ESTIMATION OF GENETIC VARIANCE COMPONENTS AND IDENTIFICATION OF TRANSGRESSIVE SEGREGANTS FOR TWO INTRASPECIFIC EXTRA-LONG STAPLE COTTON CROSSES

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ABSTRAC: The available genetic variability in the studied germplasm may be used for direct selection or hybridization program. The experimental material comprised of F_1 and F_2 populations along with their respective parents of two intra-specific cotton crosses belonging to *G. barbadense* L., to estimate heritability, genetic advance as percent of mean and transgressive segregation for boll weight, seed cotton yield per plant, lint yield per plant, lint percentage, fiber length, fiber strength, fiber fineness and uniformity ratio. Variance of parents was lowest for all the studied traits suggesting thereby homogeneity within parents. But it abruptly increased in F_2 population due to release of segregation variability. Most of the studied traits showed high heritability coupled with low genetic advance as percent of mean which indicated the predominant role of non-additive gene action in the expression of these traits. Both skewness and kurtosis had lower values and differ in the two crosses for studied traits. Lint yield / plant and lint % showed negative skewness sign and micronaire value had positive kurtosis sign for the two studied crosses. The two crosses had thrown maximum number of transgressive segregants over better parent for fiber length followed by micronaire value and boll weight, while, uniformity ratio had lowest number of transgressive segregants. The most promising transgressive segregants selected in F_2 generation also to breakdown the negative correlation between high yield and fiber quality traits. The cotton breeder could be used indirect selection to improve these traits. These desirable selected plants had higher threshold value for the eight studied traits. A track on these transgressive segregants should be maintained and forwarded to further generations up to reach to homozygosity. Most promising one could be used in further breeding programme.

Keywords: Cotton, Variability, Heritability, F_2 populations, Genetic advance, Threshold value, Transgreesive segregant.

INTRODUCTION

The main objectives of Egyptian cotton breeding program is the production of genotypes characterized by higher seed cotton and lint percentage coupled with good fiber quality, early maturity and resistance to pests and diseases. To achieving these goals the breeder should use quantitative genetic analysis for all the studied traits because most of these traits are considered as quantitative or polygenic traits. Polygenic traits exhibit continuous variation from one extreme to other, cover by several genes and highly sensitive to environmental changes, so the breeder used biometrical genetics to study these traits (Singh and Narayanan, 2013). A quantitative trait such as yield being multigenic is significantly affected by environmental factors. Thus, the overall performance of a genotype may vary due to changes in the environment (Baloch *et al.*, 2018). For that, the success of breeding program depending on the ability of plant breeder to identify and select good performing genotypes from

the breeding populations and know how to reduce environmental effect.

Genetic variability is defined as the observed phenotypic variation which occurs in plant populations and is mainly attributable to genetic differences among them. Broad sense heritability may be defined as the ratio of genotypic variance over the phenotypic variance. In other words, it determines the magnitude of transmissibility of traits from parents to their offspring (Baloch *et al.*, 2018). The additive variance, which knows as the variance of breeding values, is the important component of heritability. It is the chief source of measurement between the traits of parental and progenies. Baloch *et al.*, 2010 and 2018 reported that genetic variances coupled with higher heritability estimates of seed cotton yield and its component traits implied that these traits can be improved through hybridization and selection from segregating populations.

Selection during early generations is better for polygenic traits to reduce large number of breeding materials and increasing the possibility of picking up a desirable type in the limited screening material (Roy *et al.*, 2019). The GCV along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection. So, the progress of breeding program based on the available knowledge about nature, magnitude of gene action controlling and genetic variability controlling the target traits. Selection during transgreesive segregant in the early generations is desirable because most selected plants had gene combinations, which would be selected and advanced (Roy *et al.*, 2019).

The success of genetic improvement depends on the available knowledge of the germplasm, in order to identify the genotypes to be used as parents for hybridization to generate F_1 generation

with a high heterotic effect, allowing the appearance of transgressive variants that can be selected in segregating generations. Transgressive segregation in F_2 or later generations with phenotypes should be exceeding the range of the parents. So, plant breeders used transgressive segregation as a positive tool to improve breeding program goals (Anusha *et al.*, 2019). Reyes, 2019 highlighted that transgressive segregation is a result of a positive or negative complementation of additive alleles, epistatic interactions of unique parental attributes, unmasking of recessive alleles from a heterozygous parent, or any combination of these mechanisms.

The objectives of the present study were to determine genetic variability, broad sense heritability, skewness and kurtosis in two intra-specific F_2 populations for yield, yield components and fiber quality traits and to Select superior/transgressive segregants during F_2 generation for extra-long staple category.

