

Efficiency of Single Trait Selection for Improving Yield and Earliness in Varietal Maintenance of Giza 90 Egyptian Cotton

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Abstract

The present study was carried out at Shandaweel Res. Sta. Sohag, Cotton Res. Inst., (ARC), during the three summer seasons of 2013 -2015. The basic materials were selfed seeds of 60 single plants selected from the breeding nursery of renewal and maintenance of Giza 90 (the same materials used for producing the nucleolus of G.90). The main objective of this work was to study the possibility of selection elite high yielding plants characterized by the same fiber properties of Giza 90. To attain this goal, single trait selection for lint yield, lint percentage and earliness was applied for two cycles. Average of the ten selected families indicated that selection for LY/P ranked the first and improved LY/P by 20.30% of the check strain followed by selection for days to first flower method (15.82%), and LY/P restricted by DFF (11.54%). Generally, single trait selection is an effective method to improve selection criterion. The observed genetic gain indicated that single trait selection resulted in several superior families significant out yielded the check strain and better in one or more of the three main fiber properties; fineness, strength and Upper Half Mean length. Therefore, the official method of maintaining and renewing Egyptian cotton varieties should be modified to allow selection for yield beside preserving fiber properties.

Keywords: Maintenance of Egyptian cotton, single trait selection, observed genetic gain, genotypic and phenotypic variation, heritability.

Introduction

Cotton is one of the most important fiber crops in the world and Egypt. It is a shrub native to tropical and subtropical regions around the world, including the Americas, India, and Africa. However, virtually all of the commercial cotton grown worldwide today is grown from the two species *Gossypium hirsutum* and *Gossypium barbadense* L. Most of Egyptian cotton varieties were produced by pedigree selection. Independent culling levels selection technique can be used to improve several traits simultaneously. Selection de-

pends mainly upon genetic variability (Manning 1956, El-Kilany 1976, Abo El-Zahab and El-Kilany 1979, Mahdy 1983 a and b, Liayed and Bridges 1995, Mahdy *et al.* 2007, Tang *et al.* 2009, El-Lawendy and El-Dhan 2012 and Hassaballa *et al.* 2012). In Egyptian cotton Mustafa *et al.* (1995) evaluated 41 strains in one location (Trial A) and five locations (Trial B) and reported genetic coefficient of variation for lint yield of 9.40% for Trial A and 7.48% for Trial B. Furthermore, high heritability values were recorded in Trial B. Gomaa and Shaheen (1995) noted high estimates

of heritability for lint yield /plant, seed index and earliness index; respectively. Singh *et al.* (1995) found genotypic differences for almost all the studied traits. El-Harony (1998) in a selection experiment found that heritability in broad sense ranged from 4.32 for boll weight to 61.96% for lint percentage. Otherwise, high to moderate broad sense heritability estimates were found for all traits. Mahdy *et al.* (2001 a and b) noted high genotypic and phenotypic coefficients of variability for most traits in pedigree line and selection with intermating in intra- and interspecific crosses. Ahuja *et al.* (2004) in a selection experiment found high estimates of genetic coefficient of variation and heritability for seed cotton yield /plant, number of bolls / plant and boll weight. Basbag and Gencer (2004) stated that the characters of high heritability estimates; boll weight, seed index, fiber fineness and fiber strength could be selected in the early generations (F2 and F3), while that of low heritability as number of bolls/ plant selection should be postponed to latter generations. The phenotypic and genotypic coefficients of variation were larger in the F2 than those of the succeeding generations (Gooda 2007, Srour *et al.* 2010 and Abou El-Yazied *et al.* 2013). Large discrepancies between actual and predicted gains were obtained (El-Harony, 1998, Okasha, 1998, Youns, 1999 and El-Defrawy and El-Ameen, 2004 and Abd El-Zaheret *al.* 2007). Otherwise, Gooda (2007) found that actual genetic gain for most selected traits was higher than predicted gain except lint percentage. Khan *et al.* (2009) and Soomro *et al.* (2010) in

Upland cotton and Mahdy *et al.* (2006), Mahdy *et al.* (2009 a and b) and Srour *et al.* (2010) in Egyptian cotton recorded high genetic gain for bolls/plant, boll weight and for seed cotton yield. The main objective of this work was to evaluate the method of maintaining and renewing the breeder seeds of Giza 90 followed by Maintenance Research Section for renewing the Egyptian cotton strains and varieties, Cotton Research Institute, ARC, and the possibility of selection elite high yielding plants characterized by the same fiber properties of Giza 90. To attain this goal single trait selection for lint yield, lint percentage and earliness was applied for two cycles on the same materials used for producing Giza 90 nucleolus.

Materials and Methods

The present study was carried out at Shandaweel Res. Sta. Sohag, Cotton Res. Inst., A.R.C. during the three summer seasons of 2013 -2015. The basic materials were selfed seeds of 60 single plants selected from the breeding nursery of renewal and maintenance of Giza 90 (the same materials used for producing the nucleolus of G.90). Giza 90 is traced back to a cross between Giza 83 x Dandara, and released commercially in year 2000. G.90 is a commercial Egyptian cotton cultivar (*G. barbadense*L.) cultivated at upper and middle Egypt regions and characterized by high yielding ability, high ginning outturn (more than 120 pounds), and early maturity with staple length of about 31 mm. These materials were subjected to pedigree single trait selection for lint yield/plant, lint yield/plant restricted

by days to first flower and lint percentage. The traditional method followed by Cotton Maintenance Res. Sec. for renewing and maintenance of Egyptian cotton was represented by check strain (the newest nucleolus of Giza 90) in the experiment each year.

In season 2013; selfed seeds of the 60 selected plants were planted on March 28th, 2013, each in a plot in the breeding nursery. Each plot included five rows (10 plants in rows) 7.0 m long, 60 cm m apart and 70 cm between hills within a row. The middle row was left without planting to facilitate plant screening and selfing. The total number of selfed plants were 847. At flowering, days to first flower (DFF) was recorded for each plant. After picking at the end of the season the following characters were recorded for each single plant; seed cotton yield /plant; g (SCY/P; g), lint yield /plant; g (LY/P; g), lint percentage (lint %) [lint yield/seed cotton yield], number of bolls/plant (NB/P), number of seeds/boll (NS/B) [boll weight x (100-lint%) /seed index], Micronaire reading (Mic), fiber strength as Pressley index measured by the H.V.I instrument (PI) and Upper half mean length; mm as measured by the H.V.I. instrument (UHM). Selfedseeds of the best 20 single plants in LY/P, LY/P restricted by DFF (the best LY/P less than the population mean in DFF), Lint% and DFF were saved for season 2014.

