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Genetic Variability among Egyptian Extra-long Staple Cotton Genotypes for Some Economic Traits

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THIS INVESTIGATION was completed at Sakha Station of Agricultural Research, over 2021 and 2022 seasons to evaluate the variance among some Egyptian cotton genotypes for yielding potential and fiber quality traits. Materials comprised thirteen extra-long staple cotton genotypes (*Gossypium barbadense* L.). Genotypes were arranged in RCBD design replicated quadric. Data were collected for, boll weight, seed cotton yield, lint yield, lint%, earliness index, micronaire reading, fiber strength, fiber length and uniformity index. Genotypes (G) exhibited significant differences for all traits. Years (Y) had insignificant differences on most of traits, GxY interaction was significant for some traits. Giza 87 and Giza 88 had the lower yield while the rest of genotypes insignificantly varied. Giza 87, Giza 93 and Giza 93 x Menufi genotypes had the finest fibers, Giza 87, Giza 92 and Giza 96 had the strongest fibers. Genotypic and phenotypic exhibited broad scope of variability for all traits. Seed and lint cotton yields had moderate PCV values, while the remainder traits showed low values, GCV showed moderate value for lint yield and low values for the remainder traits. Broad-sense heritability recorded low value for boll weight to very high values for most of traits. For GS%, moderate values were recorded for seed cotton yield, lint yield and earliness index while the rest had low values. In this investigation, seed cotton yield, lint yield and earliness index exhibited high heritability together with moderate genetic advance values, subsequently, direct selection for such traits is anticipated to induce considerable improvement in next generation.

Keywords: Egyptian cotton, Genetic advance upon selection, Heritability, Variability.

Introduction

Cotton (*Gossypium* species) is extremely considered the most remarkable source of natural textile fibers worldwide. The acquaintance concerning nature and extent of genetic variability for fiber yield and its quality traits within the present germplasm of the crop is fundamental to select good genetic materials to start an effective breeding program to get superior genotypes in yield and fiber properties (Shakeel et al., 2018).

Selecting parental genotypes with superiority in fiber yield and its quality traits is fundamental procedure in the cotton breeding program. Parents are preferred for their performance as well as their combining ability. Gnanasekaran & Thiyagu (2021) found that parents that possess high mean performance coupled with significant and positive GCA are required for all plant characters except earliness traits, seed index and fiber fineness.

The existing of significant genetic variability among cotton germplasm in cotton yield, its component as well as the various fiber attributes in the upland cotton (*G. hirsutum* L.) has been recorded in many studies (Jarwar et al., 2018; Hampannavar et al., 2020; Sarwar et al., 2020; Gnanasekaran & Thiyagu, 2021; Chakholoma

et al., 2022; Bhanudas et al., 2023). Similar significant differences among Egyptian cotton (*G. barbadense* L) genotypes for most cotton yield, yield components and fiber properties were reported (Abdelmoghny et al., 2020; Amer et al., 2020; Eldessouky et al., 2021; Amer, 2022; Abdel-Aty et al., 2023; Yehia et al., 2023) that elucidate the wide range of genetic variance within these genotypes.

The various effects of genotypes, environment and growing season (year) significantly modulate fiber yield and its quality. Consequently, assessment of the effects of different environmental conditions is indispensable to pick out cultivars with high-yielding potentials and supreme fiber properties. The effect of the growing seasons (years) on the various attributes of cotton plant was recorded and found to significantly vary from one year to another over the genotypes, which point out the diversified effects of the climatic factors predominant from planting to harvest on the mean performance of the estimated traits over the studied genotypes (Amer et al., 2020; Eldessouky et al., 2021; Yasar, 2023). Moreover, Darawsheh et al. (2022) found greater effect for the year that was two to six times as compared to the environmental effect and they concluded that the year effect is deemed as remarkable source of variance in fiber quality traits in cotton. In the same connection, Imtiaz et al. (2017) resulted that genetic variability was foremost affected by the environmental factors then by years and followed by genotypes. In addition, Unay et al. (2004) resulted the prominence of the differences between environments (years/locations) and genotypes for cotton yielding characters.

The combined genetic information concerning broad-sense heritability and genetic advance over means is useful tool to the breeder to predict the behavior of the parents to be utilized in crop breeding program and the eventual effects of selection procedures (Soomro et al., 2010; Eswari et al., 2017) and to facilitate selection of appropriate breeding technique to enhance the genetic makeup in cotton plant (Aziz et al., 2014; Sun et al., 2017). Moreover, Roy et al. (2019) stated that the genetic coefficient of variation coupled with heritability offer trustworthy estimates concerning the predicted genetic advance after phenotypic selection.

