

Efficiency of Single and Multiple Traits Selection for Yield and its Components in Varietal Maintenance of Giza 90 Egyptian Cotton Variety

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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, two cycles of selection for single trait selection for lint yield/plant and 14 selection indices (desired genetic gain index) were achieved. Average observed genetic gain of the ten selected families after two cycles of selection indicated that LY/P ranged from insignificant (16.57%) for index 2 (LY/P and BW) to 21.63% ($P \leq 0.01$) for index 7 (NB/P and NS/B). Index 2 increased BW by 9.27% ($p \leq 0.05$) and UHM length by 2.23%

($p \leq 0.01$). Index 7 showed significant genetic gain of 20.26, 21.63, 3.16, 5.44 and 2.785 for SCY/P, LY/P, SI, PI, and UHM length; respectively. Index 3 showed significant genetic gain of 19.71, 21.36, 3.61, 7.82, and 2.65% for SCY/P, LY/P, SI, PI and UHM length; respectively. Index 13 gave significant genetic gain of 18.46, 20.55 and 5.76% for SCY/P, LY/P and PI; respectively. Single trait selection for LY/P showed significant genetic gain of 19.75, 20.30 and 14.01% for SCY/P, LY/P and NB/P; respectively. The results indicated that selection index was better than single trait selection in detecting the superior families in LY/P. Generally, it could be concluded that the present program for maintenance and renewing Egyptian cotton varieties is a precise and perfect program to preserve the fiber quality, but, not suitable for improving yielding ability. In consequence, this program should be modified to allow the isolation of superior high yielding off types from the breeding nursery characterized by improvement in one or more fiber quality.

Keywords: Maintenance of Egyptian cotton, multiple traits selection, observed genetic gain, heritability.

Introduction

Egyptian cotton has prevailed as one of Egypt's biggest competitive advantages. With an established reputation of being the best cotton in the world, its fineness, strength and superior characteristics, have positioned products made of Egyptian cotton as

the world's finest. Pedigree selection method has become the most common plant breeding procedure. Most of Egyptian cotton varieties were produced by this method. Both of pedigree selection and independent culling levels (ICL) were used in maintenance and renewing Egyptian

cotton varieties. Selection index techniques can be used to improve several traits simultaneously (Smith 1936), (Manning 1956) and (Pesek and Baker 1969 and 1970). Computers provide a good opportunity to use such techniques in plant breeding programs. Selection depends mainly upon genetic variability Manning (1956), El-Kilany (1976), Abo El-Zahab and El-Kilany (1979), Mahdy (1983 a and b), and Lioyed and Bridges (1995) reported significant genotypic variability for all traits. Likewise, Soomro *et al.* (2010) recorded high heritability for plant height, bolls/plant and seed cotton yield/plant ranged from 72.97 to 75.55%. Whereas, El-Lawendy and El-Dhan (2012) found that heritability obtained in both F3 and F4- generations ranged from moderate to high (51.3 to 96.3%) for all traits. After two cycles of selection for lint percentage in two segregating populations, Hassaballa *et al.* (2012) estimated broad sense heritability of 64 and 73% for two populations. Many researchers indicated that selection index techniques were mostly better than single trait selection; Walker (1960), Kamanathan (1967), Abo El – Zahab and El – Kilany (1979), Mahdy (1983a,b), Singh *et al.* (1995), Gomaa *et al.* (1999), Esmail (2007), El-Okkia *et al.* (2008), Tang *et al.* (2009), El-Lawendy and El-Dahan (2012), Kassem *et al.* (2008) and Mahrous (2008). Maintaining of the Egyptian cotton varieties is the ability to keep the cotton variety out of the genetic changes “deterioration” so that the standard characters of such variety will be stable for a long time, and providing the cotton area for each va-

riety annually by new waves of, genetically pure cottonseed stocks. The breeder mainly concerned on preservation of the known fiber properties of a variety rather than yield. Therefore, yield of the Egyptian cotton varieties is lower than that of Upland cottons. 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, A.R.C., and the possibility of selection elite high yielding plants characterized by the same fiber properties of Giza 90.

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 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 three methods of pedigree selection; single trait selection for lint yield/plant, selection index method and the traditional method followed by Cotton Maintenance Res. Sec. for renewing and maintenance of Egyp-

tian cotton varieties. This method 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 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 was 847. At flowering days to first flower (DFF) was recorded flower for each plant. Before picking 10 open sound bolls were picked from each plant to measure; average boll weight; g (BW, g), seed index; 100-seed weight (SI; g) and lint index; (LI; g), estimated as "weight of lint in a sample/ weight of seeds in this sample *seed index". 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).

