

## SELECTION OF ELITE EGYPTIAN COTTON GENOTYPE BASED ON ONE-WAY ANOVA

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### ABSTRACT

The objective of the current study was to examine a method for selecting elite Egyptian cotton genotypes used in (Trail A) within the research program in the Breeding Section of the Cotton Research Institute by using one-way ANOVA instead of the currently used randomized complete block design. 38 families from 17 new origins (*Gossypium barbadense* L.) were cultivated in addition to four genotypes representing the control, namely (G90 x CB58), [(G83 x G80) x G89] x Australian, G95 and G90 in a randomized complete block design with six replicates in Bani Sowif Governorate (Sids Research Station) during 2018 season. The two yield characteristics and weight of 50 bolls were studied using data of six replicates. The technological characteristics, fiber length, uniformity ratio, maturity, micronaire value, color, yarn strength and lint percent were studied using only one replicate data. Analysis of randomized complete block design was performed. The results showed significant differences among the treatments for these traits. Analysis of one-way ANOVA was performed. This method was able to analyze all yield data and technological traits. The results revealed that there were significant differences among the origins for the yield characteristics, in addition to the technological characteristics, namely fiber length and the yarn strength. The results also showed that the method of one-way ANOVA surpassed the method of analysis using randomized complete block design, as it was able to analyze all the studied traits, and determine the origins that were significantly superior to the control group in yield or technological traits. This study is useful for introducing a development in the program of the Cotton Breeding Section (Trail A) using the statistical foundations in the method of selecting origins that were significantly superior to the control group to increase the accuracy of selecting the origins that will be included in the (Trial B) program for evaluation in the Upper Egypt Governorates.

**Key words:** ANOVA, evaluation, *Gossypium barbadense* L., selection, statistical analysis.

### 1. INTRODUCTION

The basic premise of the recurrent selection method is increasing the frequency of desirable genes and genetic recombination in a systematic manner to enhance the opportunities of identifying superior genotypes in plant populations. Success of recurrent selection method is dependent on the original assemblies of genes in the breeding populations. If the gene frequency of the trait under selection is different among populations, response to selection may be realized but at different rates and levels. Richmond (1950) first suggested the use of recurrent selection method in cotton breeding in this respect. Opondo and Pathak (1982) mentioned that using recurrent selection was useful in increasing the frequency of favorable genes so that the populations and population

crosses are improved with each selection cycle, consequently recombination of desirable characters may be increased.

The essence of randomized complete block design is that the experimental material is divided into groups, each of which constitutes a single trial or replication. At all stages of any experiment, the objective is to keep the experimental error within each group as small as is practical. Thus, when the units are assigned to the successive groups, all units, which go in the same group, should be closely comparable. Similarly, during the course of the experiment, a uniform technique should be employed for all units in the same group. Any changes in the technique or in other conditions that may affect the results should be made between groups (Cochran and Cox, 1950).

Singh and Narayanan (2000) mentioned the concept of applied randomized complete block design in plant breeding. The randomized complete block experiment is quite flexible. Since the variability between replications can be removed from the experimental error, it is unnecessary for the replications to be contiguous. An entire variable or replication may be omitted from an analysis when, for some reasons, it either is lost or is not comparable with the others (Fowler *et al.*, 1998). One-Way Analysis of Variance (One-Way ANOVA) is a statistical method to determine if there is a difference in means between two or more *independent* groups, where the groups defined by the outcomes for a single categorical variable. Thus, it is essentially an extension of the independent samples test for a difference in means, extended to more than two groups. Like many other parametric statistical techniques, ANOVA is based on the following statistical assumptions: a) homogeneity of variance. b) Normality of data. c) Independence of observations. The One-way ANOVA compares the means of the samples or groups in order to make inferences about the population means. The One-way ANOVA also called a *single factor analysis of variance* because there is only one independent variable or factor. The independent variable has nominal levels or a few ordered levels. In the One-way ANOVA, only one independent variable is considered, but there are two or more (theoretically any finite number) levels of the independent variable. The independent variable is typically a categorical variable. The independent variable (or factor) divides individuals into two or more groups or levels. Idris *et al.* (2015) evaluated two cotton genotypes for fiber properties using one replicate. The second part of analysis was used to evaluate fiber properties using one-way ANOVA to estimate both of season and location effects. Idris *et al.* (2016) evaluated five genotypes in four locations for fiber properties. One replicate was obtained from each location to evaluate fiber properties. Mohamed *et al.* (2003) evaluated 38 families out of 16 new origins (*Gossypium barbadense* L.) in addition to five genotypes representing the control in breeding program (Trail A) at Sids Research Station. A randomized complete block design was used. The results obtained from (Trial A) showed that only two origins (G83 x G80) x G89 and (G85 x G83) exceeded three controls in both yield and fiber quality.

This study was conducted with the aim of proposing a method for selecting elite origins from Egyptian cotton used in (Trail A) within the research program of the Breeding Section in the Cotton Research Institute using one - way ANOVA instead of the currently used randomized complete block design.

## **2. MATERIALS AND METHODS**

The materials used in this study (Trail A) were 38 families from 17 new origins (*Gossypium barbadense* L.) that were cultivated in addition to four cotton genotypes representing the control, namely (G90 x CB58), [(G83 x G80) x G89] x Australian, Giza 95 and Giza 90 (Table 1).

Experimental design was randomized complete block with six replicates in Bani Sowif Governorate (Sids Research Station) during 2018 season. Each plot consisted of five rows. The row was four meters long and 0.60 m apart, and 20 cm between hills. The hills were thinned to two plants per hill. Plot size of hand harvested was 7.2 m<sup>2</sup> (3 middle rows x 4 m long x 0.60 m apart). Planting was during the last week of March. All agricultural practices were done as usual.

Studied families and control were evaluated for seed cotton yield (SCY) in (kantar / feddan), lint cotton yield (LCY) in (kantar / feddan), 50 bolls weight in grams (50 BW) and lint percent (LP). One sample was obtained from each genotype to estimate fiber and yarn properties, *viz.*, fiber length (FL) mm, uniformity ratio (UR), maturity (M), micronaire value (Mic), color (C) and yarn strength (YS). The fiber properties were tested in the Cotton Research Laboratories, Cotton Research Institute, Giza, Egypt (ASTM, 1967).

### **2.1 Statistical Analysis**

#### **2.1.1 Traditional statistical analysis in the breeding program**

The analysis of randomized complete block design (RCBD) was carried out with the data of individual families and control with respect to yield data and 50 bolls weight (Table 2). Statistical analyses were straightforward according to Little and Hills (1978) and SPSS for Windows (1997). The genotypes, means were compared by L.S.D. test as given by Steel and Torrie (1980). All comparisons were done at 0.05 and 0.01 levels of significance.