The aim of current work was to analyze the

existing variations and genetic diversity between some genotypes of the Egyptian extra-long staple cotton for some economic traits i.e. yield, its components and fiber quality traits to provide base information for these traits that may be used in improving yield potential and fiber properties during the selection of new promising genotypes.

Materials and Methods

This work was consummated during 2021-2022 seasons at Sakha Agric. Res. Station, Agric. Res. Center, Kafr El-Sheikh governorate, Egypt.

Materials
Plant materials in this study involved thirteen extra-long staple cotton genotypes belong to *Gossypium barbadense* L. These genotypes comprised five cultivated varieties and eight promising lines in F6 to F9. The origin and pedigree of these genotypes were clarified in Table 1.

Methods
In the two growing seasons, pure seeds of the thirteen cotton genotypes were arranged in a randomized complete block design (RCBD) with four replications. The plot contained five rows 4.0m long and 0.65m wide. Hills were 0.30m apart and each hill was thinned to two plants. All other cultural practices were done as recommended package for ordinary cotton cultivation.

Before Picking time a random sample of 50 open bolls were taken from the outer two rows and were used to determine the traits: Boll weight (BW) in grams, in addition to fiber quality traits, micronaire instrument reading in micron (μ/inch), fiber strength (FS, g/tex) which is the force in grams required to break a bundle of one tex unit in size of fibers, a tex unit is the weight in grams of 1000 meters of fiber length, as well as fiber length (FL) as the upper half mean length (mm), length uniformity index (UI%) which is the ratio between the mean length and the upper half mean length of the fibers, expressed as a percentage. Measurements were done via High Volume Instrument (HVI) spectrum system.

All fiber properties were measured in the laboratories of Cotton Technology Research Division, Cotton Research Institute, Agric. Res. Center, Giza, Egypt.

TABLE 1. Name and pedigree of the studied thirteen cotton genotypes

No.	Genotype	Generation	Pedigree
1	Promising line 1	F6	Giza 93 x Menufi
2	Promising line 2	F6	Giza 96 x C.B 58
3	Promising line 3	F6	(Giza 93 x Giza 92) x (Pima S$_7$ x Giza 76)
4	Promising line 4	F6	[(Giza 70 x Pima S$_6$) x Giza 92] x C.B 58
5	Promising line 5	F6	Giza 96 x (Giza 93 x Suvin)
6	Promising line 6	F7	{(G68 x G45) x[(G84 x G45) x G45]} x G.87
7	Promising line 7	F7	G.92 x [(G.84 x G.45) x S 62]
8	Promising line 8	F9	Giza 96 x Giza 93
9	Giza 87	Released variety	(G.77 x G.45) A
10	Giza 88	Released variety	(G.77 x G.45) B
11	Giza 92	Released variety	Giza 84 x (Giza 74 x Giza 68)
12	Giza 93	Released variety	Giza 77 x Pima S^6
13	Giza 96	Released variety	[Giza 84 x (Giza 70 x Giza 51 B)] x S 62

At harvest time, the three guarded rows of each plot were twice hand-picked to determine seed cotton yield (SCY)/ plot in kilograms (Plot area= 3 rows x 4m length x 0.65m width= 7.8m^2), lint yield (LY)/ plot in kilograms, lint percentage (L%) and earliness index determined as percentage of seed cotton yield at first pick to total seed cotton yield/plot.

Statistical and genetic analyses

Firstly, data of each individual year were analyzed and homogeneity of variance was tested for the possibility of combined analysis. Subsequent confirming homogenous error of variance, a combined analysis of variance was used. The obtained data was subjected to the standard analysis of variance as single year and as a combined analysis for both seasons according to Singh & Chaudhary (1999). Differences among means of genotypes for each trait were compared by using the least significant difference (LSD) test as follows:

L.S.D = t$_α$ x$\sqrt{2}$ x Error MS/r.

Moreover, the following genetic parameters were estimated for each trait from the ANOVA mean squares in the combined data: genotypic and phenotypic variances as outlined by Miller et al. (1958) as follows:

Environmental variance (Ve) = Error mean squares (EMS)

Genotypic variance (Vg)= (Genotype mean squares (GMS) – Error mean squares (EMS))/

(Number of replications (r))

Phenotypic variance (Vp) = Vg + (Ve/r)

In addition, broad sense heritability as well as coefficients of phenotypic and genotypic variability were estimated as outlined by Burton & Devane (1953) as follows: Heritability in broad sense (H^2_b): $H^2_b = \frac{vg}{vp}$ x 100

Phenotypic coefficient of variability (PCV)= ($\sqrt{\delta^2 p} / \bar{x}$) x 100

Genotypic coefficient of variability (GCV)= ($\sqrt{\delta^2 g} / \bar{x}$) x 100

Genetic advance (GA) is a measure of how much gain might be gotten from phenotypic selection for a trait in the population. The expected genetic advance under selection as percentage of the mean (GS) was estimated as outlined by Johanson et al. (1955) as follows:

Genetic advance (GA) = k x δ_p x h^2_b

Expected genetic advance as percentage: G.S%= (GA / $\bar{x}$) x 100

where: k= 1.76 (10% selection intensity); δp = Phenotypic standard deviation; h^2_b = Heritability in broad sense and $\bar{x}$= General mean of the trait.