Selection procedures

1-Single trait selection: Selfed seeds of the best 20 single plants in LY/P were saved for season 2014.

2-Selection index method: The single plants (847) were ranked using 13 models of the modified "desired

genetic gain" method (Pesek and Baker; 1969 and 1970). Selfed seeds of the 20 superior plants for each model were saved for next season.

Season 2014: The selected plants of the 14 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 the hills 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 a total of 67 selected plants from season 2014 covered all selection procedures a long with G.90 nucleolus (this nucleolus was 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:

1- Estimation of phenotypic covariance between pairs of traits of single plants in season 2013 depended on the mathematical fact:

$$\text{IF } C = A + B \text{ Then } \sigma^2_C = \sigma^2_A + \sigma^2_B + 2\text{cov}_{AB}$$

2- Estimatates of genotypic variances and covariances in the second and third seasons were

calculated from EMS and EMCP components of the selected families as outlined by Walker (1960). Calculation of selection indices was done as Pesek and Baker (1969 and 1970). The desired genetic gain was assigned as 10% increase from the population mean of each trait in the index. The phenotypic value of a family (I) was estimated using the following formula as outlined by (Smith 1936) and (Hazel 1943). Heritability was estimated as: $(H) = (\sigma_g^2 / \sigma_p^2) \times 100$. The phenotypic and genotypic coefficients of variation were estimated using the formula developed by Burton (1952). Mean comparisons were calculated by using revised L.S.D. according to El Rawi and Khalafalla (1980). The significance of observed direct and correlated response to selection was measured as deviation percentage of family mean from the check strain using L.S.D.

1- Evaluation of the selection procedures.

To compare the different selection procedures, the procedures were subjected to two ranks. The first was for number of families showed significant observed genetic gain in LY/P and the total sum of their genetic gains. The second was for number of families showed significant observed genetic gain in LY/P > 25% of the check strain and the total sum of their genetic gains.

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 (Table 1). 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 very 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	DFP	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

2-Second cycle selection; season 2015

2-1. Genetic variability and heritability estimate

The analysis of variance of the studied traits for the selected families after the second cycle selection are shown in Table 2. The analysis of variances of different traits was performed two times. The first was for the selected families to estimate GCV%, PCV%, and heritability of the traits under selection pressure. The second was for the selected families a long with check strain (the newest nucleolus Giza 90) to compare different selected families with check strain. The analysis of variance indicated that the genotypes mean squares (families) was not significant for LY/P, SCY/P and NB/P when selection practiced for LY/P. However, mean squares of genotypes of the other traits were significant. This indicates the absence of genetic variability in LY/P for further cycle of selection. Therefore, two cycles of single trait selection for lint yield /plant depleted greatly the coefficient of variability and was enough to isolate the elite families. The phenotypic coefficient of variation dropped from 39.52% in the base population to zero after two cycle of selection. The results confirmed the concept that long times of selfing (more than 16 years)

for selected families in the breeding nursery of Giza 90 resulted in a mixture of homozygous families in lint yield / plant, and selection become “pure line selection”, and two cycles of selection for LY/P was sufficient to isolate the elite families. However, selection indices which included LY/P showed GCV %larger than that of selection for LY/P per se. The genetic coefficient of variation in LY/P was 10.35, 9.75, 5.65, 12.35, 12.32, 5.33,7.61 and 0.0 for indices NO.1, NO.2, NO.3, NO.4, NO.5, NO.11, NO.12 and NO.13, respectively. It could be concluded that the genetic variability after selection indices in general was larger than that after single trait selection. Heritability estimate for LY/P ranged from 61.87% for index 4 to 90.78% for index 1. (Srouf *et al.* (2010) Found decrease in PCV and GCV% from F2 to F3, however heritability increased. Mahdy *et al.* (2006, 2007, 2009 a, b) Found decrease in variability in LY/P, earliness index, SCY/P, BW and NB/S after two cycles of selection in segregation populations. Also, Hassaballa *et al.* (2012) and Mahdy *et al.* (2013 a, b) noted remarkable decrease in genetic variability and high estimates heritability after two cycles of selection for earliness index, LY/P and NB/P.