**Table (1): Pedigree of the Egyptian cotton genotypes (*Gossypium barbadense* L.).**

Origin		Families	Control
1	G91 x C. B 58	F <sub>5</sub> 101 / 2017	
2		F <sub>5</sub> 104 / 2017	
3		F <sub>5</sub> 105 / 2017	
4	[G83 x (G75 x 5844)] x C. B 58	F <sub>5</sub> 107 / 2017	
5		F <sub>5</sub> 108 / 2017	
6	[G83 x (G72 x Dandara)] x Pima S-62 (24202)	F <sub>5</sub> 111 / 2017	
7		F <sub>5</sub> 114 / 2017	
8		F <sub>5</sub> 116 / 2017	
9		F <sub>5</sub> 124 / 2017	
10	(G91 x G90) x Pima S-62 (24202)	F <sub>5</sub> 127 / 2017	
11		F <sub>5</sub> 134 / 2017	
12		F <sub>5</sub> 135 / 2017	
13	(G91 x G90) x C. B 58	F <sub>6</sub> 138 / 2017	
14		F <sub>6</sub> 142 / 2017	
15		F <sub>6</sub> 146 / 2017	
16	(G85 x G83) x [G83 x (G75 x 5844)]	F <sub>6</sub> 155 / 2017	
17		F <sub>6</sub> 158 / 2017	
18		F <sub>6</sub> 163 / 2017	
19	(G90 x Australian) x G85	F <sub>7</sub> 165 / 2017	
20		F <sub>7</sub> 168 / 2017	
21		F <sub>7</sub> 171 / 2017	
22	(G90 x Australian) x [G83 x G72] x Dandara]	F <sub>7</sub> 181 / 2017	
23		F <sub>7</sub> 183 / 2017	
24	[(G83 x G80) x G89] x [G83 x (G75 x 5844)]	F <sub>7</sub> 192 / 2017	
25	(G91 x G90) x G85	F <sub>8</sub> 200 / 2017	
26		F <sub>8</sub> 201 / 2017	
27		F <sub>8</sub> 202 / 2017	
28		F <sub>8</sub> 205 / 2017	
29	(G91 x G90) x [G83 x (G75 x 5844)]	F <sub>8</sub> 210 / 2017	
30	(G91 x G90) x (G85 x G83)	F <sub>8</sub> 213 / 2017	
31	(G91 x G90) x [(G83 x G80) x G89]	F <sub>8</sub> 234 / 2017	
32	(G90 x Australian) x [G83 x (G75 x 5844)]	F <sub>9</sub> 236 / 2017	
33	(G91 x G90) x Karshinky	F <sub>9</sub> 243 / 2017	
34	[G83 x G80) x Dandara] x (G90 x Australian)	F <sub>10</sub> 262 / 2017	
35		F <sub>10</sub> 265 / 2017	
36	(G91 x G90) x G80	F <sub>10</sub> 269 / 2017	
37		F <sub>10</sub> 271 / 2017	
38		F <sub>10</sub> 276 / 2017	
39	G90 x C. B 58		Bulk <sub>1</sub> Families
40	[(G83 x G80) x G89] x Australian		Bulk <sub>2</sub> Families
41	[G83 x (G75 x 5844)] x G80		G95
42	(G83 x Dandara)		G90

**Table (2): Statistical technique used for selection elite genotypes in trail (A).**

Traditional analysis		Proposed analysis	
Randomized complete block design		One - WAY ANOVA	
Source of variation	df	Source of variation	df
Replications	r - 1	Among Families (cells) Origins Families within Origins Observations within Families	c - 1 t - 1 t (c - 1) c (n - 1)
Families	t - 1		
Experimental Error	(t - 1) (r - 1)		
<b>Total</b>	<b>t r - 1</b>	<b>Total</b>	<b>c n - 1</b>

**2.1.2. Proposed statistical analysis in the breeding program**

**2.1.2.1. Analysis yield and 50 bolls weight**

Two steps of one-way ANOVA with equal samples in cells were shown (Table 2). The objective of the first step was selecting families significantly surpassed within individually origins. The objective of the second step was selecting origins significantly surpassed control. Statistical analysis of the one-way ANOVA with equal samples in cells was straightforward according to Fowler *et al.*, (1998). The treatment means were compared by Tukey test as given by Steel and Torrie (1980). All comparisons were done at 0.05 significance level.

**2.1.2.2. Analysis lint percent and fiber properties**

Two steps of one-way ANOVA with unequal samples in cells to select origins significantly surpassed control. Statistical analysis of the one-way ANOVA with unequal samples in cells was straightforward according to Fowler *et al.* (1998). The treatment means were compared by Tukey test as given by Steel and Torrie (1980). All comparisons were done at 0.05 level of significance.

**3. RESULTS AND DISCUSSION**

**3.1. Traditional statistical analysis in breeding program**

The treatments used in the analysis of randomized complete block design were 38 families and four controls (Table 1). Analysis of randomized complete block design was performed where the degree of freedom for the treatments in the table of analysis of variance was 41 (Table 3).

controls in lint cotton yield. Mohamed *et al.* (2003) who evaluated 38 families from 16 new origins (*Gossypium barbadense* L.) in breeding program (Trail A) obtained similar results. The results showed that only two origins (G83 x G80) x G89 and (G85 x G83) exceeded three controls in yield.

**3.2. Proposed statistical analysis in a breeding program**

In a one-way classification, or one factor, experiment with *n* observations per cell, the total sum of squares is partitioned into two parts, one sum of squares for main effect, and a within cells sum of squares. Each sum of squares has an associated number of degrees of freedom. Sums of squares are as previously, divided by their associated degrees of freedom to obtain variance estimates, or mean squares, which are used to test the significance of main effects (Fowler *et al.*, 1998).

**3.2.1 Yield and 50 bolls weight**

Two steps of analysis of one-way ANOVA with equal samples in cells was carried out with the data of families and control (Table 5).

The aim of the first step of one-way ANOVA analysis was selecting families and genotypes significantly surpassed within individually origins and control, respectively. The aim of the second step of one-way ANOVA analysis was selecting origins significantly surpassed control.

**3.2.1.1. Selection of families within origins**

The results of the first step of one-way ANOVA analysis showed the differences between families within 11 out of 17 origins were non-significant with respect to seed and lint cotton yield (Table 6).

**Table (3): Mean squares according to the traditional analysis of RCBD.**

Source of variation	Six Replicates				One Replicate	
	df	SCY	LCY	50 BW	df	LP and Fiber properties
Replications	5	10.46**	16.31**	150.17*	--	--
Families	41	2.53**	4.09**	311.24**	--	--
Error	205	0.79	1.23	67.54	--	--
Total	251				--	

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

--: RCBD did not analyze seven traits due to one replicate only was used.

