

EFFECTIVENESS OF RECURRENT SELECTION FOR IMPROVEMENT OF SOME ECONOMIC CHARACTERS IN EGYPTIAN COTTON

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(Manuscript received 24 November 2013)

Abstract

Two cycles of recurrent selection for the improvement lint percentage and other associated characters in two cotton crosses were applied at Sakha Agricultural Research Station Kafr El-Sheikh Governorate during six successive seasons (2008 – 2013). The results were as following.

The mean values were increased with first and second cycles of recurrent selection as compared with the basic populations. Genotypic and phenotypic coefficients of variability were larger in F_2 generation than F_3 generations and GCV was reduced in later generation (second cycle) indicating that the advanced cycle was more homogenous and uniform than the basic population. In addition, moderate to high estimates of heritability in broad sense were observed for all studied traits in the two populations and increased from F_2 to F_3 generations.

There were generally close agreement between predicted and observed responses to selection and predicted over estimated the actual ones for all traits. This suggests that dominance effects were lacking or of relatively with minor importance. Additive genetic effects would appear to predominate in the two populations. Hence, the breeder can depend on the predicted values.

A comparison of direction and magnitude of associations among traits over the two recurrent selection cycles indicated that several new associations in terms of direction and magnitude were observed, these results in newer recombinants which would be due to changes in coupling to repulsion phase linkage. Lint percentage of the second cycle selection exceeded over the base population by 13.3% and 17.73% in population I and II, respectively. Response to selection was linear and is predicted to continue at approximately the same rate of gain for an additional cycle.

The correlation responses to selection for lint percentage were observed between some unselected traits measured. As selection increased lint percentage, simultaneous increases were observed for boll weight, fiber length and strength. While, micronair reading showed slight negative desirable change. Generally, recurrent selection has been very successful in increasing the population mean in the desired direction simultaneously for all studied traits without losing variability.

INTRODUCTION

The basic premise of recurrent selection method is to increase the frequency of desirable genes and genetic recombination in a systematic manner to enhance the

opportunities of identify in superior genotypes in plant population. Success of recurrent selection method is dependent on the original assemblage of genes in breeding populations. If the gene frequency of the trait under selection is different among populations, response to selection may be realized but at different rates and levels. Richmond (1950) first suggested the use of recurrent selection method in cotton breeding in this respect, Opondo and Pathak (1982) mentioned that using recurrent selection was useful increase the frequency of favorable genes so that the populations and population crosses are improved with each selection cycle. Consequently, recombination of desirable characters should be increased.

The principle objectives in the cotton breeding include high lint yield and fiber quality properties. Consequently, plant breeders consider a number of traits during the selection process. Mahdy *et al.* (1987) compared the efficiency of three selection methods and reported that magnitude of genetic variability persisted after recurrent selection was larger than that after selection index and pedigree selection. In addition, Ahmed *et al.* (2003) compared actual and predicted genetic selection gains in two cotton crosses. The actual selection gain in general coincided with predicted one for most studied traits in first cross .While, the actual gain values for the second cross were not correlated with predicted values. Abdel-Hafez *et al.*(2003) estimate the magnitudes of the genetic advance from selection indices in two populations. The genetic gains for lint percentage in population I was large for selection and appeared important in the improvement of lint percentage. The predicted advances from F_4 generation were higher than those obtained from F_3/F_4 . The actual advances were higher than expected for all indices. In the other study, Abd El-Salam (2005) used pedigree selection in three populations and found that the means of F_2 were lower than F_4 for lint percentage and halo length. The phenotypic and genotypic coefficients of variation in F_2 were higher than those of F_3 and F_4 , except for halo length and lint percentage in population II, while the coefficient of variations in F_4 were higher than F_3 generation. Heritability ratios were high for lint percentage and halo length for the three populations in different generations.

El-Lawendey *et al.* (2008) used all possible mating among four F_2 selections in three populations. The highest predicted genetic advance was achieved for lint yield/ plant, number bolls/plant, lint/seed and seed index in the three populations. High to low genetic advances were found to be associated with high to low values of GCV for most studied characters. In the same time, Abou El-Yazied *et al.*(2008) used pedigree selection in two populations. The results showed that the means of F_2 were lower than F_3 and F_4 , generations for all studied traits except fiber fineness trait .The phenotypic and genotypic coefficients of variability were larger in F_2 generation than those of the

succeeding generations for all the studied traits. However, high estimates of heritability in broad sense were observed for all studied traits. The estimates of predicted genetic advance were obviously higher in F_4 than those in F_3 generation for most studied traits except for fiber fineness and boll weight in population I as well as fiber strength and boll weight in population II. The same trend was observed for actual gains and also, the selection advance (S.A.%).