MATERIALS AND METHODS

The selfed seeds of four cotton genotypes belonging to *Gossypium barbadense* L. namely (Giza 71 x Giza 74), Giza 71, Giza 92 and CB58, were crossed to produced two intra-specific cotton crosses; cross I ((Giza 71 x Giza 74) x Giza 71) and cross II (Giza 92 x CB 58). The F_1 generation of the two cotton crosses was advanced to release F_2 generation. The present investigation was carried out at Sakha Experimental Station, Agricultural Research Center, Kafr El-Sheikh government, Egypt, during three seasons from 2017 to 2019.

Each of the parents, F_1 and F_2 plants were sown as individual plants, the distance within plants and between rows were 70 cm. The seeds were dibbled to ensure uniform plant population. All the

recommended agronomic practices and plant protection measures were adopted to obtain healthy plants. For measurement of mean, variability and other parameters, 280 plants form the F_2 populations from each cross and 20 plants from both parents and F_1 generation were used. The following quantitative traits were evaluated *viz.*, 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; fiber length (FL) measured as span length at 2.5% by the digital fibrograph, fiber strength (FS) as Presley index by stelometer, fiber fineness as micronaire value (MIC) and uniformity ratio (UR %) 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. For the F_2 populations, mean, standard deviation, standard error, range, variances, genotypic and phenotypic variances were computed according to Singh and Chaudhary, 1985 and Sharma, 1988. The procedure adopted for calculation Phenotypic and genotypic coefficient of variation were worked out as suggested by Burton and Devane 1953. Broad sense heritability (h^2_{bs}) was estimated as the ratio of genotypic variance to the total phenotypic variance for all the studied traits as suggested by Hanson *et al.*, 1956. The genetic advance and genetic advance as percent of mean was calculated and categorized following the method of Johnson *et al.*, 1955. The current study considered that both skewness and kurtosis coefficients equals zero and three, respectively for a perfectly. Normal distributed variable calculated using frequency distribution of yield, its components and fiber quality traits (De Carlo, 1997). The association

and inter-association between and within yield and fiber quality traits, respectively was worker out as genotypic correlation coefficient.

Transgressive segregation

The limiting value of standard genotypes corresponding to range of parental means at 5% probability level was calculated so that the segregants beyond this limiting value should be transgresants. Transgressive segregants showing significant deviation only in the desirable direction were considered for drawing inferences about transgression. The limiting normal deviation (ND) value calculated as described by Panse and Sukhatme, (1967).

$$\text{ND value} = \frac{\text{Threshold value} - \bar{F}2}{\sigma F2}$$

Threshold value = $P^{(+)} + 1.96 * \sigma_{p\,(+)}$

Where: - $P^{(+)}$, $\sigma_{p\,(+)}$, $\bar{F}_2$ and σ_{F2} 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.

RESULTS AND DISCUSSION

The mean performance, standard error and coefficient of variation (CV %) of the parents and their F_1 generation for eight quantitative traits of the two cotton crosses are presented in Table 1. The parental genotypes used to create the two crosses belonging to extra-long staple category which characterized by high fiber length (more than 35mm) and fiber strength, while micronaire value should be low. On the other hand, yield and its components were quite low. This is may be due to the negative correlation between yield and fiber quality traits. So, the main target for cotton breeder is to breakdown this correlation by using different biometrical techniques and

more details study for early segregating generations to select the promising plants which had both high yield and extra-long staple values.

Most of the studied traits had wide range of variability as a result of significant difference among the parents for all these traits. Vrinda and Patil, 2018 reported that their no doubt that higher variability is expected when diverse parents are used to generate segregating population. The coefficient of variation (CV %) is the ratio between standard deviation and mean performance and generally expressed as a percentage and offers a comparable rate of change in

variation. The studied traits of the two cotton crosses showed low values of CV % (less than 10%). This indicated to low variability between parents and their F_1 populations among the two cotton crosses. Also, referred to the highest homozygosity among parents used to create the studied crosses. Abdalla, 2015 reported low CV % values (less than 10 %) for fiber quality traits in Egyptian cotton genotypes. The coefficient of variation describes only the extent of variation but does not discriminate variation into heritable and non-heritable portion (Ranganatha *et al.*, 2013).

Table 1: Mean performance, standard error (SE) and coefficient of variability (CV %) of studied traits for parents and their F_1 generation

