site.

2.2. Experimental materials

Two F_2 -populations of cotton as basic materials initiated from crosses between four Egyptian cotton varieties (*G. barbadense* L.) were used. The first (Pop I) and second (Pop II) populations developed from the crosses (Giza-90 \times Giza-86) and (Giza-95 \times Giza-80), respectively.

2.3. Base populations (F_2 -generations)

In 2018 summer season, seeds of F_2 from each population were sown separately in a non-replicated trail; each in 40 rows, 4 m long, 60 cm a wide and 40 cm between hills within a row. The parents were sown in individual plots for each population. After full emergence, the hills were thinned to one plant/hill after three weeks from sowing. All other cultural practices were applied as recommended for cotton production in the three seasons. Data were registered on 268 and 232 random guarded plants from the first and second populations, respectively. For each population, the following characters were recorded on individual guarded plants of each plot: days to first flower, earliness index, number of bolls/plants, boll weight, seed-cotton yield/plant, lint yield/plant, lint percentage and seed index.

Table 1. Some physical and chemical properties of the experimental site in 2018, 2019 and 2020.

Soil property	Seasons			
	2018	2019	2020	
Sand (%)	66.70	87.00	84.02	
Silt (%)	21.30	8.00	7.98	
Clay (%)	12	5	8	
Soil texture	Sandy loam	Sandy	Sandy	
pH (1:1)	7.93	8.18	8.8	
Organic matter (%)	0.3	0.4	0.4	
EC (ds m-1)	9.95	2.07	7.5	
CaCO ₃ (%)	5.8	11.88	7.4	
Soluble ions (m mol L-1)	SO ⁻⁴	52.3	55.4	55.4
	K ⁺	0.80	0.28	0.28
	Ca ⁺⁺	11.5	2.0	2.0
	Mg ⁺⁺	11.3	1.5	1.5
	H CO ⁻³	20.00	10.0	10.0
	Cl ⁻	27.50	33.0	33.0
	SO ⁻⁴	23.2	6.9	6.9

Two pickings were done on single plants at the end of growing season. For each population, five seeds from each of the 268 plants (Pop I) and from each of the 232 plants (Pop. II) were bulked to give an unselected bulk sample. From each population, seeds of the best 20 plants in number of bolls/plant as selection criterion were saved.

2.4. F₃-generation

In 2019 summer season, the 20 F₃-families from each population along with the unselected bulk sample and the two parents were grown in a randomized complete block design (RCBD) with three replicates for each population independently. The plot size was one row as in the previous season. The traits were registered as in the previous season as an average of five guarded plants from each family. After harvest, the best plant from each of the best ten families for number of bolls/plant as selection criterion were saved for the following generation. Seeds of the unselected bulk sample were bulked without selection.

2.5. F₄-generation

In 2020 summer season, the same 10 selected families for number of bolls/plant as selection criterion along with the parents and the unselected bulk sample were grown as in the previous season. Observations were recorded on five guarded plants from each family.

2.6. Statistical analysis

Two separate analyses of variance were done according to Snedecor and Cochran (1980) by MSTAT-C computer program in a randomized complete block design. The first includes the entries (10 selected families along with the bulk samples and parents to measure the variability and the significance of the observed gain. The second included the selected families only to calculate phenotypic (PCV), genotypic (GCV) coefficients of variability and heritability in broad sense. The phenotypic (σ^2_p) and genotypic (σ^2_g) variances were calculated according to Al-Jibouri *et al.* (1958). Heritability in broad sense was estimated as (H) = (σ^2_g/σ^2_p) × 100 according to Walker (1960). The phenotypic (PCV%) and genotypic (GCV%) coefficients of variability were estimated using the formula developed by Burton (1952). Comparisons between means were calculated by using revised L.S.D (El-Rawi and Khalafalla, 1980) as follow:

Where, L.S.D = Least significant differences between random sample, the best parent, and mean of each selected family was calculated as:

$$RLSD = t'_{\alpha} \times \sqrt{\frac{2MSe}{r}}$$

L.S.D = Least significant differences between random sample, the best parent, and mean of all selected families was calculated as:

$$RLSD = t'_{\alpha} \times \sqrt{\frac{MSe}{r}} + \sqrt{\frac{MSe}{rf}}$$

Where, t'_{α} from minimum – average-risk table.
f; number of the selected families

- Deviation of the direct and correlated response to selection in percentage from the unselected bulk sample and the better parent was measured by using L.S.D. test.

