GENETIC STUDIES ON YIELD, YIELD COMPONENTS AND FIBER PROPERTIES IN SEGREGATING GENERATIONS OF AN INTRASPECIFIC COTTON CROSS

EL-ADLY, H.H. AND ABEER S. ARAFA

Cotton Research Institute, ARC, Giza

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Abstract

Estimation of gene action through partioning of genetic variance was carried out, using the parents, F_1, F_2 and F_3 populations in the cross Giza 90 x Pima S62 (24202).

Results showed that the heterotic effects relative to better parent (useful heterosis) were positive and highly significant or significant for all studied characters except for First Fruiting Node (FFN), boll weight (BW), micronair value (Mic), Fiber strength (St) and Fiber elongation (Elon %), while days to first flower (DFF) recorded highly significant better parent heterosis value. Mid-parent heterosis values were highly significant and negative for days to first flower (DFF) and boll weight (BW). On the other hand, the remaining traits revealed positive and highly significant or significant heterotic effects except for First Fruiting Node (FFN), lint percentage (L %), micronair value (Mic) and Fiber elongating (Elon %) which showed insignificant heterotic effects.

Inbreeding depression was positively significant and highly significant for all traits except for boll weight (BW), micronair value (Mic) and Fiber elongation (Elon %). On the other hand First Fruiting Node (FFN) and days to first flower (DFF) recorded negatively significant inbreeding depression.

Regarding potence ratio, partial dominance values were obtained for all studied traits except for days to first flower (DFF), seed cotton yield/plant (SCY/P), lint yield/plant (LY/P), Fiber strength (St) and upper half mean length (UHM) which recorded over dominance.

Concerning the type of gene effects, the additive gene effects were negative and highly significant for days to first flower (DFF), Fiber strength (St) and upper half mean length (UHM), while lint yield/plant (LY/P), lint percentage (L%) and Fiber elongation (Elon %) showed positive significant and highly significant for additive gene effect. Dominance gene effects were positive and highly significant or significant for days to first flower (DFF), seed cotton yield/plant (SCY/P), lint yield/plant (LY/P), Fiber strength (St) and upper half mean length (UHM) and boll weight (BW), respectively. On other hand, Fiber elongation (Elon %) trait showed highly significant negative dominance gene effect. Additive x additive gene type of epistasis effects were highly significant for seed cotton yield/plant (SCY/P), lint yield/plant (LY/P) and lint percentage (L%), while first fruiting node (FFN), days to first flower (DFF), boll weight (BW), micronair value (Mic), Fiber strength (St), uniformity index (UI), upper half mean length (UHM), seed index (SI) and lint index (LI) recorded negatively highly significant and significant epistatic of gene effects. With regarded to the dominance x dominance interaction, the values were positive and highly significant for all studied traits except for seed index (SI), lint index (LI) and uniformity index (UI).

High values of broad sense heritability (over 50%) were detected for first fruiting node (FFN), boll weight (BW) and Fiber elongation (Elon %). Moderate heritability estimates (between 30% and 50%) were found for

seed cotton yield/plant (SCY/P), lint yield/plant (LY/P), seed index (SI), lint index (LI), micronair value (Mic), uniformity index (UI) and upper half mean length (UHM). Low broad sense heritability values (less than 30%) were obtained for days to first flower (DFF), lint percentage (L %) and Fiber strength (St). Narrow sense heritability estimates were calculated for lint index (LI), Fiber strength (St), uniformity index (UI) and upper half mean length (UHM), which exceeded 50% value. Moderate heritability estimates were observed for first fruiting node (FFN), seed cotton yield/plant (SCY/P) and lint percentage (L %). On the other hand low heritability values in narrow sense were obtained for days to first flower (DFF), boll weight (BW), lint yield/plant (LY/P), seed index (SI), micronaire value (Mic) and Fiber elongation (Elon %).

The expected genetic advance from selecting the desired 5% of F_2 population was 56.098, 71.687, 29.399 and 48.12 for first fruiting node (FFN), days to first flower (DFF), lint yield/plant (LY/P) Fiber elongation (Elon %) and upper half mean length (UHM), respectively.