Selection intensity is the mean of the deviations from the population mean, measured in units of the phenotypic standard deviation of the population.

Results and Discussion

Analysis of variation

The analyses of variation for 13 Egyptian extra-long staple cotton genotypes concerning the estimated traits are displayed in Table 2.

Mean squares of genotypes (G) manifested highly significant (P≤ 0.01) or significant differences (P≤ 0.05) for all traits in this study (except for micronaire reading in first season and fiber strength in the second season), this result showing that the studied cotton genotypes differ in their genetic structure and reflecting the presence of great amount of genetic variation within such genotypes for the tested traits, that offer plenty scope for improving such traits throughout crossing followed by directing selection.

These findings are in the same line with former investigations resulted that cotton genotypes varied significantly in yielding traits as well as fiber quality traits in upland cotton by Eswari et al. (2017), Jarwar et al. (2018), Hampannavar et al. (2020), Chakholoma et al. (2022) and Bhanudas et al. (2023), and in the Egyptian cotton by Abdelmoghny et al. (2020), Eldessouky et al. (2021), Amer (2022), Abdel-Aty et al. (2023) and Yehia et al. (2023).

With respect to the different effect of growing years (Y), data revealed that most of the estimated traits showed insignificant differences from year to another over genotypes, except for seed cotton yield and lint yield, this result indicated that the tested genotypes behaved similarly over the climatic factors in the two seasons of the study for the estimated traits.

TABLE 2. Mean squares gained from the analysis of variance for 13 cotton genotypes in two years and their combined data for the estimated traits

S.O.V.	d.f	Yield and its components					Fiber quality traits			
		BW (g)	SCY (kg/plot)	LY (kg/plot)	L %	EI %	Mic. (µg/inch)	FS (g/tex)	FL (mm)	UI %
2021										
Reps	3	0.036 --	0.184 --	0.023 --	1.369 *	96.27 --	0.122 --	2.34 --	1.892 *	4.284 *
Genotypes	12	0.075 **	0.493 **	0.088 **	15.98 **	293.33 **	0.082 --	6.52 *	1.847 **	3.757 **
Error	36	0.017	0.121	0.015	0.313	23.57	0.062	2.73	0.457	1.127
2022										
Reps	3	0.003 --	0.430 --	0.057 --	0.006 --	126.81 --	0.126 --	3.92 *	1.255 --	3.205 *
Genotypes	12	0.003 *	0.642 **	0.127 **	16.329 **	162.40 **	0.148 **	6.26 --	2.520 **	2.288 *
Error	36	0.001	0.211	0.028	0.350	48.05	0.049	4.31	0.733	0.963
Combined over years										
Year (Y)	1	0.016 --	10.104 **	1.421 **	1.997 --	2045.95 --	0.270 --	4.24 --	0.031 --	0.038 --
Reps x Y	6	0.020	0.307	0.040	0.687	111.54	0.124	16.28	1.573	3.745
Genotypes (G)	12	0.039 **	0.827 **	0.169 **	27.843 **	397.15 **	0.180 **	8.34 *	2.908 **	5.016 **
Y x G	12	0.039 **	0.307 *	0.046 *	4.468 **	58.58 --	0.050 --	4.43 --	1.459 **	1.029 --
Error	72	0.009	0.166	0.022	0.331	35.81	0.056	3.52	0.595	1.045

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

BW: Boll weight, SCY: Seed cotton yield, LY: Lint yield, L%: Lint%, EI: Earliness index, Mic: Micronaire value, FS: Fiber strength, UHM: Upper half mean and UI: Uniformity index.

With regard to the (GxY) interaction, combined data over years shown in Table 2 disclosed that boll weight, seed cotton yield, lint yield, lint% and fiber length had significant G xY interactions that showing the diverse performance for the genotypes from year to another, therefore, it is demanded to test genotypes more than a year to increase efficiency of selection to improve such traits, this result may be ascribed to the reality that each genotype demands certain zone with adequate climatic status to obtain its various prospects. Our results were in the same line with those outlined by Imtiaz et al. (2017), Amer et al. (2020), Eldessouky et al. (2021), Darawsheh et al. (2022) and Yasar (2023) who resulted that growing season significantly affected the performances of cotton genotypes. Contrariwise, the rest of traits (earliness index, micronaire reading, fiber strength and uniformity index) which exhibited insignificant (G x Y) interaction, suggested that genotypes performance similarly in both years of the study. Consequently, selection at one season for improving these traits could be efficacious for vast range of planting seasons which is advantageous from the breeder point view.