Table 2. Mean squares, genotypic (GCV %) and phenotypic (PCV%) coefficients of variation and broad sense heritability estimates(H) of the studied traits of the adopted selection procedures; season 2015(ANOVA without check)

Single trait selection for LY/P;g													
S.V	df	SCY/P	LY/P	Lint%	NB/P	BW	SI	LI	NS/B	DFE	MIC	PI	UHM
Reps	2	5.13	1.64	0.15	0.97	0.02	0.01	0.09	2.03	0.40	0.02	0.25	0.38
Genotypes	9	58.91	12.47	0.87**	5.09	0.09**	0.09*	0.15*	2.09**	2.52**	0.06*	0.40**	4.67**
Exper.error	18	46.25	7.99	0.19	4.56	0.02	0.06	0.05	0.37	0.40	0.02	0.09	0.45
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%			-										
Index 1 included LY/P and NB/P													
S.V	df	SCY/P	LY/P	Lint%	NB/P	BW	SI	LI	NS/B	DFE	MIC	PI	UHM
Reps	2	5.08	0.68	0.02	0.33	0.01	0.01	0.14	0.58	1.63	0.19	1.02	0.30
Genotypes	9	392.47**	63.70**	0.88**	45.43**	0.11**	0.46*	0.39**	2.35	4.60*	0.25**	0.45**	2.34**
Exper.error	18	34.31	5.87	0.14	7.48	0.01	0.16	0.05	1.39	1.49	0.03	0.06	0.32
GCV%		10.02	10.35	1.27	9.99	5.99	3.21	5.14	-	1.51	6.95	3.61	2.63
PCV%		10.49	10.86	1.39	10.93	6.33	3.93	5.55	-	1.83	7.40	3.86	2.82
H%			90.78		83.54								
Index 2 included LY/P and BW													
Reps	2	166.28	25.88	0.09	17.97	0.09	0.40	0.03	3.63	1.63	0.02	0.34	0.02
Genotypes	9	412.43	77.89*	2.10**	52.22*	0.14*	0.12	0.08*	1.81	9.79**	0.13**	1.03**	4.52**
Exper.error	18	191.72	29.17	0.19	21.04	0.04	0.08	0.03	1.80	2.45	0.03	0.13	0.16
GCV%		-	9.75	2.05	9.76	5.52	-	2.03	-	2.30	4.74	5.67	3.90
PCV%		-	12.33	2.16	12.62	6.49	-	2.55	-	2.65	5.32	6.06	3.97
H%			62.56			72.43							
Index 3 included LY/P and NS/B													
Reps	2	31.14	3.75	1.09	5.70	0.00	0.35	0.01	1.02	1.90	0.04	0.31	0.51
Genotypes	9	146.05	28.69*	1.12**	12.15	0.06*	0.11*	0.07	1.10	7.76**	0.32	1.30**	1.24**
Exper.error	18	72.70	10.94	0.29	9.40	0.02	0.04	0.04	0.61	2.09	0.24	0.15	0.19
GCV%		-	5.65	1.34	-	3.80	1.58	-	-	2.19		6.04	1.91
PCV%		-	7.19	1.56		4.65	1.90	-	-	2.57		6.42	2.08
H%			61.87						45.08				
Index 4 included LY/P and LI													
Reps	2	19.14	3.90	0.10	5.11	0.08	0.03	3.35	0.23	0.04	0.93	0.33	0.30
Genotypes	9	224.49*	37.73**	0.57**	35.74**	0.05*	0.10	1.04	6.59**	0.07	0.57	1.42**	1.37**
Exper.error	18	75.94	10.43	0.11	7.27	0.02	0.08	1.38	0.49	0.05	0.27	0.35	0.35
GCV%		6.26	12.35	3.91	14.80	11.86	-		19.75	-	-	20.13	7.09
PCV%		7.69	14.52	4.37	16.58	15.47	-	-	20.54	-	-	23.17	8.20
H%			72.35					-					
Index 5 included LY/P and DFE													
Reps	2	121.37	15.01	0.26	28.96	0.02	0.39	0.01	1.97	4.13	0.08	0.28	0.45
Genotypes	9	556.66**	87.79**	0.98	65.16**	0.06*	0.17	0.06	1.36	11.43**	0.09**	1.15**	1.17**
Exper.error	18	95.89	13.26	0.40	15.97	0.03	0.07	0.07	1.27	3.06	0.02	0.09	0.29
GCV%		11.95	12.32	-	12.05	3.25	-	-	-	2.50	3.75	5.87	1.76
PCV%		13.13	13.37	-	13.87	4.56	-	-	-	2.93	4.41	6.12	2.03
H%			84.89							73.23			
Index 7 included NB/P and NS/P													
S.V	df	SCY/P	LY/P	Lint%	NB/P	BW	SI	LI	NS/B	DFE	MIC	PI	UHM
Reps	2	138.33	25.42	0.39	11.66	0.00	0.63	0.01	1.40	8.63	0.13	0.47	0.45
Genotypes	9	146.27	29.44	0.89**	14.18	0.06*	0.19**	0.04	1.32	10.15**	0.05*	1.27**	1.58**
Exper.error	18	92.90	14.08	0.14	10.19	0.02	0.03	0.04	0.68	2.89	0.02	0.10	0.21
GCV%		-	-	1.28	-	3.93	2.29	-	-	2.30	2.40	6.24	2.18
PCV%		-	-	1.40	-	4.68	2.49	-	-	2.72	3.19	6.51	2.34
H%					-				-				

