

Heritability and Genetic Advance as Genetic Indicators for Improvement in Two Cotton Crosses

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Abstract

The primary breeding goal for the Egyptian cotton breeding program is how to genetically improve both yield and fibre quality traits, while most of these agronomically traits are biometric traits. The objective of the present study is to evaluate variability and estimate frequency of transgressive segregants in order to isolate early superior individual plants which exceeding the better parent for some yield and fiber quality traits in two intraspecific cotton crosses in early transgressive segregating generation (F_2). The F_1 was highly significant superior than the better parent (Giza 97 and Giza 94) of the two crosses for all the studied traits except boll weight and lint %. Most of the studied traits in F_2 generation showed high values of broad sense heritability coupled with low GAM % indicated that these traits controlled by non-additive gene action. All the studied traits had positive skewness sign except for lint %. Presley index and uniformity index for the two cotton crosses and upper half mean for cross II showed negative skewness. The negative skewness indicated that the population had more plants frequency with higher mean values than population mean and controlled by dominancy alleles. While, the traits that had positive skewness are controlled by additive gene action. The two cotton crosses showed transgressive segregants for all the studied traits. Cross I has higher transgressive index for yield traits than cross II, while cross II has the same trend for fiber quality traits than cross I. These results indicated that the both parents of the two cotton crosses had different alleles and genes governing the respective studied traits, which will help cotton breeder to combine beneficial alleles into a single genotype by rigorous selection process. This strategy could be used to improve many economic biometric traits by using better and stringent selection procedure to enhance Egyptian cotton productivity which is major concern in Egypt. The breeder can use transgressive segregation as an indicator of genetic variability to select the most superior plants.

Keywords: Genetic Variability, Heritability, Threshold Value, Transgressive Segregation, Genetic Advance, Transgressive Index.

Introduction

The Egyptian cotton breeding program used intra-specific hybridization between cotton genotypes belonging to *Gossypium barbadense* L., to produce new varieties [1]. The breeder can create variability by hybridization or mutation techniques. Hybridization is a technique used to accumulate plus or favourable genes from both parents as a consequence of recombination. So, the parents involved in hybridization should have high combining ability with each other and preferably be genetically diverse that is quite different [2]. The hybridization technique has many advantages such as producing transgressive segregation for using in selection

processes of superior plants or families, to release new variety, which characterized by high yield, good fiber quality and widely adapted to different environments. Also, hybridization is used to take advantage of transient hybrid vigour, move desirable variation among lineages, and generate novel phenotypes. So, the successful breeding program is depending on estimate genetic variability, which provides the main basis for effective selection process. Most of economic traits in cotton breeding program are polygenic in nature. So, the cotton breeder should use different quantitative genetic analysis for these traits. The Quantitative traits possess continuous variation and largely affected by the environmental factors, but

can be changed by suitable breeding procedures [3-5].

Genetic variability is defined as the observed phenotypic variation happened in plant populations and is mainly attributable to genetic differences between genotypes. Heritability in broad sense is referred as the ratio between genotypic variance over the total phenotypic variance or the magnitude of transmissibility of traits from parents to their offspring [6]. So, Genetic variability coupled with heritability of a trait could indicate the possibility ratio and extent to which improvement can be achieved through selection on the phenotypic basis. Also, high heritability coupled with high genetic gain as a percentage of mean could bring out the expected progress from selection and help breeder to design future selection process. pointed that high heritability along with high genetic gain implied that the yield and fiber quality traits can be improved through hybridization and selection from early segregating generation [7-9].

Cotton yield is a complex trait governed by many genes and correlated with many other traits. So, direct selection for yield in cotton is not so easy and prediction of its performance based on aerial morphological traits, environmental factors and so many elements. The available knowledge of existing variability and degree of association between yield and its attributing traits and their relative contribution is essential for developing high yielding productive genotypes. The geneticists reported that the success in obtaining the desired genotypes depends on obtaining genetic recombination between both linked and unlinked alleles. Many cotton researchers noted that there is a significant positive correlation between yield and its components [10-12].

Transgressive segregation is one of the most important keys to improve cultivated plants. Plant breeders define transgressive segregation as the production of phenotypes that falling outside phenotypic parental range [13]. This may be often observed in F_2 or later generation (F_3) from intra-specific mating due to high ratio of heterozygosity and the superiority will not maintained in later generations. Also, interspecific transgression is a significant tool for crop improvement, when it represents a potential source of novel genetic variation. While, the improvement of self-pollinated crops is depending on the production of homozygous progeny superior to their parental genotypes. Therefore, transgressive segregation can identify the ability of hybridization process to produce novel genotypes and phenotypes. reported that transgressive segregation resulted in individuals with a higher level of adaptation than their parents [2, 12]. The number of transgressive segregants individuals of a segregating generation can be estimated from the distance between phenotypes and their parents [13].

Therefore, the present study was undertaken to find out the genetic variability, broad sense heritability, genetic advance and genetic advance as a percentage of mean of various yield, its components and fiber quality traits in two intra-specific cotton crosses. Hence, the present study was conducted to select the top 10% of transgressive segregants for all the studied traits in early segregating generation based on transgressive index.

Materials and Methods

The selfed seeds of the two new long staple cotton variety Giza 94 and Giza 97 were crossed as a female parent with the two breeding

accessions D101 and S109 as a male parent to produce two intra-specific cotton crosses (Giza 97 x D101) and (Giza 94 x S109) in 2018 growing season. The four cotton genotypes belonging to *Gossypium barbadense* L. In the growing season of 2019 the F_1 was self-pollinated to produce F_2 seeds. The four parents, F_1 hybrids and F_2 seeds were evaluated under field growing conditions at Sakha Experimental Station, Agricultural Research Center, Kafr El-Sheikh government, Egypt during the season of 2020. During the experiment the cotton crop was conducted according to the standard recommendations for cotton production to obtain healthy plants. Each of the four parents, F_1 and F_2 plants were sown as individual plants, the distance within plants and between rows were 70 cm. The number of the evaluated plants for each parents, F_1 and F_2 generations were 10, 10 and 270 plants for each cross.

