

GENETIC ANALYSIS AND PREDICTION OF NEW RECOMBINATION IN SOME COTTON (*G. barbadense* L.) CROSSES

A. M. Abd El-Moghny

Cotton Breeding Research Section, Cotton Research Institute,
Agricultural Research Center, Giza, Egypt

ABSTRACT

Improving cotton breeding programme must depend on the amount of genetic variability between the parental genotypes, which is the main source of genotypic variation among the progeny. The present study was undertaken for the estimation of genetic variability, genetic components and heritability for some yield characters in F_2 , F_3 and F_4 generations derived from two cotton crosses. Estimated Prediction of new recombinant in F_3 generation and selection was done on F_2 to select the most promising plants and the most superior F_3 families and plants within each selected family. The results showed some genetic variation among three studied generations, which reflect genetic variability between studied generations. Dominance genetic variance was more important than additive genetic variance in most studied characters. These results indicated that these characters are controlled by non-additive gene type. The analysis of variance for F_3 generation showed significant differences between F_3 families and it's greater than within families in all the studied characters over the two cotton crosses, which show presence of high genetic variability in F_3 generation. This reflects low values of intra-class variability. So, selection is more effective between families rather than within families. Correlation and regression results between generations showed that F_2 was not good indicator of F_3 progeny, while this trend changes from F_3 to F_4 generations. Prediction for new recombinant falling outside parental range through F_3 generation was higher for all the studied characters. Realized selection differential was higher between and within selected F_2 plants and F_3 families. So, the grand mean values of these selected plants and families were higher than grand mean of F_2 and F_3 population. Selection between segregating generations coupled with high heritability is a good indicator for selecting promising plants in F_2 generation and most superior families within F_3 families and within each family.

Keywords: Cotton (*G. barbadense* L.), genetic components, intra-class variability, segregating generation, new recombination, realized selection differential.

INTRODUCTION

Geneticists and cotton breeders are interested to estimate gene effects in order to formulate the most advantageous breeding procedures for improving the quantitative characters. Estimation of additive and dominance components is important for the improvement

of yield and its components. In order to develop high yielding varieties of cotton, the genetic information of different quantitative and qualitative traits may be helpful cotton breeders to improve genetic architecture of the plant in particular direction for improving and maintaining the proper crop production level. The use of existing genetic variability in the breeding material and the creation of new variability along with its genetic understanding are of crucial importance for this purpose in a breeding program **Acquaah, (2007)**.

Heritability defined as the degree of resemblance between relatives. It is one of the most important genetic parameter on which different breeding strategy depends. The knowledge of heritability is a prerequisite for the formulation of breeding plans on scientific lines as defined by **Falconer and Mackey (1996)**. Thus heritability coupled with genetic advance and genetic variability could be the suitable tool for plant breeder to select the suitable breeding method in order to improve the genetic makeup of cotton plant (**Soomro et al. 2010 and Rangantha et al. 2013**). The breeding program of any crop mainly depends on the presence of genetic variability present in the breeding materials **Aziz et al. (2014)**.

Crop improvement is based on understanding which genes are involved in a phenotype, as well as the degree of environmental variation. Thus the ability to understand the genetic basis and heritability of characters (phenotype) in breeding programmes provides the opportunity to deploy novel allelic combinations. **Abd El-Moghny and Max (2015)** studied genotypes x environments interaction and found that environmental variation caused more than 60% of the total variance on the studied genotypes, while the genotypes variations cause 37.666% and 35.073% for seed cotton yield and lint yield characters, respectively.

Selection of superior progenies is a procedure intensive process, once the characters of importance are strongly influenced by the environment and often correlated, so that a selection is one provokes in the other characters (**Ramadan et al., 2014 and El-Mansy, 2015 a**). Increasing yield is the most important aim in any breeding program. Yield is a complex character with low inheritance and involves several quantitative components, its direct selection is not usually sufficient and therefore it is suggested that its components should be investigated instead. **Abd El-Moghny et al. (2015)** and **El-Mansy (2015 b)** found highly significant positive correlation between yield and its components in Egyptian cotton.

The objective of this study is to estimate some descriptive statistics in three segregating generations F_2 , F_3 and F_4 and determine both additive and dominance genetic variances, in order to Predict new recombinant in F_3 generation in two cotton crosses. Also, the study will

be extended to use realized selection differential to select the most promising plants from F_2 generation in order to select the most superior families in F_3 generation and the promising plants in each selected family.

MATERIALS AND METHODS

The plant materials used in this study were the selfed seeds of three segregating generations F_2 , F_3 and F_4 of two intraspecific cotton crosses belonging to *Gossypium barbadense* L. with their original parents. These breeding materials were obtained from Cotton Breeding programme, Cotton Breeding section, Cotton Research Institute, Agricultural Research Center, Giza, Egypt. The present investigation was carried out at Sakha Experimental Station; Agricultural Research Center, Kafr El-Sheikh; Egypt, during the growing seasons from 2013 to 2015. The two cotton crosses namely, cross I; (Giza 75 / Sea // Giza 94) and cross II; (Giza 89 / Giza 86 // Giza 94). Origin, pedigree and characterization of these breeding materials are presented in **Table 1**.

In the growing season of 2013, all the selfed seeds of the F_2 generation were planted in unreplicated rows to produce F_2 plants. Each row consisted of 10 single plants spaced 70 cm apart between plants and rows. At maturity all plants from each cross were harvested to estimate yield characters. Twelve and fifteen superior plants were selected based on yield characters from F_2 generations to produce F_3 families seeds.