In season 2014; The selected plants of the 4 selection procedures were planted on April 1st, 2014 season. The selfed seeds of each selected plant were used in planting. A randomized complete blocks design of three replications was used. The plot

was single row 4 m in length, 60 cm apart and 50 cm between hills within a row. One row was left without planting between each two rows to facilitate selfing and screening. After full emergence seedlings were thinned to one plant/hill. The recommended cultural practices for cotton production were adopted thought the growing season. The studied characters were recorded as in the previous season. The selfed seeds of the best 10 plants for each procedure were saved for evaluation in the next season.

In Season 2015; Selfed seeds of the selected plants from season 2014 along with G.90 nucleolus (the nucleolus produced from the same basic materials) were planted on March 25th, 2015 in a randomized complete blocks design of three replications as in the previous season. The studied characters were recorded as in the previous season.

Statistical analysis

Estimates of genotypic and phenotypic variances were calculated from expected mean squares components of the selected families as outlined by Al-jibouri *et al.* (1958). The analysis of variance was done two times for each trait, the first was for the selected families only to estimate phenotypic and genotypic coefficients of variability and heritability in broad sense. The second was for the selected families along with the check strain to make mean separation between selected families and the check strain. Heritability in broad sense was estimated as: $(H) = (\sigma_g^2 / \sigma_p^2) \times 100$. The phenotypic (PCV%) and genotypic (GCV%) coefficients of variation were estimated as Burton

(1952). Mean comparisons were calculated using revised L.S.D according to (El Rawi and Khalafalla (1980).

$$R L S D\alpha = (t) \alpha * \sqrt{(2MSE / r)}$$

Where t is the t value from "minimum-average-risk t-table" at F-value of genotypes, genotypes df and experimental error df. The significance of observed direct and correlated response to selection was measured as the deviation percentage of a family mean from the newest nucleolus (check strain) using R. L. S. D.

Results and Discussion

1-Description of the base population; season 2013

Means and coefficient of variation

Seed cotton yield /plant, lint yield/plant and number of bolls /plant showed wide range of variation accompanied with high coefficients of variation of 39.70, 39.52 and 39.45% for SCY/P, Ly/p and NB/p; respectively (Table1). The coefficient of variability was medium for boll weight and number of seeds/boll and accounted for 8.40 and 8.75%; respectively. Otherwise, the coefficients of variability in seed index, lint index, days to first flower and technological properties were low and

ranged from 2.49 for days to first flower to 7.40% for Micronaire reading. These results reflect the method of renewing strains and varieties of Egyptian cotton. The breeder devotes his effort to insure technological properties; fineness, strength and fiber length, and selects the plants matched Giza 90 type in fiber properties irrespective of their yield and its components. Therefore, the coefficients of variability of Micronaire reading, Pressely index and upper half- mean length were low, reflecting the great similarity of the plants in fiber properties. Likewise, the coefficients variability in seed index, lint index and days to first flower were low as in all the Egyptian cottons. The high coefficients of variability of seed cotton yield / plant, lint yield/plant, number of bolls/plant and boll weight indicated to the feasibility of selection for these traits with good preservation of fiber properties. The results of PCV in the base population are in general agreement with those reported by Mahdy *et al.* 2006;2007; 2009a,b; and 2013a,b; and Hassaballa *et al.* (2012) respect to cotton yield and NB/P. But, low respect to SI, LI and Maturity.

Table 1. Average, maximum, minimum and coefficient of variation of the studied traits of the base population and the adopted selection procedures; season 2013.

Base Population												
	SCY/P;g	LY/P;g	Lint%	NB/P	BW;g	SI;g	LI;g	NS/b	DFF	MIC	PI	UHM
Average ± SE	150.77 ± 2.06	58.69 ± 0.80	39.00 ±0.025	47.82 ± 0.65	3.15 ± 0.01	9.86 ±0.02	6.30 ±0.01	30.00 ±0.09	68.81 ±0.06	3.82 ±0.01	9.71 ±0.02	30.17 ±0.06
Max.	430.00	167.60	42.10	138.00	3.90	12.00	7.87	37.00	75.00	4.90	11.60	39.70
Min.	24.60	9.40	37.20	9.11	2.70	8.30	5.37	19.00	64.00	2.80	8.40	21.00
C.V%	39.70	39.52	1.85	39.45	8.40	5.37	5.26	8.57	2.49	7.40	4.83	5.70

SE=standard error, c.v.= coefficient of variability, Max = maximum and Min =minimum

2-Second cycle selection

2-1. Mean squares and coefficient of variability

Genotypes mean squares (Table 2) of traits of the selected families (without the check) for LY/P was not significant for LY/P and SCY/P (not included) indicating the depletion of genetic variance among families and insufficient genetic variability for further cycles of selection. The other traits showed significant ($p \leq 0.05$ to $p \leq 0.01$) genotypes mean squares, however, the coefficients of variability were very low. The genotypic coefficient of variability ranged from 1.01 for seed index to 4.84% for BW. These results indicated that two cycles of pedigree selection for LY/P were enough to isolate the best high yielding families. This mainly due to that the materials under study were subjected to selfing for many years, which resulted in a narrow group of homozygous lines similar in pheno-

typic performance. Otherwise, genotypes mean squares of families selected for LY/P restricted by DFF was significant ($p \leq 0.01$) for all traits except for Pressley index. This indicates that selection for more than one character preserves genetic variability. The genetic coefficients of variability were medium for LY/P (8.99%) with high estimate of broad sense heritability (79.46%), and very low for DFF (2.47%) with high estimate of heritability (95.78%). The coefficient of genetic variability of the other traits was low and ranged from 1.31% for lint% to 6.22% for NB/P.