Regression of F_2/F_3 results exhibited high values for first fruiting node (FFN), seed cotton yield (SCY/P), lint yield/plant (LY/P), lint percentage (L %), uniformity index (UI) and upper half mean length (UHM), indicating that the higher values due to the additive genetic variance.

Positively highly significant or significant correlation coefficient was observed between days to first flower (DFF) with first fruiting node (FFN), seed cotton yield/plant (SCY/P) with boll weight (BW), lint yield/plant (LY/P) with seed cotton yield/plant (SCY/P), lint percentage (L%) with lint yield/plant (LY/P), lint index (LI) with lint percentage (L%) and Fiber strength (St), micronair value (Mic) with lint index (LI), Fiber elongation (Elon%) with Fiber strength (St) and upper half mean length (UHM) with days to first flower (DFF), lint percentage (L%) and uniformity index (UI). Negative significant or highly significant correlation coefficient were recorded between seed cotton yield/plant (SCY/P) with days to first flower (DFF), seed index (SI) with seed cotton yield/plant (SCY/P) and lint yield/plant (LY/P).

It could be concluded that the selection improvement of first fruiting node (FFN), seed cotton yield (SCY/P), lint percentage (L%), seed index (SI), uniformity index (UI) and upper half mean length (UHM) traits could be achieved in early segregating generations, but the other traits need intensive selection in later generations.

INTRODUCTION

The progress of any breeding program depends on the available genetic variation, it is necessary that the materials under investigation should be subject to genetic analysis in order to find out the relative magnitude of various types of genetic variance.

The present investigation deals with the determination of the genetic parameters of the population i.e. partitioning of variance, heritability estimates and expected genetic advance upon selection for yield, yield components and fiber properties.

El-Disouqi et al (2000) observed that additive gene effects were significantly positive for seed cotton yield /plant, lint yield/plant and boll weight. Mohamed et al

(2001) found that additive gene effects were significantly positive for number of bolls/plant, boll weight, seed cotton yield/plant and lint percentage. Whereas, high heritability value in broad and narrow sense and regression coefficients were noticed for boll weight. Also they reported that the expected genetic advance upon selection was high for boll weight and number of bolls /plant. El-adly (2004) reported that the additive gene effects were positively significant for boll weight, number of bolls /plant seed cotton yield /plant, lint yield /plant, Micronaire values and Upper half mean length .He reported that the expected genetic advance values from selecting the desired 5% of F2 population were 25.1, 42.1, 46.45 and 16.6 for boll weight, number of bolls /plant, seed cotton yield /plant and lint yield /plant, respectively. Herring et al., (2004) reported that the Micronaire value and fiber strength showed low heritability estimates of h 2= 0.14 to 0.19, while lint yield exhibited a very low heritability estimate of h 2= 0.03. Fiber length and strength were correlated (r= 0.58** to 0.46**) in all the three generations. Andy et al (2005) indecated that the fiber length, fiber strength and fiber fineness showed moderately to highly heritability estimates. Nazmy (2006) reported that the inbreeding depression was positive highly significant and significant for seed index and boll weight, meanwhile additive gene effects and additive x additive type of epistatic gene effects were highly significant for seed cotton yield and lint yield.

The object of this investigation was to study the genetic behavior of yield and its components in a cross between the two varieties, Giza90 and Pima S62 (24202).

MATERIALS AND METHODS

The materials used in this study were cultivar Giza90 and variety Pima S62 (24202) (Gossypium barbadense L.). The methods used in this study started a cross between two genotypes in 2004 season at Giza Agriculture Experimental Station.

F1, F2 and F3 generations were obtained from hybrid and selfed seeds in 2005, 2006 and 2007 seasons, respectively at Seds Experiment Station of the Agriculture Research Center at Banie Saufe Governorate.

Each non-segregating growing generations (P1, P2 and F1) consisted of four rows, F2 and F3 contained 12 rows. Each row was 7.5 m long, 60 cm apart with spaced hills 75 cm. All the agriculture practices were done according to the ordinary cotton culture.

The following measurements were carried out on individual plants in each of the parents, F1, F2 and F3 populations:

A- Yield characters

    1- First fruiting node (FFN).

2- Days to first flower (DFF).

3- Boll weight (BW). Average weight in grams of 10 bolls / plant.

4- Seed cotton yield/plant (SCY/P) in grams.