Index 8 included NB/P and LI													
S.V	df	SCY/P	LY/P	Lint%	NB/P	BW	SI	LI	NS/B	DFP	MIC	PI	UHM
Reps	2	105.79	15.21	0.21	18.09	0.08	0.05	0.09	0.86	1.30	0.09	0.87	0.80
Genotypes	9	216.34**	37.94**	0.66**	34.84**	0.05*	0.16	0.10	0.80	5.35**	0.19**	0.45	1.04
Exper.error	18	48.22	6.46	0.13	5.20	0.02	0.15	0.07	1.76	1.49	0.05	0.26	0.48
GCV%		7.11	7.94	1.09	8.93	3.15	-	-	-	1.66	5.50	-	-
PCV%		8.06	8.72	1.21	9.68	4.12	-	-	-	1.95	6.44	-	-
H%					85.08			-					
Index 9 included NB/P and SI													
Reps	2	101.29	8.43	1.08	16.70	0.03	0.03	0.07	0.67	3.73	0.10	0.43	0.28
Genotypes	9	498.10**	90.17**	1.50**	22.48*	0.10**	0.20	0.14	2.33	9.49**	0.16**	0.82**	2.04**
Exper.error	18	80.71	11.26	0.27	7.24	0.02	0.13	0.06	1.38	1.81	0.03	0.09	0.13
GCV%		10.81	12.04	1.64	6.59	5.11	-	-	-	2.34	5.51	5.06	2.61
PCV%		11.81	12.87	1.81	8.00	5.85	-	-	-	2.60	6.04	5.36	2.70
H%					67.81		-						
Index 10 included LI and NS/B													
Reps	2	60.48	6.26	1.66	13.63	0.01	0.08	0.09	0.20	1.60	0.07	0.07	0.16
Genotypes	9	138.46	27.60	1.02*	14.90	0.06	0.20	0.14	1.80	7.47*	0.34	2.01**	0.86*
Exper.error	18	89.42	14.13	0.32	9.45	0.03	0.09	0.07	1.14	2.27	0.27	0.15	0.24
GCV%		-	-	1.23	-	-	-	-	-	1.95	-	7.84	1.48
PCV%		-	-	1.49	-	-	-	-	-	2.34	-	8.15	1.75
H%					-				-				
Index 11 included LY/P , NB/P and NS/B													
Reps	2	50.45	8.36	0.00	11.03	0.01	0.43	0.08	0.41	2.80	0.06	0.28	0.31
Genotypes	9	164.67*	24.80*	0.63	17.45	0.05*	0.28	0.17	1.09	6.30*	0.10*	0.36**	1.04
Exper.error	18	50.71	9.35	0.46	10.31	0.02	0.20	0.11	0.71	2.02	0.03	0.11	1.04
GCV%		5.66	5.33	-	-	3.42	-	-	-	1.75	4.01	6.51	0.00
PCV%		6.80	6.75	-	-	4.25	-	-	-	2.12	4.71	6.79	1.90
H%			62.31		-				-				
Index 12 included LY/P, NB/P and LI													
Reps	2	12.82	3.43	0.20	0.63	0.04	0.04	0.04	0.84	0.93	0.08	0.77	0.57
Genotypes	9	229.76*	41.31**	0.98**	25.09*	0.04	0.29	0.23**	0.58	3.49	0.19**	0.82**	1.81**
Exper.error	18	78.78	11.31	0.09	8.15	0.02	0.16	0.06	1.66	1.56	0.04	0.21	0.41
GCV%		6.63	7.61	1.40	6.79	-	-	3.63	-	-	5.61	4.58	2.22
PCV%		8.18	8.93	1.47	8.26	-	-	4.29	-	-	6.40	5.32	2.52
H%			72.62		67.51			71.39					
Index 13 included LY/P, LI and NS/B													
Reps	2	60.48	6.26	1.66	13.63	0.01	0.08	0.09	0.23	1.60	0.07	0.07	0.16
Genotypes	9	138.46	27.60	1.02*	14.90	0.06*	0.20	0.14	1.72	7.4**	0.34	2.01**	0.86**
Exper.error	18	89.42	14.13	0.32	9.45	0.03	0.09	0.07	1.12	2.27	0.27	0.15	0.24
GCV%		-	-	1.23	-	3.29	-	-	-	1.95	-	7.84	1.48
PCV%		-	-	1.49	-	4.53	-	-	-	2.34	-	8.15	1.75
H%			-					-	-				
Index 14 included NB/P, LI and NS/B													
S.V	df	SCY/P	LY/P	Lint%	NB/P	BW	SI	LI	NS/B	DFP	MIC	PI	UHM
Reps	2	39.99	8.97	0.22	3.31	0.02	0.16	0.01	2.90	0.23	0.01	0.01	0.61
Genotypes	9	393.19**	64.65**	1.20**	32.50**	0.10*	0.40**	0.30**	2.21*	6.11**	0.09*	0.09**	0.58*
Exper.error	18	72.20	10.66	0.10	5.22	0.02	0.07	0.04	0.65	0.53	0.02	0.02	0.19
GCV%		9.88	10.41	1.56	8.87	5.25	3.31	4.53	3.82	2.01	3.98	1.57	1.18
PCV%		10.93	11.39	1.63	9.68	5.87	3.66	4.89	4.54	2.10	4.54	1.79	1.44
H%					83.95			85.99	70.71				