In the growing season of 2014, the selected plants from F_2 generation were evaluated as F_3 families in a randomized complete block design (RCBD) in two replications with their original parents. Each replicate consisted of two rows for parents and F_3 families. Each row consisted of 10 single plants spaced 70 cm apart between plants and rows. At maturity the selected plants from each family were harvested to estimate yield characters in the two crosses. 6 and 8 families from cross I and II, respectively were selected as the superior families then the superior plants from each family were select build the F_4 family seeds.

In the growing season of 2015, selfed seeds of selected plants from each selected family were evaluated in a randomized complete block design (RCBD) with two replications. The experimental lay out was the same as carried out in 2014. All other normal culture practices were applied as recommended for ordinary cotton cultivation during the three growing seasons.

At maturity, all the cotton plants were harvested for studying four yield characters, boll weight (BW) seed cotton yield per plant (SCY)

and lint yield per plant (LY) in grams and lint percentage (L%) was calculated.

Biometrical assessment

The original obtained data were statistically analyzed for the four quantitative yield characters. The mean values, standard errors and variances of different generations and their parents were subjected to weight least squares (WLS) technique to estimate simple genetic model [m, d and h] using the joint scaling test to fit models of increasing complexity until an adequate description of the observed means was found as non-significant X^2 test according to **Mather and Jinks (1982)** and **Kearsey and Pooni (1996)**. The used model is:

$$Y_i = c + b_1 * X_{1i} + b_2 * X_{2i}$$

Where Y_i , c, b_1 , b_2 , X_{1i} and X_{2i} are generation mean, m, [d], [h], the coefficients of [d] and [h], respectively. The biometrical assessment was applied when epistasis was absent and the degree of dominance was also calculated. Heritability in broad sense was estimated correlation (r) and linear regression (b) coefficients between the three studied generations were computed according to **Falconer (1989)** and **Falconer and Mackey (1996)**.

Analysis of variance and genetic components for F_3 generation

Analysis of variance was carried out to obtain between and within family variances for the studied cotton crosses. The variance values of the F_3 family mean variance (V_{F_3}) (within families), the F_3 family variance mean (V_{F_3}) (between families) and homogeneous entries generations mean variance (E_1). Genetic variance components of additive [D] and dominance [H] were estimated as described by **Hallauer et al. (1988)** and **Kearsey and Pooni (1996)**.

Prediction of new recombinant in F_3 generation

The properties of new recombinant lines derived from a series of selfing generations of a cross between two inbred lines were computed for the F_3 generation. The proportion of new recombinant likely to outperform parental $\times P_1$, $\times P_2$ and those exceeding F_1 hybrids, therefore were computed and compared with those observed ones in F_4 generation. All these calculation was done as described by **Jinks and Pooni (1976)**. The proportion of recombinant lines corresponding to the probability levels were obtained using **Fisher and Yates, (1963)** Tables. For this analysis the original data of seed cotton yield, lint yield and lint % were transformed to root square before statistical analysis as outlined by **Folwer and Cohen (1993)**.

Selection procedure among studied segregating generations

The top 5% superior plants were selected from F_2 plants and F_3 families on the basis of boll weight, seed cotton yield, lint yield and lint %. Also, realized selection differential (rs) was calculated for F_2 plants and F_3 families to detect the superiority of selected plants and families and select the top 5% superior plants in each selected family as described by **Singh and Chaudhary (1979)**.

Table 1: Origin, pedigree and characterization of the parental cotton genotypes

Genotypes	Origin	Pedigree	Characterization
Giza 75 / Sea	Egypt	Giza 67 / Giza 69 // Sea	Low boll weight, seed cotton yield and lint percentage.
Giza 89 / Giza 86	Egypt	Giza 75 / 6022 // Giza 75 / Giza 81	Low boll weight, seed cotton yield, lint yield and lint percentage.
Giza 94	Egypt	10229 / Giza 86	High boll weight, seed cotton yield, lint yield and lint percentage coupled with fiber length, fiber strength and moderate micronaire value.

RESULTS AND DISCUSSION

The genetic variability of metric characters can be studied through the use of various statistical parameters like mean, median, range and variance components. The mean performance based on the individual data points for yield characters of the three studied generations F_2 , F_3 and F_4 among two crosses are presented in **Table 2**. Mean and stander error showed significant differences among these generations for all yield characters. Cross I (Giza 75 / Sea // Giza 94) had higher values for most studied yield characters over three generations than cross II (Giza 89 / Giza 86 // Giza 94), this may be related to differences in origin or pedigree. This indicates that these breeding materials had significant differences and mean performance increasing for all yield characters during advanced generations from F_2 to F_4 in the desirable direction; it could be largely attributed to the accumulation of favorable alleles as a result of selection efficiency. Similar results have been reported by **Ramadan et al. (2014)** and **El-Mansy (2015 a and b)**.

The source of genetic variation of F_3 generation consists of three portions; non-heritable, two heritable and one co-variance as discussed by **Mather and Jinks (1982)** and **Hallauer et al. (1988)**. The non-heritable variances are E_1 is variance component due to plant environmental effects (homogeneous genotypes like parents and F_1). While, the two heritable variance components are the variance of F_3

generation means ($\sqrt{F_3}$) (between families), which reflect the genetically differences produced by segregating at gametogenesis in the F_1 and mean variances of F_3 generation ($\sqrt{F_3}$) (within families) reflects the effects of segregation at gametogenesis in the F_2 individuals. While, the co-variance (WiF_{23}) is the covariance between F_2 generation and F_3 generation means.