5- Lint cotton yield/plant (LY/P) in grams

6- Lint percentage (L %).

7- Seed index (SI) in grams.

8- Lint index (LI) in grams.

B- Fiber properties

- Fiber Physical properties

1- Upper half mean length (m.m) UHM and, Fiber uniformity index (UI) were determined using the fibrograph 630 according to (ASTM D: 1447-67).

2- Fiber strength and elongation percentage were determined on the Stelometer Tester according to the standard methods of (ASTM D: 1445- 67).

3- Micronaire reading was estimated using Micronaire 275 instrument according to [ASTM D: 1448-2006].

All fiber properties were tested in cotton Technology Research Division labs, Cotton Research Inst. (C.R.I.). under constant conditions of temperature (20+ 2°c) and relative humidity (65 + 5%).

Statistical and genetically analysis.

1- Estimates of gene effects:

Five parameters, m, d, h, I and L were given by the formula of Mather and Jinks (1971):

$$m = \overline{F_2}$$

$$d = 1/2 \, (\overline{P1} - \overline{P2})$$

$$h = 1/6 \, (4 \, \overline{F_1} + 12 \, \overline{F_2} - 16 \, \overline{F_3})$$

$$I = \overline{P1} - \overline{F_2} + 1/2 \, (\overline{P1} - \overline{P2} + \overline{h})$$

$$L = 1/3 \, (16 \, \overline{F_3} - 24 \, \overline{F_2} + 8 \, \overline{F_3})$$

Where:

m = constant mean.

d = Pooled additive effects.

h = pooled dominance effects.

I = pooled interaction between additive by additive effects.

L = pooled interaction between dominance by dominance effects.

2- Heritability estimates:

a. Heritability in broad sense (h2 b)

$$h^2 b = \frac{V\ F_2 - VE}{V\ F_2} = \frac{\frac{1}{2}\ D + \frac{1}{4}\ H}{\frac{1}{2}\ D + \frac{1}{4}\ H + E} \quad \text{(Allard, 1960)}$$

Where:

VE = Environment variance calculated as the average of P_1, P_2 and F_1

VF_2 = phenotypic variance in F_2

b. Heritability in narrow sense (h2 n)

$$h^2 n = \frac{\frac{1}{2}\ D}{\frac{1}{2}\ D + \frac{1}{4}\ H + E}$$

c. Parent - offspring regression, i.e. regression of F_3 line means on their corresponding F_2 plant values (b).

$$b = \frac{Cov.F_2 / F_3}{F_2\ variance} = \frac{\frac{1}{2}\ D + 1/8\ H}{\frac{1}{2}\ D + \frac{1}{4}\ H + E}$$

3- Expected genetic advance under selection

Genetic advance under selection was calculated according to Johanson et al (1955) as follows:

$$G.S. = K \times \acute{O}\ P \times h^2\ n$$

$$G.S\% = (G.S / F2) \times 100$$

Where:

G.S = expected genetic advance under selection.

K = selection differential with value of 2.06 under 5% selection intensity.

Ó P = Phenotypic stander deviation.

$h^2 n$ = heritability in narrow sense.

4- Degree of dominance

Potence ratio (P) was calculated from the formula given by Smith (1952) to determine the degree of dominance.

$$P = F_1 - MP / [1/2\ (P_1 - P_2)].$$

Where:

$\overline{F_1}$ = First generation mean.

$\overline{P_1}$ = Mean of the first parent.

$\overline{P_2}$ = Mean of the second parent.

M.P = Mid parent value = ½ (P₁ + P2)

5- Inbreeding depression

Inbreeding depression% (I.D %) was determined as the percentage of decrease of F2 generation mean below the F₁ hybrid mean as follow:

$$I.D \% = \frac{F1 - F2}{F1}$$

RESULTS AND DISCUSSION

Mean performances of yield and its components and coefficient of variation for Giza90, Pima S62 (24202). F₁, F₂ and F₃ generations are presented in Table (1). The results showed that Pima S62 (24202), variety recorded higher mean values for SCY/P, LY/P, L%, SI and UHM than Giza90. While Giza90 revealed higher values for FFN and DFF and for fiber Elon% than Pima S62 (24202).