Traits Variables	G	BW g	SCY/P g	LY/P g	L%	FL mm	MIC	FS	UR %
Cross I ((Giza 71 x Giza 74) x Giza 71)									
Mean±SE	P_1	2.589 ±0.057	84.420 ±0.499	28.268 ±0.632	36.401 ±0.230	34.230 ±0.293	2.720 ±0.036	12.000 ±0.142	85.440 ±0.395
	P_2	2.695 ±0.073	56.595 ±1.527	20.123 ±0.646	35.520 ±0.275	34.630 ±0.192	2.710 ±0.031	12.020 ±0.020	84.860 ±0.298
	F_1	2.589 ±0.057	81.040 ±1.909	29.784 ±0.771	36.739 ±0.198	35.130 ±0.199	2.750 ±0.037	11.780 ±0.036	86.490 ±0.124
CV %	P_1	6.975	6.975	7.067	1.998	2.706	4.174	3.835	1.462
	P_2	8.532	8.532	10.148	2.444	1.754	3.669	0.526	1.110
	F_1	4.914	7.450	8.186	1.707	1.791	4.285	0.964	0.454
Cross II (Giza 92 x CB 58)									
Mean±SE	P_1	3.087 ±0.033	102.750 ±0.608	35.065 ±0.140	34.112 ±0.336	33.590 ±0.332	2.990 ±0.077	11.980 ±0.044	85.310 ±0.217
	P_2	3.150 ±0.052	85.050 ±1.409	29.428 ±0.432	34.632 ±0.410	32.330 ±0.286	3.040 ±0.054	11.200 ±0.165	85.080 ±0.376
	F_1	3.310 ±0.048	119.160 ±1.735	41.986 ±0.526	35.250 ±0.231	34.120 ±0.181	2.750 ±0.043	12.050 ±0.052	85.320 ±0.224
CV %	P_1	3.332	3.953	3.990	3.117	3.127	8.108	1.167	0.804
	P_2	5.238	5.238	4.645	3.748	2.797	5.634	4.668	1.399
	F_1	4.604	4.604	3.958	2.072	2.138	4.924	1.369	0.830

F_2 population

Variability parameters, broad sense heritability, genetic advance and genetic advance as a percentage of mean based on the data of individual plant observation were estimated for all the studied traits in F_2 generation of the two cotton crosses are presented in Table 2. Comparing mean values of F_2 populations with their respective parents showed that there is a desirable compared to better parent for all the studied traits for two crosses. The results showed low standard deviation values for all the studied traits, except seed cotton yield for the two crosses, which reflect the opportunity for efficient selection (Abd El-Moghny *et al.*, 2016).

Table 2: Variability parameters in segregating F_2 populations of the studied traits for two cotton crosses

Traits Parameters	BW g	SCY/P g	LY/P g	L%	FL mm	MIC	FS	UR %
Cross I ((Giza 71 x Giza 74) x Giza 71)								
Mean±SE	2.714± 0.015	108.577± 0.596	38.912± 0.231	35.843± 0.091	35.552± 0.062	3.022± 0.020	11.661± 0.025	86.128± 0.056
SD	0.250	10.012	3.879	1.523	1.033	0.344	0.416	0.947
V_{ph}	0.063	100.238	15.049	2.319	1.068	0.118	0.173	0.897
V_g	0.046	63.785	9.105	1.926	0.672	0.104	0.160	0.743
PCV %	9.221	9.221	9.970	4.249	2.906	11.375	3.568	1.100
GCV %	7.877	7.356	7.755	3.872	2.306	10.686	3.432	1.001
Range	1.180	47.200	18.915	11.567	5.700	1.800	1.700	5.200
CR %	21.455	21.455	24.009	16.473	8.017	28.125	7.359	3.023
Skewness	0.016	0.01	-0.054	-0.17	-0.07	0.47	0.27	0.01
SE Skewness	0.145	0.15	0.145	0.15	0.15	0.15	0.15	0.15
Kurtosis	-0.500	-0.42	-0.415	2.04	-0.23	0.03	-0.86	-0.01
SE Kurtosis	0.289	0.29	0.289	0.29	0.29	0.29	0.29	0.29
h^2_{bs}	0.730	0.636	0.605	0.830	0.629	0.882	0.926	0.828
GA	0.591	3.262	1.931	1.660	1.037	0.838	0.967	1.305
GAM %	21.790	3.004	4.961	4.632	2.915	27.737	8.294	1.516
Cross II (Giza 92 x CB 58)								
Mean±SE	3.276± 0.017	124.582± 0.653	43.631± 0.297	35.003± 0.138	33.922± 0.066	2.921± 0.016	11.657± 0.029	84.980± 0.071
SD	0.281	10.728	4.888	2.262	1.086	0.263	0.471	1.158
V_{ph}	0.079	115.081	23.893	5.117	1.179	0.069	0.222	1.342
V_g	0.056	84.985	21.131	4.583	0.851	0.051	0.195	0.840
PCV	8.571	8.611	11.203	6.462	3.201	9.018	4.044	1.363
GCV	7.199	7.400	10.536	6.116	2.719	7.736	3.788	1.079
Range	1.700	64.600	29.447	13.153	5.800	1.300	1.900	5.900
CR %	31.902	28.571	29.287	9.194	8.053	20.635	8.772	2.295
Skewness	0.14	0.16	-0.02	-0.33	-0.15	0.62	-0.05	-0.22
SE Skewness	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15
Kurtosis	-0.19	-0.16	-0.21	0.56	-0.10	0.22	-0.92	-0.55
SE Kurtosis	0.30	0.30	0.30	0.30	0.30	0.30	0.30	0.30
h^2_{bs}	0.705	0.738	0.884	0.896	0.721	0.736	0.878	0.626
GA	0.606	3.918	3.168	2.182	1.218	0.612	0.976	1.092
GAM %	18.485	3.145	7.260	6.235	3.590	20.945	8.373	1.285

