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Using Recurrent Selection to Improve Some Economic Traits in Egyptian Cotton (*Gossypium barbadense* L.)

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THIS WORK was done at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, Egypt during three seasons (2018–2020) to assess genetic response to selection and some genetic estimates i.e. phenotypic variance, phenotypic and genotypic coefficients of variability (PCV, GCV) and heritability for boll weight, lint%, lint yield, fiber length, fiber fineness and fiber strength in two extra-long staple cotton crosses: Giza96 x Giza76 (pop.1) and Giza93 x Pima S_1 (pop.2) at three generations F_2-F_4. Results showed significant differences among generations for most traits. Phenotypic variance, PCV, GCV and heritability were decreased as generation proceeded for all traits, indicating more homogenous and uniform in advanced generations. Selected families from F_2 and F_3 generations had higher mean performance than F_3 and F_4 realized means. The predicted expected estimates of selection in F_2 to F_3 and F_3 to F_4 generations were greater than their corresponded estimates in F_3 and F_4 generations for all traits. Predicted narrow sense heritability values were higher than realized ones and pop.1 values were higher than pop.2 for all generations. The improvements obtained from the second cycle of selection were greater than that obtained from the first cycle for the traits BW, L%, Mic. and Press. in both populations, whereas, the improvements obtained from the first cycle were greater for the traits LY/P and FL in both populations. Recurrent selection improved the studied traits simultaneously in the desired direction, the two populations varied in their response to selection as the second population showed higher responses for most traits.

Keywords: *Recurrent selection, Egyptian cotton, Genetic advance, Heritability.*

Introduction

Cotton is one of the most economic crops worldwide, it demand large number of employments starting from the agricultural practices in the field to the different industries that depend on cotton products such as, the textile industries, livestock feeding, oils, soap and other industries (Stewart and Rossi 2010).

The prime destination of cotton breeders is to improve lint yield and fiber properties through selecting supreme plants in breeding programs. Selection depends primarily upon genetic variability within the breeding population (Acquaah, 2012). Breeders have been used various methods to increase genetic variability within their cotton germplasm such as, hybridization between elite genotypes to obtain new recombinations, introduction of excellent within breeding population. Accordingly, there is greater prospect of getting superior lines from the initial population. However, it is a method to improve

exotic genotypes and using it in the local breeding program, and modern techniques of genetic engineering. Consequently, breeders use different methods of selection on the genetic materials to improve the different traits of cotton plant (Singh, 2004).

Early generations testing aim to increase breeding efficiency by early discrimination of superior heterogeneous plants and early discarding inferior ones and consequent concentrate selection efforts to the superior populations (Singh *et al*., 2021). Recurrent selection that popularized first by Hull (1945) is a cyclic selection generation after generation accompanied with interbreeding of selects to improve frequency of the desired alleles for a trait population, but it does not directly drives to release of new cultivars. Selection differential measures artificial selection intensity, while response to

selection gives information about the alteration in mean performance of a trait from a generation to the next one. Hence, plant breeders treat with genetic advance or gain as the ultimate product of heritability and selection differential (Acquaah, 2012).

Many previous reports have been studied the ability of selection to improve cotton traits. Preetha and Raveendren, (2008), Basal *et al.*, (2017) and Parre and Patil (2021) used different procedures of selection from F_2 to F_4 in upland cotton, they found predominance of additive genetic variance and practiced effective selection for isolating promising lines for the studied traits. The selected populations and progenies could be further utilized for the development of parental lines or isolation of lines with new gene combinations.In Egyptian cotton, Abou El-Yazied *et al.* (2008), Hassaballa *et al.* (2012) Abou El-Yazied *et al.* (2014), Ali *et al.* (2014), Sultan and El-Hoseiny (2017) as well as Gibely (2021) found that different methods of selection procedures enhanced the mean performances of lint %, earliness, response to late planting conditions and some other traits in cotton crosses than their base populations, they also recorded different responses to selection among the studied hybrid populations. Recurrent selection has enhanced the population mean for all the studied traits without losing variability.

The destination of this study was to estimate the mean performances of some plant traits in two segregating generations F_3 and F_4 after two cycles of recurrent selection as compared to the base population (F_2) and to determine the effect of selection on the variability of these traits. In addition, to assess the predicted response (genetic advance) and the realized response to selection for the efficacy of recurrent selection procedures to improve the studied traits in two hybrid cotton populations.

1. Materials and Methods

Materials: Plant materials utilized in the present work comprised the selfed seeds of two intraspecific cotton crosses (Giza 96 x Giza 76 as population 1 and Giza 93 x Pima S_1 as population 2) belonging to *Gossypium barbadense* L. at three segregating generations i.e. F_2 - F_4 in addition to their parental genotypes. These materials were produced by Cotton Breeding Section, Cotton Research Institute, Agric. Res. Center, Egypt.

Methods: Field experiments were sown at Sakha Agric. Res. Station, Agric. Res. Center, Kafr El-Sheikh Governorate, Egypt during the three seasons (2018 – 2020).

In the first growing season (2018), F_2 selfed seeds of the two crosses were sown in rows to produce F_2 plants. Each row was 4 m long and contained 8 single plants spaced 50 cm between plants and 65 cm between rows. At maturity all plants from each cross were picked to estimate the studied traits. Selection was accomplished on F_2 plants to take out the desired individual plants in the field on the basis of plant type, number of retained open bolls and productivity. Plants were artificially self pollinated as much as possible. At harvest, all of open pollinated bolls were picked to evaluate the studied traits. While selfed seed were used for sowing the next generation (F_3). Selection was used in 5% intensity for the superior plants in performance for the traits: lint %, boll weight, lint yield/ plant, fiber fineness (Micronaire value), fiber strength (Pressley index) and fiber length. 21 and 19 families were selected from cross I and II, respectively as the superior families then the superior plants from each family were selected to consist the F_3 seeds.

In the second growing season (2019), the selected plants out of F_2 generation with their parental varieties were evaluated as F_3 families in randomized complete block design (RCBD) replicated twice. Each replicate contained three rows as in the last season. The open pollinated seeds were planted as in normal planting in three rows, 4.0 m long and 0.65 m width with 20 hills and two plants left per hill, each three rows were regarded as a family with one row skipped between families and two replicates were used. Selection was practiced between families (open pollinated) and within families (single plants) to select the best 5% of plants within best families. At maturity selected plants from each family were picked to estimate the same aforementioned traits in the two crosses. 10 and 30 families from cross I and II, respectively were selected as the superior families then the superior plants from each family were selected to consist the F_4 seeds.

In the third season (2020), the selfed seeds of F_4 generation resulted from selected plants and open pollinated seeds were sown as in the last season and used to determine the same traits. 17 and 21 families from cross I and II, respectively were selected as the superior families then the superior plants from each family were selected to be used as the F_5 seeds.

Statistical analysis:
Genetic Parameters

The analyses of variances were made according to Singh and Chaudhary (1985).