Genotypes mean squares of traits of the selected families for lint % was not significant for SCY/P, LY/P, Lint% and Pressley index indicating complete depletion of genetic variability for the selection criterion. Genetic coefficient of variation of the other traits ranged from 1.23 for DFF to 8.30% for NB/P.

Table 2. Mean squares, genotypic (GCV%), phenotypic (PCV%) coefficients of variability and broad sense heritability (H%) of different selection criteria and correlated traits after two cycle of pedigree selection; season 2015. (ANOVA with check)

S.V.	df	Mean squares											
		SCY/P	LY/P	LINT%	NB/P	BW	Seed I	Lint I	NS/B	DFE	MIC	PI	UHM
1- Pedigree selection for LY/P													
Reps	2	4.66	1.49	0.14	0.88	0.01	0.08	0.08	1.85	0.36	0.02	0.22	0.35
Genotypes	10	142.76**	25.36**	0.79**	9.73*	0.08**	0.14*	0.14*	1.88**	2.27**	0.06*	0.37**	4.23**
Exper. Error	20	41.67	7.21	0.17	4.11	0.02	0.05	0.04	0.35	0.36	0.02	0.08	0.41
GCV%		-	-	1.23	-	4.84	1.01	2.91	3.96	1.24	3.11	3.34	3.89
PCV%		-	-	1.39	-	5.51	1.74	3.54	4.36	1.35	3.78	3.79	4.09
H%													
2- Pedigree selection for LY/P restricted by DFF													
Reps	2	104.88	15.86	0.03	2.23	0.02	0.006	0.01	1.18	0.12	0.05	0.43	0.003
Genotypes	10	285.56**	47.23**	0.91**	17.69*	0.09**	0.27**	0.29**	2.28**	8.08**	0.11**	0.10	1.38**
Exper. Error	20	58.44	8.92	0.10	6.37	0.01	0.03	0.01	0.55	0.32	0.02	0.09	0.34
GCV%		8.58	8.99	1.31	6.22	5.15	3.08	4.89	3.98	2.47	4.46	-	1.65
PCV%		9.71	10.09	1.45	7.83	5.77	3.24	4.97	4.59	2.52	5.17	-	2.00
H%			79.46							95.78			
3- Pedigree selection for Lint %													
Reps	2	61.29	12.63	0.16	7.35	0.09	0.05	0.07	0.85	0.36	0.03	0.23	0.36
Genotypes	10	155.37	28.45*	0.99**	28.26*	0.12	0.38**	0.14**	5.27**	2.45**	0.17**	0.33	1.45**
Exper. Error	20	77.56	12.13	0.23	10.16	0.07	0.04	0.02	0.28	0.36	0.03	0.13	0.27
GCV%		5.33	4.96	0.38	8.30	6.76	3.30	2.25	6.90	1.23	5.81	1.01	1.84
PCV%		7.55	7.25	0.83	10.18	7.02	3.49	2.57	7.12	1.34	6.55	2.38	2.10
H%				21.16									
4- Pedigree selection for DFF													
Reps	2	24.97	3.71	0.006	9.63	0.03	0.08	0.04	0.64	0.48	0.05	0.46	0.04
Genotypes	10	160.13**	24.90**	0.70**	24.34*	0.06*	0.40**	0.13*	0.70	3.95**	0.09*	0.84**	1.19**
Exper. Error	20	45.66	5.81	0.16	7.71	0.02	0.06	0.05	1.07	0.35	0.03	0.16	0.30
GCV%		4.44	4.81	1.16	6.73	-	3.52	2.76	-	0.88	3.51	4.68	1.60
PCV%		5.89	5.99	1.31	8.35	-	3.84	3.42	-	1.04	4.60	5.28	1.93
H%								64.96					

zero or negative genotypic variance.*and**; significant at 0.05 and 0.01 levels of probability; respectively

Mean squares of genotypes for different traits was significant ($P \leq 0.05$ to $P \leq 0.01$) when selection practiced DFF. The genotypic coefficient of variability was very low for DFF with 64.96% heritability estimate. Generally, selection for DFF dropped rapidly the GCV% for all traits after two cycles of selection.

Generally, it could be concluded that two cycles of selection for the different selection procedures were enough to isolate favorable families.

Two cycles of selection dropped rapidly the genotypic and phenotypic coefficients of variability. The PCV% of LY/P decreased from 39.52% in the base population to an estimate of zero after two cycles of selection for LY/P, decreased from 1.85% to zero for lint%, and from 2.49 to 1.04% for DFF, when selection practiced for these traits. This could be due to that the system followed by Maintenance Research Section for cotton varieties devotes great attention to the varietal

type of Giza 90 respect to the fiber properties rather than yield. In consequence, selfing for many years in the breeding nursery of Giza 90 resulted in a narrow group of homozygous lines similar to large extent in fiber properties and plant phenology, but not in yield. Therefore, two cycles of selection for yield succeeded to isolate high yielding families look like Giza 90 in fiber properties which could be called pure line selection. Ahuja *et al.* (2004) found high estimates of GCV and heritability for SCY/P, NB/P and BW. Naveed *et al.* (2004) noted heritability estimates of 22, 23, 33, 35 and 38% for BW, Lint%, SCY/P, plant height and NB/P; respectively. Ahmed *et al.* (2006) showed medium to high heritability estimates for lint percentage, SCY/P, NB, boll weight and fiber length. Tang *et al.* (2009) reported high estimates of GCV and heritability for SCY/P, LY/P and NB/P. Srour *et al.* (2010) reported decrease in PCV% and GCV% from F2 to F3 for all traits. Many researchers (Mahdy *et al.* 2006; Mahdy *et al.* 2007; Mahdy *et al.* 2009a,b ; Hassaballa *et al.* 2012 and Mahdy *et al.* 2013a,b) showed high estimates of PCV and GCV% in the base populations which decreased after two cycles of selection for different selection criteria.