The information about the degree of association among different traits of cotton is of great importance. Hence, cotton breeders are concerned with the total array of all economic characteristics. Thus, it is important to know the change in one trait by selection would affect other economic traits. Therefore, predicted changes as well as observed responses to selection for lint percentage with the unselected traits is worthy of study.

The objective of this investigation was to study the shift in mean performance of lint percentage and other traits from the original population to that of the second selection cycle and to assess the effect of selection on the variability of traits. In addition, to estimate the magnitude of the genetic advance from recurrent selection of lint percentage and its relationship with some unselected traits i. e., boll weight, fiber length, fiber fineness and fiber strength in two cotton population.

MATERIALS AND METHODS

The genetic materials used in this study included two populations belonging to *Gossypium barbadense* L. The first population was derived from the cross between (Pima high percentage x Suvin) and the second population was derived from the cross between (Pima high percentage x Giza 88). At Sakha Agricultural Research Station Kafr El-Sheikh Governorate during six successive seasons (2008 – 2013).

In 2008 the F_2 seeds of both populations were sown as well as original parents in non replicated rows 7.0 m., long and 0.65 m. wide, with one skipped row between each two consecutive planted row. Each row contained 10 single plants spaced 70 cm apart to facilitate self pollinating for each plant. Selection was carried out on F_2 plants to obtain the desirable individual plants in the field mainly on the basis of plant type, number of retained open bolls and productivity.

The 10% superior plants for lint percentage as main selected trait were selected as well as, boll weight, fiber length, fiber fineness and fiber strength as associated unselected traits.

In 2009 season the selfed seeds of each F_3 single plant were planted as in F_2 . The natural seeds of F_3 plants of each population were evaluated with the two original

parents in randomized complete block design with three replications. Each plot single row, 4.0 m. in length and 0.65 m. width and 30cm.between hills. The best ten F_3 plants according to later traits were saved to produce the second recurrent selection cycle.

In 2010 season selfed seeds of best ten F_3 plants were sown in a half diallel cross procedure to produce 45 hybrids as possible combination crosses in the two population.

In 2011, Equal amount of the 45 hybrids were mixed and sown in non replicated rows to apply self pollination for producing F_2 seeds in the two population. In 2012 and 2013, the F_2 and F_3 plants of both population were sown as mentioned in first cycle with applied selection 10% intensity to obtain the best F_3 families of both populations.

The phenotypic and genotypic coefficients of variance were estimated using the formula developed by Burton (1952):

$$\text{Phenotypic coefficient of variance (PCV)} = \sigma_p / \bar{X} \times 100$$

$$\text{Genotypic coefficient of variance (GCV)} = \sigma_g / \bar{X} \times 100$$

Where: σ_p and σ_g are the standard deviation of phenotypic and genotypic families. \bar{X} is families mean of a trait.

The estimates of broad sense heritability (h^2b %) were estimated according to the following equation: $h^2b \% = \sigma^2_g / \sigma^2_p \times 100$

Where:, V_{P_1} and V_{P_2} the phenotypic variance of, first and second parent variance . σ^2_P and σ^2_g the phenotypic and genotypic, environment variance.

The predicted genetic advance in any traits based on one variable alone was estimated from the following expressions as suggested by Walker (1960) and Miller and Rawlings (1967). $(\Delta g_{x_w}) = K. \sigma^2_{g_w} / \sigma_{p_w}$.

Where, $K = A$ selection differential with a value of 1.75 under 10% selection intensity.

The analyses were made according to Cockerham (1963). The significance between any two different means were tested using the least significant differences values in F_3 (L.S.D.) at both 5% and 1% levels which can be obtained as follows:

$$\text{L.S.D.} = t_{0.05} E_{df} \times S_{d.} \quad \text{L.S.D.} = t_{0.01} E_{df} \times S_{d.} \quad S_{d.} = \sqrt{\frac{S_1^2}{n_1} + \frac{S_2^2}{n_2}}$$

Where: n_1 and n_2 were the number of single plants.

The correlation coefficient between selected and unselected traits was calculated using Minitab 13 computer package.

