

GENETIC EVALUATION OF SOME EXTRA LONG STAPLE COTTON STRAINS (*Gossypium barbadense* L.) UNDER DIFFERENT ENVIRONMENTS

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Abstract

This study aimed to clear the interaction between the genotypes and environment on the performance of genotypes. Also to identify the relationship among the current studied traits and the range of similarity between the genotypes. Thirty-five new cotton strains descending from fourteen Egyptian cotton crosses as well as five check varieties were included in Trial (A) were sown 2011 at Kafr El-Sheikh. According to the data of yield components and fiber traits, twenty strains were selected for sowing in the next season at three locations in trial (B) at 2012 season. With respect to multivariate analysis data four strains, numbered 12, 17, 19 and 20 which were derived from [(G. 70 x Pima S6) x G. 89 x G. 86], (Pima S7 x G. 92), (G. 67 x Pima S6) x G.92, G.88 x (G.86 x G. 45) genotypes. These genotypes proved to be good substitutes to the genotypes G.87, promising cross {[G.84 x (G.70 x G.51B)] x S62}, G.88 and G.93 respectively. Estimation of variance component indicated that genetic components were more important than the components of genetic interaction. Heritability of yield components was relatively high (over 50%). The genetic variability was low. Stepwise analysis indicated that boll weight and earliness were the main characters responsible for yield performance. Also the data indicated that the traits fiber length (Upper Half Mean) and fiber strength were the main components for yarn strength.

INTRODUCTION

Hybridization among cotton genotypes, followed by conventional pedigree selection is a predominant method utilized for cotton breeding. In such pedigree system the best F_2 plants and the best plants within the best lines in the following segregating generations are visually selected. Many investigators stated that visual selection in early segregating generations for yield is inefficient and that the evaluation of some strains in such programs begins from F_5 generation and continues, until satisfactory genetic stability is achieved. Many investigators (Mohamed 1991, Mohamed *et al* 2003 and El_Adly and Eissa 2010) evaluated some strains via two tests, the first test is known as Trial (A), and the second test is the advanced trial, known as Trial (B) in the next season. It should be noted that Trial (B) is usually carried out at several locations so as to study the interaction of these genotypes under different environments. This investigation was carried out to evaluate thirty-five

strains of fourteen crosses tested in Trial A and twelve crosses tested in Trial B at three locations in order to select the best lines for developing new cotton varieties of high lint yield and high fiber traits.

MATERIALS AND METHODS

In 2011 and 2012 seasons two field experiments were carried out at the Cotton Research Institute, Agricultural Research Center, Egypt in Trial A and the advanced Trial B. Trial A consisted of forty genotypes, thirty-five lines descending from fourteen crosses, one promising cross {[G.84 x (G.70 x G.51B)] x S62} and four commercial varieties: Giza 93, Giza 92, Giza 87 and Giza 88, as checks (Table 1). Trial A was cultivated at Sakha Experiment Station, Agricultural Research Center, Kafr El-Sheikh, Egypt. While, trial B was cultivated at four locations in Lower Egypt i.e. Kafr El-Sheikh, El-Dakahlia and Demiat, in private farms, except Sakha. Each trial consisted of twenty lines descending from twelve crosses and the one promising cross {[G.84 x (G.70 x G.51B)] x S62} and the four commercial varieties Giza 93, Giza 92, Giza 87 and Giza 88 were used as checks (Table 2).

The experimental design used in trial A, and trial B, was the randomized complete block design with six replications; each plot consisted of five rows. The row was four meters long, 60 cm apart, and 20 cm between hills. Each hill was thinned to two plants per hill. The middle three rows of each plot were harvested to determine the following traits.

1. Seed cotton yield (SCY): estimated as average weight of seed cotton yield in ken/fed, (Ken = 157.5 Kg and Fed = 4200 m²).
2. Lint cotton yield (LY): measured as average weight of lint yield in Ken/fed.
3. Boll weight (BW): as the weight of 50 bolls picked randomly.
4. Lint percentage (L %): calculated from the formula: Lint percentage = (Weight of lint cotton yield in the sample / Weight of seed cotton yield) X 100.
5. Earliness index (E %): expressed as yield of the first pick x 100 / total seed cotton yield.
6. Fiber fineness and maturity (Mic): measured by Micronaire apparatus in Micronaire units.
7. Fiber strength (Stel): expressed as millitex (1⁰⁻⁸g /Tex).
8. Upper half mean (UHM): determined by the digital Fibrograph.
9. Yarn strength (YST): is the product of "Lea strength x Yarn Count" (60s carded and 3.6 twist multiplier) measured by the Good Brand Tester.

