Comparison of Three Selection Procedures in Early Generations for Improving of Some Economic Characters and Earliness in Cotton

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ABSTRACT

The goal of this investigation was to estimate the efficiency of three selection procedures which were pedigree selection method (PD), single seed descent method (SSD)and bulk population selection method (BP) in order to compare the efficiency of these methods for improvement of cotton characters. These selection procedures were compared in one cross of cotton namely, Giza 70 x TNB₁

This study was designed to research the great two cycles of selection for increasing and maintaining lint cotton yield as well as fiber quality in the cross of cotton, Giza 70 x TNB₁ were completed using different selection procedures in each cycle.

The present study was carried out at Sakha Agriculture Research Station, Kafr EL-Sheikh Governorate in 2006, 2007 and 2008 seasons to study many economic characters and earliness in cotton

Thirty plants were selected from F₂ generation of the cross, Giza 70 x TNB₁ based on the mean performance of the F₂ generation proved to be superior plants since mean values of thirty plants selected from F₂ generation by density selection 10% of superior plants were selected.

Summary of the results were achieved as follows:

The mean squares showed that differences between families derived by pedigree selection method (PD) were highly significant for all the studied characters.

Mean of characters by the pedigree selection method (PD) were higher and the best than the other two selection procedures for fiber properties such as fiber staple length (F.L.), fiber strength (F.S.) and fiber fineness (F.F.).

The values of phenotypic variance and heritability using single seed descent method (SSD) were higher than bulk population selection method (BP) for all the studied characters except seed cotton yield per plant (S.C.Y./P), seed index (S.I.), fiber staple length (F.L.) and fiber strength (F.S.).But, in the pedigree selection method (PD), the results showed that the values of heritability were higher than the two other methods for height of the first fruiting branch per plant (H.F B./P), lint percentage (L.P.), seed index(S.I.), lint index (L.I.), fiber staple length (F.L.), fiber fineness (F.F.) and fiber strength (F.S.), while were higher than bulk population selection method (BP) for number of fruiting branches per plant (N.F.B./P) and number of the total nodes per plant (N.T.N./P), also was higher than single seed descent method (SSD) for boll weight (B.W.).

Estimates of phenotypic and genotypic coefficient of variability were higher in single seed descent method (SSD) than bulk population selection method (BP) for all traits except boll weight (B W.) , number of non opening bolls per plant (N.N.O.B./P), seed index (S.I.), fiber staple length (F L.) and fiber strength (F.S.) While the values of pedigree selection method (PD) were high for height of first fruiting branch per plant (H.F B./P), fiber staple

length (F.L.), fiber fineness (F.F.) and fiber strength (F.S.) for genotypic coefficient of vanability (G.C.V. %),while the values were high for height of first fruiting branch per plant (H.F.B./P), number of non opening bolls per plant (N.N.O.B./P), and lint percentage (L.P.) for phenotypic coefficient of variability (P.C.V. %).

Correlation coefficients between all studied characters for base population were positive and significant for most characters and the correlation coefficient among cotton yield and both fiber staple length (F.L.) and fiber strength (F.S.) were positive and highly significant. This indicated that the plant breeder can obtain excellent lines that combines high fiber properties with high yield. While, in pedigree selection method (PD), the correlation coefficients among cotton yield and both fiber staple length (F.L.) and fiber strength (F.S.) were negative and significant but, in single seed descent method (SSD) values were negative and insignificant for fiber staple length (F.L.) also positive and insignificant for fiber strength (F.S.).

However, correlation coefficients among cotton yield and both fiber staple length (F.L.) and fiber strength (F.S.) were negative and insignificant for fiber staple length (F.L.), also positive and insignificant for fiber strength (F.S.). Meanwhile for lint yield per plant (L.Y. /P) with fiber staple length (F.L.) was negative and significant, too negative and insignificant for fiber strength (F.S.).

This change in correlation coefficients from positive to negative was also observed by Sharma (1979) in one of the two composite crosses of Upland cotton. Miller and Rawlings (1967) and Meredith and Bridge '1971) also reported change in correlation values between lint yield and fiber strength (F.S ' in intermitted population. In the present study, there was also shift in the direction of correlation of cotton yield with fiber staple length(F.L.) and fiber strength (F.S.) from negative to positive, although these were insignificant. The change resulted in simultaneous improvement in study of {Munshi et al. (1985)}.

As general from these previous results cleared that pedigree selection method (PD) was significant and the best thr n single seed descent method (SSD) and bulk population selection method (BP).

INTRODUCTION

The present study was designed to evaluate the efficiency of some selection procedures .Several selection procedures such as pedigree selection method (PD), single seed descent method (SSD), bulk population selection method (BP), mass pedigree selection method (MP)and early generation testing have been proposed for the improvement of self fertilized crops such as cotton. So, in this research was therefore , undertaken to compare the efficiency of three selection procedures which these pedigree selection method (PD), single seed descent method (SSD) and bulk population selection method (BP) in one cross of cotton , namely Giza 70 x TNB_1.

The pedigree selection method (PD) has been widely used. The procedure is to select superior progenies from segregating generations, and maintaining records of all parent-progeny relationships.

The importance of knowledge how the change in one trait by selection may cause simultaneous changes in other economic traits. The results of this study were generally in agreement with results achieved by, Mahdy et

al (1987), Ghoneim (1989), Gooda (2001), and Lasheen (2003). Younis (1986), AL-Ameer (2004) and Abdel-Hafez et al.(2007) found that the pedigree selection method (PD)was the most efficient procedure for important lint yield/plant , number of bolls/plant and boll weight in the population .They added that phenotypic and genotypic variances uses decreased rapidly after two cycles of selection.

In addition, Lasheen (2003), Lasheen et al.(2003), AL-Ameer (2004), Abd EL-Maksoud et al.(2004) and Abdel-Hafez et al.(2007)showed that it is worthy to notice that no detectable changes occurred in the mean performances of lint yield or any of its components and fiber properties due to selection and it is useful for breeder to consider these characters in formulating his breeding programs to obtain gain in selection for single plant yield.

Munshi et al. (1985) found that the correlation coefficient was shift in the direction of correlation of ginning outturn with fiber length from negative ($r = -0.50$)in c_1 cycle to positive ($r = 0.13$)in c_2 cycle, although these values were insignificant. The change resulted in simultaneous improvement in the ginning outturn and fiber length in c_2 cycle

MATERIALS AND METHODS

This work was conducted in three growing seasons of 2006, 2007 and 2008 at Sakha Agricultural Research Station, Kafr EL-Sheikh, Governorate, Egypt to compare of different selection methods in improving some economic characters and earliness in cotton.