The change percentage was estimated according to the following equation:

$$\text{Change \% (SA\%)} = \text{mean of } C_1 - \text{mean of } C_0 / \text{mean of } C_0 \times 100$$

RESULTS AND DISCUSSION

Recurrent selection in predominantly cross-pollinated crops has been found as an effective system of selection in accumulating favorable alleles at a large number of loci and providing increased opportunities for selection of plants with favorable trait combinations in selected population.

The common experiences of cotton breeders are a reduction in genetic variability in breeding material. This poses a limitation in the choice of parental material in the development of appropriate segregating populations. By conventional breeding methods, maintenance of variability is necessary to sustain the progress in breeding for improved varieties. Thus, recurrent selection method is an important to diversity the genetic variability in conventional program.

Mean performances, phenotypic and genotypic coefficients of variation, heritability, genetic advances and selection advances estimates (Tables 1 and 2) showed that the means of lint percentage, boll weight, fiber length and fiber strength for F_2 were lower than F_3 generations of the two populations. While the means of F_2 were undesirable higher than means of F_3 generation for Micronaire reading of the two populations. Similar results were obtained by Abd El-Salam (2005) and Abou El-Yazied *et al.* (2008)

The results showed phenotypic and genotypic coefficients of variation that was larger in F_2 generation than F_3 generations for all studied traits in the two populations where the genotypic coefficient of variation reduced in later generation indicating that the advanced cycles were more homogenous and uniform than the basic population. However, moderate to high estimates of heritability in broad sense were observed for all studied traits in the two populations. These results revealed that the magnitude of the genetic variability persisted in this material was sufficient for providing substantial amount of improvement through the selection of superior progenies and high heritability values are quick and easy to accumulate when using this method of selection. The selection response is determined by the genetic and non genetic variance hence, coefficient of variation is very useful for the study of variation and heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of characters from parents to their offspring (Falconer 1981). Further, he suggested that a genetic coefficient of variation together with heritability could give the best indication of the amount of genetic variance to be expected from selection.

Table 1. Mean performances, phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability (h^2_b), genetic advances (Δg) and selection advances (SA %) in F_2 and F_3 generations through first recurrent selection cycle (C_1) in population I

Traits	Gene.	Mean (C_1)	PCV%	GCV%	h^2_b %	Δg		SA%	C_0
						Pre	Act		
Lint %	F_2	38.39±0.224	2.9	2.0	45.9	2.09	0.90	4.28	36.75
	F_3	40.66±0.225	1.8	1.3	51.2	3.90	0.64	5.45	38.5
Boll weight	F_2	2.77±0.035	6.5	2.8	20.9	0.09	0.05	0.12	2.75
	F_3	3.08±0.049	5.1	2.6	25.8	0.12	0.07	4.8	2.93
Fibre length	F_2	31.81±0.212	3.4	3.1	80.0	2.07	1.48	1.49	31.34
	F_3	31.45±0.346	3.2	2.8	82.0	1.69	1.57	0.83	31.23
Mic. reading	F_2	3.98±0.07	8.4	6.3	55.6	0.15	0.33	-0.76	4.01
	F_3	4.00±0.06	4.6	3.9	73.0	0.18	0.23	-2.38	4.1
Fiber strength	F_2	10.48±0.10	4.9	3.9	61.3	1.0	0.55	4.5	10.01
	F_3	10.32±0.12	3.7	3.3	77.1	0.77	0.52	4.33	9.87

C_0 = basic population mean

Table 2. Mean performances, phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability (h^2_b), genetic advances (Δg) and selection advances (SA %) in F_2 and F_3 generations through first recurrent selection cycle (C_1) in population II

Traits	Gene.	Mean (C_1)	PCV%	GCV%	h^2_b %	Δg		SA%	C_0
						Pre	Act		
Lint %	F_2	38.20±0.211	2.1	1.2	32.3	3.16	0.46	8.15	35.1
	F_3	39.3±0.187	1.5	1.0	44.8	2.29	0.46	3.86	38.2
Boll weight	F_2	2.89±0.041	5.5	4.1	54.7	0.32	0.15	5.60	2.77
	F_3	3.0±0.050	5.1	4.0	61.4	0.33	0.17	8.1	2.77
Fiber length	F_2	33.59±0.185	2.1	1.6	53.4	1.98	0.67	4.19	32.2
	F_3	34.59±0.213	1.9	1.5	59.0	0.97	0.69	3.07	33.7
Mic. Reading	F_2	3.93±0.064	6.3	4.2	43.0	0.19	0.10	1.98	3.85
	F_3	3.73±0.054	4.6	3.1	47.9	0.46	0.14	-4.68	3.9
Fiber strength	F_2	10.38±0.091	3.40	2.8	66.7	0.64	0.41	1.72	10.2
	F_3	10.35±0.067	2.0	1.3	70.5	0.90	0.14	2.54	10.08