The average of genotype's performance

The average performance of 13 genotypes of the extra-long staple cotton for the studied traits combined over years is shown in Table 3.

Cotton yield and its components

Boll weight: The mean of BW in grams for the tested 13 genotypes varied from 2.88g for promising line no.1 to 3.12g for Giza 96, the remainder genotypes were medium in BW. It is obvious that the boll weight within the Egyptian extra-long staple genotypes is low which consider a serious problem encounter the cotton breeder in his numerous attempts to increase yield of the plant through increasing the boll weight.

Seed cotton yield: SCY/plot in kilograms differed from 2.189kg for Giza 87 to 3.218kg obtained by promising line no.6. The remainder genotypes were medium in their yield. Data offered in Table 3 clearly indicated that Giza 87 and Giza 88 genotypes had the lowest SCY/plot which resulted in the significant differences in the studied genotypes while the remainder (11) genotypes exhibited insignificant differences in this trait.

Lint yield: LY/plot in kilograms varied from 0.721kg gained by Giza 87 to 1.210kg gained by Giza 96, the remainder genotypes were occupied intermediate possession in this trait.

Data concerning LY/plot showed that three genotypes (Giza87, Giza 88 and Giza 93) had the lowest values which resulted in the significant differences in the studied genotypes while the remaining (10) genotypes had insignificant differences between them in this respect.

Lint %: L% showed wide range from 32.94% that given by Giza 87 to 39.10% for Giza 96. Generally, the tested genotypes showed wide variance in this trait indicating the existence of plentiful amount of the genetic variance among these genotypes for such trait, that offer plenty scope for improving such trait through direct selection.

Earliness index: EI % was determined as percentage of seed cotton yield at first pick to the total seed cotton yield/plot. It varied from 58.41% for Giza 87, which indicate more lateness to 82.39% for promising line no.3, the more earliness of this genotype may be attributed to the foreign genotype involved in it (Pima S7). In general, the tested genotypes had a wide spectrum of variance in this trait which point to the existence of abundant genetic variance within these genotypes for earliness, which give the breeder a good chance to improve such trait by selecting earlier genotypes.

Fiber properties

Micronaire reading: Mic. is a measurement of the thickness of the cell walls of cotton fiber in μg/inch units and is used to represents a combined measure of cotton fineness and maturity, micronaire is lower for finer fibers.

Mic. was determined for the 13 cotton genotypes and had highly significant differences among genotypes which varied from 3.74 (less fineness) produced by Giza 92 to 3.20 (highest fineness) obtained by Giza 93. In general, all genotypes obtained fine fibers with micronaire reading less than 4.0, the finest fibers were obtained by three genotypes (Giza 93, Giza 93 x Menufi and Giza 87) with micronaire reading 3.20, 3.45 and 3.50, respectively with insignificant differences among them.

TABLE 3. Mean performance of 13 extra-long staple cotton genotypes for cotton yield, its component and fiber quality traits combined over two years

Genotypes		Yield and its components				
		B.W (g)	S.C.Y (kg/ plot)	L.Y (kg/ plot)	L %	E.I %
1	Giza 93 x Menufi	2.88	3.064	1.088	35.55	76.16
2	Giza 96 x C.B 58	2.95	3.034	1.165	38.39	71.70
3	(Giza 76 x Giza 93 x Giza 92) x Pima S$_7$	2.97	3.079	1.113	36.02	82.39
4	[(Giza 70 x Pima S$_6$) x Giza 92] x CB 58	2.92	3.016	1.089	36.06	74.87
5	Giza 96 x (Giza 93 x Suvin)	2.92	3.131	1.155	37.01	77.24
6	{(G68 x G45) x[(G84 x G45) x G45]}x G. 87	3.01	3.218	1.096	34.10	67.83
7	G.92 x [(G.84 x G.45) x S 62]	2.97	3.001	1.120	37.32	75.10
8	Giza 96 x Giza 93	2.99	2.791	1.063	37.91	80.04
9	Giza 87	2.90	2.189	0.721	32.94	58.41
10	Giza 88	3.08	2.327	0.799	34.31	65.52
11	Giza 92	3.00	3.158	1.122	35.46	77.64
12	Giza 93	3.06	2.704	0.924	34.05	81.93
13	Giza 96	3.12	3.091	1.210	39.10	67.73
Mean		2.98	2.91	1.50	36.02	73.58
LSD 5%		0.12	0.537	0.193	0.75	7.89
LSD 1%		0.13	0.542	0.196	0.77	7.96