The phenotypic and genotypic variances and heritability values in broad sense were estimated in accordance to Falconer and Mackay (1996) as follows:

-Phenotypic variance ($\delta^2 p$): Total phenotypic variance for each generation.

-Environmental variance ($\delta^2 E$): The mean variance for the parental varieties.

$\delta^2 E = (V P_1 + V P_2) / 2$.

-Genotypic variance ($\delta^2 g$) is the genetic variance of each generation. $\delta^2 g = \delta^2 p - \delta^2 E$.

-Broad sense heritability ($h^2_b \%$) = ($\delta^2 g / \delta^2 p$) x 100

The phenotypic (PCV) and genotypic (GCV) coefficients of variability were calculated as shown by Burton (1952) as follows:

$$PCV = (\delta p / \overline{X}) \times 100$$
$$GCV = (\delta g / \overline{X}) \times 100$$

Where: δp and δg are standard deviation of phenotypic and genotypic of families.

$\overline{X}$ is the general mean of a trait.

Selection Parameters
Predicted Selection Response:
The expected genetic advance and the realized selection response were calculated as popularized by Sharma (1988) and Falconer (1989) as follows:

1- pS (Predicted / Expected selection differential)
$pS = i \times \delta p$
Where: i: Constant (=2.06 at 5% selection intensity); δp: Phenotypic standard deviation.

2- pR (Predicted / Expected selection response, i.e. Genetic advance)
$pR = i \times h^2_b \times \delta p$ or $= h^2_b \times pS$
Where: h^2_b= heritability in broad sense.

3- pR% (Percentage proportion of pR in $\overline{X}_p$)
$pR\% = 100 \times pR / \overline{X}_p$.   Where:
$\overline{X}_p$=Mean of selected plants in a generation.

4- pgR (Predicted/ expected generalized selection response)
$pgR = pR / \delta p$; or $= (pS \times h^2_b) / \delta p$.

5- ph^2_{ns} (Predicted heritability in narrow-sense)
$= pR / (i \times \delta p)$.

Realised Selection Response:
1- rR (Realised selection response) $= \overline{X}_g - \overline{X}_0$
where:
$\overline{X}_g$: Mean of selected plants in generation.
$\overline{X}_0$: Mean of the same generation.

2- rR% (Percentage proportion) = ($rR / \overline{F}_n$) x 100
where: $\overline{F}_n$ is the mean of any generation.

3- rgR (Realised generalized selection response in generation) = rR x δp.

4- rh^2_{ns} (Realised heritability in narrow-sense)
$rh^2_{ns} = rR / (i \times \delta p)$.

Results and Discussion

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Recurrent selection has been proved as an effective procedure of selection that accumulate favorable alleles at a great number of loci and offers increased possibility for selecting plants with desirable trait combinations within the selected population (Hull, 1945).

The estimates of means, standard errors, phenotypic (PCV %) and genotypic (GCV %) coefficient of variability as well as broad sense heritability (h^2_b) during the three segregating generations F_2, F_3 and F_4 for all studied traits in the two hybrid populations in this study are given in Table (1).

Means and standard errors revealed significant differences among the three generations for most of the studied traits. Mean performances showed considerable increments as the generation proceeded for all traits except for fiber fineness expressed as micronaire reading that showed desirable decrease as the generation preceded which reflecting the success of recurrent selection in improving such traits. The two cotton populations varied in performance for the studied traits among the three generations which may be attributed to significant difference among the four parental varieties involved in the two crosses.

Boll weight (g) varied from 3.05 g for F_2 in the first cross (Giza 96 x Giza 76, Pop. 1) to 3.31 g for F_4 in the second cross (Giza 93 x Pima S_1, Pop. 2). The mean values of BW for (Pop. 2) were higher in magnitude as compared to that of (Pop. 1) at the three generations. Concerning lint percentage (L%), it varied from 34.47% for F_2 in pop. 2 to 36.58% for F_4 in pop. 1. The mean values of L% for (Pop. 1) were higher in magnitude than that of (Pop. 2) at the three generations.

The same trend was recorded for the trait lint yield/ plant (LY/P) as it varied from 66.21g for F_2 in pop. 2 to 86.70 g for F_4 in pop. 1. The mean values were higher in Pop. 1 as compared to those of Pop. 2 at the three generations, contrarily, the recorded increments resulted from selection were higher in pop. 2 as compared to those recorded in pop. 1.

Table 1. Means and standard errors, total variance, phenotypic (PCV) and genotypic (GCV) coefficients of variation and broad sense heritability estimated in F_2, F_3 and F_4 generations for the studied traits in two hybrid cotton populations.

Traits	Gen.	Mean ± Sd		Variance		PCV%		GCV%		h^2_b	
		Pop. 1	Pop. 2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2
BW	F_2	3.05 ±0.23	3.16 ±0.19	0.053	0.038	1.737	1.315	1.146	0.796	75.69	66.40
	F_3	3.12 ±0.20	3.23 ±0.18	0.038	0.033	1.229	0.895	0.651	0.627	72.83	62.14
(g)	F_4	3.20 ±0.17	3.31 ±0.17	0.030	0.030	0.923	0.650	0.360	0.546	70.40	60.47
L %	F_2	35.18 ±2.16	34.47 ±1.81	4.665	3.284	13.260	9.134	9.134	5.961	68.89	62.58
	F_3	35.55 ±2.07	35.00 ±1.73	4.286	2.980	12.056	7.973	7.973	5.209	66.13	61.19
	F_4	36.58 ±1.97	36.18 ±1.65	3.883	2.734	10.615	6.648	6.648	4.550	62.62	60.23
LY/p	F_2	79.43 ±11.7	66.21 ±12.2	137.43	148.50	173.02	112.88	112.88	160.58	65.24	71.60
	F_3	84.22 ±10.3	72.43 ±11.8	107.12	140.22	127.20	80.47	70.47	134.22	63.26	69.34
(g)	F_4	86.70 ±9.60	75.83 ±11.7	92.09	136.60	106.21	65.11	51.11	112.67	61.30	62.55
FL	F_2	36.23 ±0.92	35.46 ±0.83	0.855	0.688	2.359	1.328	1.093	1.086	56.28	55.98
	F_3	36.32 ±0.88	35.86 ±0.74	0.780	0.550	2.146	1.138	0.889	0.824	53.83	53.75
(mm)	F_4	36.40 ±0.82	36.21 ±0.70	0.666	0.497	1.830	0.939	0.569	0.670	51.31	48.85
Mic.	F_2	3.66 ±0.32	3.39 ±0.29	0.103	0.085	2.807	1.736	1.736	1.746	61.83	69.64
	F_3	3.45 ±0.28	3.22 ±0.27	0.081	0.075	2.421	1.419	1.249	1.361	58.62	58.82
	F_4	3.20 ±0.27	3.03 ±0.26	0.074	0.069	2.326	1.299	1.099	1.251	55.87	55.20
Press.	F_2	11.64 ±0.40	11.49 ±0.29	0.089	0.082	0.763	0.439	0.187	0.415	57.53	58.06
	F_3	11.72 ±0.28	11.65 ±0.27	0.081	0.075	0.692	0.380	0.118	0.345	54.90	54.06
	F_4	11.96 ±0.28	11.90 ±0.26	0.076	0.067	0.638	0.320	0.078	0.271	50.16	48.34

Regarding fiber properties studied which were: fiber length (FL), fiber strength expressed as Pressely index (Press.) and fiber fineness expressed as micronaire reading (Mic.); data concerning these traits showed that FL and Press. were varied from 35.46 mm and 11.49, respectively for F_2 in pop. 2 up to 36.40 mm and 11.96, respectively for F_4 in pop. 1. Means were higher in Pop. 1 than that of Pop. 2 through the three generations, although the resulted increment from F_2 to F_4 was higher for pop. 2 than that in pop. 1. With regard to Mic., results in Table (1) showed that the means values ranged from 3.03 for F_4 in pop. 2 to 3.66 for F_2 in pop. 1, the mean values were reduced (more fineness) as generation proceeded within the two populations studied. Pop. 2 showed better values for Mic. than pop. 1 for the three generations.