C_0 = basic population mean

In addition, Shaheen *et al.* (2000) found that heritability for F_2 generation was lower than F_3 for lint percentage and fiber length in three populations. Also, Gooda

(2006) studied improvement in two populations and found that, P.C.V. and G.C.V. were decreased from F_2 to F_3 generations for all studied traits and heritability estimates in broad sense increased from F_2 to F_3 generation for the same traits. Improvement of halo length, fiber length at 2.5%, Pressley index and Micronaire value were achieved by using direct phenotypic selection for seed cotton yield, lint yield, boll weight, seed index and lint index.

Comparing the predicted gains with the actual ones, it could be noticed that the predicted surpassed the actual one for all studied traits in the two populations. This may be due to the unfavorable environmental conditions which inhibitor genes which controlled these quantitative traits as well as, high estimates values of heritability in broad sense were observed in unselected traits in the two populations. Similar results were obtained by El Lawendy (2003) who mentioned that large discrepancies were observed between predicted and realized gains because genotypic variances and covariance's used to calculate predicted gains were likely biased by certain genotypic x environment interaction.

Also, selection advance (SA %) was high for the selected trait, lint percentage in the two populations and some unselected traits i.e., boll weight and fiber strength in population I as well as, boll weight and fiber length in population II. These indicated that selection for lint percentage in the two populations was effective and sufficient to improve lint percentage and subsequently improvement some unselected traits. Hence, the highest values of selection advances compared with unselected generation mean traits (the check) indicating that selection procedures applied were effective and successful for selecting the best families within the two populations with respect to these traits.

Generally, the predicted and actual gains obtained from recurrent selection were nearly similar in both populations. Improvement in lint percentage, boll weight and fiber quality could be due to high selection intensity, genotypic coefficient of variance and heritability. These three factors play a major role in genetic advances in the two populations. Similar results were obtained by Ahmed *et al.* (2003), Abdel-Hafez *et al.* (2003), El-Lawendey *et al.* (2008) and Abou El-Yazied *et al.* (2008).

The results of mean performance of F_3 selected families for five traits on the first recurrent selection cycle in the two population using L.S.D. are presented in Table 3 and 4. The best ten families in each population were chosen from F_3 generation for five phenotypic selection traits compared with their respective parents for the selected traits by using L.S.D.,. The most superior families showed significant and highly significant differences for lint percentage trait, special families numbers 8,11,20,31,and 34 in population I and families numbers 4, 9, 21 and 25 in population

II which showed best highly significant values for most studied traits in the two population.

The F_3 generation in the two populations for the first recurrent selection cycle contains amounts of genetic variation to get up best results of gains from using phenotypic selection and response of genetic advance in lint percentage through another recurrent selection cycle through hybridization procedure to produce 45 hybrids as possible combination crosses between the best ten selected families in the two population. Similar results were obtained by Abd El-Salam (2005).

Table 3. Mean performance of F_3 selected families for five traits on first recurrent Selection cycle (C_1) in population I comparative with mean it's parents

F_3 selec. Families	Lint percentage	Boll weight	Fiber length	Fiber fineness	Fiber strength
3	39.9+	2.9++	31.0	4.1	10.1
8*	43.0++	3.3++	30.3	4.0	11.3++
11*	42.2++	3.1++	30.6	4.1	10.5++
13	40.2++	3.2++	31.2	4.0	10.0
15	40.1++	3.0++	32.2	3.7+	10.0
17	40.6++	3.0++	30.7	4.0	10.2
20*	41.2++	3.4++	33.0	3.6++	10.1
22	39.1	2.9++	33.1	4.0	10.1
31*	42.9++	3.2++	31.4	4.1	10.5++
34*	41.0++	3.0++	31.1	4.2	10.5++
\bar{X}	40.83	3.08	31.57	4.0	10.32
P1 (PHP)	38.31	2.55	34.3	3.9	10.15
P2(Suven)	35.89	2.43	31.16	4.11	9.9
L.S.D _{0.05}	0.91	0.19	0.53	0.16	0.24
L.S.D _{0.01}	1.28	0.27	0.75	0.22	0.34

*,** Significant and highly significant at 5% and 1% levels, respectively.