2-2. Pedigree selection for lint yield / plant

Two cycles of pedigree selection for LY/P results in a mean of the selected families significant ($P \leq 0.05$ to $P \leq 0.01$) out yielded the check strain for SCY/P, LY/P and NB/P (Table3). The means of the other traits did not differ from the check

strain. Nine out of ten individual families showed significant increase in yields than the check strain. The observed genetic gain (Table 4) indicated that nine, 1, 7, 2, 1, 1, 2 and 4 families significant ($P \leq 0.05$ to $P \leq 0.01$) exceeded the check strain in yields, lint%, NB/P, BW, SI, LI, NS/B, PI and UHM length; respectively. The significant genetic observed gain in the selection criterion LY/P ranged from 14.59 to 27.19% of the check strain. Cotton breeder always seeks for the superior plants in the late generation. Two cycles of pedigree selection resulted in a superior family No.334. This family significant exceeded the newest check strain by 22.92, 2719, 3.46, 15.14, 8.59, - 10.26 and 4.08% for SCY/P, LY/P, Lint%, NB/P, LI, Micronaire reading and UHM length; respectively. The other traits of family No.334 did not differ from the check strain. These results ascertain that in the official system of renewing the strains and varieties of Egyptian cotton, the breeder devotes all his effort to preserve the type of Giza 90 variety in fiber properties ignoring yield. Gomaa *et al.* (1999) found high response to selection for SCY/P. Mahrous (2004) stated that the observed gain in SCY/P was correlated with significant response in LY/P, NB/P, BW and Lint%. Mahdy *et al.* (2009b) showed genetic observed gain ranged from 8.89 – 25.21% of the better parent for SCY/P after two cycles of selection. Mahdy *et al.* (2013a) achieved average observed gain in LY/P after two cycles of selection of 21.15 and 18.20% of the better parent in two populations.

2-3. Pedigree selection for lint yield/plant restricted by days to first flower

The overall means of the selected families indicated significant improvement in LY/P, Lint%, BW, LI, DFF and UHM length (Table 5). The observed genetic gain (Table 6) showed significant increase of the

overall mean than the check of 11.54% for LY/P, 1.13% for Lint%, 4.63% for BW, 2.35% for LI, -1.81% for DFF and 3.58% for UHM length. The observed gain of the individual families showed that three families were significant ($P \leq 0.01$) earlier than the check by -1.96 to -5.39%.

Table 3. Means of the studied traits after two cycles of selection for LY/P; season 2015

Ser	SCY/P;g	LY/P;g	lint%	NB/P	BW	SI;g	LI;g	NS/B	DFF	MIC	PI	UHM
334	112.90	45.10	39.94	35.69	3.17	9.57	6.95	19.67	67.33	3.50	9.80	31.43
19	113.13	44.33	39.18	32.63	3.47	10.27	6.28	20.33	68.67	3.73	10.27	27.83
31	116.07	44.77	38.56	34.73	3.35	10.17	6.18	20.33	67.33	3.83	9.80	32.10
27	100.77	38.37	38.09	34.38	2.93	10.00	6.15	18.00	68.33	3.73	9.77	30.00
690	110.97	43.07	38.82	36.18	3.07	10.00	6.47	19.00	67.67	3.73	9.57	30.17
361	112.37	43.57	38.75	36.43	3.09	9.80	6.43	19.33	67.33	3.93	9.70	31.63
767	105.60	40.63	38.46	35.99	2.93	9.93	6.29	18.00	68.33	3.73	9.77	30.00
265	111.30	42.53	38.21	36.84	3.02	9.67	6.40	19.33	70.33	3.87	8.80	31.60
32	109.77	42.33	38.58	36.27	3.03	10.03	6.27	18.67	68.00	3.77	9.50	29.97
3	107.03	41.90	39.13	34.30	3.12	10.13	6.35	18.67	67.67	4.03	9.67	30.20
Mean	109.99	42.66	38.77	35.34	3.12	9.96	6.38	19.13	68.10	3.79	9.66	30.49
check	91.85	35.46	38.60	31.00	3.00	9.80	6.40	19.00	68.00	3.90	9.50	30.20
RLSD 0.05 for mean 1	8.95	3.72	0.54	3.14	0.18	0.33	0.28	0.77	0.73	0.21	0.37	0.78
RLSD 0.01 for mean	12.66	5.27	0.74	4.62	0.25	0.48	0.39	0.98	1.00	0.30	0.51	1.04
RLSD 0.05 for families2	12.07	5.02	0.72	4.24	0.25	0.44	0.37	1.04	0.99	0.28	0.50	1.05
RLSD 0.01 for families	17.08	7.10	1.00	6.22	0.34	0.64	0.53	1.32	1.34	0.41	0.68	1.40
1- to compare mean with the check												
2- to compare a family with the check												

Significant observed gain was found for five families in lint%, BW and lint index, two families in Micronaire reading and seven families in UHM length. The best superior promising families were family No.31. Family No.334 was the superior family selected in the previous selection procedure; LY/P. Family No. 31 ex-

ceeded the check by 26.25% in LY/P, 11.56% in BW, 3.47% in Seed index, 7.02% in Ns/B and 6.29% in UHM Length.

2-4. Pedigree selection for lint percentage

The overall mean of the selected families for lint% significant ($P \leq 0.01$) exceeded the check strain in the

selection criterion (Table 7). Significant increases of the overall mean were observed for SI, LI and UHM length. The other correlated traits; SCY/P, LY/P, NB/P, BW, NS/B, Micronaire reading and Pressley index did not show significant increase than the check. The genetic observed gain (Table 8) indicated that pedigree selection is an efficient method to im-

prove the selection criterion; lint%. Nine out of the ten selected families showed significant genetic observed gain in lint % ranged from 2.77 to 5.42% of the check strain. The observed genetic gain showed 3, 3, 5, 4, 1, 2 and 4 families exceeded the check strain for LY/P, BW, SI, LI, NS/B, PI and UHM length.