Eight quantitative traits were studied; boll weight (BW), seed cotton yield per plant (SCY/P), lint yield per plant (LY/P) in grams and lint percentage (L %). Also, fiber quality traits; upper half mean (UHM) measured by the digital fibrograph, Pressley index (PI) as Presley index measured by stelometer, fiber fineness as micronaire value (MIC) and uniformity index (UI %) were tested at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

Statistical Analysis

Data were recorded on individual plant basis in each cross. Means and standard errors (SE) were determined for each trait for (P_1 , P_2 and F_1 hybrid), while descriptive statistics for the F_2 generations for all the studied traits across two cotton crosses was calculated as outlined by [14]. Mean values of the genetically uniform genotypes were compared using t test. Normality of the phenotypic distribution of all traits in the segregating generation (F_2) was done for the two cotton crosses and both skewness and kurtosis were computed. Broad sense heritability (h_2bs) was estimated as the ratio of genotypic variance to the total phenotypic variance for all the studied traits as suggested by [15]. The genetic advance (GA) and genetic advance as percent of mean (GAM %) was calculated and categorized following the method suggested by [16].

To study genetic effects, the components of generation's means of the studied populations, P_1 , P_2 , F_1 within each intra-specific cotton cross, as described by [17] used to estimate additive effects over all loci [d], average of dominance effects over all loci [h] and average phenotype of the two parents or mid-parent (MP). Degree of dominance and heterosis over mid-parent were measured as $[h] / [d]$ and $[h] - [d]$, respectively.

Transgressive segregation

The transgressive segregants is defined as the individuals which had mean values of F_2 plants exceeding their better parent or lower than their inferior parent. The limiting normal deviation (ND) value calculated as described by [18].

$$ND \text{ Value} = \frac{\text{Threshold Value} - F_2^-}{\sigma F_2}$$

Threshold value = $P^{(+)} + 1.96 * \sigma_{p^{(+)}}$
Where $P^{(+)}$, $\sigma_{p^{(+)}}$, F_2^- and σF_2 are the mean and standard deviation of increasing parent, mean of F_2 generation and standard deviation of F_2 generation, respectively. The individuals transgressed this

threshold limit were considered as the transgressive segregants.

Transgressive index (T_1) indicates the proportion of phenotypic differences between both parents and the phenotypic range in the F_2 population was calculated as described by [19].

$$T_1 = \frac{F_2 \text{max} - F_2 \text{min}}{P_1 - P_2}$$

Where T_1 = transgressive index, F_2 max = the highest value in the F_2 population, F_2 min = the lowest value in the F_2 population and $P_1 - P_2$ is the difference between the two parents.

Results and Discussions

The variability level of segregating populations based on the differences between the two parents derived from the interested trait. The two parents Giza 97 and Giza 94 are new national long staple cotton varieties, while the other parents (D101 and S109) are breeding accession. Table 1 showed that the four parents of the F_2 population have highly significant differences for all the studied traits. The behavior of F_1 's appeared to be greater than the two parents over the two studied crosses. The differences between mid parent and F_1 hybrid was highly significant for all traits except, boll weight for the two crosses and uniformity index (UI %) for the first cross (Giza 97 x D101) only. While, the differences between P_1 (Giza 97 for cross I and Giza 94 for cross II) and the F_1 hybrid showed highly significant variability for all studied traits except boll weight and lint % for the two cotton crosses. On the other hand, a highly significant difference was recorded between F_1 and P_2 (D101 for cross I and S109 for cross II). Similar findings were recorded for early segregating generations in some Egyptian cotton crosses [8, 12].

Since the variability and diversity between P_1 , P_2 and F_1 for the two crosses revealed wide divergence for the studied traits. Therefore, the genetic effects involved in the characterization of gene transfer responsible for such attributes to the studied Egyptian cotton varieties were examined. Whilst, both additive and dominance gene effects were important in the controlling studied traits as presented in Table 2. Most estimates of additive gene effect were greater than dominance effects for all traits except, boll weight, seed cotton yield / plant, lint yield / plant and micronaire value for cross I (Giza 97 x D101). Moreover, most of dominance estimates [d] showed positive direction for all traits except upper half mean and Presley index. While, cross II (Giza 94 x S109) recorded higher values of

dominance gene effect for all the studied traits except, boll weight than additive effect with positive direction. Such positive or negative estimate of dominance gene action [d] might indicate that the trait attributes progressively directed towards the better parent or the lower parent, respectively.

Estimates of degree of dominance and heterosis calculated on the basis of [d] and [h] parameters are illustrated in Table 2. Moreover, most estimates of degree of dominance were greater than unity for boll weight, seed cotton yield / plant, lint yield / plant and micronaire value for cross I (Giza 97 x D101) indicating a case of positive overdominance over the better parent (Giza 97). The traits; lint % and uniformity index had less unity values with positive sign, while upper half mean and pressley index had less unity values with negative sign indicating partial dominance. On the other hand, cross II (Giza 94 x S109) recorded higher positive values more than unity for all the studied traits except boll weight. These results showed that cross II has over-dominance effect over better parent (Giza 94). While, boll weight has positive sign and less than unity, indicated partial dominance. The evidence for dominance directional is easy to find and it is the presence of inbreeding depression [6].

Transgressive segregation and heterosis are main targets for any breeding program. Heterosis over mid-parent values showed varied estimates according to cross and trait as presented in Table 2. Most estimates of heterosis were negative for all the studied traits except, seed cotton yield / plant, lint yield / plant and micronaire value for cross I (Giza 97 x D101). While, cross II (Giza 94 x S109) showed positive sign for all the studied traits except, boll weight. This may be due to the higher values of dominance gene action controlling these traits. Also, cross II (Giza 94 x S109) had higher values with positive effect for heterosis for all traits than cross I (Giza 97 x D101) except, boll weight. Unlike heterosis or extreme phenotypes that occur as a result of transgressive segregation can be fixed after F_2 generation and played important roles in evolution. Cross I have higher values and positive heterosis direction for yield traits except, lint % than cross II. On the other hand, cross II showed positive and higher heterosis values for fiber quality traits than cross I. These results indicated that expression of heterosis effects for these traits were more tended in cross II than cross I. Similar results for different Egyptian cotton crosses were also obtained by [10, 20].

