

EVALUATION OF SOME EGYPTIAN COTTON GENOTYPES UNDER DIFFERENT ENVIRONMENTS

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ABSTRACT

The present study included 38 long staple genotypes, and two isolated hybrids in addition to two check varieties, Giza 90 and Giza 95. They were evaluated in 2019 season at Beni-sueif government (Trail A). While, Trail B consisted of 17 genotypes, selected from Trail A, with the three control genotypes, and evaluated in 2020 season at five locations (Beni-sueif, El-Fayoum, Assiut, Souhag and Luxor Governorates). Results of trail A indicated that, the two superior genotypes $[(G\ 83 \times (G\ 75 \times 5844)) \times G90] \times G91$ and $\{(G\ 83 \times G\ 80) \times Dandara\} \times (G90 \times A105)$ were significantly out-yielded the two check varieties in seed, lint cotton yields and boll weight. Results of trail B showed that, locations significantly differed for all the studied traits, The genotypes and interactions mean squares were significant for seed cotton yield, lint cotton yield and boll weight. Mean performance across all locations showed that, $[(G\ 83 \times (G\ 75 \times 5844)) \times G90] \times G91$, $\{(G\ 83 \times (G\ 72 \times Dandara)) \times S109\}$ and $(G90 \times A105) \times G85$ significantly out yielded the best check variety Giza-95 in seed cotton yield across all locations. Boll weight data indicated that, $(G91 \times G90) \times R101$ and $(G91 \times G90) \times G80$ had bolls heavier than the three checks. Results of trails A and B indicated that, the promising genotype $[(G\ 83 \times (G\ 75 \times 5844)) \times G90] \times G91$ was significantly higher yield than the check genotypes in both seed and lint cotton yield in both trail A and trail B across all locations, and this cross may be considered as a promising material for future breeding programs to develop and isolate high yielding varieties of Egyptian cotton.

Key words: Gossypium barbadense, genotype x location interaction, heritability, Advanced Trail.

INTRODUCTION

Hybridization among cotton genotypes, followed by conventional pedigree selection is a predominant method utilized for cotton breeding. In such pedigree system, the best F₂ 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 F₅ generation and continue, until satisfactory genetic stability is achieved. Many investigators (El-Moghazy *et al* 1982, Abo-Zahra *et al* 1986, Sallam *et al* 1987, Ismael *et al* 1989, Awaad and Mostafa (1996), Mohamed *et al* 2003, El_Adly and Eissa 2010, El-Adly *et al* 2013 and El-Hoseiny H.A. 2013) 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.

The ultimate objective of any cotton breeder is to develop high yielding varieties, through selection and breeding, utilizing available genetic resources. The final product of cotton plant, *i.e.* seed cotton yield is the outcome of interplay between genetic and non-genetic components and due to complex nature of the interaction and selection of plants from breeding

population. Improvement of seed and lint cotton yield is one of the focal endeavors of cotton breeding programs. The promising strains derived from the crosses of the breeding program are evaluated in different locations before recommending them for commercial production of farmers.

The promising and desired families in the fifth segregating generation of the different crosses were tested in the preliminary strain test (Trail A), along with the commercial varieties. The selected families from Trail A were tested through the advanced strain test Trail B beside the commercial varieties for comparison at different locations, to study their performance under different locations. The superior crosses over the commercial varieties will be grown in another breeding program for increasing the seeds to produce the breeder seed.

The main objective of this investigation was to evaluate 42 genotypes in Trial A and 20 genotypes in Trial B in diverse environments that represent the range of environments that are suitable for growing the present entries to recognize the promising cross which surpassed the commercial varieties for some major yield components and fiber quality traits.

MATERIALS AND METHODS

Cotton research institute carried out two field experiments in seasons 2019 and 2020 as preliminary trail A and advanced trail B. Trail A consisted of 42 long staple cotton genotypes, 38 lines descending from 17 crosses and four check genotypes, two commercial varieties (Giza 90 and Giza 95) and two isolated hybrids, $\{(G\ 83 \times G\ 80) \times G\ 89\} \times A105$ and $G\ 90 \times S109$ (Table 1), which were cultivated at Sids agricultural research station (Benisuef) in 2019 season. Strains that selected from Trail A were cultivated in Trail B in 2020 season. Trail B was carried out at five locations *i.e.* Benisuef, El-fayoum, Assiut, Souhag and Luxor as yield trials of cotton breeding program. Each trail consisted of 20 genotypes, 17 advanced strains derived from 13 crosses which were numbered from 1 to 17, and 3 check genotypes, which the commercial variety, G90 was obsoleted (Table 2).