3. RESULTS AND DISCUSSION

3.1. Description of the F_2 -populations

3.1.1. Average, phenotypic coefficient of variation (CV%), heritability in broad sense (H%) and expected genetic advance from the mean ($\Delta G/\text{Mean}$ (%))

The characteristic of the two populations (Table 2) exhibited that the average number of bolls/plant of pop. I was lower (30.06) than better parent Giza-90 (36.59) and higher than the other parent Giza-86 (20.50). This indicates that partial dominance towards the better parent Giza-90. High CV% (41.90%) was obtained for pop. I compared to moderate CV% (11.15%) for pop. I compared to moderate CV% (11.15%) for Giza-90 and low CV% (3.44%) for Giza-86. Therefore, high estimates of broad sense heritability (99.79%) and very large expected genetic advance in percentage of the mean (86.14%) were observed. In pop. II (Table 2), the average number of bolls/plant was 25.84 compared to 31.33 for Giza-95 and 21.50 for Giza-80. The phenotypic variation (CV%) of number of bolls/plant for the two parents was very low compared to high CV% (20.36%) for pop II. Hence, very high estimates of broad sense heritability of 98.19 and expected genetic advance as percentage of the mean of 40.42 were observed.

3.1.2. Correlation study

The correlation coefficients (Table 3) were positive and highly significant between number of bolls/plant with each of boll weight, seed cotton yield/plant, lint yield/plant, lint percentage and seed index in both populations except boll weight in population I was negative and insignificant. Consequently, this observation suggested that selection practiced for the improvement of the number of bolls/plant would automatically improve these characters. On the other hand, number of bolls/plant demonstrated negative and highly significant correlation with each of days to first flower and earliness index. These results were agreement with those obtained by Abo-Sen (2001), Mahdy *et al.* (2001), Ahuja *et al.* (2004), Iqbal *et al.* (2006), Khan *et al.* (2009), Mahdy *et al.* (2017), Okaz *et al.* (2017), Nikhil *et al.* (2018), Nawaz *et al.* (2019) and Chapepa *et al.* (2020).

3.2. Pedigree selection for number of bolls/plant; variability and heritability estimates

3.2.1. Analysis of variance

Differences among genotypes and F_4 -families were significant ($p < 0.01$) for selection criterion; number of balls/plant and correlated traits i.e., days to first flower, earliness index, boll weight, seed cotton yield/plant, lint yield/plant, lint percentage and seed index in pop I and II (Table 4). This indicates that the existence of sufficient variability for further improvement. These results agreed with those reported by Khan *et al.* (2009), Soomro *et al.* (2010), Mahdy *et al.* (2013b) and Ahsan *et al.* (2015).

Table 2. Means, phenotypic coefficient of variation (CV%), heritability in broad sense (H%) and expected genetic advance from the mean ($\Delta G/\text{Mean}$ (%)) of the two base populations I and II (F_2) and its parents of the studied traits; season 2018.