This method was able to analyze yield characteristics only, and it showed significant differences among the treatments for these traits (Table 4). The results showed that 17 families from 9 new origins (*Gossypium barbadense* L.) in breeding program (Trail A) exceeded all four

In contrast, the differences between genotypes within control group were significant with respect to the same two traits. G90 x CB58, [(G83 x G80) x G89] x Australian and G95 significantly surpassed G90 with respect to yield (Table 7).

**Table (4): Means in the traditional analysis in breeding program, Trial (A).**

F.	Six Replicates				One Replicate						
	SCY	LCY	S↓	50 BW	LP	FL	UR	M	Mic	C	YS
1	8.77	10.64	30	151	38.5	31.9	84.7	0.94	4.4	10.8	1880
2	8.63	10.52	34	153	38.7	31.4	84.2	0.94	4.4	11.5	1840
3	8.93	11.08	19	171	39.4	31.6	84.9	0.92	4.1	11.4	1800
4	9.12	11.45	9	139	39.9	31.7	84.3	0.92	4.2	11.9	1800
5	9.19	11.34	12	152	39.2	31.8	83.8	0.92	4.0	11.6	1800
6	8.98	12.02	4	153	42.5	32.2	83.7	0.92	4.3	12.7	1800
7	9.02	11.18	16	148	39.3	31.4	85.7	0.96	4.1	12.9	1760
8	8.82	10.88	22	146	39.2	31.1	84.3	0.95	4.3	11.8	1800
9	9.23	11.29	15	153	38.8	32.0	84.5	0.95	4.2	12.1	1840
10	8.77	10.66	29	151	38.6	31.1	83.6	0.92	4.2	11.6	1920
11	9.26	11.30	14	146	38.7	30.5	85.5	0.93	4.3	11.4	1840
12	8.97	10.75	25	164	38.1	30.9	83.6	0.92	4.4	12.5	1960
13	9.25	11.32	13	151	38.8	30.8	83.8	0.92	4.1	12.6	1720
14	9.44	11.86	5	144	39.9	30.2	84.2	0.93	4.0	11.2	1800
15	10.05	12.96	1	132	40.9	29.8	84.1	0.98	4.1	11.4	1880
16	8.42	10.62	31	161	40.0	30.7	84.3	0.92	4.2	12.3	1840
17	7.88	10.26	36	157	41.3	31.2	83.5	0.93	4.2	12.6	1840
18	7.40	9.41	41	156	40.4	31.0	83.5	0.94	4.2	12.0	1880
19	8.82	11.11	17	159	40.0	30.9	85.2	0.91	4.1	12.5	1960
20	8.44	10.75	26	158	40.4	30.7	85.2	0.90	3.9	12.6	1760
21	8.20	10.42	35	149	40.3	30.2	83.8	0.91	4.1	12.6	1760
22	9.21	11.66	8	159	40.2	31.2	85.8	0.91	3.9	11.9	1800
23	8.63	10.74	27	149	39.5	31.1	84.7	0.94	4.2	12.2	1880
24	8.82	11.05	20	149	39.7	31.3	84.3	0.94	4.2	11.8	2140
25	10.17	12.79	2	149	39.9	32.1	84.3	0.95	4.2	12.8	1940
26	9.30	11.69	7	153	39.9	31.9	84.3	0.94	4.2	10.4	1940
27	9.29	11.76	6	153	40.2	31.5	84.2	0.93	4.1	12.0	1900
28	9.69	12.38	3	153	40.6	31.2	84.5	0.93	4.2	11.4	1980
29	8.79	10.78	23	153	38.9	30.2	85.1	0.93	3.9	11.3	1860
30	8.68	10.73	28	154	39.3	32.0	84.8	0.94	4.2	12.0	2020
31	8.70	10.78	24	154	39.3	31.3	84.7	0.92	4.2	12.1	1980
32	9.24	11.44	10	151	39.3	31.0	84.6	0.93	4.1	11.1	2020
33	7.77	9.77	40	156	40.0	31.2	83.5	0.95	4.2	12.0	1920
34	8.39	10.17	38	150	38.5	29.5	83.8	0.95	4.2	13.2	1720
35	9.21	11.40	11	150	39.3	30.3	84.0	0.92	4.2	12.1	1840
36	8.38	10.23	37	168	38.8	30.4	84.9	0.94	4.2	11.1	1800
37	8.83	10.92	21	165	39.3	30.2	83.4	0.93	3.8	11.7	2040
38	8.73	10.54	33	154	38.4	30.2	84.1	0.95	4.3	12.2	1840
39	8.05	10.10	39	159	39.8	30.7	84.1	0.95	4.4	13.6	1800
40	8.16	10.61	32	165	41.3	30.7	86.2	0.96	4.2	12.4	1720
41	9.04	11.09	18	152	38.9	30.9	84.5	0.93	4.2	12.1	1680
42	6.64	8.48	42	158	40.6	30.1	83.4	0.89	3.9	11.7	1720
Mean	8.79	10.97		154	39.6	31.0	84.4	0.90	4.2	12.0	1858
LSD 5%	1.01	1.26		9							
LSD 1%	1.32	1.65		12							

**F:** Families.    **S:** Descending order.    **SCY:** Seed cotton yield.    **LCY:** Lint cotton yield.  
**BW:** Bolls weight.    **LP:** Lint percent.    **FL:** Fiber length.    **UR:** Uniformity ratio.  
**M:** Maturity.    **Mic:** Micronaire value.    **C:** Color.    **YS:** Yarn strength.

**Table (5) Layout of one-way ANOVA with equal samples in cells.**

Origin		Families / 2017 (cells)			
1	G91 x C. B 58	F <sub>5</sub> 101	F <sub>5</sub> 104	F <sub>5</sub> 105	
2	[G83 x (G75 x 5844)] x C. B 58	F <sub>5</sub> 107	F <sub>5</sub> 108		
3	[G83 x (G72 x Dandara)] x Pima S-62 (24202)	F <sub>5</sub> 111	F <sub>5</sub> 114	F <sub>5</sub> 116	F <sub>5</sub> 124
4	(G91 x G90) x Pima S-62 (24202)	F <sub>5</sub> 127	F <sub>5</sub> 134	F <sub>5</sub> 135	
5	(G91 x G90) x C. B 58	F <sub>6</sub> 138	F <sub>6</sub> 142	F <sub>6</sub> 146	
6	(G85 x G83) x [G83 x (G75 x 5844)]	F <sub>6</sub> 155	F <sub>6</sub> 158	F <sub>6</sub> 163	
7	(G90 x Australian) x G85	F <sub>7</sub> 165	F <sub>7</sub> 168	F <sub>7</sub> 171	
8	(G90 x Australian) x [(G83 x G72) x Dandara]	F <sub>7</sub> 181	F <sub>7</sub> 183		
9	[(G83 x G80) x G89] x [G83 x (G75 x 5844)]	F <sub>7</sub> 192			
10	(G91 x G90) x G85	F <sub>8</sub> 200	F <sub>8</sub> 201	F <sub>8</sub> 202	F <sub>8</sub> 205
11	(G91 x G90) x [G83 x (G75 x 5844)]	F <sub>8</sub> 210			
12	(G91 x G90) x (G85 x G83)	F <sub>8</sub> 213			
13	(G91 x G90) x [(G83 x G80) x G89]	F <sub>8</sub> 234			
14	(G90 x Australian) x [G83 x (G75 x 5844)]	F <sub>9</sub> 236			
15	(G91 x G90) x Karshinky	F <sub>9</sub> 243			
16	[G83 x G80] x Dandara] x (G90 x Australian)	F <sub>10</sub> 262	F <sub>10</sub> 265		
17	(G91 x G90) x G80	F <sub>10</sub> 269	F <sub>10</sub> 271	F <sub>10</sub> 276	
18	Control	Bulk <sub>1</sub>	Bulk <sub>2</sub>	G95	G90