All fiber tests were performed in the Laboratories of the Cotton Technology Research Division, Cotton Research Institute, Agricultural Research Center, Giza.

Table 1. Origin and pedigree of the studied cotton genotypes (Trial A), 2011 season

No.	Parent	Family	Origin
1	F ₅ 1173 /010	F ₄ 1095 /09	G. 93 x G.92
2	F ₅ 1177 /010	F ₄ 1100 /09	" " "
3	F ₅ 1179 /010	" " "	" " "
4	F ₅ 1207 /010	F ₄ 1139 /09	(G. 45 x Sea Island) x G.92
5	F ₅ 1213 /010	F ₄ 1142 /09	G. 93 x Suvin
6	F ₅ 1221 /010	F ₄ 1149 /09	" " "
7	F ₅ 1222 /010	" " "	" " "
8	F ₅ 1228 /010	F ₄ 1159 /09	" " "
9	F ₆ 1248 /010	F ₅ 1176 /09	(G. 70 x Pima S6) x G. 92
10	F ₆ 1250 /010	" " "	" " "
11	F ₆ 1254 /010	F ₅ 1178 /09	" " "
12	F ₆ 1266 /010	F ₅ 1198 /09	(G. 70 x Pima S6) x Pima high lint%
13	F ₆ 1274 /010	F ₅ 1200 /09	" " "
14	F ₆ 1275 /010	" " "	" " "
15	F ₆ 1282 /010	F ₅ 1208 /09	(G. 70 x Pima S6) x (G. 89 x G. 86)
16	F ₆ 1288 /010	F ₅ 1215 /010	" " "
17	F ₆ 1291 /010	F ₅ 1219 /09	" " "
18	F ₆ 1307 /010	F ₅ 1232 /09	G. 88 x Pima S6
19	F ₆ 1310 /010	" " "	" " "
20	F ₆ 1321 /010	F ₅ 1245 /09	" " "
21	F ₆ 1322 /010	" " "	" " "
22	F ₇ 1331 /010	F ₆ 1257 /09	Pima S7 x G. 45
23	F ₇ 1333 /010	" " "	" " "
24	F ₇ 1342 /010	F ₆ 1270/09	Pima S7 x G.76
25	F ₇ 1344 /010	" " "	" " "
26	F ₇ 1358 /010	F ₆ 1276/09	" " "
27	F ₇ 1359 /010	" " "	" " "
28	F ₇ 1370 /010	F ₆ 1290/09	Pima S7 x G.92
29	F ₇ 1372 /010	F ₆ 1291/09	" " "
30	F ₇ 1377 /010	F ₆ 1302/09	" " "
31	F ₈ 1386 /010	F ₇ 1321/09	(G. 67 x Pima S6) x G. 92
32	F ₈ 1393 /010	F ₇ 1333/09	" " "
33	F ₉ 1396 /010	F ₈ 1338/09	G.88 x (G.68 x G.45)
34	F ₉ 1398 /010	" " "	" " "
35	F ₉ 1403 /010	F ₈ 1348/09	" " "
36	{[G.84 x (G.70 x G.51B)] x S62}		{[G.84 x (G.70 x G.51B)] x S62}
37	Giza 93		(G. 77 x Pima S6)
38	Giza 92		[G.84 x (G.74 x G.68)]
39	Giza 87		G.77 x G.45
40	Giza 88		G.77 x G.45

Table 2. Origin and pedigree of the studied cotton genotypes (Trial B), 2012 season