The extent of variability is measured by GCV and PCV which gave relative amount of variation in different traits. All the studied traits had the highest values for PCV than GCV, indicating, that these traits interacted with the environments to considerable extent. In addition, the ranges of F_2 population for the two crosses were similar magnitude. The wide range of phenotypic variation in eight quantitative traits for the two crosses depends on genetic makeup. Generally, there is high amount of variation among the F_2 populations which might be due to diversity among parental genotypes. Also, the presence of variability coupled with higher PCV and GCV again supports presence of wide range of genetic variability in the F_2 population (Vrinda and Patil, 2018). Generally, low differences between PCV and GCV values were indicating that low environmental effect on the expression of these traits (Ranganatha *et al.*, 2013).

The broad sense heritability was calculated by utilizing the variability among spaced F_2 plants in relation to the variability among spaced plants of the non-segregating parents (Falconer, 1981). Broad sense heritability for all the studied traits was more than (60 %) for the studied crosses. Genetic advance as a percentage of mean was low (less than 10 %) for all the studied traits, except for boll weight and micronaire value for the two crosses. So, high broad sense heritability coupled with low GAM %, indicated that, these traits controlled by non-additive (dominance or epistasis) gene action. While, the other two traits (boll weight and micronaire value) had highly heritability coupled with high or moderate GAM %, indicated that, these traits had low environmental effect and controlled by additive gene effect for two crosses. The extent to which genetic segregation is expected in later generation of a cross is largely a reflection of the heritability. These results are in accordance with those of Vrinda and Patil, (2018).

Skewness and kurtosis reflect the nature of variability existing in a genetic population under study. Skewness explains the distribution of individuals in positive or negative side compared to the mean of population, whereas kurtosis explains the flatness of the curve for different traits in evaluated population (Preetha and Raveendren, 2008).