Table 1: Phenotypic mean performances and standard errors (SE) for all studied traits among two intraspecific cotton crosses

Traits	P ₁ ±SE	P ₂ ±SE	F ₁ ±SE	F ₂ ±SE	Contrasts			
					P ₁ /P ₂	MP/F ₁	P ₁ /F ₁	F ₁ /P ₂
Cross I (Giza 97 x D101)								
BW	3.387±0.033	3.010±0.023	3.310±0.048	3.484±0.017	**	NS	NS	**
SCY/P	202.830±0.522	125.690±0.320	212.317±2.637	210.081±1.037	**	**	**	**
LY/P	80.723±0.423	42.080±0.255	84.440±1.160	82.556±0.495	**	**	**	**
L%	39.800±0.212	33.520±0.122	39.769±0.220	39.287±0.122	**	**	NS	**
UHM	33.470±0.056	32.250±0.043	32.520±0.087	33.841±0.052	**	**	**	*
MIC	4.190±0.028	4.060±0.031	4.260±0.037	4.217±0.016	*	**	*	**
PI	10.760±0.037	10.190±0.035	10.370±0.037	10.956±0.017	**	*	**	**
UI %	86.350±0.082	84.270±0.073	85.510±0.104	85.476±0.048	**	NS	**	**
Cross II (Giza 94 x S109)								
BW	3.387±0.033	3.110±0.023	3.310±0.048	3.502±0.017	**	NS	NS	**
SCY/P	220.155±2.114	138.690±0.320	232.487±2.646	255.746±1.045	**	**	**	**
LY/P	86.674±0.847	49.206±0.280	91.747±1.175	98.645±0.495	**	**	**	**
L%	39.370±0.088	35.808±0.114	39.665±0.198	39.395±0.090	**	**	NS	**
UHM	32.380±0.085	32.100±0.071	33.990±0.125	34.021±0.062	*	**	**	**
MIC	3.890±0.028	3.360±0.031	4.260±0.037	4.338±0.017	**	**	**	**
PI	10.510±0.031	10.380±0.033	10.650±0.052	10.787±0.037	*	**	*	**
UI %	85.470±0.073	84.850±0.082	86.400±0.144	85.498±0.066	**	**	**	**

Significance for the contrasts (comparisons among means) is represented with asterisks: P < 0.05 (*), P < 0.01 (**), NS = non-significant and MP = mid-parent value.

Table 2: Genetic parameters for the studied uniform genotypes for the two cotton crosses for all studied traits

Parameters	Mid-parent MP	Additive [d]	Dominance [h]	Degree of dominance h/d	Heterosis h-d	Alleles
Traits						
Cross I (Giza 97 x D101)						
BW	3.199	0.188	0.221	1.175	0.033	+
SCY/P	164.260	38.570	54.410	1.411	15.840	+
LY/P	61.401	19.322	24.928	1.290	5.606	+
L%	36.660	3.140	2.815	0.897	-0.325	+
UHM	32.860	0.610	-0.340	-0.557	-0.950	-
MIC	4.115	0.035	0.145	4.143	0.110	+
PI	10.475	0.285	-0.105	-0.368	-0.390	-
UI %	85.310	1.040	0.200	0.192	-0.840	+
Cross II (Giza 94 x S109)						
BW	3.249	0.139	0.062	0.444	-0.077	+
SCY/P	179.423	40.733	53.065	1.303	12.332	+
LY/P	67.940	18.734	23.807	1.271	5.073	+
L%	37.589	1.781	2.076	1.166	0.295	+
UHM	32.240	0.140	1.750	12.500	1.610	+

MIC	3.625	0.265	0.635	2.396	0.370	+
PI	10.445	0.065	0.205	3.154	0.140	+
UI %	85.160	0.310	1.240	4.000	0.930	+

Hybridization of self-pollinating crops produces segregation and recombination, which starting from the F₂ generation. F₂ generation is the ideal generation in which segregation and recombination had maximum for imposing selection. The level of variability in F₂ population depends on the diversity between the two parents of the interested traits. The four parents showed highly significant differences for all the studied traits will produce high level of variability through F₂ generation (Table 1). Descriptive Statistics, broad sense heritability, genetic advance and genetic advance as a percentage of mean was calculated based on the mean of individual data of the F₂ population for the two cotton crosses as presented in Table 3. Coefficient of variation (CV %) is the percentage ratio between standard deviation and mean was less than 15 % for all the studied traits over two cotton crosses indicated good experimental precision.

The mean values of F₂ progenies for all studied yield traits among the two cotton crosses recorded higher phenotypic mean values than their homozygous grandparents (four parents) and their heterozygous immediate parents (F₁ hybrids). While, the fiber quality traits falling in the range of long staple cotton category. This indicated that the cotton breeder can select the more desirable plants exceed the better parent. Also, low values of standard deviation for all the studied traits could increase selection efficiency. Phenotypic coefficient of variation (PCV %) and genotypic coefficient of variation (GCV %) showed amount of variation for different traits. All the evaluated traits for the two cotton crosses had lower values less than 10 % indicating narrow range of variability, restricting the scope for selection. So, the breeder should exploit diverse germplasm to increase genetic variability. Also, lower differences between PCV and GCV were not much influenced by the environment, suggesting ample scope for improvement through selection procedures. This agreement between PCV and GCV showed that the variation could be due to genetics and affected by the environmental factors.

Broad sense heritability (h₂bs) values showed higher values more than 60 % for all the studied traits as classified by [15]. This indicated that the genetic factors controlling expression of these evaluated traits had a great effect. The high heritability values may be explain as the parents carry different additive alleles at the same loci controlling these traits. While, the genetic advance as a percentage of mean (GAM %) was lower than 10 % for all the studied traits among two cotton crosses except, boll weight and micronaire value for the two crosses and pressley index for cross II, which had higher values more than 10 % (Table 3). High values of broad sense heritability (h₂bs) coupled with low GAM % indicated that these traits controlled by non-additive gene action. While, the other three traits which had higher heritability with high or moderate GAM % are controlled by additive gene action with low effect of environmental factors. These results are in accordance with those of [12, 21]. This indicated that these traits with high broad sense heritability values had high rapid genetic gain that could be achieved by selection due to the presence of high additive genetic

variance to show the existence of families with different reproductive values. Therefore, these results could help plant breeder to determine the appropriate strategy for crop improvement. Crossing between parents or pure lines that had different genetic backgrounds could increase genetic variability of the segregating populations. Hybridization is result of accumulation of genes with the same direction to give high rise of the phenotype that exceeds its parents. Also, heritability estimates could used as a good indicator to predicate the improvement through selection producer.