The experimental design was a randomized complete block design with six replications. Plot size was five rows, 4m long, 60 cm width and 20 cm between hills within rows with two plants/hill (40 plants/row).

Table 1. Pedigree of the genotypes and cultivated varieties grown in trail A in 2019 season.

No.	Genotypes	Parent	Origin
1	H ₅ 72/ 2018	H ₄ 59/ 2017	[(G 83 × (G 75 × 5844)) × G90] × G91
2	H ₅ 73/ 2018	" " "	" " "
3	H ₅ 75/ 2018	" " "	" " "
4	H ₅ 92/ 2018	H ₄ 71/ 2017	{G 83 x (G 72 x Dandara)}x S109
5	H ₅ 93/ 2018	H ₄ 76/ 2017	" " "
6	H ₅ 98/ 2018	H ₄ 83/ 2017	G80 × S109
7	H ₅ 100/ 2018	H ₄ 85/ 2017	" " "
8	H ₅ 104/ 2018	H ₄ 86/ 2017	" " "
9	H ₅ 105/ 2018	" " "	" " "
10	H ₅ 111/ 2018	H ₄ 92/ 2017	G85 × S109
11	H ₅ 113/ 2018	" " "	" " "
12	H ₆ 123/ 2018	H ₅ 105/ 2017	G91 × S109
13	H ₆ 129/ 2018	H ₅ 107/ 2017	[(G 83 × (G 75 × 5844)) × S109
14	H ₆ 130/ 2018	" " "	" " "
15	H ₆ 135/ 2018	H ₅ 111/ 2017	{G 83 x (G 72 x Dandara)} × S108(24202)
16	H ₆ 147/ 2018	H ₅ 124/ 2017	" " "
17	H ₆ 152/ 2018	H ₅ 134/ 2017	(G91 x G90) x S108(24202)
18	H ₆ 153/ 2018	" " "	" " "
19	H ₇ 159/ 2018	H ₆ 138/ 2017	(G91 x G90) x S109
20	H ₇ 163/ 2018	H ₆ 146/ 2017	" " "
21	H ₈ 180/ 2018	H ₇ 165/ 2017	(G90 x A105) x G85
22	H ₈ 181/ 2018	" " "	" " "
23	H ₈ 192/ 2018	H ₇ 181/ 2017	(G90 x A105) x {G 83 x (G 72 x Dandara)}
24	H ₈ 196/ 2018	" " "	" " "
25	H ₉ 209/ 2018	H ₈ 201/ 2017	(G91 x G90) x G85
26	H ₉ 210/ 2018	" " "	" " "
27	H ₉ 228/ 2018	H ₈ 210/ 2017	(G91 x G90) x {G 83 x (G 75 x 5844)}
28	H ₉ 233/ 2018	H ₈ 234/ 2017	(G91 x G90) x {(G 83 × G 80) x G 89}
29	H ₁₀ 244/ 2018	H ₉ 243/ 2017	(G91 x G90) x R101
30	H ₁₀ 245/ 2018	" " "	" " "
31	H ₁₁ 247/ 2018	H ₁₀ 262/ 2017	{(G 83 x G 80) x Dandara}x (G90 x A105)
32	H ₁₁ 248/ 2018	" " "	" " "
33	H ₁₁ 249/ 2018	" " "	" " "
34	H ₁₁ 253/ 2018	H ₁₀ 265/ 2017	" " "
35	H ₁₁ 255/ 2018	" " "	" " "
36	H ₁₁ 256/ 2018	H ₁₀ 269/ 2017	(G91 x G90) x G80
37	H ₁₁ 257/ 2018	" " "	" " "
38	H ₁₁ 273/ 2018	H ₁₀ 276/ 2017	" " "
39	Mixed families	G 90 × S109	Hybrid isolated
40	Mixed families	{(G 83 × G 80) x G 89}x	Hybrid isolated
41	Giza 95	{G83 x (G75x 5844)} x G80	Commercial variety
42	Giza 90	Giza 83 x Dandara	Commercial variety

Table 2. Pedigree of genotypes and cultivated varieties grown in trail B in 2020 season.