The results indicated that the mean performance of F₁ was higher than parents, F₂ and F₃ for DFF, SCY/P, LY/P, L % and UI and exceeded the P₂, F₂ and F₃ for FFN trait.

It could be concluded from the results that the mean performance in F₂ and F₃ generations, the F₂ was higher value than their parents, F₁ and F₃ for SI and fiber St. The F₃ generation mean performance was higher than the parents and F₂ for SCY/P, LY/P, LI and fiber Elon% and exceeded all populations in DFF. Therefore selection could be effective in the improvement of the characters DFF, SCY/P, LY/P, LI and fiber Elon% characters in the next generation. The data also revealed that the coefficient of variation of F₃ population was larger for FFN, DFF, L%, SI and LI than their parents, F₁ and F₂ generations. This indicates that the environmental fluctuations have marked effects on the expression of these characters.

Hetrosis, inbreeding depression and potence ratio are presented in Table (2). The values of heterosis versus the mid and better parents showed significant positive heterotic effects relative to mid and better parents were founed for all characters studied except for FFN, Mic and Fiber Elon%. Significant negative heterosis relative to mid-parent and better parent for DFF. While L% character showed significant positive heterotic effect relative to mid parent and fiber St for better parent. On the other hand, BW recorded negative heterosis effect to better parent.

Significant positive values of inbreeding depression (Table 2) were found for SCY\P, LY\P, L%, SI, LI, fiber St, UI and UHM, indicating the accumulation of additive gene effects of the expression of these traits. However significant negative inbreeding depression values were noticed for FFN and DFF, suggesting that the genes controlling these traits were not completely segregated. The same results of heterotic effects were obtained by Disouqi et al (2000), Eissa (2004) and Nazmy (2006). On the other hand El-Disouqi et al (2000) showed significant negative inbreeding depression for SCY. Eissa (2004) recorded significant positive inbreeding depression for FFN.

Concerning potence ratio, Table(2) reveled over dominance for DFF, SCY\P, LY/P, fiber St and UHM traits, while the remaining traits exhibited positive or negative values of potence ratio less than unity indicating partial dominance effect.

Genetic parameters effects using generations means are shown in Table (6). The constant mean values (m) were highly significant for all studied traits, it is clear that these traits were quantitavely by inherited. Additive genetic effects (d) were positive significant and highly significant for LY/P, L% and fiber Elon%, respectively. However it was highly significant and negative for DFF and UHM. On the other hand dominance gene effects (h) were positive significant and highly significant for BW, DFF, SCY/P, LY/P, fiber St and UHM, while fiber Elon% trait recorded negatively significant dominance gene effects (Table 4).The dominance genetic effects were larger than additive gene effects for most studied traits. This indicates that dominance genetic effects were more important in the inheritance of these traits. The additive x additive type of epistasis (I) effects were highly significant and positive for SCY/P, LY/P and L% traits, the remaining traits revealed significant or highly significant epistasis gene effects. With regard to the interaction dominance x dominance (L) epistatic gene effects were highly significant and positive for most studied traits except for SI, LI and UI. From the above results, it could be concluded that the additive and dominance gene effects as well as some epistatic gene effects could have contributed to the inheritance of the studied traits. In this respect El-Helw Sayda (2002) and El-Adly (2004) obtained significant and highly significant additive x additive type of epistasis effects for LY/P and L%, while the interaction dominance x dominance

epistatic gene effects were negatively significant or highly significant for SCY/P, LY/P, Mic and UHM.

Heritability estimates in both broad and narrow senses, genetic advance upon selection as well as parent offspring (b) are presented in Table (5).the results showed that high broad sense heritability estimates (exceeded 50%) were found for FFN, BW and fiber Elon% characters. While moderate broad sense heritability estimates (30% to 50%) were detected for SCY/P, LY/P, SI, LI, Mic and UHM. On the other hand DFF, BW, L% and Fiber St showed low broad sense heritability estimate (less than 30%). High narrow sense heritability estimates were observed for LI, Fiber St, UI and UHM (more than 50%). Moderate narrow sense heritability estimates were observed for FFN, SCY/P and L%. Low narrow sense heritability estimates were recoded for DFF, BW, LY/P, fiber St, Mic and fiber Elon%. From the above results it could be concluded that high heritability estimates in broad sense indicated that the selection for phenotype could be highly effective for FFN and BW traits. High narrow sense heritability could be due to the additive genetic effect for the characters LI, Fiber St, UI and UHM, selection for these traits will be effective in early generations.