Genotypes		Fiber quality traits			
		Mic. (µg/inch)	FS (g/ tex)	UHM (mm)	UI %
1	Giza 93 x Menufi	3.45	44.31	35.64	87.72
2	Giza 96 x C.B 58	3.67	44.75	35.65	87.15
3	(Giza 76 x Giza 93 x Giza 92) x Pima S$_7$	3.71	43.71	35.64	87.47
4	[(Giza 70 x Pima S$_6$) x Giza 92] x CB 58	3.70	45.56	36.57	87.92
5	Giza 96 x (Giza 93 x Suvin)	3.70	45.71	35.66	87.60
6	{(G68 x G45) x[(G84 x G45) x G45]}x G. 87	3.72	45.11	36.27	87.89
7	G.92 x [(G.84 x G.45) x S 62]	3.65	43.99	36.47	87.65
8	Giza 96 x Giza 93	3.58	44.94	35.76	88.24
9	Giza 87	3.50	46.31	35.45	85.94
10	Giza 88	3.60	44.70	35.37	85.80
11	Giza 92	3.74	47.15	34.30	87.40
12	Giza 93	3.20	44.15	35.65	87.55
13	Giza 96	3.65	46.22	35.35	88.52
Mean		3.61	45.12	35.64	87.44
LSD 5%		0.31	2.47	1.02	1.34
LSD 1%		0.33	--	1.04	1.36

BW: Boll weight, SCY: Seed cotton yield, LY: Lint yield, L%: Lint percentage, EI: Earliness index, Mic: Micronaire; FS: Fiber strength, UHM: Upper half mean and UI: Uniformity index.

Fiber strength: FS was measured in g/tex which is the force in grams needed for breaking a fiber bundle at a specified distance.

FS ranged from 43.71g/tex for promising line no.3 to 47.15g/tex for Giza 92. This wide spectrum of variability among genotypes in their fiber strength is important from the view point of the breeder to facilitate selection procedures for increasing fiber strength in the new selected genotypes.

Fiber length: FL in millimeter units was menstruated as 2.5% fiber length (length of the upper half mean). The extra-long staple genotypes varied from 34.30mm for Giza 92 that was significantly lower than the other genotypes as it had the lowest fiber length and may be considered as long staple variety because the extra-long staple genotype must exceed 34.9mm in fiber length. Whereas the promising line no.4 gave the highest fiber length (36.57mm).

Three promising line no. 4, 6 and 7 had the higher fiber length that exceeded 36.0mm (36.57, 36.27 and 36.47, respectively), these genotypes could be used in breeding program to improve fiber length in Egyptian cotton.

Uniformity index: The uniformity of fiber length (UI) was calculated as the percentage ratio of 50% to 2.5% fiber lengths. Genotype possesses low UI% has a high discrepancy in fiber length that bring about difficulty in dealing with fibers and ultimately reduces yarn quality.

Results given in Table 3 indicated that UI% differed from 85.80% for Giza 88 that varied significantly from the remaining genotypes as it had the lowest UI%, because Giza 88 and Giza 87 are old varieties as it released earlier than the remaining genotypes, whilst Giza 96 had the highest value (88.52%). The remainder genotypes had intermediate positions in UI%.

These outcomes agreed with those reported previously which found significant variation within cotton genotypes in yielding ability traits as well as fiber traits in tetraploid upland cotton (Eswari et al., 2017; Sarwar et al., 2020; Darawsheh et al., 2022; Bhanudas et al., 2023; Yasar, 2023), and in the Egyptian cotton (Abdelmoghny et al., 2020; Amer et al., 2020; Eldessouky et al., 2021; Abdel-Aty et al., 2023; Yehia et al., 2023).

Measurements of variability

The parameters of variability estimated in this study comprised, range, phenotypic and genotypic variance (Vp and Vg), phenotypic and genotypic coefficient of variability (PCV and GCV), heritability in broad-sense and expected gain from selecting 10% of the superior plants for each trait in plant population. These parameters for each of the estimated traits in the present investigation are displayed in Table 4.

Results concerning the range of the estimated traits revealed that boll weight for the extra-long staple cotton genotypes exhibited narrow range of variability that was from 2.66g to 3.37g, this narrow range inhibits cotton breeder attempts to improve BW or to increase cotton yield through increasing boll weight.