No.	Genotypes	Parent	Origin
1	H ₅ 73/ 2018	H ₄ 59/2017	[(G 83 × (G 75 × 5844)) × G90] × G91
2	H ₅ 92/ 2018	H ₄ 71/ 2017	{G 83 x (G 72 x Dandara)}x S109
3	H ₅ 98/ 2018	H ₄ 83/ 2017	G80 × S109
4	H ₅ 113/ 2018	H ₄ 92/ 2017	G85 × S109
5	H ₆ 135/ 2018	H ₅ 111/ 2017	{G 83 x (G 72 x Dandara)} × S108(24202)
6	H ₆ 147/ 2018	H ₅ 124/ 2017	” ” ”
7	H ₆ 152/ 2018	H ₅ 134/ 2017	(G91 x G90) x S108(24202)
8	H ₇ 159/ 2018	H ₆ 138/ 2017	(G91 x G90) x S109
9	H ₈ 180/ 2018	H ₇ 165/ 2017	(G90 x A105) x G85
10	H ₈ 192/ 2018	H ₇ 181/ 2017	(G90 x A105) x {G 83 x (G 72 x Dandara)}
11	H ₈ 196/ 2018	” ” ”	” ” ”
12	H ₉ 210/ 2018	H ₈ 201/ 2017	(G91 x G90) x G85
13	H ₁₀ 245/ 2018	H ₉ 243/ 2017	(G91 x G90) x R101
14	H ₁₁ 247/ 2018	H ₁₀ 262/ 2017	{(G 83 x G 80) x Dandara}x (G90 x A105)
15	H ₁₁ 248/ 2018	” ” ”	” ” ”
16	H ₁₁ 256/ 2018	H ₁₀ 269/ 2017	(G91 x G90) x G80
17	H ₁₁ 273/ 2018	H ₁₀ 276/ 2017	” ” ”
18	Mixed families	G 90 × C.B 58	Hybrid isolated
19	Mixed families	{(G 83 × G 80) x G 89}× A105	Hybrid isolated
20	Giza 95	{G83 x (G75x 5844)} x G80	Commercial variety

Recommended cultural practices were applied for cotton production. The three central rows of each plot at each location were hand picked to determine seed and lint cotton yield in kentar/feddan. A random sample of 50 bolls was picking from the two outer rows per plot to determine boll weight and lint percentage. The following characters were recorded on each genotype: (1) Seed-cotton yield (SCY, k/fed): Determined as the total seed cotton yield, (2) Lint yield/plant(LCY, k/fed), (3) Lint percentage (LP, %): Percentage of lint to seed cotton yield, and (4) Boll weight (BW, g): Average weight of fifty sound open bolls. At maturity, a random representative sample of 50 open bolls was picked from the two outer rows per plot to determine fiber properties: Upper half mean length (UHM, mm), fiber uniformity ratio (UR, %), yarn strength (YSt., unit), Micronaire reading (Mic,unit), Yellowness (+b, unit) and Maturity. The lint cotton samples were tested at Cotton Technology Laboratory, Cotton Research Institute, ARC. High Volume Instrumentation (HVI) was used for determination of fiber traits.

Plot means were used for statistical analysis. In trail B across locations Bartlet's test for heterogeneity of error variance indicated that error terms were homogeneous. In the combined analysis across locations, genotypes and replications effects were assumed to be fixed. The genotypic (σ^2_g), phenotypic (σ^2_p) variances and broad sense heritability (H) estimates were calculated.

RESULTS AND DISCUSSION

The preliminary strain test (Trail A):

The analysis of variance (Table 3) for the studied traits of all genotypes (Trail A) indicated that, the genotypes mean squares were highly significant for seed cotton yield, lint cotton yield and boll weight, revealing the presence of the genetic variation among the genotypes in these traits. Broad sense heritability was obtained for seed cotton yield, lint yield, and boll weight, which was 73.4, 75.2, and 45.4%, respectively, indicating the presence of substantial amount of genetic variance for seed cotton yield, lint yield and boll weight. These results agreed with those obtained by Gutierre and EL- Zik (1992), EL-Feki *et al* (1995) and El-Hoseiny (2013).

Table 3. The analysis of variance, genotypic, environmental and phenotypic variances, and heritability for studied traits (Trail A).