No	Genotypes	Parent	Origin
1	F ₅ 1173 /010	F ₄ 1095 /09	G. 93 x G.92
2	F ₅ 1177 /010	F ₄ 1100 /09	" " "
3	F ₅ 1179 /010	" " "	" " "
4	F ₅ 1207 /010	F ₄ 1139 /09	(G. 45 x Sea Island) x G.92
5	F ₅ 1222 /010	F ₄ 1149 /09	G. 93 x Suvin
6	F ₅ 1228 /010	F ₄ 1159 /09	" " "
7	F ₆ 1248 /010	F ₅ 1176 /09	(G. 70 x Pima S6) x G. 92
8	F ₆ 1254 /010	F ₅ 1178 /09	" " "
9	F ₆ 1266 /010	F ₅ 1198 /09	(G. 70 x Pima S6) x Pima high lint%
10	F ₆ 1275 /010	" " "	" " "
11	F ₆ 1288 /010	F ₅ 1215 /09	(G. 70 x Pima S6) x (G. 89 x G. 86)
12	F ₆ 1291 /010	F ₅ 1219 /010	" " "
13	F ₆ 1322 /010	" " "	" " "
14	F ₇ 1331 /010	F ₆ 1257 /09	Pima S7 x G. 45
15	F ₇ 1342 /010	F ₆ 1270/09	Pima S7 x G.76
16	F ₇ 1358 /010	F ₆ 1276/09	" " "
17	F ₇ 1370 /010	F ₆ 1290/09	Pima S7 x G.92
18	F ₈ 1386 /010	F ₇ 1321/09	(G. 67 x Pima S6) x G. 92
19	F ₈ 1393 /010	F ₇ 1333/09	" " "
20	F ₉ 1396 /010	F ₈ 1338/09	G.88 x (G.68 x G.45)
21	{[G.84 x (G.70 x G.51B)] x S62}		{[G.84 x (G.70 x G.51B)] x S62}
22	Giza 93		(G. 77 x Pima S6)
23	Giza 92		[G.84 x (G.74 x G.68)]
24	Giza 87		G.77 x G.45
25	Giza 88		G.77 x G.45

The analysis of variance was performed according to Sendecor (1965).

Table 3. Form of the analysis of variance and expectations of mean squares for a single environment

S.O.V.	d.f	M.S	E.M.S
Replications	r-1		
Genotypes	g-1	M ₂	$\sigma^2e + r\sigma^2g$
Error	(r-1)(g-1)	M ₁	σ^2e

Where:

R, g, M₁, M₂, σ^2e , σ^2g : number of replications, number of genotypes, error mean squares, genotypes mean squares, error variance and genotypic variance, respectively.

Table 4. Form of the combined analysis of variances and expectations of mean squares for all genotypes over environments

S.O.V.	d.f	M.S	E.M.S
Environments(E)	L-1		
Replications/ L	L (r-1)		
Genotypes	g-1	M ₃	$\sigma^2e + r\sigma^2g L + rL\sigma^2g$
Genotypes x E	(g-1) (L -1)	M ₂	$\sigma^2e + r \sigma^2g L$
Error	L (g-1) (r-1)	M ₁	σ^2e

Where:

E: r and g : environments, replications and genotypes, respectively.

M₁, M₂ and M₃: are errors, genotypes by environments interactions and genotypes variances, respectively.

Heritability estimated, in broad sense (h^2_{bs} %) was calculated by using the formula:-

$$h^2_{bs} \% = [\sigma^2g / (\sigma^2g + \sigma^2ge + \sigma^2e)] \times 100$$

Where: σ^2g : genotypic variance component.

σ^2ge : variance component due to genotype x environment.

The cluster analysis was performed using the group average linkage Euclidean distance and lined by Anderberg (1973). All the previous estimates were performed by using SPSS computer programs (1995). Stepwise multiple regression analysis was carried out according to Draper and Smith (1966) to determine the best variables accounted for most variance in seed and lint cotton yield and yarn strength.

RESULTS AND DISCUSSION

Table (5) shows the variance analysis of 35 strains as well as the five check varieties. The data indicated the differences of the strains for seed and lint cotton yield and earliness while the boll weight exhibited insignificant difference for strains and varieties.

Table 5. The analysis of variance mean squares for Trial A in Sakha, 2011 season

S.O.V.	d.f	b.w	Seed cotton yield K/F	Lint cotton yield K/F	Earliness %
Replications	5	39.21	24.54	30.76	162.33
Genotypes	39	21.80	14.08*	19.50*	30054*
Error	195	16.75	3.72	4.6	103.87

*,** significantly different at the 0.05 and 0.01 levels of probability, respectively

With regard to the yield the data Table (6) showed that 17 out of 35 genotypes surpassed the overall means of total genotypes.

Table 6. Mean performance for yield and its components and fiber properties of genotypes in Trial A in Sakha