*and**; significant at 0.05 and 0.01 level of probability; respectively.-insignificant mean squares of genotypes and/ or negative genotypic variance.

2-2. Means and observed genetic gain

Average of the ten selected families and their observed genetic gain after two cycles of selection for different selection procedures are shown in Table 3. Mean observed genetic gain in LY/P ranged from insignificant (16.57%) for index 2 (LY/P and BW) to 21.63% ($P \leq 0.01$) for index 7 (NB/P and NS/B). Index 2 increased BW by 9.27% ($p \leq 0.05$) and UHM length by 2.23% ($p \leq 0.01$). Index 7 showed significant genetic gain of 20.26, 21.63, 3.16, 5.44 and 2.785 for SCY/P, LY/P, SI, PI, and UHM length; respectively. Index 3 showed significant genetic gain of 19.71,

21.36, 3.61, 7.82, and 2.65% for SCY/P, LY/P, SI, PI and UHM length; respectively. Index 13 gave significant genetic gain 18.46, 20.55 and 5.76% for SCY/P, LY/P and PI; respectively. Single trait selection for LY/P showed significant genetic gain of 19.75, 20.30 and 14.01% for SCY/P, LY/P and NB/P; respectively. It is of interest to indicate that the overall mean of the selected families masked the superior selected families for each selection procedures. In autogamous crops the breeder in the late generation searches for the individual superior families. Therefore, the individual superior families will be presented in Table 5.

Table 3. Mean of the ten selected families and their observed genetic gain in percentage of the check strain after two cycles of selection; season 2015.