Populations	Variable	DFP	EI	NOB/P	BW	SCY/P	LY/P	LP	SI
I	Mean \pm SE	66.40 \pm 0.51	66.02 \pm 0.87	30.06 \pm 0.42	2.47 \pm 0.002	171.12 \pm 5.09	59.71 \pm 1.81	34.47 \pm 0.18	8.15 \pm 0.05
	CV%	12.96	21.46	41.90	22.18	82.55	48.69	8.77	10.86
	H%	83.93	83.54	99.79	96.67	98.91	97.92	87.18	93.55
	ΔG	14.43	24.38	25.89	1.10	169.78	59.77	5.17	1.59
	$\Delta G/\text{Mean}$ (%)	22.41	36.93	86.14	44.36	99.22	100.11	15.00	19.51
P ₁ (Giza 90)	Mean \pm SE	65.68 \pm 1.16	78.03 \pm 2.02	36.59 \pm 0.48	2.31 \pm 0.04	38.39 \pm 0.85	13.27 \pm 0.32	36.23 \pm 0.27	8.89 \pm 0.22
	CV%	6.82	10.03	11.15	6.55	8.56	4.42	2.85	9.67
P ₂ (Giza 86)	Mean \pm SE	70.90 \pm 1.28	69.06 \pm 2.06	20.50 \pm 0.20	2.27 \pm 0.05	30.24 \pm 0.94	10.07 \pm 0.35	33.30 \pm 0.52	9.30 \pm 0.40
	CV%	5.76	9.38	3.44	6.17	4.21	4.69	4.93	14.15
II	Mean \pm SE	69.37 \pm 2.29	66.40 \pm 0.87	25.84 \pm 0.35	1.89 \pm 0.28	116.40 \pm 5.09	38.86 \pm 1.78	32.65 \pm 0.97	8.67 \pm 0.23
	CV%	50.34	19.87	20.36	28.26	66.66	69.59	45.08	40.01
	H	88.5	85.2	98.19	92.86	95.6	95.5	90.4	90.9
	ΔG	63.65	23.16	10.44	1.01	152.81	53.19	27.41	6.49
	$\Delta G/\text{Mean}$ (%)	91.77	34.88	40.42	53.64	131.28	136.87	83.95	74.88
P ₁ (Giza 95)	Mean \pm SE	70.90 \pm 0.75	78.06 \pm 2.44	31.33 \pm 0.18	2.55 \pm 0.03	79.43 \pm 1.61	29.04 \pm 0.50	36.68 \pm 0.53	8.94 \pm 0.27
	CV%	3.35	4.89	1.86	3.81	6.41	5.41	4.60	9.55
P ₂ (Giza 80)	Mean \pm SE	75.13 \pm 0.55	67.48 \pm 1.13	21.50 \pm 0.18	2.22 \pm 0.01	55.40 \pm 1.22	17.54 \pm 0.58	33.88 \pm 0.75	7.27 \pm 0.18
	CV%	2.30	5.28	2.71	0.90	6.94	10.77	7.01	7.99

ΔG ; Expected genetic advance from selection 10% superior plants.

The genotypic coefficient of variability among the ten selected families for number of bolls/plant (Table 4) was large after two cycles of selection and sufficient for further cycles of selection in both populations. GCV estimates for number of bolls/plant were 16.67 and 14.57% in populations I and II, respectively. The slight discrepancy between PCV and GCV caused high estimates of broad sense heritability for number of bolls/plant and other correlated traits in both populations. It accounted 96.97 and 96.72% (NB/P), 92.46 and 94.75% (DFF), 96.81 and

94.83% (EI), 96.08 and 95.24% (BW), 97.37 and 98.55% (SCY/P), 76.63 and 97.76% (LY/P), 96.71 and 96.76% (LP) and 95.97 and 97.83% (SI) in pop I and II, respectively (Table 4). Genetic coefficient of variation together with a heritability estimate would seem to give the best picture of the genetic advance from selection (Burton, 1952; Sanghi *et al.*, 1964). Similar results were obtained by Ahmed *et al.* (2006) and Khan *et al.* (2009) reported that broad sense heritability were high for number of bolls/plant, boll weight and seed cotton yield/plant.

Table 3. Simple correlation coefficients between each pairs of eight traits of the F₂-population I (above diagonal) and F₂-population II (below diagonal).

Traits	DFF	EI	NB/P	BW	SCY/P	LY/P	LP	SI
DFF	-	0.014	-0.865**	-0.025	-0.289**	-0.297**	-0.142*	0.036
EI	0.024	-	-0.183**	0.029	-0.160**	-0.130*	0.212**	-0.144*
NB/P	-0.287**	-0.088	-	-0.076	0.933**	0.905**	0.052	0.252**
BW	-0.137*	0.239**	0.248**	-	0.246**	0.259**	0.198**	0.239**
SCY/P	-0.296**	-0.023	0.945**	0.485**	-	0.979	0.112	0.322**
LY/P	-0.299**	-0.006	0.937**	0.493**	0.993**	-	0.268**	0.306**
LP	-0.123	0.122	0.258**	0.240**	0.282**	0.372**	-	0.046
SI	-0.122	-0.112	0.336**	0.237**	0.343**	0.313**	-0.097	-

However, the realized heritability estimates were low and accounted for 37.06 and 63.50% in pop I and II, respectively. Estimates of the realized heritability were more reliable and accurate than broad sense heritability, except for the effect of genotypes by environmental interaction caused by growing of parent and offspring at two separate seasons. Mahdy *et al.* (2013) reported that the realized heritability and parent and offspring regression were 0.3890 and 0.0886 for pop I and 0.3946 and 0.1271 for pop I and pop II, respectively.