Phenotypic distributions of the F₂ plants are shown in Figures 1 and 2 for cross I (Giza 97 x D101) and cross II (Giza 94 x S109), respectively. Number of F₁ and F₂ had higher mean values than their high (Giza 97 and Giza 94) and low (D101 or S109) mean of the parents was observed for boll weight, seed cotton yield, lint yield and micronaire value for cross I and all the studied traits for cross II except, lint %. These traits had high number of F₂ individuals with extreme values of transgressive segregation frequency or higher transgressive segregating % as presented in Table 4. Also, most of these individuals surrounded the mean value of the highest parent (Giza 97 and Giza 94) for cross I and cross II, respectively and displaying wide segregation. While, the remaining traits that had number of F₂ individuals falling beyond higher or lower parent showed narrow or low segregation. The occurrence of some extreme F₂ individuals is expected due to environmental effect rather than genetic reasons since the F₂ population was much larger than the parental populations.

Skewness and kurtosis are estimations of curves' departure from normal distribution, by inflating and narrowing the real distribution of individual data. Skewness showed the distribution of individuals in positive or negative direction compared to population mean, whereas kurtosis explains the flatness of the curve for studied traits in evaluated population [22]. The kurtosis value was less than three in F₂ generations for all the studied traits as presented in Table 3 and Figures 1 and 2 for cross I and II, respectively. This indicated that, the curve was platykurtic. Both skewness and kurtosis should be zero for a perfectly normally distributed variable as described by [23]. In fact the ideal kurtosis value is three but most statistical packages subtract 3 from the value. So that, both skewness and kurtosis ideal values are zero. Thus, value of skewness may be positive or negative indicating right or left skewness, respectively. The studied traits showed different skewness value and sign over the two cotton crosses. All the studied traits had positive skewness sign except for lint %, pressley index and uniformity index for the two cotton crosses and upper half mean for cross II showed negative skewness. These results indicated that the traits with negative skewness indicating that the population had more plants frequency with higher mean values than population mean. So, the selection efficiency for this population will lead to identify these plants that have higher mean values. This may be related to the plants with negative skewness controlled by dominance alleles. On the other hand the plants had positive skewness controlled by additive gene action, so selection for this population used to identify superior

progenies. Similar results were recorded by [12, 24].

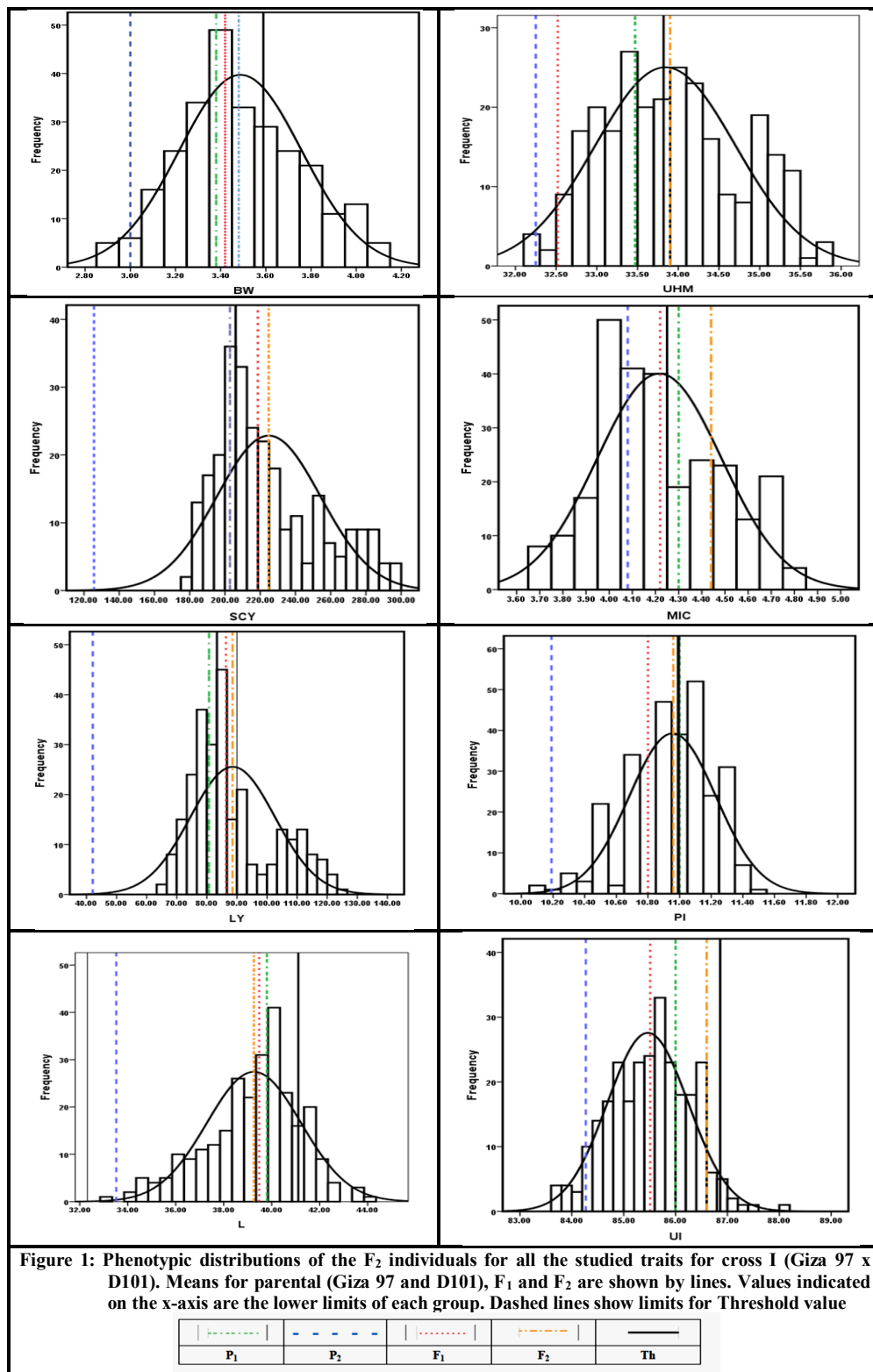
Kurtosis explains the flatness of the curve for different traits in the evaluated population. The kurtosis values are signifying the peakness or flatness of the curve. The kurtosis value was less than three for all studied traits of all the two cotton crosses indicating that, the curve was platykurtic. The two cotton crosses showed negative kurtosis sign for all the studied traits among two cotton crosses, indicating that the distribution has lighter tails and a flatter peak than