In the first growing season of 2006, the plants from the cross Giza 70 x TNB_1 were self–pollinated to obtain the F_2 seeds of this cross.

In the second growing season of 2007, the seeds of individual plants were sown separately and at the flowering time, 10% of superior plants were selected and self–pollinated in order to obtain the seeds of the F_3 generation as starting materials for application of the cycle of selection for pedigree selection method (PD), single seed descent method (SSD) and bulk population selection method (BP).

During growing season 2008, the previous three selection procedures were applied to F_3 populations of the cross Giza 70 X TNB_1. The plants having values for the important economic and earliness characters from selected F_3 plants were recorded.

The data were recorded for the following characters:
1- vegetative traits such as number of days to flowering of the first flower per plants (N.D.F /P), number of vegetative branches per plant (N.V.B./P), height of the first fruiting branch per plant (H.F.B./P), number of fruiting

branches per plant (N.F.B./P) and number of the total nodes per plant (N.T.N./P).

2- yield characters such as : seed cotton yield per plant (S.C.Y./P), boll weight (B.W.), number of opening bolls per plant (N.O.B./P), number of non opening bolls per plant (N.N.O.B./P), lint yield per plant (L.Y./p), Lint percentage (L.P.) seed index (S.I.) and lint index (L.I.).

3-Fiber properties such as fiber staple length (F. L.) which was measured by the digital fibro graph according to standard method for testing this trait, fiber fineness (F.F.) was estimated by Micronaire instrument and fineness was expressed as Micronaire value and fiber strength (F.S.) was measured for flat-bundles of fiber using the Pressley tester at zero gang length, and recorded as Pressley index value.

Analysis of variance was conducted for all characters and differences between the different families in pedigree selection method (PD) were tested for significance to the "F" test.

Means, ranges, genotypic variance (σ^2 g), phenotypic variance (σ^2 ph), heritability in broad sense (H^2_b %), genotypic coefficient of variability (G.C.V. %) phenotypic coefficient of variability (P.C.V. %), expected genetic gain (G_s) and expected genetic advance (ΔG) were conducted for each character

Heritability estimates in the broad sense were calculated according to the following equation.

$$\text{Heritability in broad sense (} H^2_b \text{ \%) } = \frac{\sigma^2 g}{\sigma^2 ph} \times 100 \text{ \{Allard (1960)\}}$$

The expected genetic gain under selection at 10% selection intensity was measured according to Johnson et al. (1955) and Allard (1960) as follows.

$$G_s = K. \sigma \text{ ph}. H^2_b$$

The expected genetic advance (ΔG) represented as a percentage of lines mean for the trait (Grand mean) was calculated according to Miller et al. (1958)

$$(\Delta G) = \frac{G_s}{\overline{X}} \times 100$$

Where:

ΔG = expected genetic advance

G_s = K. σ ph. H^2_b

G_s = expected genetic gain

K = selection differential and its value equal to 1.76 at the 10% intensity of selection.

σ ph = phenotypic standard deviation
H^2_b = heritability value in broad sense
$\overline{X}$ = grand mean.

RESULTS AND DISCUSSION
Data of the base population
The results achieved from the data of single plants of F_2 generation (Table 1) showed that six characters had high values for important parameters, compared with the remaining characters, such as genotypic variance ($\sigma^2 g$) phenotypic variance ($\sigma^2 ph$), heritability in broad sense ($H^2_b\%$), genotypic coefficient of variability (G.C.V. %), phenotypic coefficient of variability (P.C.V. %), expected genetic gain (G_s) and expected genetic advanced as a percentage of trait mean (ΔG). These characters were height of the first fruiting branch per plant (H.F.B./p), seed cotton yield per plant (S.C.Y./p), number of opening bolls per plant (N.O.B /p), number of non opening bolls per plant (N.N.O.B./p) ,Lint yield per plant (L.Y./p) and seed index (S.I.).

The heritability values provides no indication of the amount of genetic progress that would produce from selection of the best individual plants {Johnson et al. (1995)}, because the genetic parameters such as heritability and genetic correlation may vary of the presence of genotypes environment interaction {Larsson et al. (1997)}. Therefore, the genetic coefficient of variation with heritability together would give the best indication of the amount of genetic variance to be expected from selection {Burton (1952)}.

These results are in agreement with those of Katarki and Sangaiah (1966) who found, that a considerable variability for seed cotton yield and seed index of Indian cotton.

The observations of genotypic coefficient of variability (G.C.V. %), phenotypic coefficient of variability (P.C.V. %) and genetic advance (G_s) from selection of F_2 generation progenies indicated that the estimates of the expected genetic advance (ΔG) from selection was higher for the six characters than the remaining studied characters. This suggests that appreciable amount of genetic variability exists within open-pollinated F_2 generation with regards to the six characters and consequently genetic improvement could be realized for these traits.

These results in Table 1 showed that the heritability in broad sense ($H^2_b\%$) (>50) was recorded by some traits (H.F.B. /P.), (S.C.Y. /P.), (N.O.B. /P.), (N.N.O.B. /P),(L.Y./P.) and (S.I.).

Table 1 Mean, ranges, phenotypic variance (σ^2 ph), genotypic variance (σ^2 g), heritability in broad sense ($H^2{}_b\%$), genotypic coefficient of variability (G.C.V.%), phenotypic coefficient of variability (Ph.C.V.%), expected genetic gain (G_S) and expected genetic advanced(Δg) for F_2 base population in the cross (Giza70XTNB$_1$).