It is clear that the two cycles of recurrent selection used in this study resulted considerable improvement in the mean performances in the studied traits as compared to the base populations that might be mostly ascribed to the accumulation of advantageous alleles as a result of selection effectiveness. Similar findings were reported in previous works by: Abou El-Yazied *et al.*, 2008;

Hassaballa *et al.*, 2012; Abou El-Yazied *et al.*, 2014; Sultan and El-Hoseiny, 2017; Abd El Sameea *et al.*, 2020 and Gibely, 2021.

Results pertaining to the studied genetic parameters (total phenotypic variance, phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and heritability in broad sense (h^2_b) for the studied traits presented in Table (1) showed that phenotypic variance decreased as the generation proceeded, F_4 had the lowest variability followed by F_3 as compared to the base population (F_2) in both crosses which indicated more homogeneity and uniformity of F_3 and F_4 generations as compared to the base (F_2) population. Phenotypic variances ranged from 0.030 for BW in both populations to 148.50 for LY/P in pop. 2. The first cross (Pop. 1) gave higher values of total variance than the second cross (Pop. 2) for all traits (except for LY/P).

The coefficients of variability expressed as percentage at phenotypic and genotypic levels have been used to compare the variation observed among the different traits. A wider range of variability will enhance the opportunities of selecting a desired line (Shruti *et al.*, 2019). Regarding PCV and GCV, results showed that both estimates were larger in F_2 generation than F_3 and F_4 generations for all studied

traits in the two populations, the two estimates were reduced as generation progressed indicating that the advanced generations were more homogenous and uniform than the base population in the two crosses, that may be due to the effect of inbreeding that reduce heterozygosity and increase fixation of genes in the later generations (Mather, 1949). PCV and GCV ranged from 0.561 and 0.078, respectively for the trait Press. in pop. 1 and pop. 2 to 224.28 and 112.88 for LY/P in pop. 1 and pop. 2, respectively.

Sivasubramanian and Menon (1973) classified PCV and GCV to low (<10%), moderate (10-20%) and high (>20%), hence, high values of PCV and GCV were detected only for LY/P in both populations for the three generation; while intermediate values of PCV were recorded for L% in pop. 1 for all generations. Low PCV and GCV values were observed for the rest of the traits across the two crosses in all generations. The low disparity between PCV and GCV indicating that these traits were less affected by the environmental conditions, hence, selection for such traits on phenotype base would be effective (Kumar *et al*. 2019 and Gibely, 2021). Whereas the narrow range of variability detected for most traits reflect limiting efficiency of selection. Hence, cotton breeders have to create genetic variability through exploiting diverse germplasm and hybridization (Khokhar *et al*. 2018). These findings are in harmony with those of Preetha and Raveendren, 2008; Hassaballa *et al*., 2012; Abou El-Yazied *et al*., 2014; Abd El-Moghny, 2016 Sultan and El-Hoseiny, 2017; Shruti *et al*., 2019 and Gibely, 2021 who recorded low PCV and GCV for fiber quality and some other traits in cotton crosses.

Broad sense heritability (h^2_b) is the ratio between genotypic to phenotypic variances, it was divided by Robinson *et al.,* (1951) into three classes: Low (< 30%), moderate (30–60%) and high (> 60%). However, Falconer (1989) stated that heritability is a good indicator for the transmission of traits from parents to their offspring, GCV coupled with heritability might present the best indicator for the amount of genetic advance expected from selection.

Data concerning h^2_b presented in Table (1) revealed relatively moderate to high values for all traits in the two studied populations, ranged from 48.34% for Pressely index in F4 of Pop. 2 to 75.69% for BW in F_2 of Pop. 1, with higher values of Pop. 2 than Pop. 1 in most cases. These results indicated greater values of genotypic variances than environmental variances as well as the presence of sufficient amount of genetic variances in the studied material to practice effective selection for superior progenies to improve these economical traits.

However, the reduction of heritability estimates as the generation proceeded for all traits within the two populations might be ascribed to the reduction in

genetic variability and heterozygosity as a result of selection which exhausted a major part of variability (non-additive portion), in addition to the prevalence of non-additive portion of variability due to dominance and over-dominance effects in the early segregating generations which reduce with the progress of inbreeding as a result of the more homogeneity and uniformity for genes in latest generations; moreover, Wu *et al*. (2010) stated that inbreeding depression in several crosses would be expected in later generations if parents had negative homozygous dominance effects for a trait. Our findings were in accordance with those reported by: Abou El-Yazied *et al*., 2014; El-Mansy, 2015; and Mabrouk, 2020. Whereas other works detected increasing broad sense heritability with advancement of generation that was attributed to the increase in additivity of gene effects as a result of the increase in homozygosity (Preetha and Raveendren, 2008; Abd El-Moghny, 2016; Abd El Sameea *et al*., 2020 and Gibely, 2021). In the same connection, AL-Hibbiny (2020) found that yield and its attributed traits showed lower heritability with proceeding of generation, whereas fiber traits had higher values in later generations.

The selection procedure

Means of predicted and realized responses to selection for boll weight (BW) and lint% (L%) in the three cycles of selection are presented in Table (2). Results concerning BW showed that selected families from F_2 and F_3 generations had higher mean performances (3.14 and 3.19, respectively in pop. 1 and 3.36 and 3.27, respectively in pop. 2) as compared to F_3 and F_4 realized means which gave 3.12 and 3.22, respectively in pop. 1 and 3.36 and 3.37, respectively in pop. 2).

The predicted expected advance to selection (pR) in F_2 to F_3 generations (31.29 and 11.40, respectively in pop. 1 and pop. 2) and in F_3 to F_4 generations (21.37 and 6.19, respectively) were greater than realized advance (rR) in F_3 and F_4 generations as the values were 0.07 and 0.06, respectively for pop. 1 and pop. 2 in F_3 generation and 0.08 and 0.08, respectively in F_4 generation. The pR in F_4 to F_5 generations were 13.80 and 3.30, respectively in pop.1 and pop. 2. Moreover, percentage proportion for predicted response to selection (pR%) were higher than realized proportion (rR%) in all cases for the two populations except for pR% in F_3 generation of pop. 2 (1.89%) that was lower than rR% in F_4 generation (2.48%).