Table 2: Phenotypic mean performance for F_2 , F_3 and F_4 generations for quantitative yield characters of the two studied cotton crosses

Characters		Mean \pm SE	Minim	Maxim	Median
Giza 75 / Sea // Giza 94					
Boll weight (g)	F_2	3.540 \pm 0.060	2.900	4.117	3.570
	F_3	3.593 \pm 0.036	3.160	4.850	3.460
	F_4	3.730 \pm 0.034	3.320	4.860	3.620
Seed cotton yield (g)	F_2	269.575 \pm 18.363	97.400	443.000	268.250
	F_3	271.687 \pm 7.699	102.200	156.200	266.650
	F_4	325.687 \pm 7.699	613.700	667.700	320.650
Lint yield (g)	F_2	107.264 \pm 7.170	38.100	175.074	105.000
	F_3	110.568 \pm 3.156	40.100	61.553	107.874
	F_4	133.087 \pm 3.182	247.300	270.195	130.000
Lint %	F_2	39.883 \pm 0.192	38.560	42.976	39.543
	F_3	40.677 \pm 0.136	35.985	36.155	40.829
	F_4	40.847 \pm 0.136	44.900	45.070	40.999
Giza 89 / Giza 86 // Giza 94					
Boll weight (g)	F_2	3.293 \pm 0.055	2.250	3.940	3.280
	F_3	3.483 \pm 0.026	2.940	3.110	3.420
	F_4	3.753 \pm 0.026	4.340	4.510	3.590
Seed cotton yield (g)	F_2	267.777 \pm 17.253	123.500	498.400	267.000
	F_3	311.638 \pm 4.262	203.822	266.822	307.328
	F_4	374.357 \pm 4.262	453.893	516.893	370.328
Lint yield (g)	F_2	109.309 \pm 6.597	48.000	191.000	105.200
	F_3	126.838 \pm 1.749	82.146	108.044	124.892
	F_4	152.998 \pm 1.766	191.360	218.903	150.200
Lint %	F_2	39.594 \pm 0.253	37.974	43.263	39.127
	F_3	40.687 \pm 0.104	38.251	38.441	40.531
	F_4	40.883 \pm 0.104	44.542	44.732	40.721

Classification of genetic variation in F_3 generation over two crosses is shown in **Table 3**. The first portion is the non-heritable one, which showed that E_1 is less because each mean is based on (m) individuals for all the studied characters.

The second portion is the heritable one was described as the component of genetic variation and F_3 analysis of variance for quantitative yield characters as shown in **Tables 3 and 4** among two cotton crosses. The estimated variances of F_3 generation for the studied characters were high, which suggests the presence of homozygosity among the parental population and variation due to environment is very low, whereas high variance of F_3 generation for the studied characters is indication for the presence of high genetic variability within the population. While, variance between F_3 families is greater than within families in all the studied characters over the two crosses (**Table 3**). So, the F_3 segregating generation, not only has genetic variability but also had plant to plant variances (intra-class variability) as shown in **Table 3**. Therefore, the intra-class variability which is defines as the differences between plants within each family

as defined by **Kearsey and Pooni (1996)**. Low intra-class variability values were recorded in all the studied characters over two crosses as shown in **Table 3**, this indicating low variation between plants within each F_3 families (**EI-Mansy, 2005**). These results were in harmony with that obtained from the analysis of variance of F_3 generation means (V_{1F_3}) (between families) was significant and highly significant differences for all the studied yield characters over two crosses as shown in **Table 4**. This showed the presence of high genetic variability among F_3 generation and suggested that selection might be more effective between families rather than within families (**EI-Mansy, 2005** and **Aziz et al., 2014**).

Also, genetic components classified to additive and dominance genetic variances. The values of additive genetic variance [D] was smaller than the dominance genetic variance [H] overall the characters among the two crosses, except boll weight in the first cross (**Table 3**). These results indicated the relative importance of non fixable or non additive type of gene action in the inheritance of these characters, which may be had higher average degree of dominance. So, the use of intermating population or recurrent selection is better for the improvement of these characters in initial generations. Similar observations in Egyptian cotton were reported by **EI-Mansy (2005)** and **Gibely (2015)**.

The third portion is co-variance between F_2 and F_3 generation means (WiF_{23}) as shown in **Table 3** was ranged from 0.029, 3.053, 1.245 and 0.008 for cross I and 0.047, 0.713, 0.291 and 0.001 for cross II for boll weight, seed cotton yield, lint yield and lint %, respectively. Estimation average degree of dominance of the studied yield characters over the two crosses are shown in **Table 3**. The dominance relationships of a pair of alleles or the ratio between H to D; is the average degree of dominance, which is more than unity and had plus sign for all the studied characters indicating overdominance and parent with increasing alleles is dominant to the parent with decreasing genes. These results in the same trend as obtained by **Gibely (2015)**.

Two methods used to calculate heritability in broad sense (h^2b). The first one defined as the ratio between genotypic to phenotypic variations (**Falconer, 1989**) is presented in **Table 3** ranged from moderately for boll weight, seed cotton yield and lint yield to higher values for lint % over two crosses, except boll weight in the first cross. This may be due to the higher values of genotypic variance than environmental one, so heritability reflects efficiency of selection producer. **Abd EI-Moghny et al. (2015)** and **EI-Mansy (2015 b)** found higher heritability values for yield characters among F_3 generation. **Gibely et al. (2015)** found low value of heritability for boll weight among some Egyptian genotypes.