Characters		Genotype	Mean	Range	σ^2Ph	σ^2g	$H^2_a\%$	G C V %	Ph C V %	G_a	Δg
	NuBr	F2 300	2 96	1 - 6	0 97	0 16	16 50	13 50	33 40	0 28	9 62
		F2 30*	5 00	3 - 7	1 38						
		P·	1 80	0 - 3	1 03						
		P2	2 20	1 - 4	0 80						
	HPB	F2 300	7 74	6 - 9	0 80	0 45	56 00	8 64	11 60	0 88	11 31
		F2 30*	6 93	6 - 8	0 55						
		P·	7 93	7 - 9	0 50						
		P2	7 73	7 - 8	0 21						
	VPB	F2 300	25 40	16 - 33	8 35	0 95	11 40	3 84	11 40	0 58	2 27
		F2 30*	29 80	26 - 33	3 15						
		P·	20 40	1 - 25	8 97						
		P2	21 60	17 - 26	5 83						
	MN	F2 300	36 20	28 - 45	9 72	-2 40	-25 00	0 00	8 39	-1 38	-3 82
		F2 30*	41 70	39 - 45	3 73						
		P·	30 10	25 - 37	14 00						
		P2	11 50	2 - 38	9 27						
	SCYF	F2 300	175 70	100 51-361 1	2004 0	1563 20	78 00	22 50	25 50	61 10	34 80
		F2 30*	252 90	204 6 - 361 1	1334 2						
		P·	59 70	32 8 - 95 2	408 80						
		P2	69 20	42 5 - 99 7	472 80						
	F W	F2 300	2 68	2 11 - 3 89	0 12	0 00	-0 24	0 00	12 90	0 00	-0 05
		F2 30*	2 99	2 38 - 3 40	0 05						
		P·	3 15	2 46 - 3 5	0 09						
		P2	3 41	2 90 - 4	0 15						
	NOBF	F2 300	65 90	32 -	262 50	200 00	76 20	21 50	24 60	21 60	32 80
		F2 30*	85 00	66 - 28	222 70						
		P·	19 40	9 - 33	58 10						
		P2	21 50	11 - 33	66 80						
	NNOBF	F2 300	10 00	2 - 30	27 20	22 80	83 90	47 70	52 10	7 66	76 50
		F2 30*	15 60	7 - 31	49 10						
		P·	4 93	2 - 9	5 07						
		P2	6 13	4 - 1	3 70						
	T K	F2 300	57 20	30 67 - 17 3	256 1	204 20	79 70	25 00	28 00	22 30	39 00
		F2 30*	84 70	64 - 12 5	183 0						
		P·	20 50	11 8 - 30 0	31 60						
		P2	24 50	14 8 - 37 8	72 30						
	L P	F2 300	32 40	27 2 - 39 2	4 74	1 02	21 50	3 11	6 71	0 82	2 53
		F2 30*	33 50	30 4 - 37 9	4 01						
		P·	34 90	30 1 - 37 5	5 45						
		P2	35 10	33 7 - 37 9	1 99						
	S	F2 300	9 51	6 89 - 12 6	1 22	0 92	75 40	10 1	11 6	1 46	15 3
		F2 30*	10 70	9 26 - 12 0	0 76						
		P·	10 90	10 2 - 12 0	0 29						
		P2	11 20	10 2 - 12 0	0 31						
	L I	F2 300	4 59	3 09 - 6 28	0 59	0 24	41 10	10 7	16 7	0 55	12 0
		F2 30*	5 36	4 25 - 6 28	0 29						
		P·	5 86	4 9 - 6 66	0 30						
		P2	5 96	4 39 - 6 98	0 39						
	F L	F2 300	32 40	27 5 - 38 2	3 12	1 19	38 10	3 37	5 46	1 18	3 64
		F2 30*	34 30	31 5 - 38 2	1 93						
		P·	35 00	32 2 - 36 7	1 62						
		P2	32 20	30 - 35 3	2 25						
	F F	F2 300	3 40	2 6 - 4 4	0 15	0 02	14 40	4 39	11 60	0 10	2 92
		F2 30*	3 06	2 6 - 3 6	0 08						
		P·	3 42	2 6 - 4 2	0 18						
		P2	4 13	3 8 - 4 8	0 08						
	F S	F2 300	10 60	8 8 - 12 3	0 41	-0 09	-21 90	0 00	6 05	-0 25	-2 32
		F2 30*	11 40	10 5 - 12 3	0 23						
		P·	11 50	10 7 - 12 2	0 27						
		P2	10 80	8 9 - 12 1	0 73						

* Number of selected plants in F_2 generation (base population).

High heritability (H^2_b%) with high genotypic coefficient of variability (G.C.V. %) give the best indication of the amount of genetic advance expected from selection (Burton, 1952), meanwhile the low heritability with difference between genotypic coefficient of variability (G.C.V. %) and phenotypic coefficient of variability (P.C.V. %) values {for example h^2_b=16.48, G.C.V. %=13.50 and P.C.V. %=33.40 respectively} for number of vegetative branches (N.V.B. /p) in the base population. This result means that the traits may be affected by environment.

Some values of heritability were equal to zero for some traits. This may be due to the low genetic variance and the high environmental effect on these traits.

However, these parameters returned to important in the next generation F_3,such as the traits of number of the total nodes per plant (N.T.N./P), boll weight (B.W.) and fiber strength (F.S.) from the studied traits were affected by environmental conditions and increasing number of gene controlled in genetic behavior for these traits. Therefore, advance improvement of yield and some traits should be increased for numbers of plants in F_2 and F_3 families in early generations to produce elite lines.

This confirms the previously published work of ;Abo EL-Zahab and Abd-Alla(1972), Ali(1977), Younis(1986), Mahdy et al.(1987),Tian et al.(1993), EL-Harony(1999),Gomaa et al.(1999), Shaheen et al.(2000) ,Gooda(2001), Lasheen(2003), AL-Ameer(2004),Abd EL-Maksoud et al .(2004) and Abdel-Hafez et al.(2007) who found that the heritability was low in F_2, while was high in F_3 and F_4 (19.5, 80.7 and 94,0), (77.3, 85.2 and 82.0) also(50.1, 73.8 and 89.1) for lint yield for the three previous generations, respectively.

2-Selection Procedures

The mean square values which appear in Table 2 showed that the differences between families derived by pedigree selection method were highly significant for all the studied characters between families derived from the cross (Giza 70 X TNB_1).This finding suggested that the efficiency of pedigree selection method (PD) for all studied characters and the low effect of environment for these characters, this result indicated also, presence of genetic variability in these materials. The differences among families depended on selection in F_2 generation. Similar results were obtained by Salama et al. (1992) for seed cotton yield, lint percentage, boll weight, number of bolls /plant, seed index and lint index.

Mean characters of the pedigree selection method (PD) were the best and higher than seed descent method (SSD) for all studied characters except for number of non opening bolls per plant (N.N.O.B. /p), lint percentage (L.P.), seed index (S.I.) and Lint index (L.I.), while were the best and higher than bulk population selection method (BP) for fiber strength (F.S.) (Tables 3, 4, and 5).