Skewness and kurtosis values describe the symmetry and vertex of the sampled distributions relative to the normal distribution (Figures 1 and 2) for crosses I and II, respectively. They considered as an alternative test of normality. The current study is considered both skewness and kurtosis should be zero for a perfectly normally distributed variable (De Carlo, 1997). In fact the ideal kurtosis value is 3 but most statistical packages subtract 3 from the value, so that both skewness and kurtosis ideal values are zero. Thus, the negative value of skewness indicates left skewness and positive values indicated right skewness. Data presented in Table 2 differ for skewness value and sign for the eight traits for two cotton crosses. The two cotton crosses had negative values of skewness for lint yield / plant, lint % and fiber length. Also, fiber strength and uniformity ratio % had negative sign for cross II. While, boll weight, seed cotton yield / plant and micronaire value had positive value for the two cotton crosses.
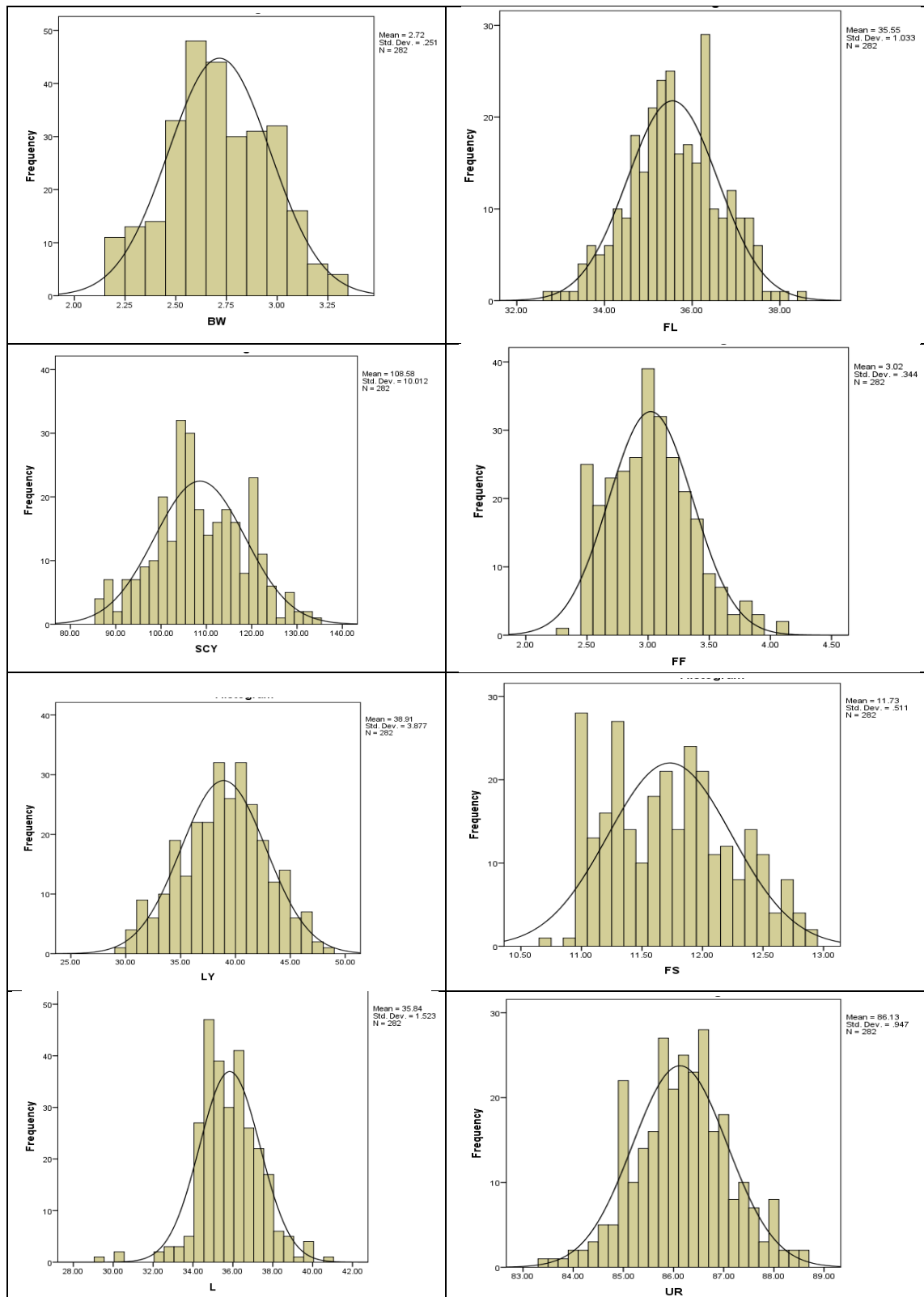
Figure. 1: Normal distribution curve for F$_2$ generation over all the studied traits for cross I ((Giza 71 x Giza 74) x Giza 71)
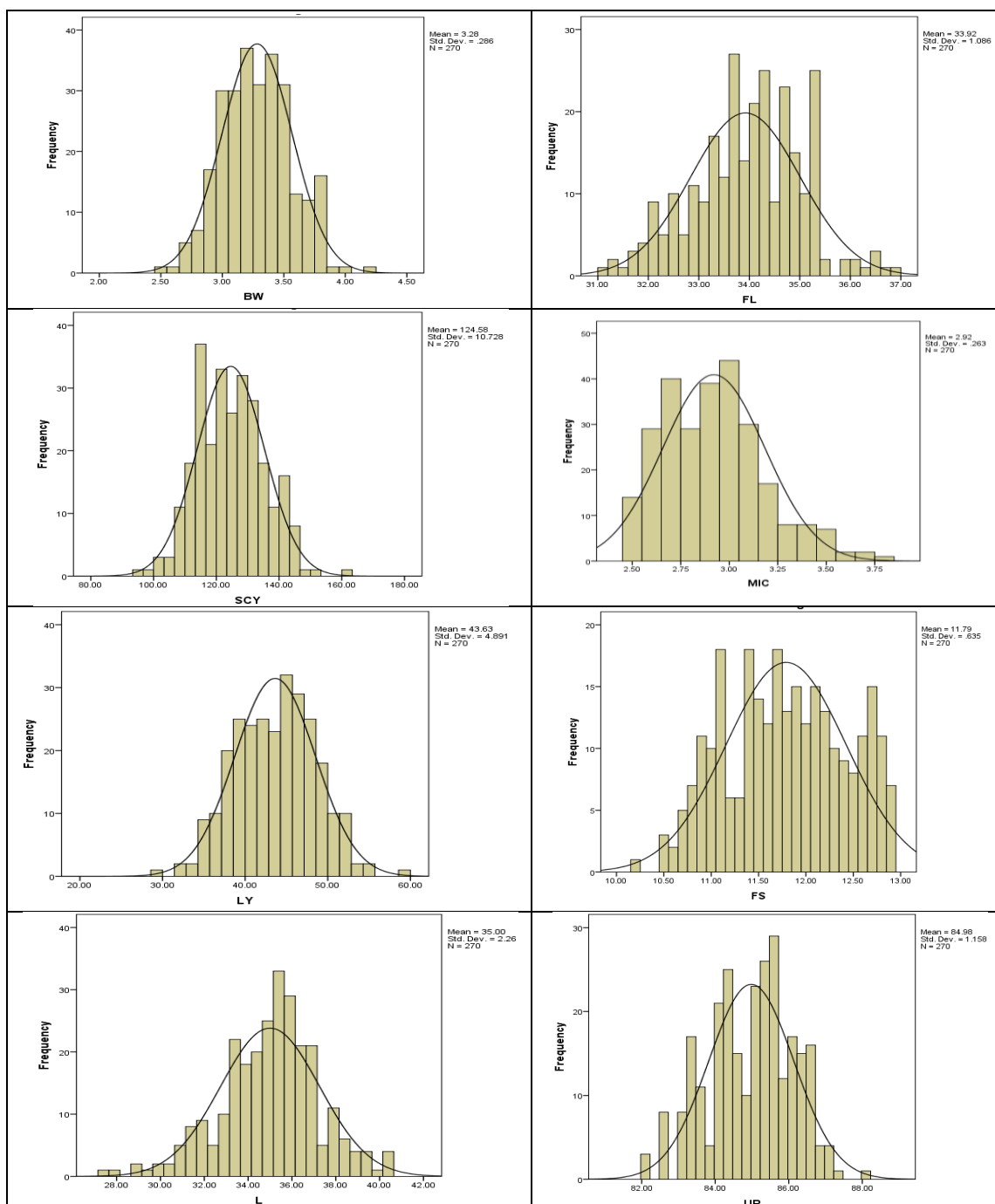
Figure 2: Normal distribution curve for F_2 generation over all the studied traits for cross II (Giza 92 x CB 58)