3.2.2. Means of the selected families for selection criterion (number of bolls/plant) and the correlated traits

In population I, mean values of number of bolls/plant of F₄-selected families after two

cycles of selection varied from 25.51 for family no. 216 to 46.70 for family no. 164 with an average of 40.66 bolls compared to 36.74 for Giza-90 and 35.68 for Giza-86. However, mean values of the correlated traits after two cycles of selection varied from 55.18 to 67.99 days, 68.45 to 80.78, 1.89 to 3.32 g., 82.38 to 117.13 g., 28.81 to 41.28 g., 34.09 to 36.69%, and 7.07 to 9.82 g. for days to first flower, earliness index, boll weight, seed cotton yield, lint yield/plant, lint percentage and seed index, respectively (Table 5). After two cycles of selection, average number of bolls/plant of F₄-selected families in population II ranged from 29.55 (family no. 51) to 43.24 (family no. 60) with an average of 34.17 bolls compared to 30.90 for Giza-95 and 25.98 for Giza-80. Such wide variation in number of bolls/plant of the 10 selected families in the F₄-generation in either population I or II encourage to do further cycles of selection,

especially, when this variation accompanied with wide variation in all correlated traits. In addition, the average of the correlated traits i.e., days to first flower, earliness index, boll weight, seed cotton yield, lint yield/plant, lint percentage and seed index ranged from 55.14 to 71.75 days, 64.64 to 84.32, 2.01 to 2.98 g., 64.94 to 106.43 g., 23.40 to 40.43 g., 35.37 to 40.15%, and 6.06 to 10.42 g., respectively (Table 6).

3.2.3. Direct and indirect observed gain of the selected families for selection criterion and the correlated traits

The average observed gain in number of bolls/plant was highly significant and recorded 10.67 and 12.41% from the better parent and the bulk sample, respectively. All the selected families exhibited highly significant highest in number of bolls/plant compared to the better parent and the bulk sample except the families no. 173 and 216 showed highly significant negative (Table 7). Two cycles of pedigree selection for increasing number of bolls/plant in population I caused favourable decrease in days to first flower by – 6.40 and – 16.18% from the better parent and the bulk sample, respectively. Desirable increase in boll weight, seed cotton yield/plant, lint yield/plant and lint percentage over the better parent and the bulk sample accompanied pedigree selection for number of bolls/plant by 28.91 and 30.14%, 12.67 and 17.44%, 18.20 and 23.21% and 3.62 and 4.97%, respectively. Undesirable decrease in seed index over the better parent and the bulk sample was resulted from pedigree selection for number of bolls/plant by – 25.00 and 17.80%, respectively (Table 7). The average observed gain in number of bolls/plant was highly significant and registered 10.58 and 17.26% from the better parent and the bulk sample, respectively. Some and most selected families illustrated highly significant highest in number of bolls/plant compared to the better parent and the bulk sample, respectively (Table 8). In population II, two cycles of pedigree selection for increasing

number of bolls/plant caused undesirable decrease in earliness index by – 1.07 and - 1.11% from the better parent and the bulk sample, respectively. Desirable increase in boll weight, seed cotton yield/plant, lint yield/plant and lint percentage over the better parent and the bulk sample accompanied pedigree selection for number of bolls/plant by 0.83 and 2.54, 6.20 and 6.29, 11.92 and 14.23 and 5.37 and 7.47%, respectively. Unfavorable increase in days to first flower over the better parent reached 6.29%, but, respective desirable decrease was observed for this trait, which reached – 4.90% from the mean bulk sample (Table 8). Similar results were reported by Mahdy *et al.* (2001), El-Okkiah *et al.* (2008), Mahrous (2008) and Mahdy *et al.* (2009). Abuja *et al.* (2004) indicated that number of bolls/plant was the most important trait for selection of genotypes with high potential of seed cotton yield. Mahdy *et al.* (2013) indicated that selection criteria based on yield components rather than yield, where effective for simultaneous improving of yield and boll weight. Abd-El- Samee *et al.* (2020) reported that improving seed cotton yield/plant could be achieved by selection for number of bolls/plant, lint yield/plant and boll weight.