Table 2: Analysis of variance and mean squares for families selected by pedigree selection method (PD) for all studied characters in the cross (Giza 70 X TNB₁)

SOV	df	Vegetative traits						Yield characters						Fiber properties		
		NVB/P	HFB/P	NFB/P	NTN/P	SCY/P	BW	NOB/P	NNOB/P	LY/P	LP%	SI	LI	FSt	Fr	rS
Replications	2	0.37	0.00	5.15	3.14	585.7	0.05	12.37	4.51	101.90	1.44	0.15	0.07	1.89	0.01	0.03
Famles F₃	29	0.93**	1.10**	7.52**	9.97**	1883.2**	0.11**	245.57**	24.31**	348.61**	15.40**	1.38**	0.58**	6.89**	0.18*	0.55**
Error	58	0.39	0.17	2.94	2.56	470.7	0.04	67.19	6.42	48.84	0.75	0.18	0.08	1.21	0.04	0.23

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

Means of characters by the pedigree selection method (PD) were higher and the best following bulk population selection method (BP) than seed descent method (SSD) for fiber properties such as fiber staple length (F.L.), fiber fineness (F.F.) and fiber strength (F.S.).

The pedigree selection method (PD) families exhibited ranges for all studied traits almost in agreed with both the ranges of the bulk population selection method (BP) and the single seed descent method (SSD).

All the previous results indicated that the pedigree selection method (PD) proved to be the best among the three selection procedures applied for most of the studied characters specially for fiber properties.

These results were generally in agreement with the results reported by Younis(1986),Mahdy et al.(1987),Ghoneim(1989),Gooda (2001),Lasheen (2003), AL-Ameer (2004), Abd El-Maksoud et al.(2004) and Abdel-Hafez et al.(2007).

The results indicated that the pedigree selection method (PD) showed higher values for phenotypic variance (σ^2ph) and genotypic variance (σ^2g) for height of the first fruiting branch per plant (H.F.B./P), boll weight (B.W.), number of non opening bolls per plant (N.N.O.B./P), lint percentage (L.P.), seed index (S.I.), Lint index (L.I.),fiber staple length (F.L.) and fiber strength (F.S) than in bulk population method (BP) and single seed descent method, respectively. On the other hand, magnitudes of genotypic variance (σ^2g) maintained among the lines within most of the three selection procedures for most traits were sufficient to lead to further appreciable improvement in the economic characters. These results suggested that genotypic variance (σ^2g) values would give the best indication of the amount of genotypic advance (ΔG) to be expected from selection procedures.

The results in Tables 3 and 4 showed that mean performance of F_3 bulk population selection method (BP) were higher than F_3 single seed descent method selection (SSD), for all traits except for number of non opening bolls per plant (N.N.O.B./P) and fiber strength(F.S.),but the heritability values were nearly similar for most traits. However, heritability values in broad sense for single seed descent method selection (SSD)were higher than bulk population selection method (BP) for all studied traits except seed cotton yield per plant (S.C.Y./P) , boll weight (B.W.), seed index(S.I.), fiber staple length (F.L.) and fiber strength (F.S.).

Expected genetic advance (ΔG) behavior was in the same trend of heritability. This means that the agreement between the two parameters

may be due to the major effect of heritability in the estimation of genetic advance because the mean performance (grand mean) was small.

Table 3: Mean, ranges, phenotypic variance (σ^2 ph), genotypic variance (σ^2 g), heritability in broad sense(H^2_b %), genotypic coefficient of variability(G.C.V.%), phenotypic coefficient of variability (Ph.C.V.%), expected genetic gain (G_S) and expected genetic advanced (Δg) for F_3 single seed descent method (SSD) in the cross (Giza70XTNB$_1$).

Characters	Genotype	Mean	Range			σ^2Ph	σ^2g	H^2_b %	G C V %	Ph C V %	G_s	Δ g
Vegetative traits	NMB/p	F_3	3.00	2	-	5	1.14	0.90	79.20	31.70	35.6	1.48	49.40
		P_1	2.33										
		P_2	2.33										
	HFB/p	F_3	7.60	6	-	9	0.69	0.44	83.90	8.71	10.90	0.93	12.20
		P_1	7.67										
		P_2	7.60										
	NFB/p	F_3	22.2	17	-	29	13.30	9.53	71.60	13.90	16.40	4.57	20.60
		P_1	21.73										
		P_2	22.27										
	NTN/p	F_3	32.80	29	-	40	13.60	9.60	70.60	9.45	11.20	4.56	13.90
		P_1	31.73										
		P_2	32.27										
Yield characters	SCY/P	F_3	164.40	97.2	-	233.9	1933.8	1665.3	86.10	24.80	26.70	66.30	40.30
		P_1	60.70										
		P_2	68.31										
	B W	F_3	2.75	2.34	-	3.24	0.10	0.034	55.70	6.68	8.96	0.24	8.73
		P_1	3.08										
		P_2	3.40										
	NO.B/P	F_3	60.10	36	-	88	295.8	265.5	89.80	27.10	28.60	27.00	45.00
		P_1	19.87										
		P_2	20.20										
	NNOB/P	F_3	9.87	5	-	16	10.70	8.39	78.40	29.40	33.20	4.49	45.50
		P_1	5.53										
		P_2	6.73										
	L Y /P	F_3	56.0	30.47	-	91.92	330.3	295.5	89.50	30.70	32.50	28.50	50.90
		P_1	22.11										
		P_2	24.49										
	L P	F_3	33.60	27.9	-	39.3	7.20	6.38	89.10	7.51	7.95	4.17	12.40
		P_1	36.58										
		P_2	35.74										
	S I	F_3	10.00	8.8	-	11.0	0.51	0.40	77.40	6.28	7.14	0.97	9.67
		P_1	10.60										
		P_2	11.31										
	L I	F_3	5.08	3.91	-	5.83	0.27	0.21	77.70	9.01	10.20	0.71	13.90
		P_1	6.12										
		P_2	6.29										
Fiber properties	F L	F_3	32.40	29.5	-	36	3.10	1.36	43.90	3.60	5.43	1.35	4.17
		P_1	35.04										
		P_2	32.39										
	F.F.	F_3	3.50	2.8	-	4.2	0.17	0.13	75.40	10.10	11.7	0.54	15.40
		P_1	3.41										
		P_2	4.06										
	F S	F_3	10.50	9.40	-	11.1	0.24	0.05	19.70	2.09	4.70	0.17	1.62
		P_1	11.12										
		P_2	10.83										

Table 4: Mean, ranges, phenotypic variance (σ^2 ph), genotypic variance (σ^2 g), heritability in broad sense (H^2_b %), genotypic coefficient of variability (G.C.V.%), phenotypic coefficient of variability (Ph.C.V.%), expected genetic gain (G_s) and expected genetic advanced (Δg) for F_3 bulk population selection method (BP) in the cross (Giza70XTNB_1).