At the end of the yield analysis, selecting all families within 11 origins with respect to seed and lint cotton yield since they showed non - significant differences among them. Also, adding six families within the other six origins. Excluding G90 from control group and keeping the remaining three genotypes within control group with respect to the same two traits, G90 had the lowest values of yield data significantly decreased than the other genotypes within control group (Table 7).

On the other hand, the differences among families within four origins viz, G9 1 x C. B 58, [G83 x (G75 x 5844)] x C. B 58, (G91 x G90) x Pima S-62 (24202) and (G91 x G90) x C. B 58 were significant with respect to 50 bolls weight. In contrast, the differences between families within the other seven origins and genotypes within control group were non - significant with respect to the same trait (Table 7).

At the end of 50 bolls weight analysis, excluding families F<sub>5</sub> 101 and F<sub>5</sub> 104 from G91 x C. B 58, F<sub>5</sub> 107 from [G83 x (G75 x 5844)] x C. B 58, F<sub>5</sub> 127 and F<sub>5</sub> 134 from (G91 x G90) x Pima S-62 (24202) and F<sub>5</sub> 146 from (G91 x G90) x C. B 58. These families had the lowest values significantly decreased within these origins (Table 7). Finally, selecting all remaining families within 17 origins and four genotypes within control group.

**3.2.1.2. Selecting origins significantly surpassed control**

The results of the second step of one-way

ANOVA analysis revealed that the differences due to origins were significant with respect to the three traits (Table 6). At the end of yield data analysis, selecting the best two origins viz., (G91 x G90) x C. B 58 and (G91 x G90) x G85 since they significantly surpassed control group with respect to seed and lint cotton yield. These results exhibited that the parent (G91 x G90) was very important to produce higher cotton yield (seed and lint) (Table 7).

Both origins [G83 x (G75 x 5844)] x C. B 58 and (G90 x Australian) x [G83 x (G75 x 5844)] were selected because they significantly exceeded control for seed cotton yield. These results revealed that the parent [G83 x (G75 x 5844)] was very important to produce higher seed cotton yield (Table 7). At the end of 50 bolls weight analysis in the second step, the origin G91 x C. B 58 was selected since it significantly surpassed control for 50 bolls weight (Table 7).

**3.2.2 Lint percent and fiber properties**

Two steps of analysis of one-way ANOVA with unequal samples in cells was carried out with the data of lint percent and fiber properties (Table 5). The objective of the first step of one-way ANOVA analysis was selecting the origins that significantly surpassed control for lint percent and fiber properties. The objective of the second step was selecting the origins that significantly surpassed control group for lint percent and fiber properties after excluding G90 from control.

**Table (6): Mean squares according to the items of the proposed analysis.**

First step of analysis One-Way ANOVA					
Source of variation		df	SCY	LCY	50 BW
			MS	MS	MS
<b>Among Families</b>		<b>41</b>	2.53**	4.09**	311.24**
	<b>Origins</b>	17	4.18**	6.46**	374.97
	<b>Families within Origins</b>	24	1.36	2.41	266.03
1	G91 x C. B 58	2	0.14	0.52	730.17**
2	[G83 x (G75 x 5844)] x C. B 58	1	0.01	0.04	481.34*
3	[G83 x (G72 x Dandara)] x Pima S-62 (24202)	3	0.17	1.41	83.17
4	(G91 x G90) x Pima S-62 (24202)	2	0.36	0.73	511.73**
5	(G91 x G90) x C. B 58	2	1.03	4.18	545.39**
6	(G85 x G83) x [G83 x (G75 x 5844)]	2	1.58	2.33	48.50
7	(G90 x Australian) x G85	2	0.59	0.72	154.17
8	(G90 x Australian) x [(G83 x G72) x Dandara]	1	1.01	2.55	341.32
9	[(G83 x G80) x G89] x [G83 x (G75 x 5844)]				
10	(G91 x G90) x G85	3	1.03	1.64	33.59
11	(G91 x G90) x [G83 x (G75 x 5844)]				
12	(G91 x G90) x (G85 x G83)				
13	(G91 x G90) x [(G83 x G80) x G89]				
14	(G90 x Australian) x [G83 x (G75 x 5844)]				
15	(G91 x G90) x Karshinky				
16	[G83 x G80] x Dandara] x (G90 x Australian)	1	2.01	4.56	0.08
17	(G91 x G90) x G80	2	0.34	0.72	331.56
18	Control	3	5.94**	7.72**	189.56
<b>Observations within Families</b>		<b>210</b>	1.02	1.59	69.50
1	G91 x C. B 58	15	0.65	0.97	114.28
2	[G83 x (G75 x 5844)] x C. B 58	10	0.31	0.48	92.93
3	[G83 x (G72 x Dandara)] x Pima S-62 (24202)	20	0.96	1.55	66.65
4	(G91 x G90) x Pima S-62 (24202)	15	0.95	1.40	70.91
5	(G91 x G90) x C. B 58	15	0.78	1.22	103.44
6	(G85 x G83) x [G83 x (G75 x 5844)]	15	0.67	1.09	50.23
7	(G90 x Australian) x G85	15	1.08	1.74	88.24
8	(G90 x Australian) x [(G83 x G72) x Dandara]	10	2.28	3.62	87.23
9	[(G83 x G80) x G89] x [G83 x (G75 x 5844)]	5	0.69	1.09	8.67
10	(G91 x G90) x G85	20	1.13	1.81	15.36
11	(G91 x G90) x [G83 x (G75 x 5844)]	5	1.23	1.85	8.97
12	(G91 x G90) x (G85 x G83)	5	0.68	1.04	16.97
13	(G91 x G90) x [(G83 x G80) x G89]	5	0.55	0.86	11.50
14	(G90 x Australian) x [G83 x (G75 x 5844)]	5	1.84	2.84	5.77
15	(G91 x G90) x Karshinky	5	1.68	2.66	65.37
16	[G83 x G80] x Dandara] x (G90 x Australian)	10	1.70	2.55	49.22
17	(G91 x G90) x G80	15	1.18	1.76	118.71
18	Control	20	0.83	1.33	94.47
<b>Total</b>		<b>251</b>			