On the other hand, kurtosis measures the apex of a distribution. A positive value typically indicates that the distribution has a sharper peak, thinner shoulders, and fatter tails than the normal distribution and negative values indicates that distribution has lighter tails and a flatter peak than normal distribution (Abdalla, 2015). Crosses I and II showed positive sign for lint % and micronaire value (Table 2). Abdalla, (2015) recorded positive values for

micronaire value for some parental cotton genotypes and their crosses. The low values of both skewness and kurtosis over all the studied traits for two cotton crosses reflect solid confirmation of data homogeneity and normality. Abdalla, 2015 and Abd El-Moghny *et al.*, 2016 found both positive and negative among skewness and kurtosis among different cotton genotypes and crosses belonging to *G. barbadense*.

Transgressive segregants

Hybridization is a breeding method often produces progenies with a wider phenotypic variation than their parents, which is referred to develop new recombination. Frequency distribution and proportion of desirable transgressive segregation, range in the values of transgressive segregants (TS) and threshold value (TV) for eight traits have been recorded on 280 individual plants in F_2 generation for the two cotton crosses.

Frequency of transgressive segregants, threshold value (TV), normal deviation value (ND), and range of the values of transgressive segregants for yield, its components and fiber quality traits during F_2 generation for the two crosses is presented in Table 3. The present investigation showed that, transgressants recorded for the two cotton crosses for eight traits which ranged from 6.028 % to 48.889 %. In case of seed cotton yield / plant ranged from 17.730 to 22.519 %, individuals transgressed beyond the increasing parent for cross I and II, respectively. Transgressive segregants were ranged from 9.220 to 40.741 % for boll weight, 14.894 to 18.519 % for lint yield / plant, 9.574 to 14.444 % lint %, 42.553 to 48.889 % for fiber length, 7.407 to 41.844 % for micronaire value, 9.839 to 11.111 % for fiber strength and 6.028 to 9.630 % for uniformity ratio for cross I and cross II, respectively. Kumar *et al.*, (2018) and

Anusha *et al.,* (2019) found different transgressive segregants frequency for yield, its components and fiber quality traits. Anupama and Mehetre, (2012) explained that the vast variation in transgressants also suggested the possibility of combining desirable genes from the parents. Roy *et al.*, (2019) reported that high transgressive segregants in F_2 generation indicted high degree of dominance and selection in early generations may not be beneficial.

Frequency of transgressive segregants varied from cross to cross for different studied traits (Table 3). The two crosses had thrown maximum number of transgressive segregates over the better parent for fiber length (252) followed by micronaire value (138), boll weight (136), seed cotton yield / plant (111), lint yield / plant (92), fiber strength (79), and lint % (66). While, minimum number of transgressive segregants was recorded for uniformity ratio % (43). These results indicating sufficient diversity among parents, hence good amount of transgression might be observed. Also, there is positively correlation between genetic divergence of the parental lines and the frequency of transgression. The F_2 will advance to F_3 by selecting the promising segregants in F_2 and lowest or undesirable plants will eliminate. So, the cotton breeder should select the most desirable plants that exceed their threshold values for all traits. The two cotton crosses had the highest transgressants values compared to their respective increasing parents as shown in Table 4 for all the studied traits. So, there was desirable shift from better parent to F_2 population towards eight quantitative traits. These results indicated that each parent is expected to contribute different desirable genes, which when brought together by recombination give rise to transgressive segregants (Anupama and Mehetre, 2012).