The second method to estimate heritability was defined as regression (slope) of offspring on the parents. So, the relationship of mean performance of F_3 progenies with its F_2 and between F_4 progenies with its F_3 was calculated as the correlation (r) and linear regression (b) coefficients as described by **Falconer (1989)** and **Falconer and Mackey (1996)** is given in **Table 5**. Correlation coefficient (r) was highly significant for all the studied characters over the two crosses between F_3 and F_4 only. While, regression coefficients (b) was non significant between F_2 and F_3 and highly significant between F_3 and F_4 over the two cotton crosses for all yield characters. These results indicated that F_2 generation was not a good indicator of F_3 progeny for such characters but this trend was changed between F_3 and F_4 generations

Table 3: Estimates of variance components for quantitative yield characters of the studied cotton crosses in F_3 generation

Variance components	Boll weight	Seed cotton yield	Lint yield	Lint %
Giza 75 / Sea // Giza 94				
Additive genetic variance [D]	0.053	4.124	1.683	0.011
Dominance genetic variance [H]	0.019	7.924	3.230	0.015
Variance of F_3 generation means ($\sigma^2_{F_3}$) (between families)	0.028	2.557	1.043	0.007
Mean variances of F_3 generation ($\sigma^2_{F_3}$) (within families)	0.016	2.022	0.825	0.005
Homogeneous entries generations mean variance (E1)	0.157	0.487	0.203	0.058
The co-variance W_{F_3}	0.029	3.053	1.245	0.008
Intra-class variability	0.446	0.025	0.026	0.165
Genotypic variance (σ^2_G)	0.044	1.607	0.657	0.006
Phenotypic variance (σ^2_{Ph})	0.201	2.094	0.860	0.064
Degree of dominance	1.420	1.386	1.385	1.149
Heritability in broad sense (h^2_b)	0.217	0.768	0.764	0.891
Giza 89 / Giza 86 // Giza 94				
Additive variance [D]	0.070	3.039	1.260	0.011
Dominance variance [H]	0.097	5.697	2.365	0.022
Variance of F_3 generation means ($\sigma^2_{F_3}$) (between families)	0.041	1.163	0.482	0.004
Mean variances of F_3 generation ($\sigma^2_{F_3}$) (within families)	0.030	0.048	0.019	0.000
Homogeneous entries generations mean variance (E ₁)	0.030	0.713	0.291	0.001
The co-variance W_{F_3}	0.047	0.807	0.334	0.003
Intra-class variability	0.419	0.073	0.039	0.010
Genotypic variance (σ^2_G)	0.071	1.211	0.502	0.004
Phenotypic variance (σ^2_{Ph})	0.101	1.924	0.792	0.005
Degree of dominance	1.176	1.369	1.370	1.415
Heritability in broad sense (h^2_b)	0.705	0.629	0.633	0.875

Table 4: Analysis of variance for yield characters of F₃ families in studied cotton crosses

Mean squares					
S.O.V	d.f	Boll weight	Seed cotton yield	Lint yield	Lint %
Giza 75 / Sea // Giza 94					
Between F ₃ families	11	0.314*	20.535**	8.429**	0.057**
Within F ₃ families	108	0.140	4.867	2.033	0.009
Giza 89 / Giza 86 // Giza 94					
Between F ₃ families	14	0.710*	18.765*	7.731*	0.047**
Within F ₃ families	135	0.298	7.132	2.908	0.006

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

Table 5: Correlation (r) and linear regression (b) coefficients between the three generations of the studied cotton crosses

Characters	Generations	Boll weight	Seed cotton yield	Lint yield	Lint %
Giza 75 / Sea // Giza 94					
Correlation (r)	F ₂ /F ₃	0.069	0.247	0.228	0.170
	F ₃ /F ₄	0.978**	1.000**	0.998**	1.000**
Regression (b)	F ₂ /F ₃	0.090	0.494	0.417	0.108
	F ₃ /F ₄	1.040**	1.000**	0.992**	1.000**
Giza 89 / Giza 86 // Giza 94					
Correlation (r)	F ₂ /F ₃	0.323	0.159	0.108	0.040
	F ₃ /F ₄	1.000**	1.000**	0.776**	0.998**
Regression (b)	F ₂ /F ₃	0.320	0.336	0.210	0.045
	F ₃ /F ₄	0.998**	0.999**	1.020**	0.995**

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

So, the breeder should focus selection on later generations. These results are in harmony with obtained by **EI-Mansy (2015 a)**, **Abd El-Salam (2005)**, **EI-Mansy (2005 and 2015 a)** reported that F₂ was not a good indicator to F₃ progeny. This may be related to; greater genetic variability within F₂ plants rather than within F₃ progeny and genotype x environment interaction. Also, dominance gene action in F₂ population may not be usable in later generations.

Predicting the proportion of new recombinant in F₃ generation

The three parameters of the simple genetic model [m], additive [d] and dominance [h] gene effects were calculated using weighted least squares (WLS) technique as shown in **Tables 6 and 7**. The estimates of mean effects (m), which reflect the contribution due to over-all mean plus the locus effects and interaction of the fixed loci indicated that these characters were quantitatively inherited and dividing

the genetic components into additive [d] and dominance [h] gene effect over all loci as defined by **Hallauer et al. (1988)**. **Abd El-Baky (2006)** used weighted least squares (WLS) technique in some segregating generations to detect genetic components among some cotton crosses and found the importance of dominance gene effects for yield character and its components.