4. Conclusion

Selection for number of bolls/plant was accompanied by desirable decrease and in days to first flower in both populations. However, desirable increase for most correlated traits i.e., boll weight, seed cotton yield/plant, lint yield/plant and lint percentage in both populations. Two families; No. 96 and 178 in population I and family No. 60 in population II could be considered the best selected families resulted from selection for number of bolls/plant. Pedigree selection for number of bolls/plant was effective in isolating genotypes for high number of bolls.

Table 4. Means squares, genotypic (GCV%), phenotypic (PCV%) coefficients of variability, broad sense heritability and realized for the selected families of number of balls/plant and correlated traits in F₄ – generation for both populations (I and II).

Populations	S.O.V	df	Selection criterion NB/P	Correlated traits							
				DFP	EI	BW	SCY/P	LY/P	LP	SI	
I	Reps	2	1.67	1.16	24.73	0.05	1.13	0.10	3.07	0.05	
	Genotypes	12	116.29**	93.17**	29.67**	0.41**	350.67**	2.30**	25.37**	4.87**	
	Selected families	9	142.32**	41.93**	36.35**	0.51**	308.86**	1.84**	30.74**	2.98**	
	Error (Genotypes)	24	3.38	3.28	1.10	0.01	6.20	0.67	0.83	0.11	
	Error (Selected families)	18	4.31	3.16	1.16	0.02	8.13	0.43	1.01	0.12	
	GCV%			16.67	5.82	4.50	14.71	9.34	1.83	8.94	11.80
	PCV%			16.95	6.06	4.58	15.07	9.47	2.07	9.08	12.04
	H _b %			96.97	92.46	96.81	96.08	97.37	76.63	96.71	95.97
	h ²			37.06	-	-	-	-	-	-	-
II	Reps	2	0.005	0.85	0.45	0.004	23.46	0.67	0.49	0.15	
	Genotypes	12	78.16**	98.53**	66.66**	0.32**	595.36**	77.13**	12.40**	3.88**	
	Selected families	9	76.84**	83.75**	88.22**	0.42**	775.47**	99.91**	10.79**	5.08**	
	Error (Genotypes)	24	2.79	4.30	4.54	0.01	11.01	2.09	0.44	0.14	
	Error (Selected families)	18	2.52	4.40	4.56	0.02	11.27	2.24	0.35	0.11	
	GCV%			14.57	7.72	6.89	14.88	20.47	18.72	4.96	14.91
	PCV%			14.81	7.94	7.07	15.29	19.86	18.91	5.04	15.03
	H _b %			96.72	94.75	94.83	95.24	98.55	97.76	96.76	97.83
	h ²			36.50	-	-	-	-	-	-	-

** : Significant at 0.01 level of probability.

Table 5. Means of number of bolls/plant and the correlated response of the other traits of the selected families (F₄-generation) for population I.

Genotypes	Selection criteria	Correlated response of the studied traits						
		NB/P	DFF	EI	BW	SCY/P	LY/P	LP
96	42.72	55.18	77.97	3.32	117.13	39.91	34.09	7.84
131	42.69	62.83	77.20	2.54	98.65	36.18	36.69	7.07
164	46.70	63.23	73.77	2.57	113.08	39.33	34.78	9.43
169	46.01	62.85	73.04	2.56	109.72	39.42	35.92	7.51
173	30.96	57.12	76.08	1.89	82.38	28.81	34.96	7.57
178	41.85	60.00	80.78	3.13	106.03	37.15	35.04	9.82
216	25.51	64.57	79.35	2.74	109.84	38.15	34.76	8.05
238	43.50	67.99	76.00	3.19	114.52	41.28	36.05	9.54
257	41.60	63.42	76.68	2.57	106.94	37.01	34.64	7.91
259	45.07	59.79	68.45	2.67	113.19	40.13	35.46	7.42
Average	40.66	61.70	75.93	2.72	107.15	37.74	35.24	8.22
Giza-90	36.74	73.90	75.94	2.11	95.1	31.93	33.58	10.96
Giza-86	35.68	65.92	72.17	2.02	86.5	29.42	34.01	9.88
Bulk' s mean	36.17	73.61	72.93	2.09	91.24	30.63	33.57	10.00
RL.S.D _{0.05}	4.15	4.02	1.35	0.01	7.61	1.02	1.02	0.13
RL.S.D _{0.01}	5.50	5.34	1.79	0.02	10.09	1.42	1.35	0.18
R. L.S.D _{0.05} Average	2.04	2.02	1.16	0.12	2.78	1.14	1.01	0.37
R. L.S.D _{0.01} Average	2.71	2.68	1.54	0.15	3.68	1.59	1.34	0.49

Table 6. Means of number of balls/plant and the correlated response of the other traits of the selected families (F₄-generation) for population II.