Characters		Genotype	Mean	Range	σ^2Ph	σ^2g	H^2_b%	G C V %	Ph C V %	G_s	Δg
Vegetative traits	NVB/p	F_3	3 25	1 - 5	0 61	0 37	61 10	18 8	24 1	0 84	25 8
		P_1	2 33								
		P_2	2 33								
	HFB/p	F_3	8.56	7 - 9	0.31	0.06	19.70	2.88	6 48	0.19	2.23
		P_1	7.67								
		P_2	7 60								
	NFB/p	F_3	24 80	19 - 30	6 20	2 42	39 00	6 26	10 0	1 70	6 84
		P_1	21 73								
		P_2	22.27								
	NTN/b	F_3	36 60	30 - 42	7.35	3.36	45.70	5.00	7.40	2 17	5.91
		P_1	31.73								
		P_2	32 27								
Yield characters	SCY/P	F_3	195 70	111 1 - 357 7	2266 3	1997 8	88.20	22 8	24 3	73 4	37 5
		P_1	60 70								
		P_2	68 31								
	B W	F_3	2 94	2.30 - 3 66	0 08	0 053	66 3	7 83	9 62	0.33	11.2
		P_1	3 08								
		P_2	3.40								
	NOB/P	F_3	66 80	37 - 121	245.5	215.2	87 70	22 0	23.5	24 0	36.0
		P_1	19 87								
		P_2	20 2								
	NNOB/P	F_3	8 15	2 - 19	8 87	6 56	74 00	31 4	36 5	3 86	47 3
		P_1	5.53								
		P_2	6 73								
	L Y /P	F_3	67 70	34 - 121 3	291.0	256 2	88.10	23 6	25 2	26 3	38 8
		P_1	22 11								
		P_2	24 49								
	L P	F_3	34 60	29 8 - 41 1	4 74	3 96	83 50	5 76	6 30	3 18	9 20
		P_1	36 58								
		P_2	35 74								
	S I	F_3	10 10	8 - 12.2	0 54	0 42	78 50	6 44	7 27	1 01	10 0
		P_1	10 6								
		P_2	11 31								
	L I	F_3	5 33	4 32 - 6 49	0.21	0 15	71 60	7 30	8 63	0 58	10 8
		P_1	6.12								
		P_2	6.29								
Fiber properties	F L	F_3	32 85	28.5 - 37.3	3.53	1 80	51 00	4.08	5 72	1.67	5 10
		P_1	35.04								
		P_2	32 39								
	F F	F_3	3.85	3 - 4.6	0.07	0 03	37.70	4 12	6 71	0 17	4 42
		P_1	3.41								
		P_2	4.06								
	F S	F_3	10.30	8.5 - 11.2	0 34	0 15	43 50	3 76	5 71	0.45	4 34
		P_1	11.12								
		P_2	10.83								

Munshi et al. (1985) showed that the coefficient of variation was the highest for progeny rows in C_2 than for the rest of the populations for boll weight, ginning outturn, seed index and fiber fineness while, in progeny-bulk populations in the C_2 cycle the coefficient of variation was less than in the C_1 cycle for most of the characters because of the force of directional selection.

The results in Table 5, revealed that the mean performance and range for all generations in pedigree selection method (PD) were in agreement with the two other selection methods for most traits ,while heritability values in broad sense were higher than the two other selection methods. This may be attributed to the fact that pedigree selection depend on plot mean. While, the two other selection methods depend on individual plants.

However, the heritability values in broad sense it-self provides no indication of the amount of genetic progress that would result from selection of the best individuals {Johnson et al. (1955)} because the estimates of heritability are influenced by various factors, viz., sample size, sampling method, conduct of experiment and method of calculation {Singh and Narayanan (2000)} an effect of linkage {Simmonds (1979)}.

Improvement in the r ean genotypic value of selected plants over the parental population is known as genetic advance. The values of expected genetic advance (ΔG) for the three selection procedures are presented in Tables 3, 4 and 5. The results indicated that expected genetic advance (ΔG) in pedigree selection methc 1 was higher than single seed descent method selection (SSD)for some tra.is such as seed index (S.I.), fiber staple length (F.L.) and fiber strength (F.S.),while it was higher than bulk population selection method (BP) for most traits .However, the high values of expected genetic advance (ΔG) in some traits were obtained in single seed descent method selection (SSD) and bulk population selection method (BP) due to the high genetic variability {(G.C.V.%), (σ^2ph) and (σ^2g)}. The differences of genetic advance under the three selection methods depends on three main factors i.e.. genetic variability, heritability and selection intensity, {Allard (1960)}.Also, the magnitude of the genetic variability presented in these materials was sufficient for providing rather substantial amounts of improvement through the selection of superior progenies for the economic characters in the three populations .The values of expected genetic advance (ΔG) as percentage of mean in the pedigree selection method (PD) were higher than their corresponding values in single seed descent method selection (SSD) and bulk population selection method (BP) for some traits indicating that the applied selection procedures were effective and successful for selecting the best lines and maintaining the traits on high standard levels. These results were generally in agreement with the results

reported by Younis (1986), Mahdy et al. (1987), Ghoneim (1989), Gooda (2001), Lasheen (2003), AL-Ameer (2004), Abd El-Maksoud et al. (2004).

Table 5: Mean, ranges, phenotypic variance (σ^2 ph), genotypic variance (σ^2 g), heritability in broad sense(H^2_b %), genotypic coefficient of variability(G.C.V.%), phenotypic coefficient of variability (Ph.C.V.%), expected genetic gain (G_S) and expected genetic advanced (Δg) for F_3 pedigree selection method (PD) in the cross (Giza70XTNB$_1$).