The results of predicting the proportion of new recombinants in F_3 generation for yield and its components is shown in **Table 6**. The proportion of recombinants of inbred lines that possible outside parental range for the studied characters were 47.608, 32.997, 26.435 and 27.425 for boll weight, seed cotton yield, lint yield and lint % for cross I (Giza 75 / Sea // Giza 94), respectively. While for cross II (Giza 89 / Giza 86 // Giza 94) it was 12.714, 41.294, 43.644 and 24.510 for the same traits respectively. These results showed that cross II had higher values than cross I. Also, **Awaad and Hassan (1996)** and **EI-Mansy (2005)** reported moderately proportion of new recombinants for yield characters among F_3 generation in some cotton crosses failing outside parental range.

However, the promising recombinant line $\times P_1$ were 44.433, 10.935 and 22.065 for cross I and 0.344, 46.414 and 43.64 for cross II for boll weight, seed cotton yield and lint yield, respectively while, lint % character was very low over the two crosses. Also, cross I had higher values than cross II, these results showed that cross II was better than cross I and will be improved rapidly through selection procedures. So, yield and its components can be improved through the Egyptian cotton breeding programme. **Awaad and Hassan (1996)** reported that the crosses which showed high predictable proportion of inbred outperform parental range and inbred $\times P_1$ will showed general slight trend when selection was practiced to the highest inbred in the F_4 generation and in a few cases for the lowest one ($\times P_2$).

Predicting the proportion of new recombinant exceeding F_1 showed higher values for all the studied characters except for lint % in cross I, but in cross II was low for seed cotton yield and lint yield and very low for lint % as presented in **Table 7**. These results may be related to wider variability between parental genotypes in cross I than cross II. So, cotton breeder should use wider genotypes in hybridization to increase genetic variation in segregating generations and focus selection on these characters to improve it through cotton breeding programme.

The potence ratio is a result value of [h] relative to [d]; showed that all studied characters had the highest values over two crosses except, seed cotton yield and lint yield in cross I and boll weight in cross II as shown in **Table 7**. These results are indicating dispersion of dominant genes which increase expression between parents and

ensure transgressive segregation for these characters. Similar conclusion was obtained by **EI-Mansy (2005)**. Finally, these results of prediction for new recombinant of F₃ generation can help cotton breeder to make great emphasis on these two crosses to improve cotton.

Table 6: Predicting the properties of the new recombination failing outside parental range in the F₃ generation of the studied cotton crosses

Characters	Probability					Range of inbreeds $m \pm 2\sqrt{D}$	Proportion of inbreeds			P max $\frac{\sqrt{H/D}}{m+h}$
	[m]	[d]	d/\sqrt{D}	$\frac{\sqrt{D}}{P_1-F_1}$	$\frac{\sqrt{D}}{P_2-F_2}$		ρP_1	ρP_2		
Giza 75 / Sea // Giza 94										
BW	3.089	0.382	0.064	-0.148	0.020	0.259± 1.209	47.608	44.433	49.202	2.964
SCY	13.676	1.238	0.439	1.332	-2.211	32.868± 44.128	32.997	10.935	1.355	17.229
LY	8.467	1.134	0.631	-0.545	-0.717	11.623± 18.812	26.435	29.460	22.065	11.677
L%	6.266	0.074	0.606	22.784	-23.997	0.522± 1.012	27.425	-	-	6.378
Giza 89 / Giza 86 // Giza 94										
BW	3.113	0.358	1.147	-3.989	-1.695	0.347± 1.595	12.714	0.344	4.551	2.837
SCY	14.690	0.224	0.094	-1.159	-0.971	30.290± 39.837	41.294	46.414	12.507	20.985
LY	9.354	0.248	0.161	1.155	-1.478	11.309± 17.460	43.644	43.64	73.525	12.121
L%	6.237	0.103	0.694	12.691	-14.078	0.628± 1.222	24.510	-	-	8.126

Table 7: Predicting the properties of the new recombination exceeding F₁ in the F₃ generation of the studied cotton crosses

Characters	[h]	Potence ratio [h]/[d]	Probability [h] / \sqrt{D}	Proportion of inbred exceeding F ₁	Actual % in F ₄
Giza 75 / Sea // Giza 94					
Boll weight	-1.247	-1.007	-0.443	15.866	49.202
Seed cotton yield	-0.039	-0.034	-0.022	48.803	49.202
Lint yield	-0.039	-0.034	-0.022	48.803	49.202
Lint %	-0.716	-9.639	-5.848	-	-
Giza 89 / Giza 86 // Giza 94					
Boll weight	0.222	0.620	0.711	26.763	23.885
Seed cotton yield	0.636	2.840	0.266	2.255	39.743
Lint yield	-0.506	-2.040	-0.329	2.067	1.969
Lint %	-0.496	-4.824	-3.346	0.00004	0.0041

Selection efficiency in segregating generations

Cotton breeder used selection parameters as a breeding tool to improve plant productivity, which more adapted with the environment. Also, estimation of genetic variability between and within generation could help cotton breeder to improve new varieties. Estimation of realized selection differential (rs) is defined as the differences between

mean phenotypic value of selected plants and mean phenotypic value of population mean, so breeder can use it as index of selection efficiency in breeding programme (**Singh and Chaudhary, 1979**).