Table 2. Predicated and realized response to selection in F₂ - F₄ generations within two cotton populations for boll weight and lint percentage.

Selection Parameters	Predicted Response in F_2 to F_3		Realized Response in F_3		Predicted Response in F_3 to F_4		Realized Response in F_4		Predicted response in F_4 to F_5	
	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2
`BW (g)										
Selection response ((G.A), pR, rR)	31.29	11.40	0.07	0.06	21.37	6.19	0.08	0.08	13.80	3.30
Percentage proportion (pR%, rR %)	10.03	3.40	2.22	2.02	6.70	1.89	2.52	2.48	42.27	9.49
Generalized selection response (pgR, rgR)	7.20	58.58	0.35	0.36	69.15	34.32	0.47	0.47	80.29	19.07
Selection differential response (Ps, rs)	0.47	0.40	0.07	0.20	0.40	0.37	0.06	0.17	0.35	0.36
ph^2_n	65.98	28.44	65.98	20.33	52.98	16.66	22.76	12.49	38.98	19.26
Realized Mean	3.05	3.16	3.12	3.23	--	--	3.20	3.31	--	--
Mean of selected families	3.14	3.36	--	--	3.22	3.34	--	--	3.26	3.37
L%										
Selection response ((G.A), pR, rR)	65.70	49.18	0.37	0.53	2.82	93.82	1.03	1.18	2.54	52.66
Percentage proportion (pR%, rR %)	17.45	1.37	1.03	1.52	7.62	2.68	2.82	3.26	6.78	13.56
Generalized selection response (pgR, rgR)	41.91	54.35	0.18	0.31	1.36	31.85	0.52	0.71	1.29	27.14
Selection differential response (Ps, rs)	4.45	3.73	2.47	1.36	4.26	3.56	0.90	2.65	4.06	3.41
ph^2_n	68.89	13.18	14.76	10.39	33.07	26.38	25.39	13.45	31.31	15.46
Realized Mean	35.18	34.47	35.55	35.00	--	--	36.58	36.18	--	--
Mean of selected families	36.15	35.11	--	--	36.99	36.32	--	--	37.48	36.43

ph^2_n: Predicted heritability in narrow-sense.

In addition, predicted generalized response to selection (pgR) of F_2 to F_3 and F_3 to F_4 generations were higher than those of realized generalized selection (rgR) in F_3 and F_4 generations, the values for pgR reached 7.20 and 58.58, respectively in pop. 1 and 2 for F_2 to F_3; 69.15 and 34.32, respectively for F_3 to F_4 generations as well as 80.29 and 19.07, respectively for F_4 to F_5 generations. While rgR values were 0.35 and 0.36, respectively in pop. 1 and pop. 2 in F_3 as well as 0.06 and 0.17, respectively in pop. 1 and pop. 2 for F_4 generation.

The predicted selection differentials (pS) were higher in magnitude than the realized differential responses (rS) in both populations, pS values were 0.47 and 0.40, respectively for pop.1 and pop.2 in F_2 to F_3 generations; 0.40 and 0.37, respectively in F_3 to F_4 generations as well as 0.35 and 0.36, respectively in F_4 to F_5 generations. While rS values were 0.07 and 0.20, respectively in F_3 generation as well as 0.06

and 0.17, respectively for pop.1 and pop. 2 in F_4 generation.

Predicted heritability values in narrow sense (ph^2_n) were higher than realized ones and in pop. 1 higher than that of pop. 2 for all generations, the values ranged from 22.76% in F_4 to 65.98% F_2 and F_3 generations for pop. 1, as well as 12.49% in F_4 generation to 28.44% in F_2 generation for pop. 2. The values of ph^2_n were decreased as generations proceeded. The aforementioned results clarify that dominance gene effects were prevalence in the inheritance of BW, in addition, greater response in second cycle than that of first cycle of selection was recorded and attributed to minor genes affecting BW in first cycle and major genes in second cycle of selection (Avery *et al.*, 1982).

The same trend was observed for lint percentage trait (L%) as the means of predicted and

realized responses to selection in the three cycles of selection clarified that selected families from F_2 and F_3 generations had higher mean performances (36.15% and 36.99%, respectively in pop.1 and 35.11% and 35.65%, respectively in pop. 2) as compared to F_3 and F_4 realized means which reached 36.15% and 36.99 %, respectively in pop.1 as well as 35.11% and 35.65%, respectively in pop. 2.

The predicted expected advance to selection (pR) in F_2 to F_3 generations (65.70 and 49.18, respectively in pop.1 and pop. 2) and in F_3 to F_4 generations (2.82 and 93.82, respectively) were greater than realized advance (rR) in F_3 and F_4 generations as the values were 0.37 and 0.53%, respectively for pop.1 and pop. 2 in F_3 generation and 1.03 and 1.18, respectively in F_4 generation. The pR in F_4 to F_5 generations were 2.54 and 52.66, respectively in pop.1 and pop.2. Moreover, percentage proportion for predicted response to selection (pR%) were higher than realized proportion (rR%) in all cases for pop.1, whereas pR% values were lower than rR% in pop. 2.

In addition, predicted generalized response to selection (pgR) of F_2 to F_3 and F_3 to F_4 generations were higher than realized generalized selection (rgR) in F_3 and F_4 generations, the values for pgR were 41.91 and 27.14, respectively in pop. 1 and 2 for F_2 to F_3; 1.36 and 54.35, respectively for F_3 to F_4 generations as well as 1.29 and 31.85, respectively for F_4 to F_5. While rgR values were 0.18 and 0.31, respectively in pop. 1 and pop. 2 in F_3 generation as well as 0.52 and 0.71, respectively in pop. 1 and pop. 2 for F_4 generation.

The predicted selection differentials (pS) were higher than the realized differential responses (rS) in both populations, pS values were 4.45 and 3.73, respectively for pop.1 and pop. 2 in F_2 to F_3 generations; 4.26 and 3.56, respectively in F_3 to F_4 generations as well as 4.06 and 3.4, respectively in F_4 to F_5 generations. While rS values were 2.47 and 1.36, respectively in F_3 as well as 0.90 and 2.65, respectively in F_4 generation.

Predicted heritability values in narrow sense (ph^2_n) for L% were higher than realized ones and pop. 1 values were higher than that of pop. 2 for all generations, the values ranged from 25.93% in F_4 to 68.89% in F_2 generations for pop. 1, as well as 10.39% in F_3 generation to 26.38 % in F_3 generation for pop. 2. The aforementioned results clarify that additive and non-additive gene effects were controlling this trait.