No	S.C.Y.	Lint Y.	Lint %	BW	E %	UHM	F.St	Mic	Yarn St.
1	13.79	15.2	35.0	150	59.96	35.9	45.9	3.3	3180
2	12.3	13.66	35.27	145	56.63	36.8	46.5	3.5	2970
3	13.11	14.47	35.04	150	43.11	36.2	44.5	3.6	2995
4	12.71	13.86	34.62	148	52.34	34.7	42.3	3.5	2840
5	10.6	11.67	34.97	150	37.04	34.7	43.7	3.3	2945
6	12.56	13.3	33.64	150	52.96	36.2	43.1	3.4	2950
7	13.70	14.19	32.88	147	42.28	36.5	46.0	3.6	3045
8	12.96	14.03	34.36	155	47.11	35.0	45.2	3.9	2945
9	12.68	14.05	35.18	149	56.04	34.8	45.2	3.7	2965
10	11.7	12.69	34.42	151	60.86	35.1	46.7	3.9	2960
11	13.06	13.67	33.24	153	54.61	36.7	46.3	3.8	3115
12	13.12	14.31	34.64	152	57.29	36.5	48.5	3.8	3185
13	10.14	10.82	33.9	145	55.94	37.6	44.0	3.9	2960
14	11.75	12.89	34.82	150	48.13	37.3	45.0	4.0	3190
15	9.45	10.86	36.48	151	34.75	36.5	42.4	4.0	2900
16	11.28	12.95	36.44	152	46.8	38.1	45.8	4.0	3195
17	11.55	12.5	34.38	153	48.84	36.4	43.6	4.0	3020
18	9.91	11.25	36.06	151	38.47	38.1	44.5	3.9	3050
19	10.95	12.75	36.97	149	43.52	35.9	44.0	3.9	3030
20	11.81	13.22	35.78	149	47.82	38.5	43.8	4.0	2980
21	11.79	13.71	36.7	152	52.02	37.2	48.5	4.0	3080
22	9.70	10.37	34.55	150	42.41	37.1	45.5	3.7	3075
23	8.79	9.48	34.13	150	40.84	38.6	45.8	3.8	3175
24	11.33	13.2	36.29	151	43.18	34.7	41.7	3.6	2880
25	9.35	10.95	37.17	152	38.67	35.2	42.0	3.7	2955
26	8.90	10.2	36.39	150	37.68	36.0	43.5	3.7	2980
27	8.53	9.14	34.03	151	42.18	37.4	45.6	3.8	2875
28	13.12	15.12	36.59	150	41.18	35.2	46.9	4	2950
29	13.88	15.82	36.19	151	55.25	34.1	40.1	4	2785
30	12.64	13.82	34.72	151	48.2	36.3	45.6	4	2850
31	11.16	11.89	33.81	152	49.39	37.8	44.6	3.9	2690
32	11.56	13.33	36.61	151	49.34	35.5	40.2	3.7	2965
33	12.05	13.83	36.46	150	44.5	37.3	43.3	4	2535
34	11.66	13.45	36.62	151	43.22	35.9	44.3	4.3	2695
35	11.05	13.11	37.66	151	38.87	37.6	44.5	4.2	2750
36	13.54	17.04	39.97	147	43.84	36.0	46.6	4.1	3545
37	11.43	12.38	34.4	150	46.05	36.5	44.5	3.0	2660
38	12.79	14.67	36.4	151	56.49	33.5	43.8	3.7	2825
39	8.48	8.94	33.48	149	34.73	36.0	40.5	3.5	2755
40	10.47	12.22	37.06	149	45.19	36.2	46.2	4.0	2965
Mean	11.53	12.88	35.43	150	46.94	36.3	44.5	3.8	2935
L.S.D. 5%	2.39	2.66		5.07	12.63				
L.S.D. 1%	3.15	3.50		6.68	16.63				

The data also indicated that 14 out of 35 exhibited mean performance of lint percentage surpassed the overall mean, while genotypes which exhibited mean performance of genotypes number 25 and 35 for lint % were superior than the variety G. 88.

With regard to the quality traits, the data indicated that the ranges of these traits were 34.7 to 37.6, from 40.1 to 46.7, 3.3 to 4 and from 2785 to 3195 for upper half mean, fiber strength, micronaire and yarn strength respectively. Regarding the data of 19 genotypes, were selected for evaluation in trial B at three locations.

Table (7) showed the combined analysis of 19 selected strain as well as the five check cultivars at three locations for yield and its components.

The data suggested that the mean squares of genetic and location were highly significant for yield, boll weight and earliness index. The data also showed that the interaction between genotypes and environment were significant. With regard to the mean performance of yield and its component and fiber properties presented in (Table 8) the results indicated the ranges of (7.79 – 11.16), (8.36 – 12.35), (33.21 – 38.28), (147 – 153) and (58.83 – 71.53) for seed cotton yield, lint yield, lint percentage and earliness index, respectively. Advanced strain number 20 of G.88 x (G. 68 x G.45) recorded the highest yield potential. It was followed by the promising hybrid which was isolated strain and genotypes number 19, 17, and 12 with insignificant differences with regard to lint percentage, the strains exhibited higher lint percentage. Also these strains did not differ significantly for earliness index.