Selection was done in two levels, the first one between F_2 plants and F_3 families to select the most superior plants and families. The second level within each F_3 family to select the most promising plants in each selected family to be F_4 families in the next season as shown in **Tables 8 and 9** for the two cotton crosses. 12 and 15 plants were selected in F_2 generation from crosses I and II, respectively, as the most promising plants from F_2 population to make up F_3 families in the next season. Most of these plants had higher values more than grand mean of the F_2 population. Among F_3 generation 6 and 8 families were selected from cross I and II, respectively which had higher phenotypic mean values than the F_3 original families mean and has positive values. From these selected families the most promising plants were selected from each selected family for making F_4 generation. The last also had higher and positive values realized selection differential (rs). This selection procedure is depending on the higher phenotypic values for seed cotton yield and lint yield for these crosses.

Realized selection differential (rs) between F_2 and F_3 generations boll weight, seed cotton yield, lint yield and lint % was 0.041, 2.112, 3.304 and 0.794, while between F_3 and F_4 generations was 0.149, 54.0, 22.519 and 0.17 for cross I, respectively. On the other hand, for Cross II was 0.122, 35.55, 17.985 and 1.093 between F_2 and F_3 , while it was between F_3 and F_4 0.239, 61.98, 25.862 and 0.196, respectively, for boll weight, seed cotton yield, lint yield and lint %. These results indicated that there was a wide range of genetic variability between these studied generations. **Ramadan et al. (2014)** and **El-Many (2015 a)** used direct and indirect selection to select the most promising plants and families during segregating generations.

Realized selection differential (rs) within selected F_2 plants and F_3 families should be high for the selected plants in F_2 and F_3 families as shown in **Table 10** for the two crosses. Within F_2 plants it was 0.153 and 0.019, 110.383 and 96.056, 43.399 and 37.057, -0.165 and -0.261 for boll weight, seed cotton yield, lint yield and lint % for cross I and II, respectively. While within F_3 families were 0.075 and -0.018, 37.874 and 11.425, 15.432 and 4.102, 0.019 and -0.209 for boll weight, seed cotton yield, lint yield and lint % for cross I and II, in the same order. Some of the selected plants or families had negative sign for boll and lint % but most of them had higher and positive sign for seed cotton yield and lint yield over the two studied crosses.

These results showed that there is a high improvement for seed cotton yield and lint yield characters through selection and some reduce in boll weight and lint %. The study focused on seed cotton

yield and lint yield characters which showed high variability. So, these results help cotton breeder to select the most superior families. On the other hand, selection must be applied within each selected family to select the most promising plants from the superior family.

Also, the results indicated that these breeding materials have good opportunity for improvement through selection tools. Cotton yield character is a complex character and selection for one reflected character may improve the others (El-Mansy, 2015). On the other hand, Ramadan *et al.* (2014); Abd El-Moghny *et al.* (2015) and El-Mansy (2015 b) found highly significant positive correlation coefficients between yield character and its components among some Egyptian cotton genotypes. Soomro *et al.* (2010) reported that selection parameters should be coupled with high heritability estimates to offers effective response to selection.

Table 8: Mean performance of F₂ plants, F₃ and F₄ families for the studied cotton cross I (Giza 75 / Sea // Giza 94)

Generations	No.	Boll weight	Seed cotton yield	Lint yield	Lint %
Selected F ₂ plants	1	3.680	350.000	139.000	39.714
	2	4.100	326.500	130.700	40.031
	3	3.900	443.000	175.074	39.520
	4	3.300	440.500	170.385	38.680
	5	3.940	319.600	128.400	40.175
	6	3.760	391.000	154.700	39.565
	7	3.040	320.300	129.300	40.368
	8	3.540	442.900	175.000	39.512
	9	3.960	351.200	149.000	42.426
	10	3.320	377.900	147.200	38.952
	11	4.117	430.500	166.000	38.560
	12	3.660	366.100	143.200	39.115
Grand mean of F ₂ plants		3.54±0.06	269.57±18.36	107.26±7.17	39.88±0.19
Selected mean of F ₂ plants		3.69±0.09	379.95±14.10	150.66±5.06	39.71±0.29
Selected F ₃ families	1	3.62±0.11	240.96±17.39	101.53±7.60	42.03±0.39
	2	3.62±0.07	292.01±15.34	120.51±6.27	41.28±0.28
	3	3.42±0.01	268.01±13.31	105.96±5.75	39.48±0.51
	4	3.45±0.03	206.62±13.12	81.07±4.84	39.33±0.35
	5	3.57±0.14	270.88±21.84	110.04±8.89	40.57±0.25
	6	3.50±0.13	227.67±17.41	95.0507.20	41.76±0.35
	7	3.60±0.15	320.07±34.55	133.89±14.67	41.67±0.60
	8	3.44±0.14	188.74±23.62	77.15±9.81	40.76±0.26
	9	3.57±0.11	297.69±20.25	123.71±9.31	41.38±0.49
	10	3.47±0.03	295.96±19.46	122.66±7.10	41.44±0.31
	11	3.56±0.10	319.46±32.87	128.63±13.30	40.26±0.33
	12	4.09±0.2	332.17±38.12	132.86±15.00	40.11±0.35
Grand mean of F ₃ families		3.58±0.06	271.68±7.69	110.56±3.15	40.67±0.13
Mean of selected F ₃ families		3.65±0.00	309.56±6.71	126.00±2.85	40.69±0.35
	2	3.78±0.079	346.01±15.34	143.40±6.31	41.45±0.28
	7	3.58±0.01	322.010±13.31	127.83±5.90	39.65±0.51
	9	3.68±0.09	324.880±21.84	132.50±8.97	40.74±0.25
	10	3.76±0.15	374.070±34.55	157.03±14.86	41.84±0.60
	11	3.73±0.11	351.690±20.25	146.65±9.53	41.55±0.49
	12	4.17±0.19	386.176±38.12	155.18±15.01	40.28±0.35
Grand mean of F ₄ families		3.73±0.03	350.839±7.69	143.76±3.18	40.92±0.13