Table 3: Threshold value (TV), normal deviation value (ND), percentage and range in the values of transgressive segregants (TS %) in the two cotton crosses

Traits	Crosses	F_2 population					
		Threshold value	ND	Frequency	Maximum No. of TS	TS %	Range in values of T.S.
Boll weight	Cross I	3.146	1.723	26	136	9.220	2.160-3.340
	Cross II	3.473	0.690	110		40.741	2.530-4.230
Seed cotton yield / plant	Cross I	120.000	1.141	50	111	17.730	86.400-133.600
	Cross II	133.000	0.785	61		22.593	96.140-160.740
Lint yield / plant	Cross I	43.000	1.054	42	92	14.894	29.933-48.848
	Cross II	48.000	0.894	50		18.519	29.746-59.192
Lint %	Cross I	37.221	0.905	27	66	9.574	30.323-40.890
	Cross II	37.176	0.961	39		14.444	27.370-40.523
Fiber length	Cross I	35.821	0.260	120	252	42.553	32.700-38.400
	Cross II	34.103	0.166	132		48.889	31.100-36.900
Micronaire value	Cross I	2.905	0.340	118	138	41.844	2.300-4.100
	Cross II	3.436	1.958	20		7.407	2.500-3.800
Fiber strength	Cross I	12.144	1.162	49	79	9.839	10.700-12.400
	Cross II	12.254	1.266	30		11.111	10.200-12.900
Uniformity ratio %	Cross I	86.706	0.610	17	43	6.028	83.500-88.600
	Cross II	86.654	1.445	26		9.630	82.100-88.000

Table 4: The upper limits achieved by transgressive segregants in respect of eight studied traits in F_2 generation of two cotton crosses

Traits	Highest intensity of traits expression of two cotton crosses for all the studied traits		
		Cross I	Cross II
Boll weight	Maximum	3.340	4.230
	Better parent mean	2.589	3.087
Seed cotton yield / plant	Maximum	133.600	160.740
	Better parent mean	84.420	102.750
Lint yield / plant	Maximum	48.848	59.192
	Better parent mean	28.268	35.065
Lint %	Maximum	40.890	40.523
	Better parent mean	36.401	34.198
Fiber length	Maximum	38.400	36.900
	Better parent mean	34.230	33.590
Micronaire value	Maximum	4.100	3.800
	Better parent mean	2.720	2.990
Fiber strength	Maximum	12.000	12.000
	Better parent mean	12.000	11.980
Uniformity ratio %	Maximum	88.600	88.000
	Better parent mean	85.440	85.310

From these data it is evident that when the desired intensity of traits is not available in the parents, the concept of transgressive segregation can be employed to extend the limit of trait expression, while the success to obtain the desired transgressive segregants depends upon obtaining genetic recombination between both linked and unlinked alleles (Anusha *et al.,* 2019). Also, the breeder could be isolatie the rare genotypes by making higher selection pressure. To increase the rate of transgressive segregants, the breeder should be select the most diverse parents with better combining ability (Anupama and Mehetre, 2012). The F_2 populations for the two cotton crosses had higher number of transgressive segregants for most studied traits which could be used in further selection procedures to establish good genetic material (Roy *et al.*, 2019).

From this investigation, it is to point out that observation on eight traits were recorded on 280 individual plants during F_2 generation for each cross. Out of the 280 F_2 plants only 33 and 40 plants give higher threshold value for one or more than one trait for cross I and II, respectively. The increasing over better parent was recorded for these selected plants as a percentage value is present in Tables 5 and 6 for cross I and II, respectively. The breeder should focus on the individual progenies which gave high frequency of transgressive segregants for yield and its components accompanied with desirable fiber properties because usually there is negatively correlation between yield and fiber quality traits especially for extra-long staple category breeding program (Preetha and Raveendra, 2008; Anupama and Mehetre, 2012 and Kumar *et al.*, 2018).

The main goal for the studied crosses is to select extra-long traits coupled with high yield and lint %. So, high selection pressure was done on the selected plants to select the desirable plants which had higher threshold value for the eight traits together as presented in Table 7. Plants No. 115, 127, 184, 193, 248 and 262 from cross I and 13, 29, 36, 38, 44, 97, 233 and 238 from cross II were found to be the most promising transgressive segregant for both yield and fiber quality traits, because these selected plants had higher threshold value for the eight studied traits. In addition to positive sign for all the studied traits which indicate that these plants had higher intensity of expression than the increasing parent. So, these selected plants may be a valuable resource for improving both yield and fiber quality traits for extra-long staple category in *G. barbadense*. The cotton breeders succeed to breakdown negative correlation between high yield and fiber quality traits. These selected plants are not stable and need to be evaluated in advanced generation with high selection intensity for desirable traits (Kumar *et al.*, 2018 and Anusha *et al.,* 2019*).*

The genotypic correlation coefficient is a good indicator of direction and strength of the relationship between traits to identify the important traits, which should be consideration during selection. Also, provide information about the effective traits (Preetha and Raveendra, 2008). Genotypic correlation coefficient between yield and fiber quality traits for F_2 population and the desirable selected plants of the two crosses is presented in Table 8. The aim of the genotypic correlation is to prove that the breeder breakdown the negative correlation between yield and fiber quality traits especially for extra-long staple breeding programs.