The expected genetic advance upon selection at 5% of F_2 population in (Table 4) ranged from 5.678 for BW to 71.687 for DFF. The results of expected genetic advance upon selection were higher for FFN, DFF, LY/P, fiber Elon% and UHM indicating that the improvement of these traits is highly effective through selection. Abou-Arab et al (1997) found that the expected genetic advance upon selection was higher for BW, SCY/P and LY/P.

Parent off spring correlation and regression are listed in Table (4). The high value of regression for FFN, SCY/P, L%, UI and UHM suggested that the F2 plants which had high values tended to give F3 lines with high values. High value regression is usually due to the additive genetic variance.

Correlation coefficient between all possible pairs of studied traits are presented in Table (5). Highly significant and positive correlations were observed between DFF with FFN, LY/P with SCY/P, L% with LY/P, LI with L%, fiber Elon% with Fiber St and UHM with DFF and UI. On the other hand significant positive correlation was detected between SCY/P with BW, LI with SI, Mic with LI and UHM with L%. While negatively significant correlation was recorded between SI and LY/P.

It could be concluded that the improvement in this material of FFN, SCY/P, L%, SI, UI and UHM traits could be achieved in early segregating generations, but the improvement of the other traits need intensive continuous selection through later generations.

Table 1. Mean performance and standard error for yield, yield components and fiber properties of studied population of cotton cross (Giza90 x PS7).

Characters	statistic	population				
		P1	P2	F1	F2	F3
FFN	x̄	6.3 ±9.330	6.6 ± 0.0973	6.4 ± 0.0922	6.7 ± 0.0856	6.5 ± 0.0672
	C.V	9.330	9.540	9.055	8.479	10.620
DFF	x̄	69.2 ± 0.565	71.5 ± 0.381	68.6 ± 0.557	69.8 ± 0.299	67.7 ± 0.348
	C.V	55.475	37.381	54.712	29.652	123.879
BW (g)	x̄	3.0 ± 0.0594	3.1± 0.0601	3.0 ± 0.0303	3.0 ± 0.0388	2.94 ± 0.0161
	C.V	5.880	5.85	3.07	2.758	5.13
SCY/P (g)	x̄	84.40 ± 1.82	91.48 ± 2.71	115.40 ± 1.91	92.69 ± 1.66	107.84 ± 1.26
	C.V	79.022	66.263	88.101	65.512	84.934
LY/P (g)	x̄	33.0 ± 0.69	36.49 ± 1.165	46.17 ± 0.801	36.37 ± 0.66	42.62 ± 0.493
	C.V	68.292	114.5	78.686	66.584	75.212
L%	x̄	39.11± 0.208	39.83 ± 0.240	40.0 ± 0.180	39.23 ± 0.177	39.62 ± 0.130
	C.V	20.398	24.026	18.907	16.983	71.973
SI	x̄	9.76 ± 0.095	9.76 ± 0.094	9.36 ± 0.133	9.88 ± 0.073	9.61± 0.071
	C.V	9.391	9.391	13.490	6.791	17.520
LI	x̄	6.27 ± 0.112	6.47 ± 0.106	6.25 ± 0.093	6.38 ± 0.068	6.61± 0.071
	C.V	8.049	8.948	11.280	6.331	12.010
Mic	x̄	4.1±0.0577	4.1 ± 0.0783	4.0 ±0.0200	4.1 ± 0.0510	4.0 ± 0.0500
	C.V	3.618	3.447	3.596	1.750	1.616
St	x̄	35.38 ± 0.3040	38.38 ± 0.4722	36.25 ± 0.3471	38.88 ± 0.1313	36.75 ± 0.5071
	C.V	0.683	0.066	0.319	0.998	0.0001
ELON%	x̄	7.9 ±0.115	7.4 ± 0.114	7.2 ± 0.073	6.8 ± 0.147	7.8 ± 0.111
	C.V	3.045	3.020	3.242	0.872	1.117
UI	x̄	82.0 ± 0.145	82.2 ± 0.158	82.8 ± 0.223	81.5 ± 0.162	82.0 ± 0.248
	C.V	2.407	2.461	1.362	0.743	0.164
UHM	x̄	30.2 ± 0.1719	31.5 ± 0.1259	31.4 ± 0.1813	30.2 ± 0.1533	29.4 ± 0.1692
	C.V	2.258	2.889	1.887	0.825	0.587