In conclusion, this study is to estimate the increase of yield characters during advanced generations, which indicating accumulation of favorable alleles as a result of selection efficiency. Non additive gene action controlling yield characters and variation among F_3 families were highly significant and greater than within family's low values of intra-class variability. Yield and its components is a complex character and indirect selection should be used for improve these characters. The cotton breeder should use selection differential coupled with high heritability aiming to improve cotton breeding programme.

Table 9: Mean performance of F_2 plants, F_3 and F_4 families for the studied cotton cross II (Giza 89 / Giza 86 // Giza 94)

Generations	No.	Boll weight	Seed cotton yield	Lint yield	Lint %
Selected F_2 plants	1	2.520	300.400	119.500	39.780
	2	3.300	445.300	169.100	37.974
	3	3.240	289.900	110.900	38.255
	4	3.400	313.000	123.100	39.329
	5	2.840	384.000	146.900	38.255
	6	3.080	447.800	172.500	38.522
	7	3.320	308.800	131.394	42.550
	8	3.440	408.200	159.000	38.951
	9	3.480	417.400	160.000	38.333
	10	3.160	498.400	191.000	38.323
	11	3.620	358.500	154.600	43.124
	12	3.700	297.900	118.800	39.879
	13	3.940	360.200	142.000	39.423
	14	3.140	415.600	159.600	38.402
	15	3.500	347.100	135.000	38.894
Grand mean of F_2 plants		3.29±0.05	276.77±17.25	109.15±6.59	39.59±0.25
Mean of selected F_2 plants		3.31±0.09	372.83±16.65	146.22±5.95	39.33±0.39
Selected F_3 families	1	3.40±0.06	282.39±16.65	112.25±7.12	39.67±0.27
	2	3.50±0.14	273.91±12.33	108.76±5.11	39.68±0.28
	3	3.48±0.12	295.09±18.47	123.02±7.18	41.79±0.35
	4	3.36±0.07	310.01±14.96	124.72±6.06	41.23±0.33
	5	3.38±0.09	317.12±16.00	126.90±6.23	40.05±0.21
	6	3.41±0.06	285.99±11.74	122.35±4.35	42.87±0.35
	7	3.47±0.09	309.86±24.01	127.20±9.47	41.12±0.27
	8	3.47±0.11	312.25±15.94	128.87±6.66	41.27±0.25
	9	3.41±0.10	323.08±18.56	129.70±7.61	40.11±0.19
	10	3.38±0.07	315.21±13.73	125.50±4.75	39.90±0.35
	11	3.59±0.08	324.26±17.26	130.48±7.59	40.15±0.30
	12	3.32±0.06	346.55±18.64	142.21±7.62	41.06±0.32
	13	3.61±0.12	321.12±13.33	129.74±6.34	40.30±0.35
	14	3.82±0.12	324.40±11.01	132.18±5.07	40.71±0.46
	15	2.56±0.56	339.32±51.48	138.03±20.92	40.35±0.28
Grand mean of F_3 plants		3.41±0.02	312.37±4.26	127.13±1.74	40.68±0.10
Mean of selected F_3 families		3.39±0.13	323.80±3.80	131.23±1.85	40.47±0.17
Selected F_4 families	5	3.57±0.06	345.39±16.65	137.90±7.27	39.86±0.27
	8	3.53±0.07	378.01±14.96	156.47±6.07	41.42±0.33
	9	3.55±0.08	380.12±16.00	152.85±6.22	40.24±0.20
	10	3.58±0.05	348.99±11.74	150.02±4.24	43.06±0.35
	11	3.58±0.10	386.08±18.56	155.71±7.69	40.30±0.18
	12	3.76±0.08	387.26±17.26	156.51±7.75	40.34±0.29
	13	3.49±0.06	409.55±18.64	168.86±7.66	41.25±0.32
	14	3.99±0.12	387.40±11.01	158.57±5.25	40.90±0.46
Grand mean of F_4 families		3.63±0.02	377.85±4.26	154.61±1.76	40.92±0.10

Table 10: Realized selection differential (rs) within F₂ plants and F₃ families for the studied cotton crosses