Means of predicted and realized responses to selection for lint yield/plant (LY/P) and fiber length (FL) in the three cycles of selection are presented in Table (3). Results concerning LY/P showed that selected families from F_2 and F_3 generations had

higher mean performances (85.27 and 87.05, respectively in pop.1 and 74.48 and 77.54, respectively in pop. 2) as compared to F_3 and F_4 realized means which were 84.22 and 86.70, respectively in pop.1 and 72.43 and 75.83, respectively in pop. 2). The predicted and realized responses to selection increased as generation progressed due to the efficiency of selection.

The predicted expected advance to selection (pR) in F_2 to F_3 generations (11.46 and 25.10, respectively in pop. 1 and pop. 2) and in F_3 to F_4 generations (11.81 and 78.04, respectively) were greater than realized advance (rR) in F_3 and F_4 generations as the values were 4.79 and 6.22, respectively for pop. 1 and pop. 2 in F_3 generation and 2.48 and 3.39, respectively in F_4 generation. The pR in F_4 to F_5 generations were 9.51and 62.52, respectively in pop.1 and pop. 2. Percentage proportion for predicted response to selection (pR%) were higher than the realized (rR%) in all cases for the two populations over all generations except for pR% in F_2 generation of pop. 2 (0.28%) that was lower than rR% in F_3 generation (8.59%).

In addition, predicted generalized response to selection (pgR) of F_2 to F_3 and F_3 to F_4 generations were higher than realized generalized selection (rgR) in F_3 and F_4 generations, the values for pgR% reached 7.20 and 58.58, respectively in pop.1 and 2 for F_2 to F_3; 69.15 and 34.32, respectively for F_3 to F_4 generations as well as 80.29 and 19.07, respectively for F_4 to F_5. While rgR values were 0.35 and 0.36, respectively in pop.1 and pop. 2 in F_3 as well as 0.06 and 0.17, respectively in pop.1 and pop. 2 for F_4 generation.

The predicted selection differentials (pS) were higher than the realized differential responses (rS) in both populations, pS values were 24.15 and 25.10, respectively for pop.1 and pop. 2 in F_2 to F_3 generations; 21.32 and 24.39, respectively in F_3 to F_4 generations as well as 19.77 and 24.08, respectively in F_4 to F_5 generations. While rS values were 4.37 and 22.27, respectively in F_3 generation as well as 2.16 and 12.73, respectively in F_4 generation.

Predicted heritability estimates in narrow sense (ph^2_n) were higher than realized ones and pop. 1 estimates were higher than pop. 2 for all generations, the range was from 12.57% in F_4 generation to 65.24% in F_2 generation for pop. 1, as well as 10.27% in F_4 generation to 32.14% in F_3 generation for pop. 2. The ph^2_n values were decreased as generations proceeded. These results clarified that dominance gene effects were prevalence in the inheritance of LY/P.

Regarding fiber length (FL) results for this trait given in Table (3) showed that selected families from F_2 and F_3 generations had higher mean performances (36.54 and 36.40, respectively in pop.1 and 35.92 and

Table 3. Predicated and realized response to selection in F_2 - F_4 generations within two cotton populations for lint yield/plant and fiber length.

Selection Parameters	Predicted response in F_2 to F_3		Realized response in F_3		Predicted response in F_3 to F_4		Realized response in F_4		Predicted response in F_4 to F_5	
	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2
LY/plant (g)										
Selection response ((G.A), pR, rR)	11.46	25.10	4.79	6.22	11.81	78.04	2.48	3.39	9.51	62.52
Percentage proportion (pR%, rR %)	13.68	0.28	5.68	8.59	13.57	9.44	2.86	4.48	10.70	7.06
Generalized selection response (pgR, rgR)	13.44	2.06	0.46	0.52	1.14	66.21	0.26	0.29	0.99	5.35
Selection differential response (Ps, rs)	24.15	25.10	4.37	22.27	21.32	24.39	2.16	12.73	19.77	24.08
ph^2_n	65.24	31.00	34.75	21.28	27.70	32.14	12.57	10.27	24.06	21.60
Realized Mean	79.43	66.21	84.22	72.43	--	--	86.70	75.83	--	--
Mean of selected families	85.27	74.48	--	--	87.05	77.54	--	--	88.86	80.00
FL (mm)										
Selection response ((G.A), pR, rR)	44.11	75.59	0.09	0.40	0.75	46.17	0.08	0.36	0.52	33.10
Percentage proportion (pR%, rR %)	120.72	2.05	0.24	1.12	2.06	1.30	0.21	0.98	1.43	8.98
Generalized selection Response (pgR, rgR)	47.70	91.15	0.10	0.54	0.85	62.28	0.09	0.50	0.64	46.97
Selection differential response (Ps, rs)	1.90	1.71	0.30	1.44	1.82	1.53	0.04	0.63	1.68	1.45
ph^2_n	46.31	44.25	23.16	20.28	20.56	30.23	24.52	16.56	15.55	22.80
Realized Mean	36.23	35.46	36.32	35.86	--	--	36.36	36.21	--	--
Mean of selected families	36.54	35.92	--	--	36.40	36.26	--	--	36.44	36.43

ph^2_n: Predicted heritability in narrow-sense.

36.26, respectively in pop. 2) as compared to realized means in F_3 and F_4 generations (36.32 and 36.36, respectively in pop.1 and 35.86 and 36.21, respectively in pop. 2).

The predicted expected advance to selection (pR) in F_2 to F_3 generations (44.11 and 75.59, respectively in pop. 1 and pop. 2) and in F_3 to F_4 generations (0.75 and 46.17, respectively) were greater than realized advance (rR) in F_3 and F_4 generations as the values were 0.09 and 0.40, respectively for pop. 1 and pop. 2 in F_3 generation as well as 0.08 and 0.36, respectively in F_4 generation. The pR in F_4 to F_5 generations were 0.52 and 33.10, respectively in pop.1 and pop. 2. However, proportion for predicted response (pR%) were higher than realized proportion (rR%) in most cases for the two populations and all generations.

However, predicted generalized response to selection (pgR) of F_2 to F_3 and F_3 to F_4 generations were higher than the reialzed ones (rgR) in F_3 and F_4 generations, the values for pgR were 47.70 and 91.15, respectively

in pop. 1 and 2 for F_2 to F_3; 0.85 and 62.28, respectively for F_3 to F_4 generations as well as 0.64 and 46.97, respectively for F_4 to F_5. While rgR% values were 0.10 and 0.54, respectively in pop. 1 and pop. 2 in F_3 as well as 0.09 and 0.50, respectively in pop. 1 and pop. 2 for F_4 generation.

The predicted selection differentials (pS) were higher than the realized differential responses (rS) in both populations, pS values were 1.90 and 1.71, respectively for pop.1 and pop. 2 in F_2 to F_3 generations; 1.82 and 1.53, respectively in F_3 to F_4 generations; 1.68 and 1.45, respectively in F_4 to F_5 generations. While rS values were 0.30 and 1.44, respectively in F_3; 0.04 and 0.63, respectively in F_4 generation. Predicted heritability in narrow sense (ph^2_n) were higher than realized ones in most cases, the values ranged from 15.55% in F_4 to 46.31% in F_2 for pop.1, as well as 16.56% in F_4 to 44.25% in F_2 for pop. 2. The values of ph^2_n were decreased as generations proceeded that may due to the prevalence of dominance gene effects in the inheritance of FL.