Table 4. Observed genetic gain from selection for LY/P after the second cycle in percentage from the check strain; season 2015

Ser	SCY/P;g	LY/P;g	lint%	NB/P	BW	SI;g	LI;g	NS/B	DFE	MIC	PI	UHM
334	22.92**	27.19**	3.46**	15.14*	5.56	-2.38	8.59**	3.51	-0.98	-10.26*	3.16	4.08*
19	23.17**	25.02**	1.51	5.26	15.56**	4.76*	-1.93	7.02**	0.98	-4.27	8.07**	-7.84**
31	26.37**	26.25**	-0.09	12.03	11.56**	3.74	-3.49	7.02**	-0.98	-1.71	3.16	6.29**
27	9.71	8.20	-1.33	10.90	-2.22	2.04	-3.85	-5.26	0.49	-4.27	2.81	-0.66
690	20.81**	21.45**	0.57	16.72*	2.22	2.04	1.04	0.00	-0.49	-4.27	0.70	-0.11
361	22.34**	22.86**	0.38	17.51*	3.11	0.00	0.42	1.75	-0.98	0.85	2.11	4.75**
767	14.97*	14.59*	-0.35	16.09*	-2.22	1.36	-1.67	-5.26	0.49	-4.27	2.81	-0.66
265	21.18**	19.95*	-1.02	18.82*	0.67	-1.36	0.05	1.75	3.43	-0.85	-7.37	4.64**
32	19.51**	19.38*	-0.06	17.01*	0.89	2.38	-2.08	-1.75	0.00	-3.42	0.00	-0.77
3	16.53*	18.16*	1.38	10.63	4.11	3.40	-0.83	-1.75	-0.49	3.42	1.75	0.00
Mean	19.75**	20.30**	0.44	14.01*	3.92	1.60	-0.38	0.70	0.15	-2.91	1.72	0.97
RLSD 0.05% for mean 1	9.745	10.500	1.391	10.138	6.137	3.357	4.333	4.054	1.079	5.336	3.876	2.567
RLSD 0.01% for mean	13.788	14.856	1.915	14.890	8.449	4.850	6.131	5.166	1.464	7.707	5.336	3.445
RLSD 0.05% for families 2	13.141	14.159	1.875	13.670	8.275	4.527	5.843	5.466	1.455	7.195	5.227	3.461
RLSD 0.01% for families	18.592	20.032	2.582	20.077	11.393	6.539	8.267	6.966	1.974	10.392	7.196	4.645
1- to compare mean with the check												
2- to compare a family with the check												

- *and **; significant at 0.05 and 0.01 % levels of probability; respectively.

2-5. Pedigree selection for days to first flower (DFE)

Mean days to first flower (Table 9) of the selected families for two cycles of selection ranged from 64.33 to 65.67 with an earlier ($P \leq 0.05$) average of 64.83 compared to 68.0 days for the check strain.

The observed genetic gain (Table 10) of the selection criterion; DFE was earlier ($p \leq 0.01$) than the check strain for all the selected families and ranged

from -2.45 to -5.39% of the check. Six families showed significant observed genetic gain in SCY/P ranged from 14.43 to 26.15 with an average of 15.43% of the check. Seven families showed significant genetic gain in LY/P ranged from 14.59 to 29.44% of the check. Respect to the other correlated gains; 1, 4, 2, 3, 1, 3 and 5 families showed significant genetic gain from the check strain for lint%, NB/P, BW, SI, LI, PI, and UHM length; respectively.

Table 5. Means of the studied traits after two cycles of selection for LY/P restricted by DFF; season 2015

Ser	SCY/P;g	LY/P;g	lint%	NB/P	BW	SI;g	LI;g	NS/B	DFF	MIC	PI	UHM
334	112.900	45.100	39.936	35.692	3.167	9.567	6.950	19.667	67.333	3.500	9.800	31.433
54	98.833	38.700	39.155	32.956	3.000	9.267	6.943	19.667	64.667	3.533	9.633	31.567
31	116.067	44.767	38.564	34.728	3.347	10.167	6.177	20.333	67.333	3.833	9.800	32.100
700	96.400	37.300	38.694	31.770	3.033	9.867	6.400	19.000	68.333	3.733	9.900	31.533
699	103.900	40.400	38.883	34.680	3.000	9.633	6.603	19.000	66.667	4.067	9.833	31.267
3	107.033	41.900	39.132	34.296	3.123	10.133	6.347	18.667	67.667	4.033	9.667	30.200
105	101.367	40.533	39.998	29.515	3.433	9.667	6.897	21.333	64.333	3.733	9.600	31.100
354	80.900	31.667	39.143	28.546	2.833	9.467	6.797	18.333	64.667	3.933	9.767	30.233
362	95.833	36.767	38.352	30.165	3.173	10.067	6.183	19.667	67.333	3.800	9.500	31.500
48	99.800	38.400	38.510	30.484	3.280	10.100	6.207	20.333	69.333	4.000	10.133	31.867
mean	101.303	39.553	39.037	32.283	3.139	9.793	6.550	19.600	66.767	3.817	9.763	31.280
Check	91.850	35.460	38.600	31.000	3.000	9.800	6.400	19.000	68.000	3.900	9.500	30.200
RLSD 0.05% for mean 1	9.952	3.888	0.387	3.714	0.122	0.202	0.117	0.966	0.634	0.184	-	0.759
RLSD 0.01% for mean	13.702	4.955	0.525	5.364	0.166	0.272	0.157	1.329	0.846	0.253	-	1.045
RLSD 0.05% for families 2	13.420	5.243	0.522	5.008	0.165	0.273	0.158	1.302	0.854	0.248	-	1.024
RLSD 0.01% for families	18.476	6.682	0.707	7.233	0.224	0.366	0.211	1.792	1.141	0.342	-	1.409
1- to compare mean with the check												
2- to compare a family with the check												

The best promising families were family No.73, No. 75, No. 156 and No. 335. Families No. 73 and No. 75 were earlier and out yielded ($P \leq 0.01$) the check strain. Family No. 156 was earlier, out yielded the check and better in Pressley index. Family No. 335 was earlier, high yielding and better than the check strain in both of Pressley index and UHM length. Mahdy *et al.* (2006) increased earliness index after two cycles of selection from 3.85 to 15.38%, and from 16.67 to 23.61% of the better parent in two populations. Hassaballa *et al.* (2012) increased earliness index in a population by 14.17% of the better parent after two cycles of selection.