Genotypes	Selection criteria NB/P	Correlated response of the studied traits						
		DFP	EI	BW	SCY/P	LY/P	LP	SI
51	29.55	59.49	70.97	2.98	92.84	31.50	39.98	9.58
60	43.24	65.93	78.08	2.46	106.43	40.43	35.37	8.79
62	32.72	71.17	80.78	2.01	65.88	24.40	36.55	7.65
75	32.43	67.08	76.96	2.74	72.50	28.19	40.15	7.68
96	30.67	55.14	64.64	2.90	104.72	37.11	39.35	7.95
108	29.74	67.80	79.42	2.19	64.94	23.67	36.45	9.28
127	43.16	67.68	76.90	2.09	90.13	34.75	36.62	6.06
181	32.52	71.75	78.19	2.70	71.18	26.55	35.79	9.73
192	35.57	69.63	76.51	2.06	73.34	26.95	36.74	10.42
202	32.06	69.69	84.32	2.11	67.60	25.57	39.80	9.36
Average	34.17	66.54	76.68	2.42	80.96	30.51	37.68	8.65
Giza-95	30.90	77.51	77.72	2.40	76.23	27.26	35.76	9.12
Giza-80	25.98	62.60	77.51	2.26	72.62	24.90	34.29	8.47
Bulk's mean	29.14	69.97	77.54	2.36	76.17	26.71	35.06	8.55
RL.S.D _{0.05}	3.42	5.27	5.78	0.01	13.51	2.56	0.54	0.17
RL.S.D _{0.01}	4.54	6.99	7.69	0.02	17.91	3.40	0.72	0.23
R. L.S.D _{0.05} Average	1.86	2.32	2.46	0.12	4.05	1.62	0.74	0.40
R. L.S.D _{0.01} Average	2.46	3.07	3.28	0.15	5.37	2.15	0.98	0.54

Table 7. The observed direct gain and correlated response as percentage from the better parent and the bulk sample of the selected families (F₄ – generation) for population I.

Item	Families no.	Selection criterion			Correlated response of the studied traits				
		NB/P	DFP	EI	BW	SCY/P	LY/P	LP	SI
Better parent	96	16.28**	-16.29**	2.67*	57.35**	23.17**	24.99**	0.24	-28.47**
	131	16.19**	-4.69*	1.66	20.38**	3.73	13.31**	7.88**	-35.49**
	164	27.11**	-4.08	-2.86*	21.80**	18.91**	23.18**	2.26	-13.96**
	169	25.23**	-4.66*	-3.82	21.33**	15.37**	23.46**	5.62*	-31.48**
	173	-15.73**	-13.35**	0.18	-10.43*	-13.38**	-9.77**	2.79	-30.93**
	178	13.91**	-8.98**	6.37**	48.34**	11.49**	16.35**	3.03	-10.40**
	216	-30.57**	-2.05	4.49**	29.86**	15.50**	19.48**	2.21	-26.55**
	238	18.40**	3.14	0.08	51.18**	20.42**	29.28**	6.00**	-12.96**
	257	13.23**	-3.79	0.97	21.80**	12.45**	15.91**	1.85	-27.83**
	259	22.67**	-9.30**	-9.86**	26.54**	19.02**	25.68**	4.26	-32.30**
	Average	10.67**	-6.40**	-0.01	28.91**	12.67**	18.20**	3.62*	-25.00**
Bulk	96	18.11**	-25.04**	6.91**	58.85**	28.38**	30.30**	1.55	-21.60**
	131	18.03**	-14.64**	5.85**	21.53**	8.12**	18.12**	9.29**	-29.30**
	164	29.11**	-14.10**	1.15	22.97**	23.94**	28.40**	3.60	-5.70*
	169	27.20**	-14.62**	0.15	22.49**	20.25**	28.70**	7.00**	-24.90**
	173	-14.40**	-22.40**	4.32**	-9.57	-9.71**	-5.94*	4.14	-24.30**
	178	15.70**	-18.49**	10.76**	49.76**	16.21**	21.29**	4.38	-1.80
	216	-29.47**	-12.28**	8.80**	31.10**	20.39**	24.55**	3.54	-19.50**
	238	20.27**	-7.63**	4.21**	52.63**	25.52**	34.77**	7.39**	-4.60
	257	15.01**	-13.84**	5.14**	22.97**	17.21**	20.83**	3.19	-20.90**
	259	24.61**	-18.77**	-6.14**	27.75**	24.06**	31.02**	5.63*	-25.80**
	Average	12.41**	-16.18**	4.11**	30.14**	17.44**	23.21**	4.97**	-17.80**
L.S.D _{0.05}		3.10	3.05	1.75	0.21	4.19	1.38	1.53	0.54
L.S.D _{0.01}		4.20	4.14	2.38	0.28	5.68	1.87	2.07	0.73
L.S.D _{0.05} Average		2.29	2.27	1.30	0.13	3.12	1.03	1.14	0.41
L.S.D _{0.01} Average		3.10	3.08	1.76	0.18	4.22	1.40	1.54	0.56