	Characters	Genotype	Mean	Range	σ^2Ph	σ^2g	H^2_b %	G.C.V.%	Ph.C.V.%	G_s	Δ g
		F_3	3.18	1.67 – 4.18	0.31	0.18	58.06	13.34	17.61	0.57	17.89
	NVB/p	P_1	2.33								
		P_2	2.33								
		F_3	8.43	6.33 - 9.00	0.37	0.31	84.55	6.60	7.18	0.90	10.69
Vegetative trait	HFB/p	P_1	7.67								
		P_2	7.60								
		F_3	23.24	18.25 – 25.79	2.51	1.53	60.90	5.32	6.81	1.70	7.30
	NFB/p	P_1	21.73								
		P_2	22.27								
		F_3	34.84	30.75 – 37.39	3.32	2.47	74.32	4.51	5.23	2.38	6.84
	NTN/p	P_1	31.73								
		P_2	32.27								
		F_3	167.83	104.47 – 219.00	627.73	470.83	75.01	12.93	14.93	33.07	19.71
	S C Y /P	P_1	60.70								
		P_2	68.31								
		F_3	2.80	2.47 – 3.37	0.04	0.02	63.64	5.46	6.84	0.21	7.66
	B W	P_1	3.06								
		P_2	3.40								
		F_3	60.29	40.00 – 76.27	81.86	59.46	72.64	12.79	15.01	11.57	19.19
	N O B /P	P_1	19.87								
Yield characters		P_2	20.2								
		F_3	8.40	2.75 – 13.33	8.10	5.96	73.59	29.07	33.89	3.69	43.89
	NNOB/P	P_1	5.53								
		P_2	6.73								
		F_3	66.27	29.69 -77.49	116.20	99.92	85.99	17.76	19.16	16.31	28.99
	L Y /P	P_1	22.11								
		P_2	24.49								
		F_3	33.35	28.37 – 38.97	5.13	4.88	95.13	6.63	6.79	3.79	11.37
	L P	P_1	36.58								
		P_2	36.74								
		F_3	9.92	8.82 – 11.20	0.46	0.40	86.96	6.38	6.84	1.04	10.46
	S I	P_1	10.6								
		P_2	11.31								
		F_3	4.97	3.98 – 5.74	0.19	0.17	86.21	8.21	8.85	0.67	13.42
	L I	P_1	6.12								
		P_2	6.29								
		F_3	32.84	30.44 – 35.95	2.30	1.89	82.44	4.19	4.61	2.20	6.70
	F L	P_1	35.04								
Fiber properties		P_2	32.39								
		F_3	3.70	3.07 – 4.03	0.06	0.05	77.78	5.84	6.62	0.34	9.06
	F F	P_1	3.41								
		P_2	4.06								
		F_3	10.59	9.90 – 11.33	0.18	0.11	58.18	3.08	4.04	0.44	4.14
	F S	P_1	11.12								
		P_2	10.83								

3-Correlation coefficient

The informations about the degree of association among different traits of cotton are of great importance to plant breeding program designed to combine the desirable expression of several characters. Simple correlations for all pairs of studied traits in F_2 generation are presented in Table 6.

Genotypic correlation coefficients between all studied characters for base population (Table 6) were positive and significant for most characters and the correlation coefficients among cotton yield and both fiber staple length (F.L.) and fiber strength (F.S.) were positive and highly significant. This indicating that the plant breeder can obtain excellent lines combining both high fiber properties with high yield. However, the pedigree selection method(PD) in the F_3 generation showed negative and significant correlation coefficients among cotton yield and both fiber staple length (F.L.) and fiber strength (F.S.)(Table 7).On the other hand, single seed descent method (SSD) revealed insignificant correlation coefficients which were negative and positive, respectively among cotton yield and both fiber staple length (F.L.) and fiber strength (F.S.)(Table 8).The same trend was found for bulk population selection method (BP)(Table 9). Meanwhile, lint yield per plant (L.Y./P) was negatively and significantly correlated with fiber staple length (F.L.),whereas its correlation with fiber strength (F.S.) was negative and insignificant. These finding were in agreement with EL-Harony et al. (2000).

This change in correlation coefficients from positive to negative was also observed by Sharma (1979) in one of the two composite crosses of Upland cotton. Miller and Rawlings (1967) and Meredith and Bridge (1971) also reported change in correlation values between lint yield and fiber strength (F.S.) in intermitted population. In the present study there was also shift in the direction of correlation of cotton yield with fiber staple length (F.L.) and fiber strength (F.S.) from negative to positive, although these were insignificant. That change resulted in simultaneous improvement in the studied traits of {Munshi et al. (1985)}.

4- Mean performance for F_3 families in pedigree selection method (PD)

The data in (Table 10) showed that the mean performance for same F_3 families in pedigree selection method (PD) was higher than the better parent for some traits in vegetative traits, yield characters and fiber fineness. While these mean performance were low in the families in the same method for boll weight (B.W.), seed index (S.I.), lint index (L.I.), fiber staple length (F.L.) and fiber strength (F.S.). Therefore, the breeder can select elite lines characterized by high yield, short season and with fiber properties similar to that of Giza 70 variety (Extra long staple variety).

Table 6: Correlation coefficients between the characters for F_2 base population for all studied characters in the cross (Giza70X TNB_1).

Characters		Vegetative traits						Yield characters						Fiber properties		
		NLBp	HBp	NFBp	NTNp	SCp	BW	NOBP	NOBP	LYP	LP	SI	LI	F L	F F	F S
Vegetative traits	NLBp	100	044*	008	043*	042*	028**	027*	015*	040*	018*	020*	024*	020**	-019	022*
	HBp		100	-034*	005	-014	018*	018*	022*	006	027**	012*	024*	-019*	035*	020*
	NFBp			100	050*	032*	005	027*	046*	028*	-010*	009*	003	013*	-015*	018*
	NTNp				100	043*	021*	031*	044**	042*	009	020*	017*	018*	-023*	020*
	SCp					100	003*	057*	024*	050*	021*	028*	003*	025*	-006	013*
	BW						100	-017*	007	039**	034*	068**	057*	042*	035*	013*
	NOBP							100	015*	012*	005	005	005	001	-025*	023*
Yield characters	NOBP								100	020*	-010	013*	002	015*	-024*	012*
	LYP									100	040*	012*	045*	023*	-003	025*
	LP										100	022*	075*	007	015*	002*
	SI											100	060*	052*	037*	021*
	LI												100	035*	043*	015*
Fiber properties	F L													100	000	048*
	F F														100	020*
	F S															100

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

Table 7 Correlation coefficients between the characters for F_3 pedigree selection method (PD) for all studied characters in the cross (Giza70X TNB_1).