Table 2. Hetrosis (H), inbreeding depression (I.D) and potence ratio (P.R) estimates for yield characters and fiber properties studied.

| Characters | Heterosis (H) | | I.D | P.R |
	H.MP	H.BP		
FFN	-1.908	-3.904	-4.969**	-0.066
DFF	-2.445**	3.994**	-1.666*	-1.805
BW	-1.653	-3.474*	0.238	-0.011
SCY	31.221**	26.156**	19.680**	1.783
LY	32.897**	26.524**	21.238**	2.003
L%	1.372*	0.461	1.949**	0.774
SI	4.070*	4.090*	5.557**	0.001
LI	4.676*	4.44*	5.158**	-0.048
Mic	1.235	2.439	2.500	-0.001
St	1.695	5.537**	7.241**	-2.400
Elon%	5.882	0.017	0.0171	0.350
UI	0.853**	1.5700**	1.570**	0.280
UHM	1.783*	3.822**	3.822**	1.430

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

Table 3. Estimation of gene action for yield, yield components and fiber properties of cotton cross (Giza90 x PS7).

Characters	Gene action				
	m	d	h	i	L
FFN	6.67 ± 0.08562**	-0.135 ± 0.1827	0.380 ± 0.2554	-36.560 ± 0.8113**	36.295 ± 1.7062**
DFF	69.75 ± 0.2994**	-1.1350 ± 0.341**	4.8133 ± 1.667**	-387.706 ± 3.376**	388.418 ± 5.301**
BW	3.00 ± 0.02784*	-0.060 ± 0.0423	0.167 ± 0.0735*	-16.648 ± 0.253**	16.670 ± 0.437**
SCY	92.690 ± 1.6712**	-3.530 ± 1.6360	25.26 ± 4.912**	410.32 ± 15.816**	385.89 ± 23.159**
LY	36.359 ± 0.0672**	1.750 ± 0.6799*	10.152 ± 1.957**	160.877 ± 6.359**	150.682 ± 9.349**
L%	39.230 ± 0.171**	0.36 ± 0.160*	-0.306 ± 0.503	209.173 ± 1.619**	208.54 ± 2.346**
SI	9.880 ± 0.0685**	0.001 ± 0.0677	0.373 ± 0.250	-53.813 ± 0.759*	53.88 ± 1.122
LI	6.390 ± 0.0639**	-0.100 ± 0.0613	0.1733 ± 0.212	-34.826 ± 0.668*	34.693 ± 0.968
Mic	4.100 ± 0.0511**	-0.05 ± 0.0486	0.200 ± 0.169	-22.4 ± 0.492**	22.35 ± 0.762**
St	31.100 ± 0.135**	-1.20 ± 0.283**	5.267 ± 1.397**	-178.133 ± 3.057**	176.766 ± 5.795**
Elon%	6.800 ± 0.148**	0.250 ± 0.0811**	-2.4 ± 0.419**	-32.533 ± 1.335**	32.683 ± 1.774**
UI	81.50 ± 0.162**	-0.10 ± 0.1127	-0.466 ± 0.751	-433.866 ± 1.946*	434.033 ± 3.053
UHM	30.200 ±0.153**	-0.65 ±0.1065**	2.933 ± 0.559**	-168.8 ± 1.597**	169.616 ± 2.344**

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

Table 4. Hertability estimates (h%), Parent-offspring (b) and expected genetic advanced (Δg %) of cotton cross (Giza90 x PS7)