Table 7. Form of the combined analysis of variances and expectations of mean squares for all genotypes over environments

S.O.V.	d.f	b.w	Seed cotton yield K/F	Lint cotton yield K/F	Earliness %
Environments(E)	2	2205.9	1489.2	1777.8	32504.7
Replications/ L	15	24.16	17.4	21.064	830.2
Genotypes	24	184.19*	10.75*	14.9*	235.5*
Genotypes x E	48	56.3	6.40	7.0	81.5
Error	360	29.8	3.6	4.4	72.6

*,** significantly different at the 0.05 and 0.01 levels of probability, respectively

With regard to fiber quality, the derived strains exhibited similar level to extra-long cultivars. The mean performance of differ traits showed differences with range of (37.2 – 35.2), (3.1– 4.0), (46.3 – 49.1) for upper half mean, micronaire value, and fiber strength while yarn strength the derived strains exhibited insignificant differences. The highest mean values of upper half mean and finest micronaire reading were recorded by cultivars Giza 93, while the derived strains from cross G.88 x (G.68 x G.45) exhibited higher upper half mean and a micronaire value of 3.8 and fiber strength of 46.6. Therefore the best four derived strain were numbered with 12, 17, 19, 20 as well as isolated promising cross {[G.84 x (G.70 x G.51B)] x S62}.

Table 8. Mean performance for yield and its components and fiber properties of genotypes in Trial (B) at four locations

No	S.C.Y	L.C.Y	Lint %	B.W	E %	F.L	MIC	F.S	Yarn St
1	10.09	11.11	35.25	149	65.81	35.8	3.8	49	3193
2	9.89	10.78	34.64	147	66.32	35.3	3.8	47.7	3188
3	9.40	10.28	34.74	147	66.28	35.5	3.8	46.9	3105
4	10.07	10.86	34.60	150	70.80	35.2	3.8	49.1	3198
5	10.00	10.46	33.37	151	71.67	35.9	3.8	49.2	3207
6	10.31	10.95	33.60	153	70.17	35.2	3.8	49.1	3110
7	9.48	10.35	34.66	152	67.02	35.2	3.8	47.9	3102
8	10.76	11.52	33.97	152	71.53	36.3	3.8	49.1	3227
9	10.67	11.24	33.49	153	71.19	36.1	4	47.9	3163
10	10.00	10.83	34.30	152	58.83	36.1	4	47.4	3135
11	9.37	10.40	35.16	152	65.17	36.5	4	47.4	3185
12	10.53	11.18	33.72	153	64.39	36.1	3.9	45.9	3110
13	9.70	10.85	35.60	154	64.00	35.6	3.9	47.5	3108
14	7.79	8.36	33.93	148	62.73	35.5	4	46.9	3108
15	10.39	11.53	35.30	151	67.62	36.4	3.9	48.5	3123
16	8.71	9.75	35.46	153	63.82	36.2	3.9	47.1	3173
17	10.21	11.40	35.33	152	62.54	35.4	4	46.7	3142
18	9.02	9.61	33.86	153	69.20	36.1	3.8	47.5	3150
19	9.99	11.09	35.23	153	69.86	35.4	3.8	49.5	3210
20	11.16	12.35	35.09	152	65.30	37.2	3.8	46.4	3190
21	9.54	11.52	38.28	151	60.30	35.4	4	46.6	3137
22	10.18	10.99	34.41	153	67.54	36.8	3.1	46.3	3172
23	10.05	11.23	35.54	151	71.02	34.9	3.8	46.8	3065
24	8.28	8.66	33.21	153	62.32	35.4	3.7	46.5	3112
25	8.50	11.98	35.84	153	62.84	36.8	3.9	48.7	3212
Mean	9.76	10.77	34.74	151.4	66.33	35.9	3.8	47.7	3153
L.S.D. 5%	1.20	1.33		3.45	5.39				
L/S.D. 1%	1.20	1.33		3.45	5.39				

Similarity and taxonomic distance

The best four derived as well as the cultivars {[G.84 x (G.70 x G.51B)] x S62}, G.93, G.92, G.87, G88 were used in hierarchical cluster to determine the relative similarity and diversity or taxonomic distance with regard to the above mentioned results. The best four lines were represented by F₆ 1291/2010 belonging to cross (G. 70 x Pima s6) x (G.89 x G.86), F₇ 1370/010 belonging to cross (Pima s7 x G.92, F81393/010 belonging to cross (G. 67 x Pima s6) x G.92, F₉ 1396 /010 belonging to cross G.88 x (G.68 x G.45). These four lines as well as the four cultivars. G.93, G.92, G87 and G.88 in addition the promising cross {[G.84 x (G.70 x G.51B)] x S62} were used in hierarchical cluster to determine the relative similarity and diversity or taxonomic distance