PHP = Pima high percentage

Table 4. Mean performance of F₃ selected families for five traits on first recurrent Selection cycle (C₁) in population II comparative with mean it's parents

F ₃ selec. Families	Lint percentage	Boll weight	Fiber length	Fiber fineness	Fiber strength
2	39.4+	3.0	33.9	4.2	10.1
4*	40.0++	3.0	35.7	3.6++	11.1+
5	38.7	3.1	34.6	4.1	10.3
9*	40.1++	3.1	34.9	3.8	10.6
11	38.6	3.2	34.9	4.5	10.2
14	38.4	2.9	33.6	4.3	10.0
16	39.0	2.9	34.5	4.2	10.1
17	39.3	2.8	34.8	4.2	10.5
21*	39.6+	2.9	33.4	4.2	10.8
25*	39.7+	2.8	33.5	4.2	10.5
\bar{X}	39.3	3.1	34.59	4.13	10.35
P1 (PHP)	38.31	2.55	34.3	3.9	10.15
P2(Giza 88)	37.8	3.2	35.22	4.0	10.81
L.S.D _{0.05}	1.18	0.18	0.58	0.18	0.25
L.S.D _{0.01}	1.66	0.26	0.81	0.26	0.35

*,** Significant and highly significant at 5% and 1% levels, respectively.

PHP = Pima high percentage

The mean performances, phenotypic and genotypic coefficients of variation, heritability, genetic advances and selection advances estimates in Tables 5 and 6 showed the same trend as in first selection cycle with a further boost on mean performances in second cycle for all studied traits in the two populations. The results for lint percentage and other correlated trait clearly indicated that there has been a positive shift in the population means for both populations.

Table 5. Mean performances, phenotypic (PCV) and genotypic (GCV) coefficient of variation and broad sense heritability (h^2_b), genetic advances (Δg) and selection advances (SA %) in F_2 and F_3 generations through second recurrent selection cycle (C_2) in population I

Traits	Gene.	Mean (C_2)	PCV%	GCV%	h^2_b %	Δg		SA%	C_0
						Pre	Act		
Lint %	F_2	40.89±0.161	1.7	1.2	57.0	2.47	0.65	5.05	38.79
	F_3	41.27±0.142	1.3	1.1	66.7	2.64	0.67	5.17	39.15
Boll weight	F_2	3.11±0.042	5.8	3.3	33.6	0.47	0.11	4.31	2.99
	F_3	3.17±0.040	4.0	2.8	37.2	0.15	0.08	3.14	3.09
Fiber length	F_2	33.63±0.189	1.8	1.2	36.5	1.55	0.45	2.47	32.72
	F_3	34.12±0.168	1.6	1.0	40.0	0.67	0.39	0.80	33.84
Mic. reading	F_2	4.13±0.044	4.5	3.2	51.1	0.37	0.17	-3.32	4.28
	F_3	3.97±0.97	4.2	3.1	59.0	0.36	0.17	0.62	3.95
Fiber strength	F_2	10.02±0.062	2.6	2.2	72.8	1.16	0.34	3.90	9.62
	F_3	10.34±0.066	2.5	2.1	76.0	1.12	0.35	6.18	9.07

C_0 = basic population mean

Table 6. Mean performances, phenotypic (PCV) and genotypic (GCV) coefficients of variation and broad sense heritability (h^2_b), genetic advances (Δg) and selection advances (SA %) in F_2 and F_3 generations through second recurrent selection cycle (C_2) in population II