Means of predicted and realized responses to selection for fiber fineness as micronaire reading (Mic.) and fiber strength as Pressely index (Press.) for the two hybrid populations in the three cycles of selection were presented in Table (4). Results concerning Mic. showed that selected families from F_2 and F_3 generations had undesirable higher mean performances (3.52 and 3.33, respectively in pop.1; 3.25 and 3.11, respectively in pop. 2) as compared to F_3 and F_4 realized means which gave desirable lower values i.e. 3.35 and 3.20, respectively in pop.1 as well as 3.22 and 3.03, respectively in pop. 2).

The realized advance (rR) in F_3 and F_4 showed desirable negative values that reached -0.313 and -0.166, respectively for pop. 1 and pop. 2 in F_3 generation as well as -0.149 and -0.191, respectively in F_4 generation. The pR in F_2 to F_3 generations (40.83 and 17.87, respectively in pop.1 and pop.2)

and in F_3 to F_4 generations (0.303 and 30.66, respectively), while in F_4 to F_5 generations were 0.266 and 7.102, respectively in pop.1 and pop.2. Moreover, Percentage proportion for realized response to selection (rR%) were lower and desired than predicted proportion (pR%) in all cases for both populations. Concerning the realized generalized response to selection (rgR) in F_3 and F_4 generations were favourably lower than predicted generalized selection (pgR), the rgR values were -1.101 and -0.608, respectively in pop.1 and pop.2 in F_3 generation as well as -0.546 and -0.727, respectively in F_4 generation. While pgR reached 57.37 and 61.30, respectively for both populations in F_2 to F_3 generation; 1.063 and 56.13, respectively in F_3 to F_4 generations; 0.974 and 27.089, respectively for F_4 to F_5 generation. These results clarified the efficiency of recurrent selection in improving such trait.

Table 4. Predicated and realized response to selection in F_2 - F_4 generations within two cotton populations for Micronaire reading and Pressely index.

Selection Parameters	Predicted response in F_2 to F_3		Realized response in F_3		Predicted response in F_3 to F_4		Realized response in F_4		Predicted response in F_4 to F_5	
	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2
Mic.										
Selection response ((G.A), pR, rR)	40.83	17.87	-0.313	-0.166	0.303	30.66	-0.149	-0.191	0.266	7.102
Percentage proportion (pR%, rR %)	11.60	5.59	-9.363	-5.151	9.032	10.75	-4.658	-6.286	8.487	24.094
Generalized selection response (pgR, rgR)	57.37	61.30	-1.101	-0.608	1.063	56.13	-0.546	-0.727	0.974	27.089
Selection differential response (Ps, rs)	0.66	0.60	-0.142	-0.195	0.586	0.56	-0.069	-0.086	0.562	0.540
ph^2_n	61.83	29.76	61.83	22.85	25.80	54.50	-26.51	12.23	23.63	13.15
Realized Mean	3.66	3.39	3.35	3.22	--	--	3.20	3.03	--	--
Mean of selected families	3.52	3.25	--	--	3.33	3.11	--	--	3.15	3.00
Press.										
Selection response ((G.A), pR, rR)	15.02	34.29	0.226	0.264	2.10	30.51	0.300	0.147	1.069	25.72
Percentage proportion (pR%, rR%)	12.55	2.85	0.227	2.248	0.835	2.595	2.509	1.234	0.574	21.38
Generalized selection response (pgR, rgR)	50.43	62.61	0.093	0.964	0.350	55.68	1.087	0.569	0.251	59.58
Selection differential response (Ps, rs)	0.61	0.59	0.335	0.543	0.585	0.564	0.131	0.129	0.569	0.532
ph^2_n	24.48	58.06	24.49	20.49	28.49	54.06	52.75	51.14	6.10	48.34
Realized Mean	11.64	11.49	11.66	11.75	--	--	11.96	11.90	--	--
Mean of selected families	11.97	11.85	--	--	12.00	11.96	--	--	12.09	11.95

ph^2$_n$: Predicted heritability in narrow-sense.

The realized differential responses (rS) showed lower and desired values than predicted selection differentials (pS) in both populations, both estimates showed low values that did not reach the unity. The values of rS were -0.124 and -0.195, respectively in F$_3$ generation as well as -0.069 and -0.086, respectively in F$_4$ generation. The pS values were 0.66 and 0.60, respectively for pop.1 and pop. 2 in F$_2$ to F$_3$ generations; 0.586 and 0.560, respectively in F$_3$ to F$_4$ generations as well as 0.562 and 0.540, respectively in F$_4$ to F$_5$ generations.

Predicted heritability values in narrow sense (ph^2$_n$) were higher than realized ones and values of pop.1 were higher than that of pop. 2 in most cases, the values ranged from 0.00% (negative value that theoretically equal zero) in F$_4$ generation to 61.83% in F$_2$ to F$_3$ generations for pop.1, as well as 12.23% in F$_4$ generation to 54.50 in F$_3$ to F$_4$ generation for pop. 2. The values of ph^2$_n$ were decreased as generations preceded due to the dominance gene effects.

Regarding fiber strength (Press.) results showed that selected families from F$_2$ and F$_3$ generations had desirable higher means (11.97 and 12.00, respectively in pop.1 as well as 11.85 and 11.96, respectively in pop.2) as compared to F$_3$ and F$_4$ realized means which gave lower values reached 11.66 and 11.96, respectively in pop.1 as well as 11.85 and 11.96, respectively in pop.2). The predicted responses to selection (pR) in F$_2$ to F$_3$ generations (15.02 and 34.29, respectively in pop.1 and pop.2) and in F$_3$ to F$_4$ generations (2.10 and 30.51, respectively) were greater than realized response (rR) in F$_3$ and F$_4$ generations as the values were 0.226 and 0.264, respectively for pop.1 and pop.2 in F$_3$ generation and 0.300 and 0.147, respectively in F$_4$ generation.

The pR in F$_4$ to F$_5$ generations were 1.069 and 25.72, respectively in pop.1 and pop. 2. Similarly, percentage predicted proportion (pR%) were higher than realized proportion (rR%) for the two populations over all generations. However, The predicted expected advance to selection (pR) and its proportion (pR%) were higher in magnitude for pop. 2 than pop.1 that may be attribute to the higher variance in the second population due to the exotic genotype involved in this population.