SOV	df	MS		
		Seed cotton yield (K/f)	Lint yield. (K/f)	Boll weight
Replications	5	35.75**	54.82**	64.91 ^{ns}
Genotypes	41	6.96**	11.40**	130.57**
Error	205	1.85	2.83	71.26
Geno. Var. (σ^2_g)		0.85	1.43	9.89
Envi. Var. (σ^2_e)		0.31	0.47	11.88
Phen. Var. (σ^2_p)		1.16	1.90	21.77
Heritability (H^2),%		73.42	75.18	45.42

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

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). The data indicated that the heritability value (over 50%) for seed and lint cotton yieldm except for boll wieght. 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.

The results of seed cotton yield trait (Table 4) showed that, all the 38 tested genotypes surpassed the best check isolated hybrid G 90 × C.B 58. The increase ranged from 0.23 k/ fed for genotype no. 27 to 3.12 k/fed for genotype no. 31. Moreover, 24 genotypes were surpassed the best check genotypes and grand mean. Three genotypes (no. 2, 16 and 31) were significantly out-yielded the grand mean by 17.11, 18.98 and 20.37%, respectively. These superior genotypes could be considered promising genotypes which had a high yielding ability more than the four check genotypes and belonged to the best crosses in Trail A.

Regarding lint cotton yield trait (Table 4), the best check isolated hybrid {(G 83 × G 80) x G 89} × A105 which gave 9.39 k/fed and all the tested genotypes exceeded it in lint yield except genotypes no. 7, 9 and 27.

Table 4. Mean performance of yield and yield components for the tested genotypes and cultivated varieties grown in Trail A at Sids station in season 2019.

No.	Genotypes	SCY (k/f)	LCY (k/f)	Bw (g)	LP,%	U.H.M
1	H ₅ 72 / 2018	7.76	9.91	162	40.6	30.9
2	H ₅ 73/ 2018	10.06	12.73	165	40.2	30.9
3	H ₅ 75/ 2018	8.39	10.52	162	39.8	30.2
4	H ₅ 92/ 2018	9.00	11.04	165	39.0	30.1
5	H ₅ 93/ 2018	8.22	10.10	161	39.0	31.2
6	H ₅ 98/ 2018	8.92	10.72	164	38.2	30.7
7	H ₅ 100/ 2018	7.67	9.33	158	38.6	31.0
8	H ₅ 104/ 2018	9.02	10.36	155	36.5	30.2
9	H ₅ 105/ 2018	7.75	9.29	156	38.0	30.6
10	H ₅ 111/ 2018	8.65	10.55	161	38.7	30.8
11	H ₅ 113/ 2018	9.11	11.16	159	38.9	30.3
12	H ₆ 123/ 2018	8.54	10.51	158	39.1	30.9
13	H ₆ 129/ 2018	7.69	9.41	161	38.8	30.8
14	H ₆ 130/ 2018	8.48	10.23	157	38.3	30.9
15	H ₆ 135/ 2018	9.44	11.97	159	40.3	30.5
16	H ₆ 147/ 2018	10.22	12.51	151	38.9	30.4
17	H ₆ 152/ 2018	8.21	10.01	162	38.7	30.1
18	H ₆ 153/ 2018	8.37	9.95	161	37.7	30.5
19	H ₇ 159/ 2018	9.21	11.30	156	38.9	31.2
20	H ₇ 163/ 2018	7.91	10.10	148	40.5	28.4
21	H ₈ 180/ 2018	9.51	12.28	154	41.0	30.3
22	H ₈ 181/ 2018	9.49	11.79	151	39.5	31.0
23	H ₈ 192/ 2018	8.81	10.73	152	38.7	32.2
24	H ₈ 196/ 2018	9.12	11.13	154	38.7	31.0
25	H ₉ 209/ 2018	8.91	10.94	149	39.0	29.9
26	H ₉ 210/ 2018	8.98	11.40	158	40.3	30.2
27	H ₉ 228/ 2018	7.45	9.13	153	38.9	29.6
28	H ₉ 233/ 2018	9.03	11.09	156	39.0	29.1
29	H ₁₀ 244/ 2018	8.24	10.45	155	40.3	30.3
30	H ₁₀ 245/ 2018	9.44	11.47	158	38.6	31.7
31	H ₁₁ 247/ 2018	10.34	12.90	161	39.6	30.0
32	H ₁₁ 248/ 2018	9.83	12.38	158	40.0	29.5
33	H ₁₁ 249/ 2018	8.92	11.05	157	39.3	30.3
34	H ₁₁ 253/ 2018	8.89	11.05	153	39.5	29.3
35	H ₁₁ 255/ 2018	9.42	12.04	149	40.6	30.1
36	H ₁₁ 256/ 2018	9.63	12.06	157	39.8	29.1
37	H ₁₁ 257/ 2018	8.34	10.16	151	38.7	30.1
38	H ₁₁ 273/ 2018	8.70	10.67	159	39.0	30.1
39	G 90 × C.B 58	7.22	9.00	149	39.6	29.0
40	{(G 83 × G 80) × G 89} × A105	7.20	9.39	161	41.4	29.7
41	Giza 95	6.16	7.82	150	40.3	30.4
42	Giza 90	4.58	5.44	153	37.7	30.1
	Mean	8.59	10.62	157	39.2	30.3
	L S D_{0.05}	1.29	1.60	8.02		
	L S D_{0.01}	1.82	2.26	11.34		