Traits	Gene.	Mean (C_2)	PCV%	GCV%	h^2_b %	Δg		SA%	C_0
						Pre	Act		
Lint %	F_2	40.83±0.147	1.7	1.4	68.7	3.51	0.83	5.93	38.36
	F_3	41.57±0.152	1.5	1.3	72.2	3.17	0.79	6.56	38.83
Boll weight	F_2	3.27±0.035	5.0	4.0	63.7	0.30	0.18	4.15	3.14
	F_3	3.16±0.037	4.8	3.9	66.4	0.38	0.17	1.53	3.10
Fiber length	F_2	34.4±0.178	2.4	2.0	64.5	2.27	0.94	2.14	33.66
	F_3	34.65±0.182	2.2	1.8	66.6	1.29	0.87	0.64	34.45
Mic. reading	F_2	4.22±0.041	4.9	2.8	32.4	0.24	0.11	-2.32	4.34
	F_3	3.7±0.042	4.7	2.8	35.2	0.19	0.11	-2.60	3.81
Fiber strength	F_2	10.25±0.093	4.2	3.6	74.6	1.14	0.56	2.97	9.96
	F_3	10.42±0.095	2.7	2.0	75.6	0.80	0.28	4.05	10.0

C_0 = basic population mean

The results of mean performance of F_3 selected families for five traits in second recurrent selection cycle for the two population using L.S.D. are presented in Table 7 and 8. The best eighteen families in population I were chosen from F_3 generation for five phenotypic selection traits compared with mean it's parents for selected traits by using L.S.D., the best families showed significant and highly significant differences for lint percentage trait, especially families numbers 70,80,120,148 and 165 in population I. While, seventeen best families in population II especially families numbers 28, 83, 88, 121, 137, 138 and 163 showed highly significant values for most studied traits .

The superior of such families as a result of using recurrent selection in each population may be due to increased in the frequencies of favorable genes so that the populations and population crosses are improved with each selection cycle. In this phase recombination of desirable traits should be increased Opondo and Pathak (1982).

Table 7. Mean performance of F_3 selected families for five traits on second recurrent selection cycle (C_2) in population I comparative with mean it's parents

F_3 selec. Families	Lint percentage	Boll weight	Fiber length	Fiber fineness	Fiber strength
26	40.9**	3.1**	33.8	4.0	9.9
48	41.1**	3.2**	34.2	4.0	10
59	40.5**	3.2**	34.3	4.0	10.4
70*	41.9**	3.3**	34.6	3.6*	10.8**
80*	41.6**	3.1**	34.4	3.7*	10.7**
92	41.1**	3.2**	34.4	4.1	10.2
98	41.0**	2.9	34.2	4.0	10.4
120*	41.8**	3.4**	34.7	3.6+	10.7**
165	40.6**	3.2**	33.5	4.1	9.9
148*	42.4**	3.4**	34.8	3.6+	10.5*
151	41.5**	3.3**	33.1	4.0	10.0
165*	41.9**	3.4**	34.5	3.9	10.6**
166	41.3**	3.2**	33.6	4.0	9.8
169	40.7**	3.0+	34.6	4.0	10.4
170	41.6**	3.2**	34.2	4.0	10.5*
171	41.6**	3.2**	33.3	4.2	9.8
183	40.5**	3.1**	34.7	4.0	10.5*
189	40.7**	3.2**	33.2	4.0	10.0
\bar{X}	41.27	3.17	34.12	3.93	10.28
P1 (PHP)	38.31	2.55	34.3	3.9	10.11
P2(Suven)	35.89	2.4	31.06	4.01	9.8
L.S.D _{0.05}	0.94	0.25	0.46	0.20	0.32
L.S.D _{0.01}	1.33	0.36	0.64	0.29	0.45

*,** Significant and highly significant at 5% and 1% levels, respectively.

PHP = Pima high percentage

Table 8. Mean performance of F₃ selected families for five traits on second recurrent selection cycle (C₂) in population II comparative with mean it's parents

F ₃ selec. Families	Lint percentage	Boll weight	Fiber length	Fiber fineness	Fiber strength
23	41.4**	3.1	33.7	3.9	10.5
25	40.1**	2.9	34.1	4.0	10.5
26	40.8**	3.1	34.1	3.8	10.1
28*	42.4**	3.13	35.8*	3.5*	10.7
29	40.5**	3.1	34.5	3.5*	10.0
30	41.8**	3.0	33.4	3.9	10.2
42	41.1**	3.0	35.0	3.7*	10.7
44	40.5**	2.9	33.4	4.0	10.2
55	40.9**	3.2	34.2	3.9	10.4
83*	43.4**	3.6++	35.9*	3.6*	10.8
88*	42.1**	3.2	35.2	3.5*	10.5
121*	42.9**	3.5++	35.9*	3.6*	10.6
122	41.5**	3.1	34.1	3.7*	10.2
137*	42.3**	3.2	34.6	3.4**	10.5
138*	42.2**	3.3	35.2	3.6+	10.5
163*	42.0**	3.3	36.2**	3.3**	10.8
167	40.8**	3.0	34.1	3.9	10.2
\bar{X}	41.57	3.16	34.65	3.7	10.42
P1 (PHP)	38.31	2.5	34.3	3.9	10.11
P2(Giza 88)	37.7	3.1	35.2	3.98	10.76
L.S.D _{0.05}	1.21	0.26	0.55	0.18	0.22
L.S.D _{0.01}	1.70	0.36	0.78	0.28	0.30

*,** Significant and highly significant at 5% and 1% levels, respectively.