Characters		Vegetative traits						Yield characters						Fiber properties		
		NVBp	HFBp	NFBp	NTNp	SCVp	BV	NCBP	NKBP	LYP	LP	Si	U	F L	F F	F S
Vegetative traits	NVBp	100	003	0011	023	023	-029	028	012	010	-012	009	-014	-003	-003	004
	HFBp		100	-004	024	00	-009	005	000	008	019	-019	003	010	-013	009
	NFBp			100	091	008	019	027	003	035	009	029	012	003	002	006
	NNp				100	044	013	003	04	00	002	005	002	004	-005	004
	SCVp					100	011	008	028	008	023	005	021	010	004	011
	BV						100	-004	011	008	008	052	044	017	016	006
Yield characters	NBP							100	021	008	020	-025	000	-017	009	008
	NKBP								100	020	011	010	009	012	-015	006
	LYF									100	048	-012	037	-022	002	-015
	LP										100	-004	000	-041	023	-019
	S											100	009	003	020	009
	U												100	-012	003	-020
Fiber properties	F L													100	-005	010
	F F														100	004
	F S															100

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

Table 8: Correlation coefficients between the characters for F_3 single seed descent method (SSD) for all studied characters in the cross (Giza70X TNB_1).

Characters		Vegetative traits						Yield characters						Fiber properties		
		NLB	HB	NFB	NTN	SCY	BW	NCBP	NMBP	LYP	LP	SI	U	F L	F F	F S
Vegetative traits	NLB	1.00	0.323	-0.421	-0.054	0.077	-0.417	0.229	-0.306	0.124	0.007	-0.429	-0.161	0.057	0.046	0.041
	HB		1.00	0.194	-0.507	0.320	-0.228	0.398	0.401	0.276	0.092	-0.077	0.053	-0.074	-0.029	-0.014
	NFB			1.00	0.817**	0.094	0.524**	0.116	0.634**	0.250	-0.021	0.667**	0.431	0.155	0.239	0.077
	NTN				1.00	0.415	0.344	0.271	0.627**	0.345	0.008	0.538**	0.392	0.153	0.272	0.006
	SCY					1.00	0.102	0.925**	0.408	0.978**	0.550	-0.134	0.553**	-0.003	0.304	0.259
	BW						1.00	-0.282	0.363	0.063	-0.167	0.666**	0.245	0.552	0.063	-0.224
Yield characters	NCBP							1.00	0.290	0.932**	0.625**	-0.065	0.448	-0.437	0.007	0.337
	NMBP								1.00	0.312	-0.160	0.554**	0.165	0.235	-0.098	0.154
	LYP									1.00	0.733**	-0.245	0.666**	-0.416	0.131	0.293
	LP										1.00	-0.457	0.606**	-0.746**	0.473	0.242
	SI											1.00	0.155	0.547	0.242	-0.210
	U												1.00	-0.463	0.667**	0.106
Fiber properties	F L													1.00	-0.283	-0.308
	F F														1.00	-0.019
	F S															1.00

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

Table 9 Correlation coefficients between the characters for F_3 bulk population selection method (BP) for all studied characters in the cross (Giza 70X TNB_1).

Characters		NLBt	HPB	NFBD	NTNL	SCXD	BW	NOBP	NNOF	LYIP	LP	SI	L	FL	FF	FS
		Vegetative traits							Yield characters					Fiber properties		
Vegetative traits	NLBt	1.00	0.87**	0.41**	0.65**	0.60**	0.21**	0.41**	0.00**	0.50**	0.14*	0.05	0.102	0.089	0.088	0.083
	HPB		1.00	0.49**	0.06**	0.58**	0.01	0.60**	0.05	0.54**	-0.009	0.013	0.02**	0.046	0.013	0.088
	NFBD			1.00	0.80**	0.72**	0.20**	0.89**	0.60**	0.70**	0.04	0.012	0.101	0.029	0.009	0.010
	NTNL				1.00	0.70**	0.047**	0.57**	0.54**	0.58**	0.02	0.040	0.07	0.046	0.021	0.082
	SCXD					1.00	0.20**	0.60**	0.75**	0.60**	0.07	0.037	0.184	0.119	0.021	0.005
	BW						1.00	0.012	0.05	0.250**	0.040	0.073**	0.05**	0.081	0.088	0.088
	NOBP							1.00	0.90**	0.60**	0.07	0.007	0.112	-0.148**	0.027	0.040
Yield characters	NNOF								1.00	0.06**	0.048	-0.080	0.067	0.063	-0.120	0.010
	LYIP									1.00	0.273**	0.016	0.102**	-0.020**	0.070	0.000
	LP										1.00	-0.060**	0.59**	-0.60**	0.019**	0.088
	SI											1.00	0.287**	0.040**	0.016	0.02**
	L												1.00	-0.022**	0.029**	-0.073
Fiber properties	FL													1.00	0.111	0.223**
	FF														1.00	-0.021
	FS															1.00

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

Table 10: Mean performance of characters for families F_3 generation by pedigree selection method (PD) in the cross (Giza 70 X TNB$_1$).