Table 4. Cont.

No.	Genotypes	U.R.(%)	Maturity	Mic.(unit)	+b (unit)	Y.St. (unit)
1	H ₅ 72 / 2018	84.5	0.95	4.5	11.0	2070
2	H ₅ 73/ 2018	84.7	0.94	4.4	12.0	2110
3	H ₅ 75/ 2018	86.1	0.96	4.5	9.8	2070
4	H ₅ 92/ 2018	85.7	0.94	4.6	11.3	2270
5	H ₅ 93/ 2018	83.8	0.95	4.5	11.8	2110
6	H ₅ 98/ 2018	85.0	0.95	4.3	11.6	2270
7	H ₅ 100/ 2018	84.3	0.96	4.4	11.3	2070
8	H ₅ 104/ 2018	84.4	0.99	4.6	11.8	2070
9	H ₅ 105/ 2018	85.8	0.98	4.4	11.4	2150
10	H ₅ 111/ 2018	85.5	0.94	4.2	11.3	2030
11	H ₅ 113/ 2018	84.6	0.95	4.4	11.9	1943
12	H ₆ 123/ 2018	85.9	0.96	4.5	12.8	1990
13	H ₆ 129/ 2018	84.8	0.95	4.6	11.0	1750
14	H ₆ 130/ 2018	84.7	0.96	4.3	11.1	1830
15	H ₆ 135/ 2018	84.7	0.97	4.5	12.6	1790
16	H ₆ 147/ 2018	84.9	0.97	4.6	12.4	2030
17	H ₆ 152/ 2018	86.1	0.94	4.3	12.3	1990
18	H ₆ 153/ 2018	84.4	0.94	4.4	12.0	1950
19	H ₇ 159/ 2018	82.6	0.95	4.3	11.8	1830
20	H ₇ 163/ 2018	85.3	0.96	4.2	11.5	1910
21	H ₈ 180/ 2018	84.6	0.95	4.4	11.9	1943
22	H ₈ 181/ 2018	83.7	0.94	4.4	12.9	1830
23	H ₈ 192/ 2018	86.2	0.94	4.4	10.9	1780
24	H ₈ 196/ 2018	83.7	0.95	4.4	11.5	1910
25	H ₉ 209/ 2018	85.2	0.96	4.2	11.9	1830
26	H ₉ 210/ 2018	83.7	0.96	4.4	12.0	1790
27	H ₉ 228/ 2018	83.9	0.94	4.3	11.4	1830
28	H ₉ 233/ 2018	84.0	0.95	4.4	12.1	1750
29	H ₁₀ 244/ 2018	83.8	0.95	4.4	12.4	1950
30	H ₁₀ 245/ 2018	85.7	0.94	4.5	11.5	1870
31	H ₁₁ 247/ 2018	83.8	0.95	4.4	12.6	1830
32	H ₁₁ 248/ 2018	84.2	0.95	4.5	13.2	2030
33	H ₁₁ 249/ 2018	84.0	0.94	4.3	11.7	1790
34	H ₁₁ 253/ 2018	84.2	0.95	4.3	13.2	1750
35	H ₁₁ 255/ 2018	84.7	0.94	4.3	13.7	2030
36	H ₁₁ 256/ 2018	83.9	0.96	4.2	10.7	1950
37	H ₁₁ 257/ 2018	84.4	0.97	4.4	11.8	1990
38	H ₁₁ 273/ 2018	83.6	0.94	4.4	10.9	1950
39	G 90 × C.B 58	84.1	0.95	4.4	12.9	1870
40	{(G 83 × G 80) × G 89} × A105	83.8	0.93	4.4	11.8	1790
41	Giza 95	84.6	0.95	4.5	11.9	1830
42	Giza 90	83.8	0.93	4.0	12.4	1990
Mean		84.6	0.95	4.4	11.9	1943
L S D _{0.05}						
L S D _{0.01}						