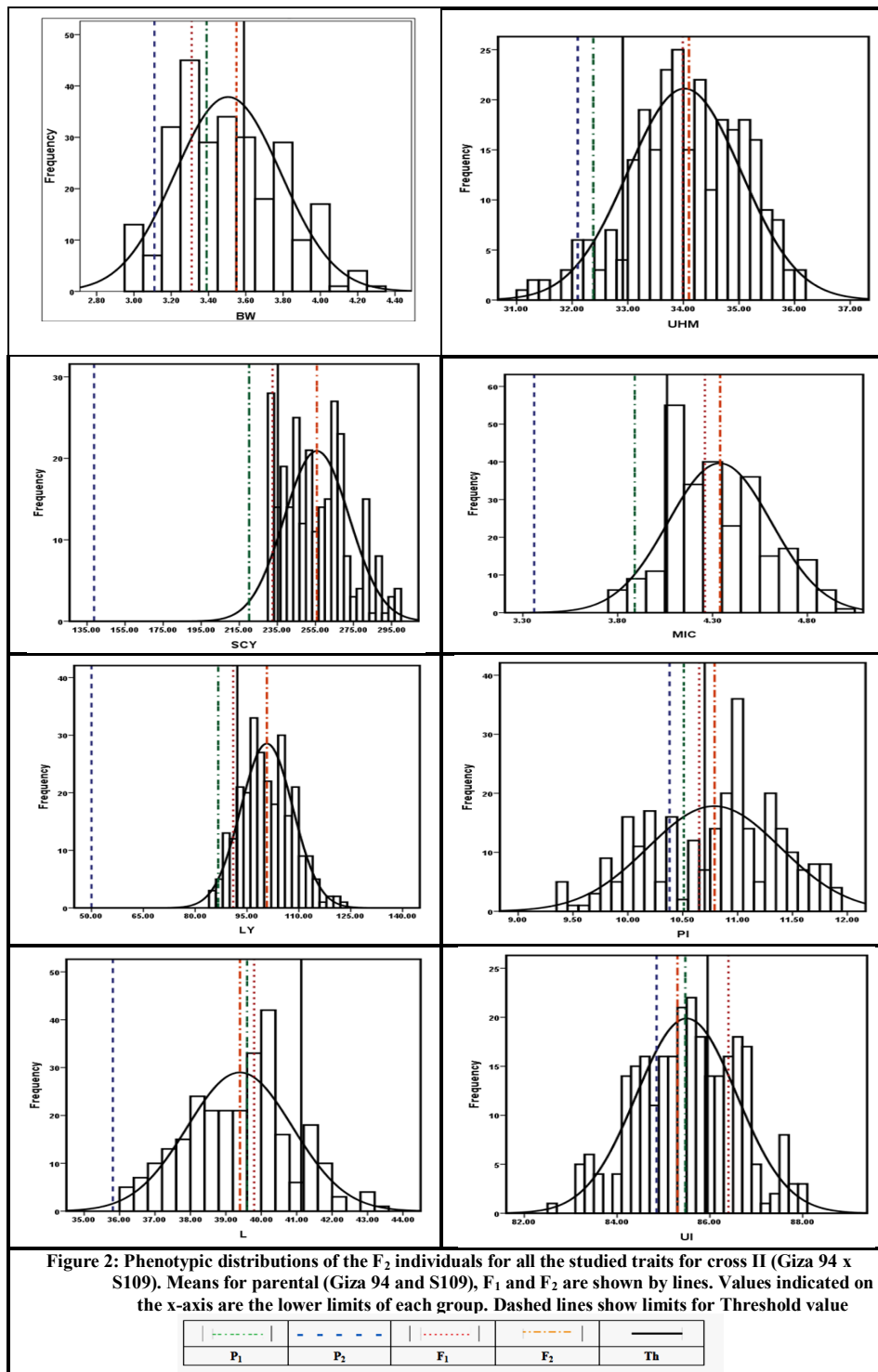
normal distribution. While, two traits lint % and pressley index for cross I had positive kurtosis sign indicates that the distribution has a sharper peak, thinner shoulders, and fatter tails than the normal distribution. Also, all the studied traits had lower skewness and kurtosis values across cross I and II, reflecting solid confirmation of data homogeneity and normality. Recorded different skewness and kurtosis sign and values for yield and fiber quality traits among different Egyptian cotton genotypes [12, 24, 25].

Table 3: Descriptive Statistics in segregating F₂ populations of the studied traits for the two intra specific cotton crosses

Traits	BWg	SCY/Pg	LY/Pg	L%	UHM mm	MIC	PI	UI %
Parameters								
Cross I (Giza 97 x D101)								
Mean	3.487	224.833	88.540	39.261	33.841	4.217	10.956	85.464
SE	0.017	1.793	0.856	0.119	0.052	0.016	0.017	0.048
Median	3.500	216.500	84.400	39.600	33.800	4.200	11.000	85.500
SD	0.271	29.460	14.060	1.963	0.861	0.269	0.274	0.781
Variance	0.074	867.909	197.691	3.852	0.741	0.072	0.075	0.610
Skewness	0.211	0.785	0.796	-0.532	0.129	0.316	-0.689	-0.023
Kurtosis	-0.448	-0.345	-0.378	0.122	-0.683	-0.689	0.078	-0.208
Range	1.200	121.700	60.600	10.800	4.000	1.100	1.400	4.400
Minimum	2.900	176.100	65.200	33.100	31.800	3.700	10.100	83.700
Maximum	4.100	297.800	125.800	43.900	35.800	4.800	11.500	88.100
CV %	7.716	13.104	15.881	5.100	2.543	6.378	2.504	0.927
GCV %	7.124	11.722	14.546	4.650	2.411	5.738	2.270	0.844
PCV %	7.716	13.104	15.881	5.100	2.543	6.378	2.504	0.927
h ₂ bs	0.852	0.800	0.839	0.831	0.899	0.809	0.821	0.828
GA	0.778	7.645	5.536	2.071	1.467	0.739	0.757	1.298
GAM %	22.326	3.400	6.253	5.271	4.336	17.522	6.911	1.518
Cross II (Giza 94 x S109)								
Mean	3.504	255.746	100.738	39.396	34.021	4.338	10.787	85.498
SE	0.017	1.045	0.459	0.090	0.062	0.017	0.037	0.066
Median	3.500	253.400	100.150	39.560	34.050	4.300	10.900	85.500
SD	0.285	17.174	7.543	1.487	1.020	0.272	0.604	1.084
Variance	0.081	294.932	56.896	2.210	1.041	0.074	0.365	1.174
Skewness	0.359	0.395	0.301	-0.001	-0.394	0.440	-0.256	-0.046
Kurtosis	-0.499	-0.632	-0.276	-0.365	-0.155	-0.257	-0.762	-0.393
Range	1.300	68.600	37.120	7.350	4.900	1.300	2.500	5.300
Minimum	3.000	230.100	85.300	36.090	31.100	3.800	9.400	82.600
Maximum	4.300	298.700	122.420	43.440	36.000	5.100	11.900	87.900
CV %	8.113	6.715	8.239	3.771	2.998	6.269	5.605	1.268
GCV %	6.847	5.864	7.328	3.421	2.764	5.655	5.392	1.151
PCV %	8.113	6.715	8.239	3.771	2.998	6.269	5.605	1.268
h ₂ bs	0.712	0.763	0.791	0.823	0.850	0.814	0.926	0.824