3- General comparison between the adopted selection procedures

It should be recalled that one of the goals of this work was to identify high yielding families matched the type of Giza 90 cultivar in fiber prop-

erties. Average of the ten selected families (Table11) indicated that selection for LY/P ranked the first and improved LY/P by 20.30% of the check strain followed by DFF method (15.82%), and LY/P restricted by DFF (11.54%). Generally, single trait selection is an effective method to improve selection criterion. Respect to the observed genetic gain in LY/P of the individual families, the best families were family No. 73 (29.44% - DFF), family No. 334 (27.91% - LY/P). Family NO.334 showed significant observed genetic gain in SCY/P, LY/p, lint %, NB/p, Si, UHM length and Micronaire reading. Among these superior families, family No. 590 (lint% procedure), family No.165 and family No.335(DFF procedure) characterized by strongest fiber beside cotton yields. It could be concluded that the adopted selection procedures identified superior high yielding families and better than the

newest check strain derived from the same materials in one or more of the main fiber properties. Therefore, the official method of maintaining and

renewing Egyptian cotton varieties should be modified to allow selection for yield beside preserving fiber properties.

Table 6. Observed genetic gain from selection for LY/P restricted by DFF after the second cycle in percentage from the check strain; season;2015

Ser	SCY/P;g	LY/P;g	lint%	NB/P	BW	SI;g	LI;g	NS/B	DFF	MIC	PI	UHM
334	22.92**	27.19**	3.46**	15.14	5.56*	-2.38	8.59**	3.51	-0.98	-10.26**	3.16	4.08*
54	7.60	9.14	1.44*	6.31	0.00	-5.44	8.49**	3.51	-4.90**	-9.40**	1.40	4.53*
31	26.37**	26.25**	-0.09	12.03	11.56**	3.74**	-3.49	7.02*	-0.98	-1.71	3.16	6.29**
700	4.95	5.19	0.24	2.48	1.11	0.68	0.00	0.00	0.49	-4.27	4.21	4.42*
699	13.12	13.93	0.73	11.87	0.00	-1.70	3.18*	0.00	-1.96**	4.27	3.51	3.53*
3	16.53*	18.16*	1.38*	10.63	4.11	3.40*	-0.83	-1.75	-0.49	3.42	1.75	0.00
105	10.36	14.31	3.62**	-4.79	14.44**	-1.36	7.76**	12.28**	-5.39**	-4.27	1.05	2.98
354	-11.92	-10.70	1.41*	-7.92	-5.56	-3.40	6.20**	-3.51	-4.90**	0.85	2.81	0.11
362	4.34	3.68	-0.64	-2.69	5.78*	2.72	-3.39	3.51	-0.98	-2.56	0.00	4.30*
48	8.66	8.29	-0.23	-1.66	9.33**	3.06*	-3.02	7.02*	1.96	2.56	6.67	5.52**
Mean	10.29	11.54*	1.13*	4.14	4.63*	-0.07	2.35*	3.16	-1.81**	-2.14	2.77	3.58**
RLSD 0.05% for mean 1	10.84	10.97	1.00	11.98	4.08	2.07	1.83	5.08	0.93	4.72	-	2.51
RLSD 0.01% for mean	14.92	13.97	1.36	17.30	5.53	2.77	2.45	7.00	1.24	6.50	-	3.46
RLSD 0.05% for families 2	14.61	14.79	1.35	16.15	5*.50	2.79	2.46	6.85	1.26	6.37	-	3.39
RLSD 0.01% for families	20.12	18.84	1.83	23.33	7.46	3.74	3.30	9.43	1.68	8.76	-	4.67
1- to compare mean with the check												
2- to compare a family with the check												

and*, significant at 0.05 and 0.01 levels of probability, respectively.- Insignificant genotypes mean squares

Table 7. Means of the studied traits after two cycles of selection for Lint %; season 2015.

Ser	SCY/P;g	LY/P;g	lint%	NB/P	BW	SI;g	LI;g	NS/B	DFE	MIC	PI	UHM
226	105.07	42.03	40.00	29.16	3.60	10.13	6.59	21.00	69.67	3.63	10.17	30.90
193	91.37	36.50	39.94	28.85	3.17	9.83	6.76	19.33	68.67	3.60	9.97	31.83
633	105.33	42.87	40.69	35.50	2.97	9.97	6.89	17.67	69.67	3.63	10.03	30.10
435	88.90	35.63	40.10	30.01	2.97	10.57	6.34	16.67	70.33	3.60	9.97	30.57
209	95.83	37.87	39.50	30.17	3.17	10.17	6.42	19.00	67.33	3.80	9.50	31.50
847	99.37	39.43	39.67	34.01	2.92	10.10	6.51	17.33	68.67	4.23	10.10	31.03
712	106.73	42.83	40.13	35.91	2.98	10.17	6.59	18.33	69.00	4.03	9.53	32.40
836	106.20	41.43	39.03	37.01	2.88	9.40	6.81	18.33	68.33	3.60	9.93	31.13
590	107.67	43.20	40.14	36.01	2.99	10.03	6.68	17.67	68.67	4.03	10.27	30.67
624	93.23	37.13	39.83	31.79	2.93	10.70	6.19	16.33	67.67	4.10	10.53	30.60
Mean	99.97	39.89	39.90	32.84	3.06	10.11	6.58	18.17	68.80	3.83	10.00	31.07
Check	91.85	35.46	38.60	31.00	3.00	9.80	6.40	19.00	68.00	3.90	9.50	30.20
RLSD 0.05 for mean1	13.65	5.40	0.64	4.69	0.12	0.24	0.17	0.62	0.73	0.23	0.53	0.68
RLSD 0.01 for mean	20.05	7.93	0.88	6.77	0.16	0.33	0.23	0.88	1.00	0.29	0.77	0.86
RLSD 0.05 for families2	18.41	7.28	0.86	6.32	0.16	0.33	0.23	0.83	0.99	0.30	0.72	0.91
RLSD 0.01 for families	27.04	10.69	1.18	9.13	0.21	0.45	0.32	1.18	1.34	0.39	1.03	1.16
1- to compare mean with the check												
2- to compare a family with the check												

Table 8. Observed genetic gain from selection for Lint % after the second cycle in percentage from the check strain; season 2015.