ns = non-significant

The highest increase was obtained by genotype no. 31 which surpassed the check genotype by 3.51 k/fed. While the lowest increase was obtained by genotype no. 13 which gave 0.02 k/fed increase in lint yield. The results showed that 21 genotypes (no. 2, 4, 6, 11, 15, 16, 19, 21, 22, 24, 25, 26, 28, 30, 31, 32, 33, 34, 35, 36 and 38) were out-yielded the best check isolated hybrid and grand mean in lint yield. Three genotypes (no. 2, 21 and 31) were significantly out-yielded the grand mean by 19.87, 15.63 and 21.47%, respectively. These promising 21 genotypes were significantly out-yielded the four check genotypes in both seed and lint cotton yield, and their crosses could be used in the breeding program to produce new high yielding cultivars. So 17 genotypes were selected from them for Trial B in next year. Boll weight values (Table 4) showed that, 9 genotype (no.2, 3, 4, 5, 6, 10, 17, 18 and 31) were equal or higher than the best check isolated hybrid {(G 83 × G 80) × G 89} × A105. Based on three traits under study, it was found that the two genotypes no. 2 ([(G 83 × (G 75 × 5844)) × G90] × G91) and 31({(G 83 × G 80) × Dandara} × (G90 × A105)) were superior.

The advanced strain test (Trail B)

Trail B is the advanced strain test for the promising genotypes that were selected from trail A and evaluated under five locations, *i.e.* Beni Sueif, El-Fayoum, Assiut, Sohag and Luxor, in order to study breeding behavior, yield performance and to evaluate genotypes are interaction under these locations. The combined analysis of variance for the studied traits of all genotypes across the five locations (Table 5) indicated that, locations were significantly differed for all the studied traits, indicating the presence of wide range of variation. The genotypes mean squares were highly significant for seed cotton yield, lint cotton yield and boll weight, indicating the presence of high genetic variation among the genotypes for these traits.

Genotype × location interactions were significant for all traits, it could be due to that these traits were highly responded to the environmental changes and the genotypes performance varied from location to another. Broad sense heritability was obtained for seed cotton yield, lint yield, and boll weight, which was 18.16, 26.64, and 5.56%, respectively, indicating the presence of low amount of genetic variance because of environmental factor.

Table 5. The combined analysis of variance across the five locations for all the studied traits of all genotypes (Trail B).

SOV	df	MS		
		Seed cotton yield	Lint yield	Boll weight
Rep./ Loc.	25	14.43**	22.64**	127.9 ns
Locations (L)	4	1,858.18**	3,165.11**	5,359**
Genotypes (G)	19	4.07*	7.78**	158.2*
G x L	76	3.25*	4.96*	258.0*
Error	475	2.35	3.71	95.0
Geno. Var. (σ^2g)		0.06	0.14	2.11
Inter. Var. (σ^2gl)		0.18	0.25	32.60
Envir. Var. (σ^2e)		0.08	0.12	3.17
Phen. Var. (σ^2p)		0.32	0.51	37.88
Heritability (H^2),%		18.16	26.64	5.56

*, ** significant at 0.05 and 0.01 probability levels, respectively

The results presented in Table 6 indicated that the three genotypes no.1 ((G 83 × (G 75 × 5844)) × G90) × G91), 2 ((G 83 × (G 72 × Dandara)) × S109) and 9 ((G90 × A105) × G85) were significantly superior than the best check variety Giza-95 in seed cotton yield across all locations by 1.21, 3.67 and 2.48%, respectively. And most of the other genotypes were better than or comparable to the check genotypes in seed cotton yield.

Lint cotton yield values (Table 6) showed that, 10 from 17 tested genotypes were significantly better than the best check variety Giza-95 in lint yield. These genotypes were (no. 1, 2, 5, 6, 9, 11,12,15,16 and 17) were better than Giza-95 by 5.43, 4.91, 4.29, 1.23, 6.57, 1.05, 0.96, 1.75, 1.49, 1.75 and 0.18%, respectively. These superior 3 genotypes out-yielded the check genotype Giza-95 in both seed and lint cotton yield across the five locations and considered promising materials for breeding programs to develop and isolate high yielding varieties of Egyptian cotton. Similar conclusion was obtained by Awaad and Mostafa (1996), El-Moghazy *et al* (1982) and Mohamed *et al* (2003).