Seed cotton yield/plot showed wide disparity between the minimum and maximum values as it ranged from 1.54kg to 4.26kg. The same trend was recorded for lint yield/plot that had wide disparity ranged from 0.52kg to 1.63kg. This wide range in the yielding potential of the tested genotypes indicating that cotton breeder has the chance to improve the total yield for these genotypes by the directional selection towards the higher yielding plants.

Similarly, lint percentage trait varied widely from 31.95% to 41.00%, this trait is remarkable from the textile view point because as it increased the lint yield increase from the same weight of seed cotton yield, so it is a primary goal for cotton breeder to select plants with high lint% to increase the fiber yield.

Earliness index% displayed enormous scope among genotypes as it ranged from 51.64% to 93.22% that facilitates selection for earlier plants within genotypes in this study. Genotypes with more earliness are economically desired as it save a part of the growing season with its equipment (labor, water, fertilizers and pesticides) and enable the grower to plant a winter crop in the proper time.

Regarding to fiber quality traits, the tested genotypes exhibited broad ranges for all fiber traits, indicating that breeder can select finer and more strength, taller and more uniform fibers within these genotypes.

TABLE 4. The genetic estimates evaluated in cotton genotypes for the tested traits

Parameter		Yield and its components					Fiber quality traits			
		BW	SCY	LY	L%	EI%	Mic.	F.S	FL	UI%
Range	Min.	2.66	1.54	0.52	31.95	51.64	2.70	37.70	33.80	84.10
	Max.	3.37	4.26	1.63	41.00	93.22	4.20	49.60	38.60	89.90
Mean		2.98	2.91	1.50	36.02	73.58	3.61	45.12	35.64	87.44
Vp		**0.0052**	**0.1034**	**0.0211**	**3.480**	**49.644**	**0.0225**	**1.043**	**0.363**	**0.627**
Vg		0.0004	0.0650	0.0154	2.922	42.322	0.0163	0.488	0.181	0.469
Vge		0.0075	0.0353	0.0060	1.0343	5.6915	0.0015	0.228	0.216	0.004
Ve		0.0011	0.0208	0.0028	0.0414	4.4764	0.0070	0.440	0.074	0.131
PCV%		**2.425**	**11.060**	**13.831**	**5.179**	**9.575**	**4.159**	**2.263**	**1.692**	**0.906**
GCV%		0.638	8.774	11.778	4.745	8.841	3.534	1.549	1.194	0.807
h^2_b		6.92	62.93	72.52	83.95	85.25	72.22	46.85	49.83	79.49
GA		0.009	0.356	0.185	2.756	10.572	0.191	0.842	0.529	1.108
G.S%		**0.295**	**12.245**	**12.358**	**7.652**	**14.367**	**5.286**	**1.866**	**1.484**	**1.267**

Vp: Total phenotypic variability, Vg: Genotypic variability, Vge: variability of GxY interaction, Ve: Environmental variability, PCV and GCV: Phenotypic and genotypic coefficient of variability, h^2_b: Heritability in broad-sense, GA: Expected genetic gain from selection and GS: Expected genetic gain as percent of the general mean of the trait.

With regard to micronaire reading, the range was wide and expanded from 2.70 μg/inch to 4.20 μg/inch, however, micronaire value is lower for finer fibers.

With concern to fiber strength, genotypes showed broad range that extended from 37.70(g/tex) to 49.60(g/tex), more strength is desired in textile industry.

Concerning fiber length estimated as the length of the upper half mean of fibers, genotypes varied widely from 33.80mm 38.60mm. Similarly, length uniformity index ranged from 84.10% to 89.90%.

The wide range among cotton genotypes for the different plant characters were outlined by Jarwar et al. (2018), Bhatti et al. (2020), Sarwar et al. (2020), Amer et al. (2021), Gibely (2021), Balarabe et al. (2022) and Yasar (2023).

Knowledge concerning extent and nature of variance obtainable within cotton germplasm for various plant traits is fundamental for selecting better traits to gain noteworthy amelioration.

The inherited part of variability (genetic part) is persuasive within the non-inherited part, which reasons hurdle in selecting the desired genotype. Phenotypic (Vp) and genotypic (Vg) variances for the tested 13 cotton genotypes exhibited broad scope of variation for cotton yielding traits the range expanded from 0.0052 and 0.0004 for both Vp and Vg, respectively in BW to 49.644 and 43.322, respectively in EI%. Furthermore, fiber properties cleared that Vp and Vg varied from 0.0225 and 0.0163, respectively for the micronaire reading to 1.043 and 0.488, respectively for the fiber strength.

As the variability values are affected by magnitude of the units used in measuring the various traits, hence, the coefficient of phenotypic and genotypic variance (PCV and GCV) were proposed. PCV% ranged from 0.906% obtained by length uniformity index to 13.831% for lint yield, while GCV% expanded from 0.638% for boll weight to 11.778% for lint yield.