Sel.For	Item	SCY/P;g	LY/P;g	Lint%	NB/P	BW;g	SI;g	LI;g	NS/B	DFE	MIC	PI	UHM
LY/P	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
	Gain	19.75**	20.30**	0.44	14.01*	3.92	1.60	-0.38	0.70	0.15	-2.91	1.72	0.97
Index1	Mean	108.99	42.42	38.91	35.61	3.08	10.02	6.47	18.70	67.57	3.88	9.98	31.24
	Gain	18.66**	19.63**	0.81	14.86**	2.50	2.20	-1.15	-4.62	1.19	-0.52	5.01*	3.44**
Index2	Mean	106.60	41.34	38.80	33.05	3.28	10.21	6.38	19.48	68.13	3.93	9.68	30.87
	Gain	16.06	16.57	0.52	6.61	9.27*	4.15	-2.64	-0.62	2.04	0.85	1.89	2.23**
Index3	Mean	109.95	43.03	39.13	35.00	3.15	10.15	6.40	18.91	66.99	4.00	10.24	31.00
	Gain	19.71**	21.36**	1.37	12.90	4.84	3.61*	-2.23	20.47	-6.10	2.65	7.82**	2.65**
Index4	Mean	105.64	40.80	38.62	35.20	3.01	9.89	6.37	18.70	68.60	3.92	9.68	30.74
	Gain	15.01*	15.05*	0.04	13.55*	0.20	0.88	-2.69	-4.59	2.74**	0.54	1.94	1.78
Index5	Mean	103.75	40.45	39.00	33.60	3.10	10.11	6.38	18.70	66.70	3.93	10.10	30.74
	Gain	12.95*	14.06*	1.03	8.39	3.33	3.11	2.60-	-4.59	-0.10	0.77	6.33*	1.80
Index7	Mean	110.46	43.13	39.02	35.20	3.14	10.11	6.40	19.00	67.60	3.91	10.02	31.04
	Gain	20.26*	21.63**	1.09	13.55	4.60	3.16**	-2.37	-3.06	1.24	0.33	5.44**	2.78*
Index8	Mean	105.35	40.80	38.73	35.20	2.99	9.90	6.36	18.60	68.50	3.87	9.89	30.61
	Gain	14.69**	15.06**	0.32	13.55**	-0.27	1.04	-2.93	-5.10	2.59*	-0.82	4.07	1.35
Index9	Mean	109.10	42.61	39.03	34.20	3.17	10.08	6.43	19.10	68.50	3.86	9.78	30.51
	Gain	18.78**	20.16**	1.12	10.32	5.73	2.82	-1.82	-2.55	2.59*	-1.10	2.91	1.03
Index 10	Mean	108.81	42.75	39.28	34.40	3.16	10.17	6.47	18.90	67.40	4.00	10.05	30.55
	Gain	18.46*	20.55**	1.75	10.97	5.20	3.73	-1.16	-3.57	0.94	2.64	5.76*	1.16
Index 11	Mean	108.89	42.59	39.12	35.5	3.07	10.18	6.52	18.4	68.2	3.921	9.92	31.047
	Gain	18.55	20.11*	1.34	14.52	2.33	3.90	-0.53	-6.12	2.14	0.54	4.42	2.80
Index 12	Mean	107.04	41.564	38.82	35	3.064	10.06	6.381	18.7	68.2	3.884	9.84	30.811
	Gain	16.54*	17.21**	0.57	12.90*	2.13	2.62	-2.58	-4.59	2.14	-0.41	3.58	2.02
Index 13	Mean	108.81	42.75	39.28	34.40	3.16	10.17	6.47	18.90	67.40	3.94	10.05	30.55
	Gain	18.46*	20.55**	1.75	10.97	5.20	3.73	-1.16	-3.57	0.94	0.92	5.76*	1.16
Index 14	Mean	104.71	40.76	38.92	34.00	3.08	9.97	6.52	18.90	68.00	3.81	9.65	30.53
	Gain	14.00*	14.94**	0.83	9.68*	2.80	1.77	-0.49	-3.57	1.84*	-2.33	1.53	1.11
Check	Mean	91.85	35.46	38.60	31.00	3.00	9.80	6.40	19.00	68.00	3.90	9.50	30.20

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

3- Comparison between selection procedures

It should be recalled that the main goal of this work was to study the possibility of isolation high yielding strains characterized by the same fiber properties of Giza 90. The genetic materials were subjected to single trait selection for LY/P and 14 selection indices involved two or three characters. It is difficult to compare the efficiency of all these procedures, because a procedure could improve a character and affect adversely the others. Therefore, selection procedures were subjected to

two ranks. The first was for the number of detected families showed significant genetic gain in LY/P. The second rank was for the number of detected families showed significant genetic gain in LY/P $\geq 25\%$ of check strain. A problem was encountered; how you can measure the efficiency if two or more procedures of selection detected the same number of families which showed significant genetic gain in LY/P?. To solve this problem, the observed genetic gain of the detected families was summed to give total genetic gain.

Table 4. Number of detected families showed significant observed genetic gain in LY/P and observed genetic gain $\geq 25\%$ of the check strain after two cycles of selection.