Characters	Hertability estimates		Genetic advanced (Δg %)	Parent-offspring (b) (corr coeff)	Regression F2/F3 %
	$H^2._{b.s\%}$	$H^2._{N..s\%}$			
FFN	-57.22	-31.806	56.098	-0.715	71.5
DFF	-15.46	-11.623	71.687	-3.070	30.7
BW	-90.01	10.29	5.678	-0..041	4.1
SCY	49.00	33.44	11.512	0.587	58.7
LY	36.84	21.23	29.399	0.682	68.2
L%	21.70	44.31	15.658	0.505	50.5
SI	42.55	11.31	15.985	0.190	19.0
LI	30.77	65.91	8.679	0.102	10.2
Mic	48.77	10.21	10.763	0.103	10.3
St	24.19	60.54	16.856	0.402	40.2
Elon%	74.45	15.77	48.121	0.132	13.2
UI	37.25	50.39	16.853	0.601	60.1
UHM	43.42	76.28	24.079	0.731	73.1

Table 5. Correlation among yield, yield components and fiber properties of the cross (Giza90 x Pima S7).

Characters	FN	DFF	BW	SCY	LY	L%	SI	LI	Mic	St	ELON%	UI
DFF	0.211**											
BW	0.057	0.112										
SCY	-0.079	-0.147*	-0.147*									
LY	-0.085	-0.137	-0.141	0.983**								
L%	-0.033	0.015	-0.001	0.123	0.299**							
SI	-0.039	0.093	-0.068	-0.161*	-0.159*	-0.042						
LI	-0.052	0.084	-0.055	-0.046	0.069	0.610**	0.762*					
Mic	0.114	0.050	0.024	-0.075	-0.051	0.133	0.119	0.162*				
St	0.066	0.140	0.041	-0.125	-0.129	-0.064	0.005	-0.042	-0.070			
Elon%	0.127	-0.140	-0.055	0.053	0.048	-0.011	0.007	0.005	0.032	-0.246**		
UI	-0.004	0.126	0.010	0.068	0.093	0.142	-0.065	0.036	0.001	-0.081	0.039	
UHM	0.134	0.208**	0.136	0.013	0.043	0.151*	-0.027	0.074	-0.015	0.089	-0.091	0.426**

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

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دراسات وراثية على المحصول ومكوناته وصفات التيلة للاجيال الانعزالية
فى هجين صنفى من القطن

حسن حسين العدلى ، عبير سمير عرفه

معهد بحوث القطن – مركز البحوث الزراعية – جيزة

تم اجراء هذا البحث بمزرعة محطة البحوث الزراعية بالجيزة موسم ٢٠٠٥ – ٢٠٠٦ – ٢٠٠٧ وفى موسم ٢٠٠٨ تم تقييم الاباء جيزة٩٠ و بيما س٦٢ (٢٤٠٢٠) والاجيال الثلاثة F1 و F2وF3 بمحطة البحوث الزراعية بسدس وذلك لدراسة السلوك الوراثى للمحصول ومكوناته ويمكن تلخيص اهم النتائج المنحصل عليها فيما يلى:

١. اثبتت النتائج ان قوة الهجين منسوبة الى متوسط الابوين كانت معنوية وموجبه لجميع الصفات المدروسه عدا صفة ارتفاع عقدة اول فرع ثمرى ومتوسط وزن اللوزة وقرأة الميكرونير ومتانة التيله والنسبة المنوية لأستطالة التيلة. بينما كانت قوة الهجين منسوبه الى متوسط الابوين سالبة المعنوية لصفة تاريخ تفتح اول زهرة. كذلك اوضحت النتائج ان قوة الهجين منسوبة الى افضل الاباء معنوية موجبه لكل الصفات المدروسه عدا صفة ارتفاع عقدة اول فرع ثمرى وتصافى الحليج وقرأة الميكرونير والنسبة المنوبه لاستطالة التيله. بنما اظهرت صفة ناريخ تفتح اول زهرة ومتوسط وزن اللوزة معنوية سائبة نقوة الهجين منسوبة لافضل الآباء.

٢. اظهرت النتائج ان ألانخفاص الراجع الى النربية الداخليه كان موحب نمعنوية لجميع الصفات المدروسة عدا صفة متوسط وزن اللوزة وقرأة الميكرونير والنسبة المنوية لأستطالة النيلة. بينما اظهرت صفة ارتفاع عقدة اول فرع ثمرى وتاريخ تفتح اول زهرة معنوية سالبة لمعامل التربية الداخلية.