PHP = Pima high percentage

The coefficient of correlation provides a measure of the genotypic association between pairs of traits to identify the traits which could be used as indicator for improvement of other traits through the selection programs. Table 9 revealed that the correlation between lint percentage (selected trait) and the other unselected traits in F₃ selected families in first cycle was significant for boll weight in population I. Also, positive and highly significant correlation relative to fiber strength in the two

populations. While, negative and desirable highly significant association with fiber fineness were observed in population II only. In spite of, second recurrent selection cycle the lint percentage showed positive and highly significant correlation with boll weight in both population and fiber length in population II only as well as, positive significant correlation for fiber strength in both populations. On the other hand, negative and desirable highly significant correlation observed for fiber fineness in population I and significant correlation with same trait in population II.

A comparison of direction and magnitude of association among traits in the two recurrent selection cycles Table 9 indicate that, several new associations in terms of direction and magnitude of association was observed. For example association of lint percentage with fiber length (-0.51 and 0.21) in population I and II respectively in the first cycle but changed to positive 0.47 and significant 0.71** in the second cycle .Also, between fiber length with each of fiber fineness and fiber strength, the associations were changed in sign and magnitude. It was thus evident that the reshuffling of genes responsible for correlations amongst some characters resulted in newer recombinants, which presumably, were due to changes a coupling to repulsion phase linkages. Abdel Salam *et. al.*(2013) found that the correlation between seed index and lint percentage was negative and significant in pedigree selection but it was changed to non significant in recurrent selection .This changed in correlation was due to the changes in relationship by random intermatting.

Table 9. Correlation coefficient between selected and unselected traits through the two recurrent selection cycles in the two populations

Population	Population I F ₃ selected families					Population II F ₃ selected families			
Selection	Traits	L%	B.W	F.L	F.F	L%	B.W	F.L	F.F
First cycle (C ₁)	B.W	0.65*				-0.16			
	F.L	-0.51	-0.01			0.21	0.48		
	F.F	0.31	-0.32	-0.69*		-0.74**	-0.07	-0.55	
	F.S	0.79**	0.38	-0.58	0.48	0.78**	-0.09	0.34	-0.69*
Second cycle (C ₂)	B.W	0.83**				0.84**			
	F.L	0.47	0.21			0.71**	0.75**		
	F.F	-0.76**	-0.65*	-0.69*		-0.61*	-0.58*	-0.79**	
	F.S	0.62*	0.41	0.82**	-	0.64*	0.56*	0.71**	-0.44
					0.75**				

*, ** Significant and highly significant at 5% and 1% levels, respectively

The responses to selection were relatively good, having regard to the selection pressures used. Table 10 showed the superiority of advanced cycles (SA%) for studied traits in the two recurrent selection cycles over the base population in the two populations. The superiority of advanced cycles for lint percentage in F3 selected families (second recurrent selection cycle) exceeded the base population (F2 in first recurrent selection cycle) by 13.13% and 17.73% in population I and II respectively. simultaneous increases were observed for unselected traits, boll weight by 14.92% and 13.63%, fiber length by 8.84% and 7.59% and fiber strength by 3.28% and 2.14%. While, Micronair reading showed slight negative desirable change by -1.0% and - 3.92% in population I and II respectively. Hence, response to selection was linear and is predicted to continue at approximately the same rate of gain for an additional cycle. The superiority of advanced cycles for lint percentage and other studied traits was further substantiating from the comparisons of individual S1 progeny. These results clearly demonstrate that with increase in the mean of lint percentage of the two populations, the opportunity of deriving high lint percentage lines is also attainable. These results are in accordance with those obtained by Eberhart (1972) who reported that the improvement in breeding populations results in parallel improvement in the lines derived from the population at the end of each selection cycle. Based on, the observation from these results it can be concluded that recurrent selection in the two populations has been very successful in increasing the population mean in the desired direction simultaneously for all traits without losing variability.