Selection procedure	NO. of families (*)	Total gain	Rank	NO. of families (**)	Total gain	Rank
LY/P	9	194.85	3	3	8.46	9
Index 1	9	206.97	1	4	1.53	3
Index 2	4	117.39	12	2	74.3	10
Index 3	8	194.93	2	4	116.64	4
Index 4	3	60.3	13	1	34.88	12
Index 5	6	145.99	7	3	93.03	5
Index 7	6	162.06	5	5	142.13	1
Index 8	7	136.4	10	1	34.88	12
Index 9	7	188.41	4	4	135.9	2
Index 10	5	133.11	11	3	90.39	6
Index 11	6	137.61	9	3	80.06	8
Index 12	6	139.2	8	2	64.7	11
Index 13	5	133.11	11	3	90.39	6
Index 14	7	154.54	6	3	83.26	7

(*) Number of detected families showed significant observed genetic gain in LY/P. (**) Number of detected families showed significant observed genetic gain $\geq 25\%$ in LY/P.

In the first rank (Table 4) in which significant genetic gain were summed, index 1 (LY/P and NB/P) ranked the first and scored total gain of 206.97 % followed by index 3 (LY/P and NS/B), selection for LY/P per se, index 9 (NB/P and SI) and selection index 7 (NB/P and NS/B). In the second rank, the sig-

nificant genetic gain in LY/P more than 25 % of the check strain, the genetic gain of the superior families in LY/P were summed. Selection index 7 ranked the first, index 9 ranked the second, index 1 ranked the third, index 3 ranked the fourth, and selection for LY/P per se ranked the ninth. It could be concluded that selection in-

dex was better than single trait selection in detecting the superior families in LY/P. Many researchers indicated that selection index techniques were mostly better than single trait selection; Walker (1960), Kamalanathan (1967), Abo El – Zahaband El – Kilany (1979), Mahdy (1983a,b), Singh *et al.* (1995), Gomaa *et al.* (1999), Esmail (2007), El-Okkia *et al.* (2008), Tang *et al.* (2009), El-Lawendy and El-Dahan (2012), Kassem *et al.* (2008) and Mahrous (2008).

4- General Discussion

Egyptian cotton varieties have a world reputation for its high quality properties. Each variety has its own fiber and yarn characteristics. The exportation of a cotton variety depends mainly upon its own fiber and yarn characteristics rather than its yielding ability. Therefore, Cot.Var.Main. Res. Sec, CRI. ARC. follows certain steps for many decades for renewing and maintaining and increase the breeder seeds of different Egyptian cotton varieties (materials and methods). The breeder devotes all his efforts during the steps of the maintenance program to preserve fiber and yarn qualities of the variety using independent culling levels method (ICL) during fiber tests. Yielding ability is not the main issue in maintenance program. This program is a good, précised and perfect method for preserving fiber and yarn qualities rather than yield. Therefore, the phenotypic coefficient of variation of the basic materials of this work was very high and accounted to 39.70, 39.52 and 39.45 % for SCY/P, LY/P, and NB/P compared to 2.49 ,7.40 ,4.83 and 5.70 %

for DFF, Micronair reading, pressley index and UHM length; respectively. Artificial selfing of Giza 90 plants in the breeding nursery for more than 16 year ago (Giza 90 released in year 2000) could be resulted in a mixture of homozygous strains similar to great extent in fiber properties and differ in yielding ability. The main goal of this work was to isolate and detect elite high yielding families matched Giza 90 type in fiber properties and /or high yielding families improved for one or more of three main fiber properties; fineness, strength and length. The basic materials of Giza 90 in year 2013 in the breeding nursery were subject to single trait selection for LY/P and 14 models of desired gain index for two cycles of selection. Table 5 indicated that many models of selection index were superior to single trait selection for LY/P. Furthermore; the results indicate the possibility of isolate high yielding families out yielded Giza 90 with remarkable favorable increase in one or more of the three main fiber properties. Index 1, 2 and 12 succeeded to isolate four high yielding families with remarkable increase in UHM length. The four families were family NO.803, NO.806, NO.585 and NO.630. Significant ($P \leq 0.01$) genetic gain in LY/P ranged from 22.58 (family NO .630) to 38.84 % (family NO.585). Furthermore, significant genetic gain in length was achieved of 6.51% (32.17mm), 8.28% (32.70mm), 6.73 % (32.23mm) and 6.95% (32.20mm) for the four respective families. It is a great opportunity to isolate new strain from Giza 90 (30.2mm) out yielded it and improved G90 to higher category in fi-

ber length. Family NO .766, NO. 706 and NO.334 are promising strain out yielded ($P \leq 0.01$) Giza 90 and characterized by fine fibers. Family NO.766 recorded genetic gain ($P \leq 0.01$) of

12.32, -15.38 (3.3) and 10.84% for LY/P, Micronair reading and PI; respectively.