٣. اوضحت النتائج ان كل الصفات المدروسه اظهرت سيادة حزئية عدا صفة ناريخ نفتح اول زهرة ومحصول القطن الزهر والشعر للنبات ومتانه التيلة و طول التيلة حيث اظهروا سيادة فائقة.

٤. كان تأثير الفعل الوراثى المصيف معنوى وموحب نصفة محصول القطن الشعر للنبات وتصافى الحليج والنسبة المنوية لأستطاله التيلة بينما اظهرت صفة ناريخ تفتح اول زهرة ومتانة وطول التيلة معنوية سالبة للفعل الاضافى للجين. كذلك اظهرت صفة تاريخ تفتح اول زهرة ومتوسط وزن اللوزة ومحصول القطن الزهر وانشعر للنبات ومتانه وطول النبلة معنوية موجبة للفعل السيادى للجين اما صفة أستطالة النيلة فقد اظهرت معنوية سالبه للفعل السيادى للجين. كذلك اوضحت النتائج ان تأثير نفوق الفعل انجبى الراجع الى الفعل الجينى نمصيف × المصيف معنوى وسالب لمعظم الصفات المدروسه عدا صفة محصول القطن الزهر والشعر للنبات وتصافى الحليج حيث اظهروا معنوبه موجده للفعل الجبنى المصيف × المصيف. ابضا اوضحت النتائج ان التفاعل الراجع الى الفعل السيادى × السيادى نحير كان معنوى وموجب لكل الصفات المدروسة عدا صفه معامل البذرة ومعامل الشعر للنبات ومعامل انبطاد التبنة.

٥. كانت قيم المكافئ الوراثى فى المعنى الواسع (اكبر من ٥٠%) عالية لكل الصفات المدروسة عدا ارتفاع عقدة اول فرع ثمرى ومتوسط وزن اللوزة ومعدل استطالة التيلة بينما كان المكافئ الوراثى متوسطة (من ٣٠% الى ٥٠%) لصفة محصول القطن الزهر والشعر للنبات وتصافى الحليج ومعامل البذرة والشعر وقرأة الميكرونير ومتانة التيلة ومعامل انتظام التيلة و طول التيلة. بينما اظهرت صفة تاريخ تفتح اول زهرة وتصافى الحليج مكافئ وراثى منخفض فى المعنى الواسع (اقل من ٣٠%).اما المكافئ الوراثى فى المعنى الضيق كانت عالية لصفتى معامل انتظام وطول التيلة كذلك اظهرت صفات ارتفاع عقدة اول فرع ثمرى ومحصول القطن الزهر للنبات وتصافى الحليج مكافئ وراثى متوسط فى المعنى الضيق اما باقى الصفات فقد سجلت مكافئ وراثى فى المعنى الضيق منخفضة.

٦. اظهر التحسين المتوقع من الانتخاب قيم عالية لصفات ارتفاع عقدة اول فرع ثمرى وتاريخ تفتح اول زهرة ومعدل استطالة التيلة وقد تراوحت النسبة مابين ٨,٦٧% لصفة معامل الشعر الى ٧١,٦٨% لصفة تاريخ تفتح اول زهرة.

٧. اظهرت النتائج ان هناك علاقة قوية بين النباتات فى الاجيال الانعزالية (الجيل الثانى والثالث) وان انتخاب النباتات ذات الصفات المحصولية والتكنولوجية العالية سوف يؤدى الى الحصول على نباتات ممتازة فى الجيل الثالث.

٨. اوضحت النتائج ان هناك علاقة معنوية وموجبة بين كل من تاريخ تفتح اول زهرة وارتفاع عقدة اول فرع ثمرى وبين محصول القطن الزهر للنبات ومتوسط وزن اللوزة وبين كل من محصول القطن الشعر والزهر للنبات وكذلك بين تصافى الحليج ومحصول القطن الشعر للنبات وبين معامل الشعر وكل من تصافى الحليج ومعامل البذرة كذلك كان الارتباط موجب بين استطالة ومتانة التيلة وكذلك بين متوسط طول التيلة وكل من تاريخ تفتح اول زهرة وتصافى الحليج ومعامل انتظام التيلة. بينما اظهرت النتائج ان هناك ارتباط معنوى وسالب بين كل من معامل البذرة ومحصول القطن الشعر للنبات.