Ser	SCY/P;g	LY/P;g	lint%	NB/P	BW	SI;g	LI;g	NS/B	DFE	MIC	PI	UHM
226	14.39	18.54	3.63**	-5.93	20.00**	3.40*	2.92	10.53**	2.45**	-6.84	7.02	2.32
193	-0.53	2.93	3.46**	-6.95	5.56*	0.34	5.68**	1.75	0.98	-7.69	4.91	5.41**
633	14.68	20.89*	5.42**	14.51	-1.11	1.70	7.60**	-7.02	2.45**	-6.84	5.61	-0.33
435	-3.21	0.49	3.89**	-3.20	-1.11	7.82**	-0.94	-12.28	3.43**	-7.69	4.91	1.21
209	4.34	6.79	2.33*	-2.69	5.78*	3.74*	0.36	0.00	-0.98	-2.56	0.00	4.30**
847	8.18	11.21	2.77*	9.71	-2.67	3.06	1.72	-8.77	0.98	8.55*	6.32	2.76
712	16.20	20.79*	3.97**	15.85	-0.67	3.74*	3.02	-3.51	1.47*	3.42	0.35	7.28**
836	15.62	16.85	1.13	19.40	-4.00	-4.08	6.46**	-3.51	0.49	-7.69	4.56	3.09*
590	17.22	21.83*	3.98**	16.16	-0.22	2.38	4.43*	-7.02	0.98	3.42	8.07*	1.55
624	1.51	4.72	3.19**	2.56	-2.22	9.18**	-3.28	-14.04	-0.49	5.13	10.88**	1.32
Mean	8.84	12.50	3.38**	5.94	1.93	3.13*	2.80*	-4.39	1.18*	-1.88	5.26	2.89**
RLSD 0.05 for mean 1	-	15.23	1.65	15.13	3.90	2.50	2.70	3.25	1.08	5.78	5.58	2.24
RLSD 0.01 for mean	-	22.36	2.27	21.85	5.23	3.39	3.67	4.62	1.46	7.37	8.07	2.85
RLSD 0.05 for families2	-	20.53	2.23	20.40	5.25	3.37	3.64	4.39	1.46	7.80	7.53	3.02
RLSD 0.01 for families	-	30.15	3.07	29.47	7.05	4.57	4.94	6.23	1.97	9.94	10.88	3.85
1- to compare mean with the check												
2- to compare a family with the check												

*and**, significant at 0.05 and 0.01 levels of probability; respectively. - insignificant genotypes mean squares

Table 9. Means of the studied traits after two cycle of selection for DFF; season 2015

Ser	SCY/P;g	LY/P;g	lint%	NB/P	BW	SI;g	LI;g	NS/B	DFF	MIC	PI	UHM
529	106.33	41.67	39.21	32.23	3.32	10.43	6.18	19.67	64.33	4.17	11.03	31.13
54	98.83	38.70	39.15	32.96	3.00	9.27	6.94	19.67	64.67	3.53	9.63	31.57
341	96.20	37.43	38.91	30.64	3.16	10.13	6.29	19.33	66.33	3.97	9.97	31.67
39	105.10	40.63	38.67	32.16	3.27	10.03	6.29	20.00	64.33	3.70	9.87	30.13
83	103.17	40.17	38.93	30.64	3.37	10.27	6.21	20.00	64.33	3.83	9.77	31.37
73	115.87	45.90	39.63	37.30	3.11	10.33	6.36	18.33	64.67	4.03	9.83	30.50
75	113.17	43.33	38.30	37.76	3.01	9.63	6.45	19.33	65.00	3.90	9.57	30.30
156	108.93	41.37	37.99	36.96	2.95	9.50	6.46	19.33	65.67	3.83	10.47	30.87
335	110.63	42.40	38.33	36.79	3.01	9.93	6.26	19.00	64.67	4.00	10.77	31.50
358	102.00	39.10	38.35	33.02	3.09	9.80	6.35	19.33	64.33	3.83	9.50	31.80
Mean	106.02	41.07	38.75	34.05	3.13	9.93	6.38	19.40	64.83	3.88	10.04	31.08
Check	91.85	35.46	38.60	31.00	3.00	9.80	6.40	19.00	68.00	3.90	9.50	30.20
RLSD 0.05 for mean 1	9.37	3.14	0.52	3.85	0.21	0.30	0.33	-	0.69	0.25	0.52	0.77
RLSD 0.01 for mean	13.26	4.32	0.72	5.45	0.30	0.41	0.48	-	0.93	0.37	0.66	1.09
RLSD 0.05 for families2	12.63	4.23	0.70	5.19	0.28	0.40	0.44	-	0.93	0.34	0.70	1.04
RLSD 0.01 for families	17.88	5.83	0.97	7.35	0.41	0.55	0.64	-	1.25	0.50	0.89	1.47
1- to compare mean with the check												
2- to compare a family with the check												

-Insignificant genotypes mean squares

Table 10. Observed genetic gain from selection for DFF after the second cycle in percentage from the check strain; season 2015

Ser	SCY/P;g	LY/P;g	lint%	NB/P	BW	SI;g	LI;g	NS/B	DFF	MIC	PI	UHM
529	15.77*	17.50**	1.58	3.95	10.67*	6.46**	-3.39	3.51	-5.39**	6.84	16.14**	3.09
54	7.60	9.14	1.44	6.31	0.00	-5.44	8.49*	3.51	-4.90**	-9.40	1.40	4.53*
341	4.74	5.56	0.81	-1.15	5.33	3.40	-1.77	1.75	-2.45**	1.71	4.91	4.86*
39	14.43*	14.59*	0.19	3.76	8.89	2.38	-1.77	5.26	-5.39**	-5.13	3.86	-0.22
83	12.32	13.27*	0.87	-1.15	12.22*	4.76*	-2.92	5.26	-5.39**	-1.71	2.81	3.86*
73	26.15**	29.44**	2.66**	20.33*	3.56	5.44*	-0.68	-3.51	-4.90**	3.42	3.51	0.99
75	23.21**	22.20**	-0.77	21.82*	0.22	-1.70	0.78	1.75	-4.41**	0.00	0.70	0.33
156	18.60*	16.66**	-1.58	19.22*	-1.56	-3.06	0.99	1.75	-3.43**	-1.71	10.18**	2.21
335	20.45**	19.57**	-0.70	18.68*	0.44	1.36	-2.14	0.00	-4.90**	2.56	13.33**	4.30*
358	11.05	10.27	-0.65	6.53	2.89	0.00	-0.78	1.75	-5.39**	-1.71	0.00	5.30**
Mean	15.43**	15.82**	0.38	9.83	4.27	1.36	-0.32	2.11	-4.66**	-0.51	5.68	2.92*
RLSD 0.05% for mean 1	10.20	8.85	1.35	12.42	6.94	3.06	5.14	-	1.02	6.53	5.48	2.56
RLSD 0.01% for mean	14.43	12.18	1.86	17.57	10.02	4.15	7.43	-	1.36	9.44	6.99	3.62
RLSD 0.05% for families 2	13.76	11.93	1.82	16.75	9.35	4.12	6.93	-	1.37	8.81	7.39	3.45
RLSD 0.01% for families	19.46	16.43	2.50	23.70	13.51	5.59	10.01	-	1.84	12.73	9.42	4.88
1- to compare mean with the check												
2- to compare a family with the check												