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

**SCY:** Seed cotton yield. **LCY:** Lint cotton yield. **BW:** Bolls weight.

**Table (6): Cont.**

Second step of analysis One-Way ANOVA						
Source of variation		df	SCY	LCY	50 BW	
			MS	MS	df	MS
<b>Among Families</b>		<b>40</b>	1.88**	3.24**	<b>35</b>	228.27**
	<b>Origins</b>	17	3.34**	5.40**	17	324.68*
	<b>Families within Origins</b>	23	0.79	1.64	18	137.16
1	G91 x C. B 58	2	0.14	0.52		
2	[G83 x (G75 x 5844)] x C. B 58	1	0.01	0.04		
3	[G83 x (G72 x Dandara)] x Pima S-62 (24202)	3	0.17	1.41	3	83.17
4	(G91 x G90) x Pima S-62 (24202)	2	0.36	0.73		
5	(G91 x G90) x C. B 58	2	1.03	4.18	1	140.09
6	(G85 x G83) x [G83 x (G75 x 5844)]	2	1.58	2.33	2	48.50
7	(G90 x Australian) x G85	2	0.59	0.72	2	154.17
8	(G90 x Australian) x [(G83 x G72) x Dandara]	1	1.01	2.55	1	341.32
9	[(G83 x G80) x G89] x [G83 x (G75 x 5844)]					
10	(G91 x G90) x G85	3	1.03	1.64	3	33.59
11	(G91 x G90) x [G83 x (G75 x 5844)]					
12	(G91 x G90) x (G85 x G83)					
13	(G91 x G90) x [(G83 x G80) x G89]					
14	(G90 x Australian) x [G83 x (G75 x 5844)]					
15	(G91 x G90) x Karshinky					
16	[G83 x G80) x Dandara] x (G90 x Australian)	1	2.01	4.56	1	0.08
17	(G91 x G90) x G80	2	0.34	0.72	2	331.56
18	Control	2	1.78	1.45	3	189.56
<b>Observations within Families</b>		<b>205</b>	1.00	1.56	<b>180</b>	66.92
1	G91 x C. B 58	15	0.65	0.97	5	81.77
2	[G83 x (G75 x 5844)] x C. B 58	10	0.31	0.48	5	31.60
3	[G83 x (G72 x Dandara)] x Pima S-62 (24202)	20	0.96	1.55	20	66.65
4	(G91 x G90) x Pima S-62 (24202)	15	0.95	1.40	5	186.97
5	(G91 x G90) x C. B 58	15	0.78	1.22	10	120.68
6	(G85 x G83) x [G83 x (G75 x 5844)]	15	0.67	1.09	15	50.23
7	(G90 x Australian) x G85	15	1.08	1.74	15	88.24
8	(G90 x Australian) x [(G83 x G72) x Dandara]	10	2.28	3.62	10	87.23
9	[(G83 x G80) x G89] x [G83 x (G75 x 5844)]	5	0.69	1.09	5	8.67
10	(G91 x G90) x G85	20	1.13	1.81	20	15.36
11	(G91 x G90) x [G83 x (G75 x 5844)]	5	1.23	1.85	5	8.97
12	(G91 x G90) x (G85 x G83)	5	0.68	1.04	5	16.97
13	(G91 x G90) x [(G83 x G80) x G89]	5	0.55	0.86	5	11.50
14	(G90 x Australian) x [G83 x (G75 x 5844)]	5	1.84	2.84	5	5.77
15	(G91 x G90) x Karshinky	5	1.68	2.66	5	65.37
16	[G83 x G80) x Dandara] x (G90 x Australian)	10	1.70	2.55	10	49.22
17	(G91 x G90) x G80	15	1.18	1.76	15	118.71
18	Control	15	0.49	0.76	20	94.47
<b>Total</b>		<b>245</b>			<b>215</b>	

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

**SCY:** Seed cotton yield. **LCY:** Lint cotton yield. **BW:** Bolls weight.



**Table (7): Means of traits for proposed analysis in breeding program, Trial (A).**

Seed cotton yield (First step)						
Origin		Families				Tukey
1	8.78	8.77 ✓	8.63 ✓	8.93 ✓		ns
2	9.16	9.12 ✓	9.19 ✓			ns
3	9.01	8.98 ✓	9.02 ✓	8.82 ✓	9.23 ✓	ns
4	9.00	8.77 ✓	9.26 ✓	8.97 ✓		ns
5	9.58	9.25 ✓	9.44 ✓	10.05 ✓		ns
6	7.90	8.42 ✓	7.88 ✓	7.40 ✓		ns
7	8.49	8.82 ✓	8.44 ✓	8.20 ✓		ns
8	8.92	9.21 ✓	8.63 ✓			ns
9	8.82	8.82 ✓				
10	9.61	10.17 ✓	9.30 ✓	9.29 ✓	9.69 ✓	ns
11	8.79	8.79 ✓				
12	8.68	8.68 ✓				
13	8.70	8.70 ✓				
14	9.24	9.24 ✓				
15	7.77	7.77 ✓				
16	8.80	8.39 ✓	9.21 ✓			ns
17	8.65	8.38 ✓	8.83 ✓	8.73 ✓		ns
Control	7.97	8.05 ✓	8.16 ✓	9.04 ✓	6.64	1.47
Tukey	0.83					
Second step (Excluding G90 from control group)						
Origin		Families				Tukey
1	8.78	8.77	8.63	8.93		ns
2	9.16 ✓✓	9.12 ✓	9.19 ✓			ns
3	9.01	8.98	9.02	8.82	9.23	ns
4	9.00	8.77	9.26	8.97		ns
5	9.58 ✓✓	9.25 ✓	9.44 ✓	10.05 ✓		ns
6	7.90	8.42	7.88	7.40		ns
7	8.49	8.82	8.44	8.20		ns
8	8.92	9.21	8.63			ns
9	8.82	8.82				
10	9.61 ✓✓	10.17 ✓	9.30 ✓	9.29 ✓	9.69 ✓	ns
11	8.79	8.79				
12	8.68	8.68				
13	8.70	8.70				
14	9.24 ✓✓	9.24 ✓				
15	7.77	7.77				
16	8.80	8.39	9.21			ns
17	8.65	8.38	8.83	8.73		ns
Control	8.42	8.05	8.16	9.04	----	ns
Tukey	0.65					

✓ : Selection of families.