Table 6. Mean performance of yield and yield components for the tested genotypes and cultivated varieties grown in Trail B across five locations in season 2020.

No.	Genotypes	SCY (k/f)	LCY (k/f)	Bw (g)	LP, %	U.H.M (mm)	U.R. (%)	Mic. (unit)	Maturity	+b (unit)	Y.St. (unit)
1	H ₅ 73/ 2018	9.39	12.03	152	40.2	29.3	84.5	4.2	93.6	12.1	2070
2	H ₅ 92/ 2018	9.61	11.97	149	39.3	29.1	84.6	4.3	94.6	12.6	1998
3	H ₅ 98/ 2018	9.27	11.43	146	38.8	29.2	84.9	4.2	93.4	12.5	2102
4	H ₅ 113/ 2018	8.95	11.19	148	39.4	29.7	85.3	4.5	95.4	12.6	2142
5	H ₆ 135/ 2018	9.29	11.90	149	40.4	29.1	84.2	4.3	93.8	12.8	2118
6	H ₆ 147/ 2018	9.25	11.55	151	39.4	28.8	84.6	4.3	94.8	12.8	2174
7	H ₆ 152/ 2018	8.58	10.58	147	38.8	29.0	85.3	4.3	94.0	12.6	2150
8	H ₇ 159/ 2018	9.12	11.51	146	39.7	28.8	78.1	4.3	93.2	12.4	2134
9	H ₈ 180/ 2018	9.50	12.16	151	40.4	30.0	78.0	4.0	94.4	12.0	2078
10	H ₈ 192/ 2018	8.89	11.14	149	39.5	29.0	85.4	4.2	94.0	12.1	2170
11	H ₈ 196/ 2018	9.21	11.53	149	39.5	29.2	84.5	4.3	93.0	12.3	2078
12	H ₉ 210/ 2018	9.01	11.52	146	40.3	29.6	85.1	4.4	94.4	12.5	2110
13	H ₁₀ 245/ 2018	8.67	10.86	153	39.5	30.0	85.5	4.4	94.4	11.8	2014
14	H ₁₁ 247/ 2018	8.55	10.71	148	39.4	28.6	85.1	4.3	95.0	12.6	1990
15	H ₁₁ 248/ 2018	9.20	11.61	149	39.8	29.0	84.1	4.4	93.2	12.5	1998
16	H ₁₁ 256/ 2018	9.20	11.58	153	39.8	29.2	84.7	4.2	94.0	12.2	1998
17	H ₁₁ 273/ 2018	9.22	11.61	151	39.6	28.4	84.6	4.4	94.2	11.9	2094
18	Mixed families	9.10	11.43	152	39.7	29.2	85.1	4.4	94.8	12.8	1958
19	Mixed families	8.05	10.12	148	39.5	28.5	84.8	4.2	94.0	12.3	2078
20	Giza 95	9.27	11.41	152	38.6	29.1	84.0	4.2	94.0	12.5	20.62
Mean		9.07	11.39	150	39.6	29.1	84.1	4.3	94.1	12.4	2076
L S D _{0.05}		0.65	0.82	4.93							
L S D _{0.01}		ns	1.16	ns							

ns = non-significant

Boll weight data presented in Table 6 indicated that, from the 17 tested genotypes no. 13 ((G91 x G90) x R101) and 16 ((G91 x G90) x G80) had bolls heavier than the two check varieties, and significantly surpassed

the three checks. Consequently, It could be concluded that, genotype (no. 4 (H₆146/2017)) was better than the two controls in all the studied traits until now, indicating that, these five hybrids, ((G 83 × (G 75 × 5844)) × G90] × G91), ((G 83 × (G 72 × Dandara)) × S109), ((G90 × A105) × G85), ((G91 × G90) × R101) and ((G91 × G90) × G80) performed well under the five locations in seed cotton yield, lint yield, and boll weight.

Concerning fiber quality in both trails, results showed that all genotypes were exactly in the same category of long staple cotton varieties, which have been cultivated in Upper and Middle Egypt.