The linkage dendrogram provides visual idea about clustering and variability among the oboe mentioned entries. Figure (1) and Table (9) showed that the studies entries were divided at distance level 45.59 with similarity level of 69.04 % into two group the first group represented by cultivars G.92 the second groups represented by the rest genotypes and cultivar. The groups was divided into two subgroups at distance level 30.5 with similarity level of 79.29 %

The first sub groups by 12 (F₆ 1291/010) and cultivars G.88 exhibited similarity level of 96.90% as sub-sub grouped and other sub-sub group repressed by 17 (F₇ 1370/010) and promising cross {[G.84 x (G.70 x G.51B)] x S62} with similarity of 95.7% and distance level 6.34. the second sub groups as follow 19 (F₈1393 /010) and G.88 with similarity level of 94.17% and distance level 7.70 and other group represented by genotypes 20 (F₉1396/010) and Giza 93 with similarity level of 87.59% with distance level 18.27

Table 9. Euclidean method for nine genotypes including two groups for genotypes, distance and similarity for yield and fiber characters.

Node	Cluster joined		Similarity%	Distance	No. of obs.
	Group 1	Group 2			
1	12	24	96.90	4.566	2
2	17	21	95.70	6.340	2
3	19	25	94.77	7.699	2
4	20	22	87.59	18.274	2
5	Node 3	Node 4	85.80	20.919	4
6	Node 1	Node 2	82.44	25.858	4
7	Node 6	Node 5	79.29	30.495	8
8	Node 7	23	69.04	45.593	9

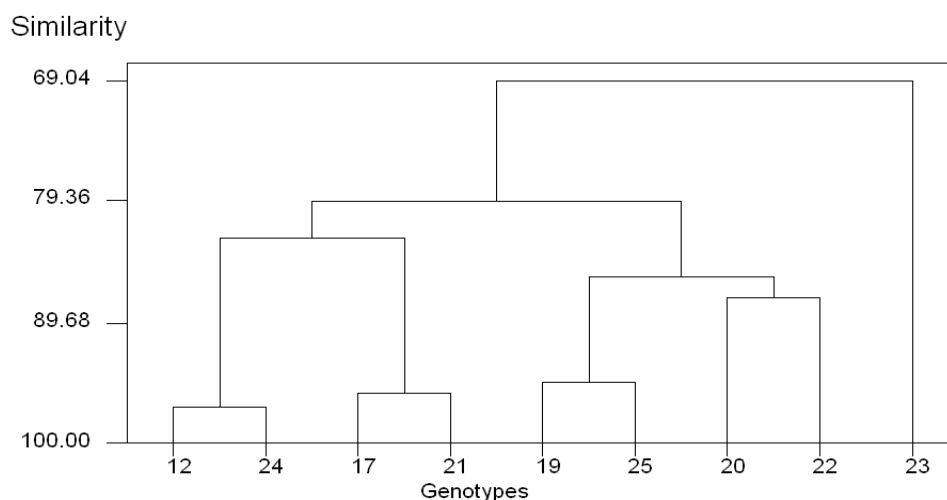


Fig. 1. Dendrogram of taxonomic similarity of nine extra-long cotton genotypes

12	(G. 70 x Pima s6) x (G. 89 x G. 86)	Derived line (F ₆ 1291 /010)
17	Pima s7 x G.92	Derived line (F ₇ 1370 /010)
19	(G. 67 x Pima s6) x G. 92	Derived line (F ₈ 1393 /010)
20	G.88 x (G.68 x G.45)	Derived line (F ₉ 1396 /010)
21	{[G.84 x (G.70 x G.51B)] x S62}	
22	Giza 93	
23	Giza 92	
24	Giza 87	
25	Giza 88	

Estimates of variance components and heritability

Estimates of variance components and their standard error, heritability and genotypic variability (GCV) for yield and its components are presented in Table (10). The data indicated the presence of substantial amount of genetic variance for boll weight, seed cotton yield, lint yield and earliness index. These results agreed with those obtained by Gutierre and EL- Zik (1992) , EL-Feki *et al.*, (1995) and Sultan (2012) . Also the results showed that all traits exhibited significant genotypes x environment interaction variance (σ^2_{ge}) the results agreed with those obtained by EL-Feki *et al.*, (1995) and Sultan (2012).