GA	0.668	5.563	3.969	1.766	1.510	0.747	1.267	1.510
GAM %	19.082	2.175	4.024	4.483	4.439	17.217	11.742	1.766





Estimation of transgressive segregation in F₂ generation

Transgressive segregation is defined as the segregation of alleles in F₂ generation with phenotypic values exceeding the two parents. Each parent contributes by different increasing (plus) or decreasing (minus) alleles, which brought together by recombination to give transgressive segregation. So that, the trait intensity appeared in the new variety is greater than their parents. So, allele's combination from both parents with the same effect direction (plus or

minus) is called complementary gene action and these individuals had extreme phenotypes [2]. The analysis of transgressive segregation in F₂ generation could help breeder to determine potential populations to be selected and reduces population size in the later generations. If the breeding program did not show high progeny better than their parents or transgressive segregation, the breeding program would not work [26].

The frequency of transgressive segregants classified the individuals of F₂ generation into phenotypes greater than better parent and lower than lower parent based on threshold value (TV) as a critical value. The phenotypes that had values more or low than better or low parents know as positive or negative transgressive segregants, respectively. While, the rest individuals know as non- transgressive ones. Table 4 presented threshold value (TV), frequencies of transgressive segregants and its percentage (TS %). The progenies of cross II (Giza 94 x S 109) recorded higher number of transgressive segregant frequency for all the studied traits than cross I. This indicated that the parent of cross II had different alleles and genes controlling these traits. So, hybridization technique followed by selection procedures is used to collect the beneficial alleles into a single genotype. The better and stringent selection procedure can pyramid the desirable quantitative alleles into a single genotype to enhance the productivity of Egyptian cotton. The maximum number of transgressive segregation was recorded for seed cotton yield / plant > lint yield / plant > Pressley index > fiber length > micronaire value > boll weight > uniformity index > lint % across the two cotton crosses. This order arranges the studied traits from difficult to improve to the east one depending on the maximum number of transgressive segregation exceeding the better parent as presented in the F₂ generation. Lint % showed the lowest number of transgressive segregation 46 and 39 plants for cross I and II, respectively. The other traits had large number of transgressive plants for evaluation in F₃ generation.

Transgressive index is used to estimate transgressive segregation in the F₂ population. The transgressive index is defined as the proportion of the F₂ population difference to the difference between the two parents. The transgressive index for the two F₂ populations ranges from 1.269 to 15.714 for lint yield / plant and micronaire value in cross I (Giza 97 x D101) and from 0.842 to 19.315 for seed cotton yield and Pressley index in cross II (Giza 94 x S109) as presented in Table 4. These results showed that highest transgressive

index is due to the small differences between the two parents and the wide distribution of the F₂ population. The range of F₂ generation had the highest value for 49.053 and 68.60 for lint yield / plant and seed cotton yield / plant for cross I and II, respectively. Cross I (Giza 97 x D101) had the highest transgressive index for yield traits more than cross II (Giza 94 x S109), while cross II has higher values for fiber quality traits. This is the reflection of wide distribution of yield traits in F₂ population for cross I more than cross II. On the other hand, cross II has wide F₂ distribution for fiber quality traits than cross I. While, lint % and uniformity index (UI %) for cross I had the lowest number of transgressive segregant frequency (46 and 12 plants) than cross II (100 and 154 plants), respectively. While, their parents were significantly different for lint % and uniformity index as presented in Table 1. These results indicated that Giza 97 and D101 for cross I had large variance 39.80, 86.350 and 33.52 , 84.270 than Giza 94 and S109 for cross II 39.37, 85.470 and 35.808, 84.850, for lint % and uniformity index, respectively.

Three traits upper half mean and pressley index for cross II and micronaire value for cross I recorded higher values for transgressive index 17.500, 19.315 and 15.714, respectively. The variability between these traits showed only significant differences (32.380 and 32.100), (10.510 and 10.380) for Giza 94 and S109 for cross II, respectively and (4.190 and 4.060) between Giza 97 and D101 for cross I. while, these traits showed the highest values of total number of transgressive segregant (TS) was 294, 258 and 312 for upper half mean, pressley index for cross II and micronaire value for cross I, respectively. [19] reported that the greater value of transgressive index could make the greater chance of getting transgressive segregation in F₂ population. The more transgressive index, the more transgressive segregant and the higher similarity between parents may produce higher transgressive segregation in F₂ generation. However, the highest percentage of transgression does not always imply a greater index.

Table 4: Threshold value (TV), normal deviation value (ND), percentage, transgressive index (TI) and range in the values of transgressive segregants (TS %) in the two cotton crosses

Traits	Crosses	F ₂ population						
		Threshold value TV	ND	Transgressive index TI	Frequency of TS	TS %	TS %	Range in values of T.S.
Boll weight	Cross I	3.589	0.370	4.430	101	211	37.407	2.850-4.520
	Cross II	3.589	0.303	4.549	110		40.741	3.000-4.260
Seed cotton yield / plant	Cross I	206.064	-0.236	1.305	153	391	56.667	171.855-272.556
	Cross II	233.259	-1.309	0.842	238		88.148	230.000-298.700
Lint yield / plant	Cross I	83.343	0.097	1.269	130	345	48.148	60.463-109.516
	Cross II	91.925	-0.827	1.103	215		79.630	80.534-121.862
Lint %	Cross I	41.113	0.912	2.050	46	85	17.037	33.103-45.976
	Cross II	39.917	0.351	2.064	39		14.444	36.091-43.442
Upper half mean	Cross I	33.816	33.816	-0.029	3.279	100	294	37.037
	Cross II	32.543	-1.449	17.500	194		71.852	31.000-36.000