Fmte	Mean	Vegetative traits					Yield characters						Fiber properties			
		NLBD	HFBD	NFBD	NMD	SCYD	BW	NBP	NMBP	LY/P	LP	SI	U	FL	FF	FS
Fam1	Mean	357+	814	231	349+	180+	286	573+	729+	557+	339	977	489	315	383	11
Fam2	Mean	325	667+	236	351+	1541+	304	513+	917+	524+	340	969	514	335	351+	113
Fam3	Mean	418+	809	242	355+	206+	289	763+	124	676+	330	949	467	342	376	108
Fam4	Mean	308	717	237	339	1502+	294	91+	106	456+	304	106	464	343	381	113
Fam5	Mean	289	633	223	316	1626+	280	580+	133	506+	312	100	453	345	359+	106
Fam6	Mean	410+	740	214	329	1677+	247	686+	350+	582+	353	901	487	335	382	107
Fam7	Mean	329	757	222	331	1681+	298	584+	571+	513+	323	110	525	351	368	106
Fam8	Mean	317	860+	222	308	1399+	258	503+	317+	424+	310	862	398	729	397	112
Fam9	Mean	363+	857+	233	356+	157+	275	572+	117	487+	310	108	485	148	371+	108
Fam10	Mean	340+	780	242	354+	1877+	286	65+	860+	583+	311	106	478	380	373+	108
Fam11	Mean	400+	860+	203	328	1889+	255	747+	4+	670+	356	912	501	319	363	102
Fam12	Mean	400+	860+	183	708	1857+	286	583+	275+	586+	326	108	524	344	408	111
Fam13	Mean	257	865+	240	351+	154+	278	559+	471+	549+	356	956	528	315	391	106
Fam14	Mean	308	854+	258+	374+	1752+	337	522+	777+	556+	322	112	533	349	380	109
Fam15	Mean	417+	865+	245	375+	1896+	287	602+	107	516+	304	111	488	394	335+	104
Fam16	Mean	293	827+	233	345	1929+	288	639+	947+	647+	354	992	543	311	353+	995
Fam17	Mean	289	869+	232	346	1664+	298	575+	709+	582+	350	998	537	324	371+	109
Fam18	Mean	347+	863+	245	355+	1697+	313	611+	118	666+	351	108	574	399	399	104
Fam19	Mean	275	900+	225	343	1346+	270	505+	950+	418+	312	928	423	325	370+	102
Fam20	Mean	309	869+	252+	371+	1657+	283	697+	100	662+	337	100	503	304	390	104
Fam21	Mean	280	900+	247	355+	1762+	256	691+	990+	581+	329	965	473	342	366+	110
Fam22	Mean	167	900+	220	327	1045+	259	400+	557+	297	284	103	3.98	318	307+	104
Fam23	Mean	323	869+	242	352+	2024+	294	697+	877+	735+	363	951	543	317	350	106
Fam24	Mean	320	860+	249	356+	1998+	262	757+	940+	775+	390+	891	571	314	392	990
Fam25	Mean	273	867+	227	341	1705+	286	641+	798+	599+	351	952	516	326	357+	110
Fam26	Mean	329	866+	226	347	1457+	259	547+	119	482+	329	984	485	331	399+	103
Fam27	Mean	266	864+	258+	373+	219+	305	725+	103	772+	352	994	540	323	351+	101
Fam28	Mean	275	860+	203	315	120	263	456+	700+	404+	336	915	464	312	325+	990
Fam29	Mean	246	885+	226	339	1623+	286	559+	769+	558+	350	928	501	320	352+	106
Fam30	Mean	300	900+	242	352+	1821+	277	661+	110	575+	316	100	463	399	311+	998
BP	Mean	233	780	2227	3227	6831	340	2020	553	2449	3558	1131	629	3504	341	1112
LSD	005	1.02	0.67	2.80	2.60	354	0.33	133	4.14	11.4	1.41	0.69	0.46	1.80	0.33	0.78
	001	1.36	0.90	3.72	3.48	47.1	0.43	17.8	5.50	15.2	1.88	0.92	0.61	2.39	0.43	1.04

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الملخص العربي

مقارنة ثلاث طرق من الانتخاب في الأجيال المبكرة لتحسين الصفات الاقتصادية والتبكير في القطن

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إن الغرض من هذه الدراسة هو إجراء مقارنة لثلاث طرق وهى طريقة انتخاب النسب ، طريقة انتخاب الجورة الواحدة و طريقة الانتخاب التجميعي لتحسين بعـ ٮ الصفات الاقتصادية في القطن .وقد اشتملت الدراسة الحالية على هجين من القطن بين جيزة ٧٠ و ٮ TNB وقد أجريت هذه الدراسة في مزرعة محطة سخا للبحوث الزراعية بمحافظه كفر الشيخ لمعهد بحوث القطن– مركز البحوث الزراعية عبر المواسم الزراعية ٢٠٠٦، ٢٠٠٧ و٢٠٠٨ وذلك لمقارنه ثلاث طرق انتخاب مختلفة لتحسين بعض الصفات الاقتصادية في الهجين(جيزة ٧٠× ۱ TNB) ويمكن تلخيص نتائج الدراسة في النقاط التالية : -

•اختبارات المعنوية أوضحت أن هناك اختلافات بين السلالات الناتجة بطريقه انتخاب النسب وكانت معنوية لكل الصفات المدروسة .

•أشارت النتائج إلى أن طريقه انتخاب النسب برهنت على أنها الأفضل والأحسن من بين الثلاث طرق المستخدمة لمعظم الصفات المدروسة وخاصة صفات التيلة وكذلك طريقه الانتخاب التجميعي أظهرت وبينت أداء عالي للمتوسط لمعظم الصفات .

•إن قيم التباين الوراثي كانت عاليه لبعض الصفات في طريقه انتخاب النسب مقارنه بالقيم في طريقتي الانتخاب التجميعي وانتخاب الجورة الواحدة على التوالي وعموما فإن أفضل وأحسن الطرق جاءت بطريقتي انتخاب النسب والانتخاب التجميعي مقارنه بطريقه انتخاب الجورة الواحدة .

•وبناءً على هذه النتائج تبين أن قيم التباين الوراثي سوف تعطى أفضل دليل على التحسين الوراثي المتوقع والمكتسب من طرق الانتخاب.والقيم العالية للمكسب الانتخابي وّجدت أنها تكون مصاحبه

للقيم العالية , المتوسطة من معامل التوريث في المدى الواسع لمعظم الصفات المدروسة وهذا يدل على أن التعبير المظهري لهذه الصفات دليل على سلوكها الوراثي ولهذا فان الانتخاب لهذه الصفات يكون أفضل .

● وهذه الدراسة توضح أن الانتخاب ولو لدورة واحدة في الأجيال المبكرة مع شدة ودقة الانتخاب يساعد على زيادة تكرار الجينات المرغوبة أثناء عملية الانتخاب .

● أما معاملات الارتباط فقد أظهرت أن هناك معنوية موجبة لمعظم الصفات في الجيل الثاني أما في الجيل الثالث فقد أظهرت طريقة انتخاب النسب قيماً معنوية وسالبة ما بين محصول القطن الزهر و صفتي طول التيلة ومتانة التيلة كما أظهرت طريقة الانتخاب التجميعي قيماً غير معنوية وسالبة لطول التيلة ومتانة التيلة مع صفة محصول القطن الزهر و قيماً معنوية وغير معنوية وسالبة لصفة متانة التيلة مع صفة محصول القطن الشعر .