Predicted generalized response to selection (pgR) of F$_2$ to F$_3$ and F$_3$ to F$_4$ were higher than the realized ones (rgR) in F$_3$ and F$_4$ generations, the values for pgR were 50.43 and 62.61, respectively in pop.1 and pop.2 for F$_2$ to F$_3$; 0.350 and 55.68, respectively for F$_3$ to F$_4$ generations; 0.25 and 59.58, respectively for F$_4$ to F$_5$generations. While rgR% values reached 0.093 and 0.964, respectively in pop.1

and pop.2 in F$_3$; 1.087 and 0.569, respectively in pop.1 and pop.2 for F$_4$ generation. Predicted selection differentials (pS) values were higher than the realized differential responses (rS) in both studied hybrid populations, pS values were 0.61 and 0.59, respectively for pop.1 and pop. 2 in F$_2$ to F$_3$ generation; 0.585 and 0.564, respectively in F$_3$ to F$_4$ generation as well as 0.569 and 0.532, respectively in F$_4$ to F$_5$ generation. While rS values were 0.335 and 0.543, respectively in F$_3$ generation, 0.131 and 0.129, respectively in F$_4$ generation.

Predicted heritability estimates in narrow sense (ph^2$_n$) were higher than realized ones in most cases, the values ranged from 6.10% in F$_{4-5}$ to 52.75% in F$_4$ generations for pop.1, as well as 20.49% in F$_3$ generation to 58.06% in F$_2$ to F$_3$ generations for pop.2. The values of ph^2$_n$ were higher in pop.2 as compared to those of pop.1 that may ascribed to the exotic genotype (Pima S$_1$) involved in pop. 2.
Our finding concerning recurrent selection on the evaluated estimates of selection were in accordance with the previous reports of Abou El-Yazied *et al.*, 2008; Ali *et al.*, 2014; Abou El-Yazied *et al.*, 2014; El-Mansy, 2015; Abd El-Moghny, 2016; Sultan and El-Hoseiny, 2017; Abd El Sameea *et al.*, 2020; AL-Hibbiny, 2020; Mabrouk, 2020 and Gibely, 2021.

Selection responses as percentage of the mean of base population (selection advance %, SA %) recorded in this study through two cycles of recurrent selection for the two hybrid populations are presented in Table (5). Results clarified that recurrent selection were relatively effective and induced appreciable improvement for all studied traits within the two hybrid populations.

With regard to BW, the first selection cycle obtained 2.274% improvement in the mean performance as compared to the base population and the total improvement after the two cycles reached 4.915% in pop.1, while in pop. 2 the improvement was 2.062% and 4.656% for both cycles of selection, respectively.
Concerning L%, the first cycle obtained 1.045% improvement in the mean performance as compared to the base population and the total improvement after the two cycles reached 3.975% in pop.1, while in pop. 2 the obtained improvement was 1.548% and 3.372% for both cycles of selection, respectively. Regarding LY/P, the first cycle obtained 6.025% improvement in the mean performance over the base population and the total cumulative improvement

after the two cycles reached 9.153% in pop.1, while in pop. 2 the obtained improvement was 9.396% and 14.528%, respectively for both cycles of selection.

Table 5. Superiority of recurrent selection cycles (SA%) as percentage over the base population for the studied traits in the two hybrid cotton populations.

| Traits	Cycle	Pop. 1	Change % (SA%)		Pop. 2	Change % (SA%)	
			One cycle	Total		One cycle	Total
BW (g)	C_0	3.05	--	--	3.16	--	--
	C_1	3.12	2.274	2.274	3.23	2.062	2.062
	C_2	3.20	2.582	4.915	3.31	2.541	4.656
L%	C_0	35.18	--	--	34.47	--	--
	C_1	35.55	1.045	1.045	35.00	1.548	1.548
	C_2	36.58	2.900	3.975	36.18	3.372	4.972
LY/plant (g)	C_0	79.43	--	--	66.21	--	--
	C_1	84.22	6.025	6.025	72.43	9.396	9.396
	C_2	86.70	2.950	9.153	75.83	4.692	14.528
FL (mm)	C_0	36.23	--	--	35.46	--	--
	C_1	36.32	0.242	0.242	35.86	1.131	1.131
	C_2	36.40	0.209	0.452	36.21	0.991	2.133
Mic.	C_0	3.66	--	--	3.39	--	--
	C_1	3.45	-5.698	-5.698	3.22	-4.899	-4.899
	C_2	3.20	-7.351	-12.631	3.03	-5.914	-10.523
Press.	C_0	11.64	--	--	11.49	--	--
	C_1	11.66	0.227	0.227	11.65	1.399	1.399
	C_2	11.96	2.574	2.807	11.90	2.149	3.578

C_0: Mean of base population; C_1, C_2: Means of first and second selection cycles; SA%: Genetic advance of selection as percentage of base population.

Fiber quality traits i.e. FL, Mic. and Press. showed similar cumulative improvement over the two cycles of selection. FL had 0.242% improvement after the first selection cycle than the base population and the total improvement after two cycles was 0.452% in pop.1, while in pop.2 the improvement was 1.131% and 2.133% for both cycles of selection, respectively. With regard to Mic., results revealed improvement over the base population (F_2) reached -5.698% and -12.631%, respectively for first and second cycles of selection in pop.1as well as -4.899% and -10.523%, respectively in pop. 2. Pressely index improved by 0.227% and 2.807% both cycles of selection respectively in pop.1, while the ratios were 1.399% and 3.578%, respectively in pop.2.

The improvements obtained from the second cycle of selection as compared to the first cycle were greater than that obtained from the first cycle as compared to the base population for the traits BW, L%, Mic. and Press. in both populations as shown in Table (5) and Figure (1). These results indicating additive effects of genes on these traits that increase in the advanced generations in the two crosses, which may be due to the effect of inbreeding that reduce heterozygosity and increase fixation of genes (Mather, 1949); furthermore, greater response in second cycle than that of first one might be attributed to minor genes affecting these traits in first cycle and major genes affecting in second cycle of selection (Avery *et al.*, 1982).

On the contrary, the improvements obtained from the first cycle of selection as compared to the base population was greater than that obtained from the second cycle for the traits LY/P and FL in both populations indicating prevalence of non-additive effects (dominance) over the additive effects of gene action on controlling such traits, which reduce with the proceeding of generations due to reduced heterozygosity and increased fixation of genes in the later generations (Mather, 1949).