CONCLUSION

Results of trails A and B indicated that, the promising cross ((G 83 × (G 75 × 5844)) × G90] × G91) was significantly higher in yield than the check genotypes in both seed and lint cotton yield in trail A and trail B across all locations, and this cross is considered promising materials for breeding programs to develop and isolate high yielding varieties of Egyptian cotton.

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تقييم بعض التراكيب الوراثية للقطن المصري تحت بيئات مختلفة

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تهدف هذه الدراسة الى دراسة سلوك التراكيب الوراثية لبعض هجن القطن المصري طويل التيلة للوجه القبلى من حيث المحصول ومكوناته مع مقارنتها مع الاصناف التجارية المنزرعة وهما الصنف جيزة ٩٠ والصنف جيزة 95. واشتملت هذه الدراسة على ٣٨ تركيب وراثى بالاضافة الى صنفى المقارنة بجانب تركيبين وراثيين للهجن المعزوله فى تجربة المحصول الاولية(أ) بمحطة بحوث سدس (بنى سويف) موسم ٢٠١٩. حيث تم الأنتخاب بداخل التجريه الاوليه(أ) ١٧ تركيب لتقييمهم الموسم التالى بتجربة ب. وكذلك اشتملت الدراسة على ١٧ تركيب وراثى بالاضافة الى صنف المقارنة (جـ ٩٥) بجانب تركيبين وراثيين للهجن المعزوله فى تجارب المحصول المتقدمة (ب) التى زرعت فى خمس مناطق وهى بنى سويف والفيوم واسيوط وسوهاج وقنا فى موسم ٢٠٢٠ كتجارب لقسم تربية القطن بمعهد بحوث القطن. وكانت اهم النتائج كما يلى: ١. كان التباين الراجع للتراكيب الوراثية معنوى للصفات المدروسة فى تجربة المحصول الاولية(أ) ومعنوي لكل الصفات المدروسة فى تجارب المحصول المتقدمة (ب) مما يدل على ان هناك اختلافات بين التراكيب الوراثية داخل كل بيئة. ٢. اظهرت النتائج وجود اختلافات عالية المعنوية بين البيئات لكل الصفات التى تم دراستها فى تجارب المحصول المتقدمة (ب). ٣. كان التفاعل بين البيئة والتراكيب الوراثية معنوى لصفة محصول القطن الزهر والشعر ووزن اللوزة مما يدل على ان التراكيب الوراثية كانت متباينة السلوك فى كل البيئات لهذه الصفات فى تجارب المحصول المتقدمة (ب). ٤. وجد ان هناك عدد من الهجن المباشرة من حيث المحصول هى الهجين [(جـ ٨٣ × (جـ ٧٥ × ٥٨٤٤)] × (جـ ٩٠) × (جـ ٩١) ، والهجين [(جـ ٨٣ × ٨٠) × (جـ ٩٠ × A107)] ، التى اعطت تفوقاً محصوليا على التركيب الوراثية المقارنة فى تجربة المحصول الاولية(أ). ٥. التراكيب الوراثية الناتجة من الهجين [(جـ ٨٣ × (جـ ٧٥ × ٥٨٤٤)] × (جـ ٩٠) × [(جـ ٩١ × (جـ ٨٣ × (جـ ٧٢ × دندرة)) × S109] والهجين (جـ ٩٠ × A107) × (جـ ٨٥) تفوقت على التراكيب الوراثية الناتجة من باقى الهجن وكذلك تفوقت محصوليا على التراكيب المقارنة فى تجربة (ب) . بجانب الهجينين (جـ ٩١ × ٩٠) × R101 و الهجين (جـ ٩١ × ٩٠) × (جـ ٨٠) المتفوقين فى وزن اللوزة على التراكيب المقارنه. ٦. ضرورة الاستمرار فى تربية وتقييم السلالات المباشرة والتراكيب الوراثية الناتجة من الهجن المتفوقة سابقة الذكر فى عدة مناطق بحيث يتمكن المربى من تحديد افضل السلالات المباشرة التى تتفوق على الاصناف المحلية المزروعة فى المحصول ومكوناته وخاصة الهجين [(جـ ٨٣ × (جـ ٧٥ × ٥٨٤٤)] × (جـ ٩١) المتفوق فى كلا التجريبتين خلال عامي البحث.

المجلة المصرية لتربية النبات ٢٥(١): ١٥-٩٨ (٢٠٢١)