Micronaire value	Cross I	4.253	0.136	15.714	104	258	38.519	3.700-4.800
	Cross II	4.062	-1.015	2.453	234		86.667	3.8-5.100
Pressley index	Cross I	10.990	0.126	2.456	154	312	57.037	10.100-11.500
	Cross II	10.690	-0.160	19.315	158		58.519	9.400-11.911
Uniformity index %	Cross I	86.858	1.745	2.116	12	166	4.444	83.700-88.100
	Cross II	85.358	-0.129	8.548	154		57.037	82.600-87.900

The main targets of the cotton breeder for these two long staple cotton crosses is increasing yield traits and maintain fiber quality traits in the range of this cotton category. Transgressive frequency for the two crosses had less number of F_2 plants (46 and 39 for cross I and cross II, respectively) that recorded higher values than their threshold value (41.113 % and 39.917 % for cross I and II, respectively) for lint %. Then the selection of the top 10 % plants 27 and 23 plants for cross I and II, respectively are shown in Table 6. The top 10 % plants had higher values for seed cotton yield /plant, lint yield / plant and lint %. These three traits had positive values for increasing % than threshold value as estimated in Table 7. This indicated that these selected plants exceed their parents or F_2 mean

and could be used as the superior families in F_3 generation. On the other hand, phenotypic mean performance of fiber quality traits ranged from positive or negative values as shown in Table 7 for the two cotton crosses, but the fiber quality traits falling in the range of long staple category. So, these promising plants are desirable to the breeder for this category and should focusing selection to increase yield traits. For this purpose the breeder used direct selection to maximize lint % and indirect selection to increase most positive correlated traits with lint %. Many cotton investigators noted that most of the cotton yield and its components had highly significant positive correlation among different cotton crosses [10-12].

Table 6: The top selected 10 % plants from the F_2 generation which exceed threshold value for yield traits for the two cotton crosses

No. of F_2 plants	BW g	SCY/P g	LY/P g	L%	UHM mm	MIC	PI	UI %
Cross I (Giza 97 x D101)								
F_2 mean	3.48	224.83	88.54	39.28	33.84	4.21	10.95	85.47
TV	3.58	206.06	83.34	41.11	33.81	4.25	10.99	86.85
8	3.61	271.68	113.58	41.81	35.20	3.90	10.70	86.00
20	3.20	282.96	116.76	41.26	33.40	4.00	10.90	86.20
28	3.45	280.00	115.08	41.20	34.40	4.00	10.90	85.40
48	3.21	293.56	123.18	41.96	32.80	3.90	11.20	84.60
49	4.00	261.20	108.13	41.40	34.20	4.40	11.10	86.10
52	3.44	270.43	112.19	41.48	34.90	4.30	10.50	86.40
67	3.50	281.05	117.23	41.71	34.90	3.80	11.30	85.80
78	3.10	286.93	119.78	41.75	35.10	4.40	11.00	85.20
83	3.43	260.83	108.01	41.41	34.80	4.40	11.00	86.00
84	3.80	269.14	110.97	41.23	35.10	4.40	10.90	86.20
105	3.50	265.50	111.23	41.90	35.30	4.10	11.10	87.10
113	3.55	275.30	115.27	41.87	33.10	4.20	11.00	85.10
128	3.30	279.09	115.62	41.43	34.30	4.00	10.40	85.70
129	3.40	284.52	116.67	41.48	33.30	4.20	10.50	84.90
151	3.36	262.61	108.35	41.26	32.90	4.50	10.90	84.90
156	3.03	282.71	116.94	41.36	32.80	4.00	11.30	85.10
158	3.25	295.98	123.35	41.68	33.90	4.20	10.90	85.70
163	3.17	291.15	121.36	41.68	32.90	4.10	11.30	84.70
165	3.30	276.68	116.28	42.03	32.90	4.00	11.20	84.80
179	3.36	262.61	108.72	41.40	34.90	4.30	11.00	86.20

199	4.00	261.20	108.33	41.47	35.40	4.20	10.90	86.50
209	3.70	263.11	110.82	42.12	33.50	3.70	11.10	84.70
217	3.10	286.93	120.85	42.12	33.60	4.10	11.10	85.40
228	3.50	271.05	117.51	43.35	33.20	4.00	10.30	83.90
230	3.42	260.23	107.54	41.33	32.80	4.40	11.10	84.70
233	3.71	263.71	112.82	42.78	33.40	4.60	11.00	84.70
266	3.22	294.17	125.80	42.77	33.70	4.60	10.90	85.20
Selected plants mean	3.430	275.345	114.903	41.749	33.952	4.174	10.944	85.452
Cross II (Giza 94 x S109)								
F₂ mean	3.50	255.74	100.73	39.39	34.02	4.33	10.78	85.49
TV	3.58	233.25	91.92	41.13	32.90	4.06	10.70	85.92
14	3.77	263.90	108.73	41.20	33.40	4.30	11.00	84.40
17	3.23	267.80	112.29	41.93	33.20	4.10	11.00	85.40
19	3.60	252.00	104.20	41.35	34.00	4.50	11.00	86.50
31	3.24	269.80	111.94	41.49	32.80	4.10	11.80	86.80
90	3.72	260.40	109.12	41.90	33.20	4.10	10.60	86.70
93	3.90	273.00	113.58	41.61	34.40	4.70	10.90	86.60
94	3.74	261.80	108.88	41.59	32.00	4.50	10.00	86.60
97	3.68	257.60	108.94	42.29	33.70	4.20	10.60	84.50
99	3.36	235.20	98.70	41.96	33.90	4.40	10.80	85.20
100	3.80	266.00	110.47	41.53	33.90	4.40	10.20	84.50
105	3.60	252.00	108.35	43.00	34.50	4.10	11.50	86.50
133	3.58	250.60	104.77	41.81	36.00	4.40	10.90	84.20
137	4.20	294.00	121.86	41.45	34.30	4.10	10.90	84.30
142	3.90	273.00	112.61	41.25	36.00	4.00	11.10	86.80
157	3.20	256.80	106.99	41.66	32.00	5.10	11.00	85.70
176	3.60	252.00	104.29	41.39	32.10	4.10	11.40	86.20
188	4.20	294.00	122.42	41.64	34.90	4.40	10.90	85.70
192	3.26	265.80	114.12	42.94	33.10	4.20	10.40	84.60
194	3.20	289.50	119.74	41.36	34.30	4.20	11.30	84.70
198	3.23	289.70	121.75	42.03	33.60	4.50	10.10	84.50
200	3.20	256.70	110.50	43.05	34.60	4.70	10.40	84.70
238	3.00	277.20	115.18	41.55	34.50	4.20	10.20	83.40
259	3.64	254.80	105.39	41.36	34.30	4.30	11.30	83.20
Selected plants mean	3.56	265.81	111.08	41.80	33.86	4.33	10.84	85.29