✓✓ : Selection of origin.

----: Exclude genotypes from control group.

ns: Not significant at 0.05 level.

**Table (7): Cont. (I):**

<b>Lint cotton yield (First step)</b>						
<b>Origin</b>		<b>Families</b>				<b>Tukey</b>
<b>1</b>	10.75	10.64 ✓	10.52 ✓	11.08 ✓		ns
<b>2</b>	11.40	11.45 ✓	11.34 ✓			ns
<b>3</b>	11.34	12.02 ✓	11.18 ✓	10.88 ✓	11.29 ✓	ns
<b>4</b>	10.90	10.66 ✓	11.30 ✓	10.75 ✓		ns
<b>5</b>	12.05	11.32 ✓	11.86 ✓	12.96 ✓		ns
<b>6</b>	10.10	10.62 ✓	10.26 ✓	9.41 ✓		ns
<b>7</b>	10.76	11.11 ✓	10.75 ✓	10.42 ✓		ns
<b>8</b>	11.20	11.66 ✓	10.74 ✓			ns
<b>9</b>	11.05	11.05 ✓				
<b>10</b>	12.16	12.79 ✓	11.69 ✓	11.76 ✓	12.38 ✓	ns
<b>11</b>	10.78	10.78 ✓				
<b>12</b>	10.73	10.73 ✓				
<b>13</b>	10.78	10.78 ✓				
<b>14</b>	11.44	11.44 ✓				
<b>15</b>	9.77	9.77 ✓				
<b>16</b>	10.79	10.17 ✓	11.40 ✓			ns
<b>17</b>	10.56	10.23 ✓	10.92 ✓	10.54 ✓		ns
<b>Control</b>	10.07	10.10 ✓	10.61 ✓	11.09 ✓	8.48	1.87
<b>Tukey</b>	1.10					
<b>Second step (Excluding G90 from control group)</b>						
<b>Origin</b>		<b>Families</b>				<b>Tukey</b>
<b>1</b>	10.75	10.64	10.52	11.08		ns
<b>2</b>	11.40	11.45	11.34			ns
<b>3</b>	11.34	12.02	11.18	10.88	11.29	ns
<b>4</b>	10.90	10.66	11.30	10.75		ns
<b>5</b>	12.05 ✓✓	11.32 ✓	11.86 ✓	12.96 ✓		ns
<b>6</b>	10.10	10.62	10.26	9.41		ns
<b>7</b>	10.76	11.11	10.75	10.42		ns
<b>8</b>	11.20	11.66	10.74			ns
<b>9</b>	11.05	11.05				
<b>10</b>	12.16 ✓✓	12.79 ✓	11.69 ✓	11.76 ✓	12.38 ✓	ns
<b>11</b>	10.78	10.78				
<b>12</b>	10.73	10.73				
<b>13</b>	10.78	10.78				
<b>14</b>	11.44	11.44				
<b>15</b>	9.77	9.77				
<b>16</b>	10.79	10.17	11.40			ns
<b>17</b>	10.56	10.23	10.92	10.54		ns
<b>Control</b>	10.60	10.10	10.61	11.09	----	ns
<b>Tukey</b>	0.93					

✓ : Selection of families.

----: Exclude genotypes from control group.

✓✓ : Selection of origin.

ns: Not significant at 0.05 level.

**Table (7): Cont.(II)**

<b>50 Bolls weight (First step)</b>						
<b>Origin</b>		<b>Families</b>				<b>Tukey</b>
<b>1</b>	158	151	153	171 ✓		16
<b>2</b>	146	139	152 ✓			12
<b>3</b>	150	153 ✓	148 ✓	148 ✓	153 ✓	ns
<b>4</b>	154	151	146	164 ✓		13
<b>5</b>	142	151 ✓	144 ✓	132		15
<b>6</b>	158	161 ✓	157 ✓	156 ✓		ns
<b>7</b>	155	159 ✓	158 ✓	149 ✓		ns
<b>8</b>	154	159 ✓	149 ✓			ns
<b>9</b>	149	149 ✓				
<b>10</b>	152	149 ✓	153 ✓	153 ✓	153 ✓	ns
<b>11</b>	153	153 ✓				
<b>12</b>	154	154 ✓				
<b>13</b>	154	154 ✓				
<b>14</b>	151	151 ✓				
<b>15</b>	156	156 ✓				
<b>16</b>	150	150 ✓	150 ✓			ns
<b>17</b>	162	168 ✓	165 ✓	154 ✓		ns
<b>Control</b>	158	159 ✓	165 ✓	152 ✓	158 ✓	ns
<b>Tukey</b>	ns					
<b>Second step (Excluding Families from origins)</b>						
<b>Origin</b>		<b>Families</b>				<b>Tukey</b>
<b>1</b>	171 ✓✓	----	----	171 ✓		
<b>2</b>	152	----	152			
<b>3</b>	150	153	148	148	153	ns
<b>4</b>	164	----	----	164		
<b>5</b>	148	151	144	----		ns
<b>6</b>	158	161	157	156		ns
<b>7</b>	155	159	158	149		ns
<b>8</b>	154	159	149			ns
<b>9</b>	149	149				
<b>10</b>	152	149	153	153	153	ns
<b>11</b>	153	153				
<b>12</b>	154	154				
<b>13</b>	154	154				
<b>14</b>	151	151				
<b>15</b>	156	156				
<b>16</b>	150	150	150			ns
<b>17</b>	162	168	165	154		ns
<b>Control</b>	158	159	165	152	158	ns
<b>Tukey</b>	9					

✓ : Selection of families.

✓✓ : Selection of origin.

----: Exclude families from origins.

ns: Not significant at 0.05 level.

**3.2.1.3. Selection of origins significantly surpassed control**

The analysis of variance of the first step showed the differences due to origins were significant with respect to two traits, viz., and fiber length and yarn strength (Table 8). The best five origins viz., [(G83 x G80) x G89] x [G83 x (G75 x 5844)], (G91 x G90) x G85, (G91 x G90) x (G85 x G83), (G91 x G90) x [(G83 x G80) x G89] and (G91 x G90) x Karshinky were selected since, they significantly surpassed control for fiber length and yarn strength (Table 9).

The three origins viz., G91 x C. B 58, [G83 x (G75 x 5844)] x C. B 58 and [G83 x (G72 x Dandara)] x Pima S-62 (24202) were selected because they significantly surpassed control group for fiber length (Table 9).