- Insignificant genotypes mean squares. *and**; significant at 0.05 and 0.01 levels of probability; respectively

Table 11. The observed genetic gain of the three superior families in yield from each selection procedure with favorable or no effect on fiber properties; season 2015.

Sel.for	Ser.	Scy/P;g	Ly/P;g	Lint%	NB/P	Bw;g	Sl;g	LI;g	NS/B	DFE	MIC	PI	UHM
LY/P	334	22.92**	27.19**	3.46**	15.14*	5.56	-2.38	8.59**	3.51	-0.98	-10.26*	3.16	4.08*
	31	26.37**	26.25**	-0.09	12.03	11.56**	3.74	-3.49	7.02**	-0.98	-1.71	3.16	6.29**
	361	22.34**	22.86**	0.38	17.51*	3.11	0.00	0.42	1.75	-0.98	0.85	2.11	4.75**
	Mean☼	19.75**	20.30**	0.44	14.01*	3.92	1.60	-0.38	0.70	0.15	-2.91	1.72	0.97
LY/P re-stricted By DFF	334	22.92**	27.19**	3.46**	15.14	5.56*	-2.38	8.59**	3.51	-0.98	-10.26**	3.16	4.08*
	31	26.37**	26.25**	-0.09	12.03	11.56**	3.74**	-3.49	7.02*	-0.98	-1.71	3.16	6.29**
	3	16.53*	18.16*	1.38*	10.63	4.11	3.40*	-0.83	-1.75	-0.49	3.42	1.75	0.00
	Mean	10.29	11.54*	1.13*	4.14	4.63*	-0.07	2.35	3.16	-1.81**	-2.14	2.77	3.58**
Lint %	633	14.68	20.89*	5.42**	14.51	-1.11	1.70	7.60**	-7.02	2.45**	-6.84	5.61	-0.33
	712	16.20	20.79*	3.97**	15.85	-0.67	3.74*	3.02	-3.51	1.47*	3.42	0.35	7.28**
	590	17.22	21.83*	3.98**	16.16	-0.22	2.38	4.43*	-7.02	0.98	3.42	8.07*	1.55
	Mean	8.84	12.50	3.38**	5.94	1.93	3.13*	2.80*	-4.39	1.18*	-1.88	5.26	2.89**
DFF	73	26.15**	29.44**	2.66**	20.33*	3.56	5.44*	-0.68	-3.51	-4.90**	3.42	3.51	0.99
	156	18.60*	16.66**	-1.58	19.22*	-1.56	-3.06	0.99	1.75	-3.43**	-1.71	10.18**	2.21
	335	20.45**	19.57**	-0.70	18.68*	0.44	1.36	-2.14	0.00	-4.90**	2.56	13.33**	4.30*
	Mean	15.43**	15.82**	0.38	9.83	4.27	1.36	-0.32	2.11	-4.66**	-0.51	5.68	2.92*

*and**, significant at 0.05 and 0.01 levels of probability; respectively. Mean☼; mean of the ten selected families.

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كفاءة الانتخاب لصفه واحده لتحسين المحصول والتكبير والمحافظة على صنف القطن المصرى جيزه ٩٠

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الملخص

أجريت هذه الدراسة بمحطه بحوث شندويل بسوهاج - مركز البحوث الزراعيه- معهد بحوث القطن خلال مواسم ٢٠١٥، ٢٠١٤، ٢٠١٣. وكانت مواد التربية المستخدمه هى نسل ٦٠ نبات فردى منتخب من حقل التربية الخاص بصنف القطن جيزه ٩٠ (وهى نفس مواد التربية المستخدمه للمحافظة على الصنف وانتاج النويه). والهدف الرئيسى من هذه الدراسه هو دراسه امكان انتخاب سلالات عاليه فى محصول الشعير من صنف جيزه ٩٠ مع المحافظه على صفاته التكنولوجيه الرئيسيه وهى النعومه والمتانه وطول النيله. تم اجراء الانتخاب لدورتين متتاليتين لكل صفه على حده. وتظهر النتائج بعد الدور الثانى تفوق الانتخاب لصفه محصول الشعير للنبات وكان ترتيبها الاول ووصل التحسين الوراثى المشاهد الى ٣٠,٢٠% من احدث نويه للصنف (التي استتبطت من نفس مواد الدراسه) - تبعها فى الترتيب الانتخاب لصفه عدد الايام حتى تفتح اول زهره (١٥,٨٢%) ثم الانتخاب للمحصول المقيّد بصفه التكبير (١١,٥٤%). وتظهر النتائج ان الانتخاب لصفه ما هو الافضل لتحسينها. كما تشير نتائج التحسين الوراثى المشاهد الى عزل وتحديد عدد من السلالات المتفوقه فى المحصول مع واحد او اثنين من صفات الجوده عن النويه المنتجه من نفس مواد التربية. لذلك ينصح بتعديل طريقه انتاج النويه المتبعه حالياً لتسمح بانتخاب سلالات عاليه المحصول ولها نفس صفات الصنف التكنولوجيه.