Table 7: The increasing percentage of the top 10 % selected plants from F₂ generation over their threshold values for the two cotton crosses

No. of F ₂ plants	BW g	SCY/P g	LY/P g	L%	UHM mm	MIC	PI	UI
Cross I (Giza 97 x D101)								
8	0.60	31.84	36.28	1.69	4.09	-8.31	-2.64	-0.99
20	-10.83	37.32	40.09	0.37	-1.23	-5.96	-0.82	-0.76
28	-3.86	35.88	38.08	0.21	1.73	-5.96	-0.82	-1.68
48	-10.55	42.46	47.80	2.06	-3.01	-8.31	1.91	-2.60
49	11.46	26.76	29.74	0.69	1.13	3.45	1.00	-0.87
52	-4.14	31.24	34.61	0.90	3.20	1.10	-4.46	-0.53
67	-2.47	36.39	40.66	1.46	3.20	-10.66	2.82	-1.22
78	-13.62	39.24	43.72	1.54	3.80	3.45	0.09	-1.91
83	-4.42	26.58	29.60	0.72	2.91	3.45	0.09	-0.99
84	5.89	30.61	33.15	0.29	3.80	3.45	-0.82	-0.76
105	-2.47	28.84	33.46	1.90	4.39	-3.60	1.00	0.28
113	-1.08	33.60	38.31	1.85	-2.12	-1.25	0.09	-2.02
128	-8.04	35.44	38.73	0.76	1.43	-5.96	-5.37	-1.33
129	-5.26	38.07	39.98	0.88	-1.53	-1.25	-4.46	-2.25
151	-6.37	27.44	30.00	0.36	-2.71	5.80	-0.82	-2.25
156	-15.57	37.19	40.31	0.61	-3.01	-5.96	2.82	-2.02
158	-9.44	43.63	48.00	1.37	0.25	-1.25	-0.82	-1.33
163	-11.66	41.29	45.62	1.39	-2.71	-3.60	2.82	-2.48
165	-8.04	34.27	39.52	2.22	-2.71	-5.96	1.91	-2.37
179	-6.37	27.44	30.45	0.70	3.20	1.10	0.09	-0.76
199	11.46	26.76	29.98	0.87	4.68	-1.25	-0.82	-0.41
209	3.10	27.68	32.97	2.45	-0.94	-13.01	1.00	-2.48
217	-13.62	39.24	45.01	2.45	-0.64	-3.60	1.00	-1.68
228	-2.47	31.54	40.99	5.45	-1.82	-5.96	-6.28	-3.41
230	-4.70	26.28	29.04	0.52	-3.01	3.45	1.00	-2.48
233	3.38	27.98	35.37	4.06	-1.23	8.15	0.09	-2.48
266	-10.27	42.75	50.94	4.02	-0.34	8.15	-0.82	-1.91
Cross II (Giza 94 x S109)								
14	5.06	13.14	18.28	0.16	1.49	5.87	2.76	-1.77
17	-9.99	14.81	22.16	1.94	0.88	0.95	2.76	-0.61
19	0.32	8.03	13.36	0.52	3.31	10.79	2.76	0.67
31	-9.71	15.67	21.77	0.86	-0.33	0.95	10.23	1.02
90	3.66	11.64	18.70	1.87	0.88	0.95	-0.98	0.90
93	8.68	17.04	23.56	1.14	4.53	15.72	1.82	0.79
94	4.22	12.24	18.45	1.11	-2.76	10.79	-6.58	0.79
97	2.55	10.44	18.51	2.81	2.40	3.41	-0.98	-1.66
99	-6.37	0.83	7.37	2.01	3.01	8.33	0.89	-0.84
100	5.89	14.04	20.17	0.96	3.01	8.33	-4.72	-1.66

105	0.32	8.03	17.87	4.52	4.83	0.95	7.43	0.67
133	-0.24	7.43	13.97	1.63	9.39	8.33	1.82	-2.01
137	17.04	26.04	32.57	0.76	4.23	0.95	1.82	-1.89
142	8.68	17.04	22.50	0.28	9.39	-1.52	3.69	1.02
157	-10.83	10.09	16.39	1.28	-2.76	25.57	2.76	-0.26
176	0.32	8.03	13.45	0.61	-2.46	0.95	6.49	0.32
188	17.04	26.04	33.18	1.23	6.05	8.33	1.82	-0.26
192	-9.16	13.95	24.15	4.38	0.58	3.41	-2.85	-1.54
194	-10.83	24.11	30.26	0.55	4.23	3.41	5.56	-1.42
198	-9.99	24.20	32.45	2.17	2.10	10.79	-5.65	-1.66
200	-10.83	10.05	20.21	4.65	5.14	15.72	-2.85	-1.42
238	-16.40	18.84	25.30	1.01	4.83	3.41	-4.72	-2.94
259	1.43	9.24	14.64	0.55	4.23	5.87	5.56	-3.17

Conclusion

Variability is a pre-requisite for successful selection of superior progenies from the segregating generations. Transgressive segregation is a fast and large method to evolve hybridization products as a combination of genes and alleles that can be tested through selection. Transgression is defined as the appearance of individuals that fall beyond their parental phenotypes. Hybridization between national cotton varieties and breeding accessions give a great potential to generate new phenotypes with important traits due to their transgressive segregation. Thus, the use of breeding accessions as a parent in Egyptian cotton breeding programme becomes an alternative for increasing yield traits especially lint % and maintain fiber quality traits in the range of long staple cotton category. The increasing of genetic variability was found in F_2 generation as indicated by transgressive variation for yield traits. The present study indicated that, most of the studied traits were predominantly controlled by non-additive genes action and presence of little influence of additive gene action.

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