The seven origins viz., (G91 x G90) x Pima S-62 (24202), [(G83 x G80) x G89] x [G83 x (G75 x 5844)], (G91 x G90) x [G83 x (G75 x 5844)], (G91 x G90) x [(G83 x G80) x G89], (G90 x Australian) x [G83 x (G75 x 5844)], (G91 x G90) x Karshinky and (G91 x G90) x G80 were selected. They are significantly surpassed control

**Table (8): Mean squares for lint percent and fiber properties in proposed analysis, Trial (A).**

First step								
Source of variation	df	LP	Fiber properties					
			FL	UR	M	Mic	C	YS
Among Origins	17	0.962	0.866**	0.373	0.084	0.029	0.459	17711**
Within Origins	24	0.725	0.133	0.532	0.051	0.020	0.395	4527
<b>Total</b>	<b>41</b>							
Second step (Excluding G90 from control group)								
Source of variation	df	LP	FL	UR	M	Mic	C	YS
Among Origins	17	0.921	0.837**	0.418	0.069	0.022	0.498	16579**
Within Origins	23	0.745	0.125	0.478	0.045	0.017	0.379	4719
<b>Total</b>	<b>40</b>							

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

LP: Lint percent.

FL: Fiber length.

UR: Uniformity ratio.

M: Maturity.

Mic: Micronaire value.

C: Color.

YS: Yarn strength.

The four origins viz., G91 x C. B 58, [G83 x (G75 x 5844)] x C. B 58, [G83 x (G72 x Dandara)] x Pima S-62 (24202) and (G90 x Australian) x [(G83 x G72) x Dandara] were selected because they significantly exceeded control group for fiber length (Table 9).

The five origins viz., (G91 x G90) x Pima S-62 (24202), (G85 x G83) x [G83 x (G75 x 5844)], (G91 x G90) x [G83 x (G75 x 5844)], (G90 x Australian) x [G83 x (G75 x 5844)] and (G91 x G90) x G80 were selected because they significantly surpassed control group for yarn strength (Table 9).

**3.2.1.4. Selection of origins significantly surpassed control after excluding G90**

The results of the second step of the analysis revealed that the differences due to origins were significant with respect to the same two traits, viz., and fiber length and yarn strength (Table 8). The best two origins viz., (G91 x G90) x G85 and (G91 x G90) x (G85 x G83) were selected since, they significantly exceeded control group for fiber length and yarn strength (Table 9)

group with respect to yarn strength (Table 9).

**3.3 The final recommended selection of origins in trail (A)**

The results in Table (10) showed that the origins significantly surpassed control group with respect to yield and fiber properties after excluding G90 from control. These origins could be divided into three groups.

The first group included three origins that significantly surpassed control with respect to yield and fiber properties. The first origin (G91 x G90) x G85 exceeded control for seed, lint cotton yield, fiber length and yarn strength. The second origin [G83 x (G75 x 5844)] x C. B 58 significantly surpassed control with respect to seed cotton yield and fiber length. The third origin (G90 x Australian) x [G83 x (G75 x 5844)] exceeded control for seed cotton yield and yarn strength.

The second group contained one origin, i.e., (G91 x G90) x C. B 58 that significantly surpassed control with respect to cotton yield (seed and lint).

**Table (9): Means of lint percent and fiber for proposed analysis, Trial (A).**

First step							
Origin	LP	Fiber properties					
		FL	UR	M	Mic	C	YS
1	38.9	31.6√	84.6	0.93	4.3	11.2	1840
2	39.6	31.7√	84.1	0.92	4.1	11.8	1800
3	40.0	31.7√	84.6	0.94	4.2	12.4	1800
4	38.5	30.8	84.2	0.92	4.3	11.8	1907√
5	39.9	30.3	84.0	0.94	4.1	11.7	1800
6	40.6	31.0	83.8	0.93	4.2	12.3	1853√
7	40.2	30.6	84.7	0.91	4.0	12.6	1827
8	39.9	31.2√	85.3	0.93	4.1	12.1	1840
9	39.7	31.3√	84.3	0.94	4.2	11.8	2140√
10	40.2	31.7√	84.3	0.94	4.2	11.6	1940√
11	38.9	30.2	85.1	0.93	3.9	11.3	1860√
12	39.3	32.0√	84.8	0.94	4.2	12.0	2020√
13	39.3	31.3√	84.7	0.92	4.2	12.1	1980√
14	39.3	31.0	84.6	0.93	4.1	11.1	2020√
15	40.0	31.2√	83.5	0.95	4.2	12.0	1920√
16	38.9	29.9	83.9	0.93	4.2	12.7	1780
17	38.8	30.3	84.1	0.94	4.1	11.7	1893√
Control	40.2	30.6	84.6	0.93	4.2	12.5	1730
Tukey	ns	0.6	ns	ns	ns	ns	117
Second step (Excluding G90 from control group)							
Origin	LP	FL	UR	M	Mic	C	YS
1	38.9	31.6√	84.6	0.93	4.3	11.2	1840
2	39.6	31.7√	84.1	0.92	4.1	11.8	1800
3	40.0	31.7√	84.6	0.94	4.2	12.4	1800
4	38.5	30.8	84.2	0.92	4.3	11.8	1907√
5	39.9	30.3	84.0	0.94	4.1	11.7	1800
6	40.6	31.0	83.8	0.93	4.2	12.3	1853
7	40.2	30.6	84.7	0.91	4.0	12.6	1827
8	39.9	31.2	85.3	0.93	4.1	12.1	1840
9	39.7	31.3	84.3	0.94	4.2	11.8	2140√
10	40.2	31.7√	84.3	0.94	4.2	11.6	1940√
11	38.9	30.2	85.1	0.93	3.9	11.3	1860√
12	39.3	32.0√	84.8	0.94	4.2	12.0	2020√
13	39.3	31.3	84.7	0.92	4.2	12.1	1980√
14	39.3	31.0	84.6	0.93	4.1	11.1	2020√
15	40.0	31.2	83.5	0.95	4.2	12.0	1920√
16	38.9	29.9	83.9	0.93	4.2	12.7	1780
17	38.8	30.3	84.1	0.94	4.1	11.7	1893√
Control	40.0	30.8	84.9	0.95	4.3	12.7	1733
Tukey	ns	0.6	ns	ns	ns	ns	122

√: Origin significantly surpassed control. ns: Not significant at 0.05 level.  
**LP:** Lint percent. **FL:** Fiber length. **UR:** Uniformity ratio.  
**M:** Maturity. **Mic:** Micronaire value. **C:** Color. **YS:** Yarn strength.

The third group consisted of nine origins that significantly surpassed control with respect to fiber properties. (G91 x G90) x (G85 x G83) was exceeded control for fiber length and yarn strength. Two of them, namely G91 x C. B 58 and [G83 x (G72 x Dandara)] x Pima S-62 (24202) were exceeded control for fiber length.

The other six origins, namely (G91 x G90) x Pima S-62 (24202), [(G83 x G80) x G89] x [G83 x (G75 x 5844)], (G91 x G90) x [G83 x (G75 x 5844)], (G91 x G90) x [(G83 x G80) x G89],

(G85 x G83) exceeded three controls in both yield and fiber quality.