With regard to the ratio $\sigma^2_g / \sigma^2_{ge}$ presented in Table (6) the results indicated high ratios. Thus these traits were controlled by heritable system/ The data in Table (10) indicated that the heritability value (over 50%) for all yield and its components and earliness index. These results agreed with those obtained by Iqbal

et al. (2011) who revealed that estimates of heritability for boll weight, seed cotton yield and lint percentage were high. Sultan (2012) obtained moderate values of heritability for seed cotton yield and lint yield.

The genotypic variability coefficient (GCV %) is important in plant breeding since it helps in the assessment of the range of genetic variability in traits and helps in comparing the genetic variance of various traits (Johanson *et al.* 1955).

Table 10. genetic components and genetic variability and heritability for yield and its component

	B.w	Seed cotton yield K/F	Lint cotton yield K/F	Earliness %
σ^2_g	0.8526 \pm 0.0369	0.0290 \pm 0.0068	0.0527 \pm 0.0092	1.0267 \pm 0.0405
σ^2_{ge}	0.1767 \pm 0.00280	0.0187 \pm 0.00091	0.0173 \pm 0.00088	0.0593 \pm 0.00162
$\sigma^2_g / \sigma^2_{ge}$	4.826	1.554	3.038	17.303
Heritability (bs)	82.84	60.84	75.24	94.54
G.C.V %	0.563	0.297	0.489	1.548

The GCV% values are shown in Table (10). The data indicated that boll weight, seed cotton yield and lint yield exhibited low value of GCV %. Burton (1952) , suggested that genetic coefficient of variability together with heritability estimate gave the best picture of advance expected from selection. Sultan (2012) obtained moderate value of GCV % for seed cotton yield and lint yield.

Prediction of seed, lint yield and yarn strength

The regression analysis of variance presented in Table (11). The results indicated that the four variables model was the best equation to determine the prediction of seed cotton and lint yield because they had highly significant mean variance in trial A. The equation determining the prediction of yarn strength depends upon three variable.

Table 11. The analysis of variance for multi-regression of accepted variables according to stepwise regression analysis.

Variable	Variance	A		B	
		d.f	M.s	d.f	M.s
Seed cotton yield K/F	Regression	4	9.126	4	0.8730
	Residual	35	1.572	20	0.6081
Lint cotton yield K/F	Regression	4	14.796	4	1.7396
	Residual	35	1.931	20	0.6657
Yarn strength	Regression	3	95786	3	8874.6
	Residual	36	27196	21	966.2

For trial B the data in Table (11) showed that the four variable mode for seed and lint cotton yield were not the best equation to determine the prediction of seed and lint cotton yield because they had insignificant values so it could be found the other variable in this equation Table (12) shows the regression equation for predicting seed and lint cotton yield in trial (A) the regression equation of seed yield and lint yield, respectively, are:

$$SCY = -9.8 + 0.118 X_1 + 0.0546 X_2 + 0.108 X_3 - 0.004 X_4$$

$$LCY = -28.8 + 0.499X_1 + 0.103 X_2 + 0.0950 X_3 - 0.0.73 X_4$$

The data in Table (12) showed that the earliness index was more important for predicting seed cotton yield and followed by boll weight while agreed with those obtained in trial (A). While, from lint cotton yield the data indicated that boll weight was more important and followed by lint percentage although this equation was not the best equation.

For yarn strength the best equation was as follow

$$\text{Yarn strength} = 666 + 39.0 X_5 - 18.7 X_6 + 24.1 X_7$$

The data in Table (12) showed that the earliness index was more important in predicting the seed cotton yield. While, for prediction are lint yield, the boll weight and earliness index were more important to predict the lint cotton yield.

Table 12 .The best regression equation for predicting seed cotton yield, lint cotton yield and yarn strength in two trials A and B.

Variable	A			B		
	Seed cotton yield K/F	Lint cotton yield K/F	Yarn strength	Seed cotton yield K/F	Lint cotton yield K/F	Yarn strength
Constant	-7.38	-20.81	995.9	-9.76	-28.79	665.8
Boll weight	0.2252	0.6311	-	0.1181	0.4987	-
Lint %	0.0360	0.0345	-	0.05464	0.10330	-
Earliness %	0.14114	0.15729	-	0.10790	0.09502	-
Mic	-0.2896	-0.3253	1.71	-0.0042	0.0727	39.36
U.H.M	-	-	42.90	-	-	-18.70
Fiber strength	-	-	-1.9	-	-	24.081