Table 10. The superiority of advanced cycles (SA%) for studied traits in the two Recurrent selection cycles over the base population in the two populations

Traits	Cycle	Pop.I	Change %(SA%)		Pop.II	Change %(SA%)	
			Over cycle	Cumulative		Over cycle	Cumulative
Lint %	C ₀	36.75	-	-	35.1	-	-
	C ₁	40.66	10.63	10.63	39.3	11.96	11.96
	C ₂	41.27	10.5	13.13	41.57	5.77	17.73
Boll weight	C ₀	2.75	-	-	2.77	-	-
	C ₁	3.08	14.01	12.0	3.0	8.30	8.30
	C ₂	3.17	2.92	14.92	3.16	5.33	13.63
Fiber length	C ₀	31.34	-	-	32.2	-	-
	C ₁	31.35	0.35	0.35	34.59	7.42	7.42
	C ₂	34.12	8.48	8.84	34.65	0.17	7.59
Mic. reading	C ₀	4.01	-	-	3.85	-	-
	C ₁	4.0	-0.25	-0.25	3.73	- 3.12	- 3.12
	C ₂	3.97	-0.75	- 1.0	3.7	- 0.80	-3.92
Fiber strength	C ₀	10.01	-	-	10.2	-	-
	C ₁	10.32	3.09	3.09	10.35	1.47	1.47
	C ₂	10.34	0.19	3.28	10.42	0.67	2.14

C₀ = basic population mean, C₁ = First selection cycle mean, C₂ = Second selection cycle mean

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كفاءة الانتخاب المتكرر لتحسين بعض الصفات الاقتصادية في القطن المصرى

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تم إجراء دورتين من الانتخاب المتكرر في هجينين من القطن المصرى لتحسين صفة تصافى الحليج وبعض الاقتصادية الأخرى بمحطة البحوث الزراعية بسخا- كفر الشيخ خلال ستة مواسم (٢٠٠٨-٢٠١٣م) وكانت اهم النتائج كالاتى :-

- سجلت زيادة فى المتوسط من دوره الاولى الى الدورة الثانيه من الانتخاب المتكرر بالمقارنة بمتوسط العشيرة الاصليه.
- كان معامل التباين المظهري والوراثي كبير في الجيل الثاني بالمقارنة بالجيل الثالث.بالإضافة إلى إن قيم معامل التوريث في المدى الواسع كانت متوسطه إلى عالية لكل الصفات المدروسة في كلا العشيرتين.
- لوحظ بصفة عامة تقارب بين التحسين الوراثي المتوقع والمشاهد مما يدل على انخفاض تأثير التباين السياتي بالمقارنة بتأثير التباين الاضافى الذي ظهر تحكمه في كلا العشيرتين ومن ثم يمكن للمربى الاعتماد على قيم التحسين الوراثي المتوقع.
- مقارنة اهمية واتجاه الارتباط بين الصفات المختلفة تحت دورتين من الانتخاب المتكرر لوحظ وجود ارتباطات جديدة سواء فى الاهميه او فى الاتجاه وهذا نتيجته وجود الاتحادات الجديد الناتجه عن تغير حالة الارتباط المتقابل الى الارتباط المتنافر.
- لوحظ زيادة تصافى الحليج في الدورة الثانية للانتخاب المتكرر عن متوسط العشيرة الاصلية بنسبة ١٣,٣ % و ١٧,٧٣% فى العشيرة الأولى والثانية على الترتيب.
- كانت الاستجابة للانتخاب شبة خطيه نسبيا ويتوقع استمرار هذه الاستجابة بنفس المعدل في الدورة التالية.
- لوحظ وجود ارتباط واستجابة للانتخاب لصفة تصافى الحليج وبعض الصفات غير المنتخبه. حيث أنه بزيادة تصافى الحليج نتيجة للانتخاب حدثت زيادة بالتتابع في صفات متوسط وزن اللوزة وطول ومثانة التيلة. بينما كانت زيادة سالبه قليله ومرغوبة لصفة نعومة التيلة.

وبالتالى يستطيع المربى الاعتماد على طريقة الانتخاب المتكرر حيث تبين إنها فعالة في تحسين تصافى الحليج في القطن للحصول على عائلات متفوقة.