Characters	No.	Boll weight	Seed cotton yield	Lint yield	Lint %
Giza 75 / Sea // Giza 94					
Realized selection differential (rs) for selected F ₂ plants	1	0.140	80.425	31.736	-0.169
	2	0.560	56.925	23.436	0.148
	3	0.360	173.425	67.810	-0.363
	4	-0.240	170.925	63.121	-1.203
	5	0.400	50.025	21.136	0.292
	6	0.220	121.425	47.436	-0.318
	7	-0.500	50.725	22.036	0.485
	8	0.000	173.325	67.736	-0.371
	9	0.420	81.625	41.736	2.543
	10	-0.220	108.325	39.936	-0.931
	11	0.577	160.925	58.736	-1.323
	12	0.120	96.525	35.936	-0.768
Realized selection differential (rs) for selected F ₃ families	1	0.046	-30.727	-9.034	1.357
	2	0.043	20.323	9.952	0.608
	3	-0.153	-3.677	-4.608	-1.192
	4	-0.127	-65.067	-29.490	-1.346
	5	-0.006	-0.807	-0.528	-0.100
	6	-0.074	-44.017	-15.518	1.089
	7	0.021	48.383	23.322	1.000
	8	-0.139	-82.947	-33.418	0.082
	9	-0.010	26.003	13.147	0.703
	10	-0.103	24.273	5.817	-1.232
	11	-0.016	47.773	18.062	-0.410
	12	0.516	60.489	22.293	-0.559
Giza 89 / Giza 86 // Giza 94					
Realized selection differential (rs) for selected F ₂ plants	1	-0.773	23.623	10.349	0.186
	2	0.007	168.523	59.949	-1.620
	3	-0.053	13.123	1.749	-1.339
	4	0.107	36.223	13.949	-0.265
	5	-0.453	107.223	37.749	-1.339
	6	-0.213	171.023	63.349	-1.072
	7	0.027	32.023	22.243	2.956
	8	0.147	131.423	49.849	-0.643
	9	0.187	140.623	50.849	-1.261
	10	-0.133	221.623	81.849	-1.271
	11	0.327	81.723	45.449	3.530
	12	0.407	21.123	9.649	0.285
	13	-0.773	23.623	10.349	0.186
	14	0.007	168.523	59.949	-1.620
	15	-0.053	13.123	1.749	-1.339
Realized selection differential (rs) for selected F ₃ families	1	-3.586	-28.962	-15.090	-1.023
	2	-3.519	-37.441	-18.595	-1.013
	3	-3.535	-16.258	-2.966	1.098
	4	-3.585	3.659	3.472	0.538
	5	-3.568	5.771	-0.139	-0.643
	6	-3.598	-25.363	-2.974	2.183
	7	-3.564	-1.489	0.820	0.429
	8	-3.549	0.896	2.596	0.582
	9	-3.552	11.724	2.716	-0.579
	10	-3.579	3.862	-1.629	-0.785
	11	-3.573	12.910	3.518	-0.536
	12	-3.593	35.200	15.869	0.370
	13	-3.532	9.769	2.869	-0.388
	14	-3.535	13.047	5.573	0.019
	15	-3.550	12.674	3.962	-0.251

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الملخص العربي
التحليل الوراثي والتنبؤ بالاتحادات الجديدة في بعض هجن القطن
(*G. barbadense* L.)
أحمد محمد عبد المغنى

قسم بحوث تربية القطن ، معهد بحوث القطن ، مركز البحوث الزراعية ، الجيزة ، مصر

يتوقف تحسين برنامج تربية القطن على مقدار التباين الوراثي بين السلالات الأبوية والتي تعد المصدر الرئيسي للتنوع الوراثي بين النسل. وقد أجريت هذه الدراسة لتقدير التباين الوراثي ومكوناته ودرجة التوريث لبعض صفات المحصول في الأجيال الثاني والثالث والرابع لاثنين من هجن القطن المصري. وقد تم تقدير درجة التنبؤ بالاتحادات الوراثية الجديدة في الجيل الثالث وكذلك الانتخاب للنباتات المبشرة في الجيل الثاني والعائلات المتفوقة في الجيل الثالث والنباتات الأكثر تفوقاً داخل كل عائلة. أظهرت النتائج بعض الاختلافات الوراثية بين الأجيال الثلاثة تحت الدراسة والتي تعكس درجة الاختلاف الوراثي بينها. كان التباين الوراثي لدرجة السيادة أعلى من الفعل المضيف لمعظم الصفات التي شملتها الدراسة بما يعكس تحكم الفعل الجيني السيادة في هذه الصفات. أظهر تحليل التباين للجيل الثالث وجود فروق معنوية بين العائلات وانها أكبر من داخل العائلات في جميع الصفات تحت الدراسة، والتي تظهر ان التباين الوراثي كبير بين هذه العائلات. وهذا يعكس القيم المنخفضة للتباين داخل المجموعات. لذلك فان الانتخاب بين العائلات أكثر فعالية من الانتخاب داخلها. استخدمت طريقة الانحدار الخطي لتقدير درجة التوريث والتي عكست ان الجيل الثاني لم يكن مؤشر جيد للجيل الثالث بينما تغير هذا الاتجاه بين الجيل الثالث والرابع. ارتفعت درجة التنبؤ بنسبة الاتحادات الوراثية الجديدة خارج نطاق الابوين للجيل الثالث في جميع الصفات تحت الدراسة. استخدمت طريقة *Realized selection differential* بين وداخل نباتات الجيل الثاني والعائلات المنتخبة في الجيل الثالث. فكان متوسط هذه النباتات والعائلات المنتخبة أعلى من المتوسط العام لعشيرة الجيلين الثاني والثالث. ويعد الانتخاب في الأجيال الانعزالية والمرتبطة بدرجة التوريث المرتفعة دليل جيد لكفاءة الانتخاب لانتخاب النباتات المبشرة في الجيل الثاني والعائلات المتميزة في الجيل الثالث والنباتات الأكثر تميز داخل كل عائلة منتخبة.