PCV and GCV were assorted by Sivasubramanian & Menon (1973) to three

categories: low, moderate and high (<10%, 10-20% and >20%, respectively). Therefore, moderate PCV% values were obtained by two traits i.e. seed cotton yield and lint yield (11.06% and 13.83%, respectively) while the remnant of traits obtained low values. Otherwise, GCV exhibited low values for all measured traits except for lint yield that had moderate GCV% value (11.778%).

The low values for GCV and PCV observed for most of the estimated traits clarified the hardness of improving these traits by direct selection.

In this study, there was an approach between Vp and Vg as well as between GCV and PCV (more than 60%) for seed cotton yield, lint yield, lint%, earliness index, micronaire reading and uniformity index, suggesting that the total variance is mainly attributed to genetic factors and by lesser degree by environmental factors, thus high heritability estimates will achieved, such traits were mainly controlled by the additive genes. The remnant of traits (boll weight, fiber strength and fiber length) showed wide gap between phenotypic and genotypic variance (less than 50%) suggesting the participation of environmental factors and genetic factors on the inheritance of such traits. These outcomes were similar to those resulted by Eswari et al. (2017), Jarwar et al. (2018), Kumar et al. (2019), Amer et al. (2020), Kumbhar et al. (2020), Gibely (2021), Abo Sen et al. (2022) and Balarabe et al. (2022).

Heritability coupled with the genetic advance illustrate the genetic portion of variance and anticipate the genotype's performance for utilizing in breeding programs to obtain superior genotypes (Soomro et al., 2010). However, broad-sense heritability (h^2_b) assesses the genetic part of phenotypic variance. High heritability value for traits facilitate selection for individual plants in early generations effectively as compared to traits with less heritability values.

Hallauer & Miranda (1981), classified heritability values of <30% as low, 30-50% as moderate, 50-70% high and >70% as very high. Accordingly, the tested genotypes, showed low h^2_b value (6.92%) for boll weight, moderate values for fiber strength and fiber length (46.85% and 49.83%, respectively), high value (62.93%) for seed cotton yield and very high values for the traits lint yield, lint%, earliness index, micronaire

reading and length uniformity index with values of 72.52%, 83.95%, 85.25%, 72.22% and 79.49%, respectively.

To sum, h^2_b values estimated for most traits point to the slight environmental contribution to the total variance and heritability is mainly attributed to genetic factors. Many other works reported moderate to high h^2_b in cotton for various plant characters (Eswari et al., 2017; Kumar et al., 2019; Amer et al., 2020; Kumbhar et al., 2020; Gibely, 2021; Balarabe et al., 2022).

The expected genetic gain under selection (GA) indicates the genetic improvement in the trait as compared to the main population after a cycle of selection at particular intensity of selection (Johanson et al., 1955). In this investigation, GA for yield and its component traits presented in Table 4 showed that GA was neglible for boll weight 0.009g which emphasize the difficulty to improve this trait via selection among the Egyptian cotton. Seed cotton and lint yield/ plot showed moderate GA as it gave 0.356Kg and 0.185kg, respectively, while lint % had higher value (2.756%) and earliness index showed the highest GA with 10.572%.

For fiber quality traits, data in Table 4 showed that GA values were 0.191 μg/inch for micronaire reading, 0.842 g/tex for fiber strength, 0.529mm for the upper half mean and 1.108% for length uniformity index.

Johanson et al. (1955) assorted the genetic gain upon selection as percent of the trait's mean (GS%) to: low, moderate and high for the values (<10%, 10-20% and >20%, respectively). Thus, results related to GS% after choosing the preferable 10% of plants within the population are given in Table 4. Results exhibited moderate GS% values for seed cotton yield, lint yield and earliness index with values of 12.245%, 12.358% and 14.367%, respectively while the remaining traits exhibited low GS%.

Johanson et al. (1955) proposed that high value of heritability coupled with high value of genetic advance (GS%) offer an evident base for the trustworthy of a specific trait in selection for improving this trait than heritability only. In this work, high heritability jointly with moderate genetic advance were observed for the traits seed cotton yield, lint yield and earliness index, and

subsequently it is expected that selection for such traits will induce considerable improvement in next generation. The remnant traits had various values of heritability along with low GS% indicating non additive gene action controlling these traits and proposing the powerless of simple selection for improving these traits. Our findings are in harmony with those previously obtained by Jarwar et al. (2018), Shakeel et al. (2018), Kumar et al. (2019), Amer et al. (2020), Gibely (2021) and Balarabe et al. (2022).