The improvement in advanced cycles for the studied traits was further emphasized by the differentiation of individual progenies in F_3 and F_4 generations over the base population (F_2), and the opportunity for inducing lines with high performance for these traits increase with proceeding selection cycles in the two cotton populations. These results are in the same line with those popularized by Eberhart (1972) who stated that the improvement in breeding population outcomes in corresponding improvement in the derived lines out of this population after each selection cycle. Results also clarified simultaneous improvements due to selection cycles for all studied traits. Therefore, responses to selection for these traits were linear and is expected to proceed at approximately the same manner for an additional selection cycle (Abou El-Yazied *et al.*, 2014; Abd El-Moghny, 2016; Sultan and El-Hoseiny, 2017; AL-Hibbiny, 2020 and Gibely, 2021).
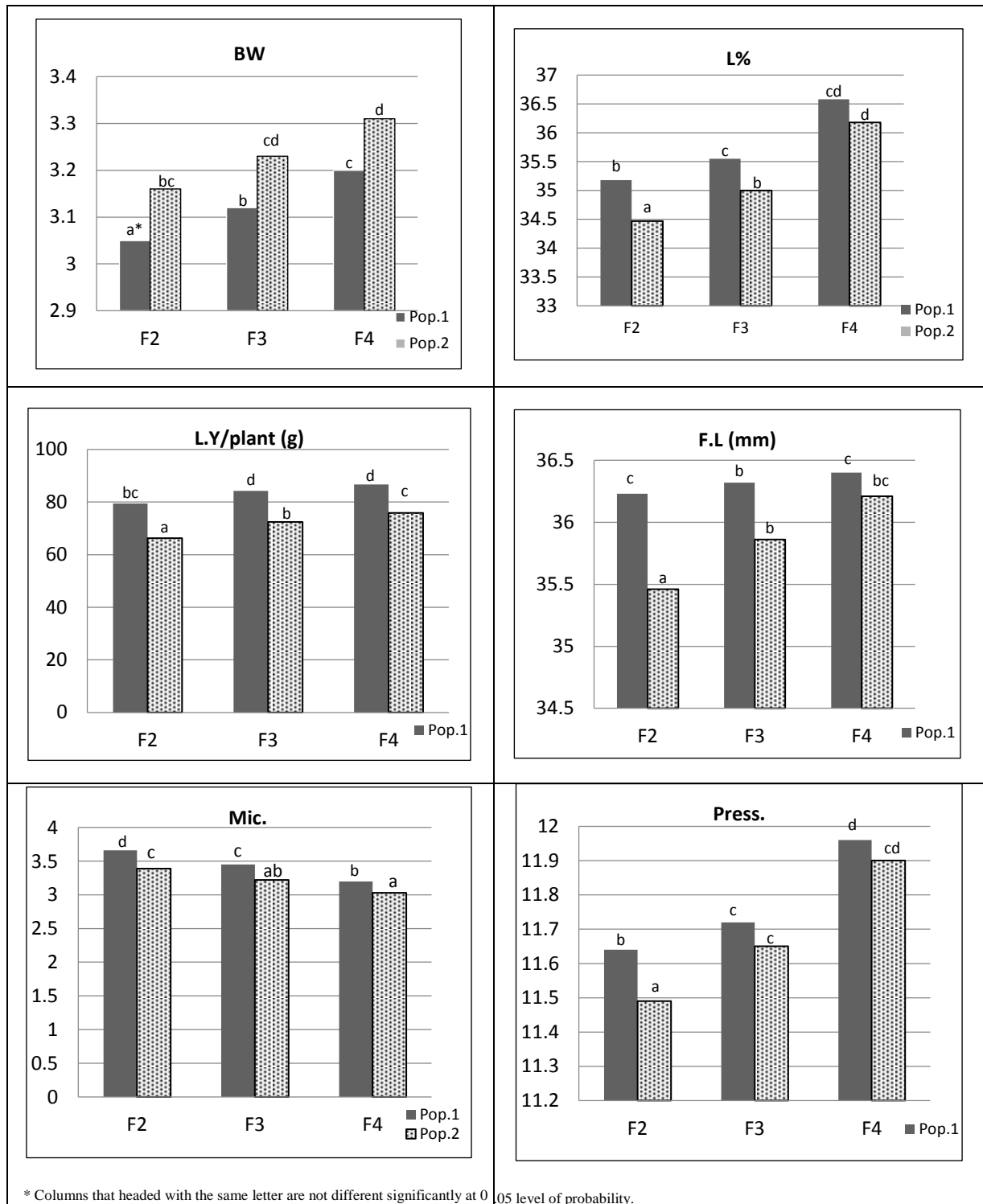
Fig. 1. Effect of two cycles of recurrent selection in two hybrid cotton populations for the studied traits.

Conclusion

Out of this study it may be concluded that recurrent selection was effective in improving the mean performance of the studied traits simultaneously in the desired direction, the two populations varied in their response to selection as the second population (Giza 93 x Pima S$_1$) showed higher responses for most traits than the first one (Giza 96 x Giza 76) that might be attributed to the origin and characterization of the parental genotypes involved in this population especially the exotic genotype which increase

variability within such population and increase efficiency of selection.

Ethics approval and consent to participate

This article does not contain any studies with human participants or animals performed by any of the authors.

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استخدام الانتخاب المتكرر في تحسين بعض الصفات الاقتصادية في القطن المصري

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أقيمت هذه الدراسة بهدف تقدير التحسين الوراثي المتوقع للانتخاب والتحسين الوراثي الفعلي والفارق الانتخابي وكذلك نسبة التوريث ومعامل التباين الوراثي والمظهري لبعض صفات المحصول (وزن اللوزة وتصافى الحليج ومحصول القطن الشعر للنبات) وبعض صفات التيلة (الطول والمتانة والنعومة) بعد ثلاث دورات من الانتخاب في الجيل الثاني والثالث والرابع لهجينين من الأقطان فائقة الطول، وهما (جيزة ٩٦ x جيزة ٧٦) العشيرة الأولى و(جيزة ٩٣ x بيما س١) العشيرة الثانية. وأقيمت التجربة بمحطة البحوث الزراعية بسخا بمحافظة كفر الشيخ – مصر خلال ثلاثة مواسم (٢٠١٨-٢٠٢٠م). ويمكن تلخيص النتائج فيما يلي: – أظهرت النتائج وجود إختلافات معنويه بين الأجيال الثلاثة فى العشيرتين لمعظم الصفات المدروسة. حدث انخفاض ملحوظ فى قيم التباين الكلى ومعاملى التباين المظهرى والوراثى وكذلك القيمه الوراثية مع تقدم الأجيال فى العشيرتين لكل الصفات المدروسة وذلك بسبب زيادة التجانس الوراثى مع تقدم الأجيال. كان متوسط العائلات المنتخبة في كل جيل أعلي من متوسط الجيل التالي في جميع الصفات كما حدث ارتفاع فى المتوسط الفعلي مع تقدم الأجيال كنتيجة لفاعلية الإنتخاب على الصفات المدروسة. وجد أن التحسين الوراثي المتوقع للانتخاب اكبر من التحسين الوراثي المتحصل عليه في الجيل التالي لكل القياسات المستعمله وكل الصفات المدروسة مما يشير الى أن تأثير التباين السيادى هو الذي يتحكم في هذه الصفات. كذلك فان تقديرات نسبة التوريث المتوقعه أعلى من المتحصل عليها فى الجيل التالى لكل الصفات والأجيال وكذلك كانت القيم فى العشيرة الأولى اعلى منها فى العشيرة الثانيه. كما اختلفت العشيرتان تحت الدراسه فى الاستجابة للانتخاب حيث أظهرت العشيرة الثانية استجابة اكبر وتحسين اعلى لمعظم الصفات المدروسة لوجود تباين أكبر بها نظرا للصنف الأجنبى الداخل فى تركيبها (بيما س١). وقد ثبت من الدراسة فعالية الانتخاب المتكرر فى احداث تحسين وراثى متزامن لجميع الصفات المدروسة وكذلك وجود امكانية لحدوث مزيد من التحسين لدورة انتخابية اخرى.