Table 5. Observed genetic gain in percentage of the check strain for lint yield and fiber properties.

Fam. NO.	Selection for	Observed genetic gain			
		LY/P	MIC	PI	UHM
803	Index1,12	29.82**	NS	NS	6.51**
806	Index1	25.49**	NS	NS	8.28**
766	Index1,8,12	12.32*	-15.38**	10.84**	NS
811	Index1	32.77**	NS	8.07**	5.58**
805	Index1	16.66**	NS	10.18**	NS
585	Index2	38.84**	NS	NS	6.73**
630	Index 2	22.58**	NS	NS	6.95**
437	Index3,10,11,13	25.49**	NS	14.39**	NS
586	Index3,10,13	20.84**	NS	22.81**	NS
803	Index5	25.84**	NS	14.42**	NS
529	Index5	17.51*	NS	16.1**	3.08*
706	Index9	38.83**	-11.03**	NS	NS
673	Index9	28.6**	NS	10.21**	NS
737	Index9	27.66**	NS	10.84**	NS
334	LY/P, Index 14	29.82**	-10.26**	3.16	4.07**

NS; insignificant observed genetic gain from the check strain.

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

Family NO.766 is a promising high yielding and convert Giza 90 from coarse (3.9 Mic) to more fine 3.3 Mic and strongest fiber. Families NO.437, NO.586, NO.803 and NO.529 are another great opportunity to increase yield of Giza and increase fiber strength by 14.39 to 16.11%. Table 5 shows 15 promising elite strains characterized by high yielding ability with improve in one or more of the three main fiber properties. Generally, it could be concluded that the present program for maintenance and renewing Egyptian cotton varieties is a precise and perfect program to preserve the fiber quality, but, not suitable for improving yielding ability. In consequence, this program should be modified to allow the isola-

tion of superior high yielding off types from the breeding nursery characterized by improvement in one or more fiber quality.

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كفاءة الانتخاب لصفه واحده وعده صفات للمحصول ومكوناته فى المحافظه على صنف القطن جيزه ٩٠

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الملخص

اجريت الدراسه بمحطه بحوث شندويل بسوهاج -مركز البحوث الزراعيه فى مواسم ٢٠١٣، ٢٠١٤، ٢٠١٥. كانت مواد البحث هى نسل ٦٠ نبات فردى من حقل التربيه الخاص بالمحافظه على الصنف جيزه ٩٠ (نفس مواد التبيه لاستنباط نويه الصنف). وهدف هذا العمل الى دراسه امكانيه استنباط سلالات عاليه المحصول من نفس الصنف مع المحافظه على صفاته التكنولوجيه. لتحقيق ذلك تم اجراء دورتين من الانتخاب لصفه محصول الشعر واربعه عشر دليلا للانتخاب. أظهرت النتائج الى تحسين وراثى مشاهد ومعنوى فى محصول الشعر يتراوح بين ١٦,٥٧% لدليل الانتخاب الثانى (يضم محصول الشعر/نبات ووزن اللوزه) الى ٢١,٦٣% للدليل السابع (محصول الشعر + عدد البذور فى اللوزه). زاد الدليل الثانى وزن اللوزه بمقدار ٩,٢٧%. اما الدليل السابع فقد أدى الى تحسين وراثى مشاهد ومعنوى وصل الى ٢١,٣٦، ١٩,٧١، ٣,٦١، ٧,٨٢، ٢,٦٥% فى محصول الزهر ومحصول الشعر ودليل البذره ودليل البرسلى ومتوسط النصف الاعلى على الترتيب. أدى الانتخاب لصفه محصول الشعر/النبات الى تحسين وراثى مشاهد ومعنوى مقداره ٢٠,٣٠، ١٩,٧٥، ١٤,٠١% لمحصول الزهر ومحصول الشعر وعدد اللوز على النبات على التتیب. كما توضح النتائج افضليه ادله الانتخاب على الانتخاب لصفه محصول الشعر فى التعرف على السلالات المبشره. وعموما توضح النتائج ان برنامج المحافظه على الاصناف وانتاج النويات برنامجا جيدا للمحافظه على صفات التيله دون المحصول. لذلك يجب تطوير البرنامج ليسمح بتحسين المحصول مع المحافظه على صفات الجوده للصنف.