Conclusion

The tested extra-long staple genotypes varied in their genetic potential reflecting the reasonable part of genetic diversity present within this germplasm for the estimated traits that offer plenty scope for improving such traits throughout artificial hybridization followed by simple selection. High heritability values together with moderate values of genetic gain were observed for seed cotton yield, lint yield and earliness index, thus selection for the aforementioned traits is prophesied to induce considerable improvement in next generation.

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التباين الوراثى لبعض الصفات الاقتصادية فى الأقطان المصرية فائقة الطول

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أقيمت هذه الدراسة بهدف معرفة كمية ونوع التباين الموجود بين بعض التراكيب الوراثية للقطن المصرى فائقة الطول لبعض الصفات المحصولية وصفات جودة التيلة للاستفادة منها فى برنامج التربية لتحسين هذه الصفات. ولتحقيق هذا الهدف تم زراعة ثلاثة عشر تركيب وراثى من القطن المصرى فائق الطول منها خمسة أصناف وثمانية سلالات مبشرة فى الأجيال من السادس الى التاسع لتقييمها بمزرعة محطة التجارب الزراعية بسخا بمحافظة كفر الشيخ خلال موسمين زراعيين (2021، 2022 م). تمت زراعة التراكيب الوراثية فى تصميم قطاعات كاملة العشوائية فى أربعة مكررات وتم دراسة الصفات التالية: متوسط وزن اللوزة بالجرام، محصول القطعة التجريبية من القطن الزهر والشعر بالكيلوجرام، تصافى الحليج، معدل التبكير، الى جانب الصفات التيلة وتشمل النعومة، المتانة، الطول ومعدل انتظام الطول. أظهرت النتائج المتحصل عليها ما يلى: وجود فروق عالية المعنوية بين التراكيب الوراثية لكل الصفات المدروسة. لم تختلف معظم الصفات معنويا من موسم لآخر كما أن التفاعل بين التراكيب الوراثية والسنوات كان معنويا لصفات وزن اللوزة ، محصول القطن الزهر والشعر للقطعة التجريبية ، تصافى الحليج وطول التيلة. أعطى الصنفان جيزة 87 وجيزة 88 أقل القيم للصفات المحصول ومكوناته بينما باقى التراكيب الوراثية لم تختلف معنوياً فى هذه الصفات. التراكيب الوراثية جيزة 87 ، جيزة 93 و(جيزة 93 x منوفى) أعطت أفضل قيم النعومة بينما أظهرت الأصناف جيزة 87، جيزة 92 وجيزة 96 أفضل قيم للمتانة. أعطت كل التراكيب الوراثية طول تيلة أعلى من 35ملم (فائقة الطول) فيما عدا الصنف جيزة 92 الذى أظهر أقل القيم (34.30 ملم) . أظهرت التراكيب الوراثية مدى واسع لكل الصفات المدروسة ماعدا صفة وزن اللوزة التى أظهرت مدى ضيق مما يوضح صعوبة الإنتخاب لتحسين هذه الصفة فى الأقطان المصرية فائقة الطول. أظهرت النتائج معنوية عالية للتباين الكلى والوراثى لكل الصفات المدروسة بما يعكس الاختلاف بين هذه التراكيب الوراثية تحت الدراسة. أعطى معامل التباين المظهرى قيماً متوسطه لصفات محصول القطن الزهر والشعر للقطعة التجريبية، بينما كانت القيم منخفضة لباقى الصفات، وقد كانت قيم معامل التباين الوراثى منخفضه لكل الصفات فيماعدا صفة محصول القطن الشعر التى أعطت قيمة متوسطة. أعطت الكفاءة الوراثية بالمعنى العام قيمة منخفضة لصفة وزن اللوزة وقيماً متوسطة لصفتى المتانة وطول التيلة وقيمة عالية لصفة محصول القطن الزهربينما كانت القيم عالية جداً لباقى الصفات مما يدل على إمكانية الإنتخاب المباشر لهذه الصفات فى برامج التربية.التحسين المتوقع نتيجة إنتخاب 10٪ أعلى من المتوسط العام للصفة أعطى قيماً متوسطة لصفات محصول القطن الزهر والشعر للقطعة التجريبية ومعدل التبكير، أما باقى الصفات فقد أعطت قيماً قليلة فى هذا الشأن. من هذه الدراسة يتضح أن القيمة الوراثية أعطت قيماً عالية مقترنةً بقيم متوسطة من التحسين المتوقع نتيجة الإنتخاب لصفات محصول القطن الزهر والشعر ومعدل التبكيرمما يوضح أن الإنتخاب لهذه الصفات من المتوقع أن يؤدى الى تحسين هذه الصفات فى الجيل التالى.