The final regression equation of seed cotton yield, lint cotton yield and leaf product (yarn strength) respectively are:-

$$SCY = -7.4 + 0.225 X_1 + 0.036 X_2 + 0.141X_3 - 0.290 X_4$$

$$LCY = -20.08 + 0.631 X_1 + 0.034 X_2 + 0.157X_3 - 0.325X_4$$

$$\text{Yarn strength} = 995.9 + 1.7 X_3 + 42.9 X_6 - 2.0 X_7$$

According to aforementioned equation of the bulk of total variance in seed cotton yield in Trial (A) was attributed to earliness index followed by boll weight. While lint yield was attributed to boll weight and followed by earliness index. These results were partially in harmony with those obtained by Ismail *et al.* (1994) who reported that a number of bolls per plant followed by boll weight were the major contributors to seed and lint yield and these results agreed with those obtained by El-Feki *et al.* 2002 for yarn strength in Trial (A).

From the obvious results, it may be summarized that the major cause of differences among genotypes in relation to production stabilities is the genotypes x environment (GE) interaction, so that the performance of the genotypes depends on the specific environmental conditions this explained the part of genotypes x environment interaction. While, the most of GE interaction cannot be explained by the major factor of environment.

Also the results identified that the relationships among the current studied traits, is very important and this gives the breeder a highly useful tool for planning a breeding program by providing relevant information on the potential gains that will be achieved as the breeding process advances.

The results identified that genotypes [(G. 70 x Pima S6) x G. 89 x G. 86], (Pima S7 x G.92), (G. 67 x Pima S6) x G.92, G.88 x (G.86 x G. 45) could replace varieties G.87, promising cross {[G.84 x (G.70 x G.51B)] x S62}, G.88 and G.93 in future respectively.

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التقييم الوراثي لبعض سلالات القطن فائقة الطول تحت بيئات مختلفة

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يهدف هذا البحث الى تقييم 35 سلالة ناتجة من 14 هجين مقارنة بأربعة أصناف منزرعة هي جيزة 93 ، جيزة 92، جيزة 87، جيزة 88 بالإضافة الى الهجين المبشر [ج 84 × (ج 70 × ج 51) × س 62] اختبرت في تجربة المحصول الاولية (أ) لقسم بحوث تربية القطن حيث زرعت هذه التجربة في محطة البحوث الزراعية بسخا موسم 2011م ومن نتائج المحصول والتيلة لهذه التجربة تم انتخاب 20 سلالة بالإضافة الى الاصناف المقارنة والهجين المبشر السالفة الذكر وتم تقييمها في تجربة المحصول المتقدمة (ب) في ثلاث مناطق مختلفة هي (كفر الشيخ، الدقهلية، دمياط،) للموسم الزراعى 2012م.

كانت الصفات المدروسة هي محصول الزهر، ومحصول الشعر وتصافى الحليج والتبكير وطول التيلة (متوسط الربيع الاعلى) وقراءة الميكرونير ومتانة التيلة وكذلك متانة الغزل، وبالنظر الى نتائج التحليل التجميى لهذه الصفات في التجربة المتقدمة (ب) تم انتخاب اربع سلالات تم ادخالها في تحليل التقسيم الهرمى لبيان مدى تشابه هذه السلالات مع الاصناف التى يمكن ان تحل محلها وكانت النتائج كالاتى

- اوضحت النتائج ان افضل التراكيب الوراثية هي التراكيب رقم 12، 17، 19، 20 في تجربة (ب) حيث ان التركيب الوراثى رقم 12 والنتاج من الهجين (ج 70 × بيما س 6) × (ج 89 × ج 86) يمكن ان يكون بديلا جيد للصنف جيزة 87 ، والتركيب الوراثى رقم 17 الناتج من الهجين (بيما س 6 × ج 92) بديلا للهجين المبشر [ج 84 × (ج 70 × ج 51) × س 62] ، والتركيب الوراثى رقم 19 والنتاج من الهجين (ج 67 × بيما س 6) × ج 92 بديلا للصنف جيزة 88، والتركيب الوراثى رقم 20 والنتاج من (ج 88 × ج 68 × ج 45) بديلا للصنف جيزة 93.
- اشار تحليل التباين الى ان المكون الوراثى اكثر اهمية من التفاعل بين البيئة والوراثة في توريث صفات المحصول ومكوناته
- كانت درجة التوريث اكبر من 50% بينما كانت قيم معامل الاختلاف الوراثى اقل القيم.
- اظهر تحليل stepwise ان صفتى وزن اللوزة والتبكير هما المسئولتان عن زيادة المحصول و ان صفتى طول التيلة ومتانة التيلة كانتا اهم الصفات المسئولة عن متانة الغزل.