**3.4. Recommended remark**

Trail (A) should be cultivated at least in two locations in Middle and Upper Egypt. The first one in Bani Sowif Governorate (Sids Research Station) and the other one in Sohag Governorate. This gives a chance to select origins under the effect of the interaction conditions. In addition, it allows deciding on the suitable origins for each zone.

**Table (10): Final selection of elite genotypes in breeding program, Trial (A).**

Origin	Yield				Fiber properties					
	SCY	LCY	50 BW	LP	FL	UR	M	Mic	C	YS
1	8.78	10.75	171 ✓	38.9	31.6 ✓	84.6	0.93	4.3	11.2	1840
2	9.16 ✓	11.40	152	39.6	31.7 ✓	84.1	0.92	4.1	11.8	1800
3	9.01	11.34	150	40.0	31.7 ✓	84.6	0.94	4.2	12.4	1800
4	9.00	10.90	164	38.5	30.8	84.2	0.92	4.3	11.8	1907 ✓
5	9.58 ✓	12.05 ✓	148	39.9	30.3	84.0	0.94	4.1	11.7	1800
6	7.90	10.10	158	40.6	31.0	83.8	0.93	4.2	12.3	1853
7	8.49	10.76	155	40.2	30.6	84.7	0.91	4.0	12.6	1827
8	8.92	11.20	154	39.9	31.2	85.3	0.93	4.1	12.1	1840
9	8.82	11.05	149	39.7	31.3	84.3	0.94	4.2	11.8	2140 ✓
10	9.61 ✓	12.16 ✓	152	40.2	31.7 ✓	84.3	0.94	4.2	11.6	1940 ✓
11	8.79	10.78	153	38.9	30.2	85.1	0.93	3.9	11.3	1860 ✓
12	8.68	10.73	154	39.3	32.0 ✓	84.8	0.94	4.2	12.0	2020 ✓
13	8.70	10.78	154	39.3	31.3	84.7	0.92	4.2	12.1	1980 ✓
14	9.24 ✓	11.44	151	39.3	31.0	84.6	0.93	4.1	11.1	2020 ✓
15	7.77	9.77	156	40.0	31.2	83.5	0.95	4.2	12.0	1920 ✓
16	8.80	10.79	150	38.9	29.9	83.9	0.93	4.2	12.7	1780
17	8.65	10.56	162	38.8	30.3	84.1	0.94	4.1	11.7	1893 ✓
<b>Control</b>	8.42	10.60	158	40.0	30.8	84.9	0.95	4.3	12.7	1733
<b>Tukey</b>	0.65	0.93	9	ns	0.6	ns	ns	ns	ns	122

✓: Origin significantly surpassed control. **SCY:** Seed cotton yield. **LCY:** Lint cotton yield.  
**BW:** Bolls weight. **LP:** Lint percent. **FL:** Fiber length. **UR:** Uniformity ratio.  
**M:** Maturity. **Mic:** Micronaire value. **C:** Color. **YS:** Yarn strength.

(G91 x G90) x Karshinky and (G91 x G90) x G80 significantly surpassed control with respect to yarn strength. The promising families that were selected from trail (A) will be grown with control in trail (B) in the next season. Similar results were obtained by Mohamed *et al.* (2003) who evaluated 16 new origins (*Gossypium barbadense* L.) and five genotypes representing the control in breeding program (Trail A). The results showed that only two origins (G83 x G80) x G89 and

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## انتخاب التراكيب الوراثية المباشرة من القطن المصري اعتمادا على تحليل التباين أحادي الاتجاه

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### ملخص

أجريت الدراسة بهدف اقتراح طريقة لانتخاب التراكيب الوراثية المباشرة من القطن المصري المستعملة في (تجربة أ) ضمن البرنامج البحثي لقسم التربية بمعهد بحوث القطن وذلك باستعمال تحليل التباين في اتجاه واحد بدلا من طريقة تحليل القطاعات الكاملة العشوائية المستخدمة حاليا. تم زراعة 38 عائلة من أصل 17 تركيب وراثي جديد، بالإضافة إلى 4 تراكيب وراثية تمثل الكونتروول وهي (ج90 × س. س. ب 58)، [(ج83 × ج80) × ج89] × أسترالي، جيزة 95، جيزة 90 في تصميم القطاعات الكاملة العشوائية في 6 مكررات (بمحطة بحوث سدس) محافظة بنى سويف في موسم 2018. درست الصفات المحصولية وهي (المحصول الزهر، المحصول الشعير، وزن 50 لوزة) باستخدام بيانات 6 مكررات وكذلك دراسة الصفات التكنولوجية وهي (طول الليفة، الانتظام، النضج، قراءة الميكرو نير، اللون، متانة الشلة) بالإضافة إلى معدل الحليج باستعمال بيانات مكرر واحد فقط. تم إجراء تحليل القطاعات الكاملة العشوائية حيث كانت درجة الحرية للمعاملات بجدول تحليل التباين هي 41. وقد استطاعت هذه الطريقة من تحليل الصفات المحصولية فقط، كما أظهرت وجود فروق معنوية بين المعاملات لهذه الصفات. أجري تحليل التباين في اتجاه واحد حيث كانت درجة الحرية للمعاملات بجدول تحليل التباين هي 17 (الأصل الوراثي 17 معاملة واعتبار تراكيب الكونتروول معاملة واحدة). أيضا استطاعت هذه الطريقة تحليل جميع الصفات المحصولية والتكنولوجية. وأظهرت النتائج وجود فروق معنوية بين المعاملات للصفات المحصولية بالإضافة إلى طول الليفة، متانة الشلة من الصفات التكنولوجية. وأوضحت النتائج أن طريقة تحليل التباين في اتجاه واحد تفوقت على طريقة التحليل باستعمال القطاعات الكاملة العشوائية حيث أمكن تحليل جميع الصفات المدروسة وتحديد الأصول الوراثية المتفوقة معنويا على الكونتروول في الصفات المحصولية والتكنولوجية. هذا بالإضافة إلى تحديد الأصول الوراثية التي تتفوق معنويا على الكونتروول في الصفات المحصولية والأخرى التي تتفوق معنويا على الكونتروول في الصفات التكنولوجية كل على حده. ويستفاد من هذه الدراسة بإدخال تطوير برنامج قسم تربية القطن (تجربة أ) باستعمال الأسس الإحصائية في طريقة انتخاب التراكيب الوراثية المتفوقة معنويا على الكونتروول لزيادة دقة انتخاب التراكيب التي سوف يتم إدخالها بعد ذلك في برنامج تجربة (ب) لتقييمها في محافظات الوجه القبلي.

المجلة العلمية لكلية الزراعة- جامعة القاهرة، المجلد (72) العدد الرابع (أكتوبر 2021): 107-121.