*, **: Significant at 0.05 and 0.01 levels of probability, respectively.

Table 8. The observed direct gain and correlated response as percentage from the bulk sample of the selected families (F₄ – generation) from single seed descent method for population II.

Item	Families no.	Selection criterion			Correlated response of the studied traits				
		NOB/P	DFP	EI	BW	SCY/P	LY/P	LP	SI
Better parent	51	-4.37	-4.97	-8.44**	24.17**	21.79**	15.55**	11.80**	5.04
	60	39.94**	5.32	0.74	2.50	39.62**	48.31**	-1.09	-3.62
	62	5.89	13.69**	4.22	-16.25**	-13.58**	-10.49*	2.21	-16.12**
	75	4.95	7.16*	-0.71	14.17**	-4.89	3.41	12.28**	-15.79**
	96	-0.74	-11.92**	-16.60**	20.83**	37.37**	36.13**	10.04**	-12.83**
	108	-3.75	8.31**	2.46	-8.75*	-14.81**	-13.17**	1.93	1.75
	127	39.68**	8.12**	-0.79	-12.92**	18.23**	27.48**	2.40	-33.55**
	181	5.24	14.62**	0.88	12.50**	-6.62	-2.60	0.08	6.69
	192	15.11**	11.23**	-1.29	-14.17**	-3.79	-1.14	2.74	14.25**
	202	3.75	11.33**	8.79**	-12.08**	-11.32**	-6.20	11.30**	2.63
	Average	10.58**	6.29**	-1.07	0.83	6.20*	11.92**	5.37**	-5.15*
Bulk	51	1.41	-14.98**	-8.47**	26.27**	21.89**	17.93**	14.03**	12.05**
	60	48.39**	-5.77*	0.70	4.24	39.73**	51.37**	0.88	2.81
	62	12.29*	1.72	4.18	-14.83**	-13.51**	-8.65	4.25	-10.53
	75	11.29*	-4.13	-0.75	16.10**	-4.82	5.54	14.52**	-10.18**
	96	5.25	-21.19**	-16.64**	22.88**	37.48**	38.94**	12.24**	-7.02
	108	2.06	-3.10	2.42	-7.20	-14.74**	-11.38*	3.96	8.54*
	127	48.11**	-3.27	-0.83	-11.44*	18.33**	30.10**	4.45	-29.12**
	181	11.60*	2.54	0.84	14.41**	-6.55	-0.60	2.08	13.80**
	192	22.07**	-0.49	-1.33	-12.71**	-3.72	0.90	4.79	21.87**
	202	10.02*	-0.40	8.74**	-10.59*	-11.25**	-4.27	13.52**	9.47*
	Average	17.26**	-4.90*	-1.11	2.54	6.29*	14.23**	7.47**	1.17
L.S.D _{0.05}		2.81	3.49	3.59	0.21	5.59	2.44	1.78	0.62
L.S.D _{0.01}		3.80	4.73	4.87	0.28	7.58	3.30	2.41	0.84
L.S.D _{0.05} Average		2.08	2.60	2.66	0.13	4.54	1.82	0.83	0.45
L.S.D _{0.01} Average		2.82	3.52	3.61	0.18	6.15	2.46	1.12	0.62

*, **: Significant at 0.05 and 0.01 levels of probability, respectively

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