Table 5: Promising transgressive segregants (TS) having combinations of desirable traits more than threshold value (TV) for all the studied traits of cross I ((Giza 71 x Giza 74) x Giza 71)

Traits / Plant No.	Increased over better parent %							
	BW g	SCY/P g	LY/P g	L%	FL mm	Mic	FS	UR%
20	23.600	51.623	65.317	0.299	4.294	21.324	-2.813	-0.632
21	26.690	55.413	72.800	2.282	2.834	32.353	-2.813	-0.164
31	27.462	56.361	60.850	-5.368	6.632	21.324	5.712	0.421
90	19.737	46.885	58.402	-0.796	3.126	25.000	-4.518	0.772
115	18.965	45.937	60.957	1.454	9.261	2.941	2.302	2.879
127	16.261	42.620	56.005	0.630	10.722	43.382	2.302	2.879
144	8.150	32.670	37.650	-4.556	5.755	17.647	-0.256	1.007
146	15.875	42.146	56.284	1.141	3.710	17.647	-6.223	1.709
169	18.192	44.989	55.319	-1.455	3.418	17.647	4.007	1.241
176	13.171	38.830	47.830	-2.045	12.182	13.971	2.302	3.347
181	15.875	42.146	51.193	-2.155	3.126	10.294	1.449	0.304
183	15.875	42.146	51.800	-1.762	3.126	13.971	2.302	0.187
184	17.806	44.516	61.046	2.513	1.373	10.294	1.449	0.890
190	20.124	47.358	58.835	-0.844	2.542	21.324	2.302	-0.515
193	17.806	44.516	63.461	4.051	5.463	25.000	2.302	2.996
202	23.600	51.623	63.572	-0.759	3.710	6.618	-3.666	0.890
203	19.737	46.885	55.708	-2.483	6.339	2.941	-0.256	0.538
220	19.351	46.411	53.939	-3.279	2.542	10.294	-0.256	0.538
222	23.600	51.623	65.113	0.176	5.755	21.324	-2.813	0.655
223	23.986	52.097	58.229	-4.300	5.755	10.294	0.597	0.538
229	18.192	44.989	50.462	-4.536	3.710	2.941	2.302	0.890
236	23.214	51.149	58.813	-3.344	3.418	6.618	-0.256	2.177
241	19.737	46.885	53.528	-3.848	4.587	-0.735	4.007	0.421
248	15.875	42.146	58.432	2.531	0.789	25.000	2.302	1.007
259	15.875	42.146	46.703	-5.060	6.047	-4.412	-3.666	1.007
260	15.875	42.146	45.855	-5.609	5.755	21.324	1.449	1.592
262	15.875	42.146	60.005	3.548	3.418	6.618	2.302	0.538
264	15.875	42.146	45.746	-5.680	3.126	-8.088	-2.813	0.538
268	15.875	42.146	49.219	-3.432	3.418	6.618	-2.813	1.358
271	15.875	42.146	49.637	-1.612	6.339	2.941	2.302	1.007
272	15.875	42.146	58.021	2.264	4.002	6.618	-0.256	1.592
275	15.875	42.146	46.615	-5.117	6.339	13.971	4.007	0.304
281	17.420	44.042	47.161	-6.017	6.924	25.000	-3.666	1.241

Table 6: Promising transgressive segregants (TS) having combinations of desirable traits more than threshold value (TV) for all the studied traits of cross II (Giza 92 x CB 58)

Traits Plant No.	Increased over better parent %							
	BW g	SCY/P g	LY/P g	L%	FL mm	Mic	FS	UR%
13	14.674	30.920	35.234	3.080	0.030	-6.355	0.167	0.457
21	17.266	33.878	48.599	10.764	1.518	0.334	-7.346	0.340
22	21.801	39.056	57.053	12.707	-0.863	13.712	-9.850	-1.301
28	6.900	22.044	14.950	-6.009	1.221	3.679	-9.850	0.457
29	15.970	32.399	34.466	1.349	3.900	-3.010	1.836	0.926
31	21.801	39.056	48.642	6.670	8.961	-13.043	-5.676	3.153
32	18.562	35.358	30.950	-3.458	0.625	10.368	1.002	0.926
34	14.027	30.180	40.185	7.460	3.900	0.334	-0.668	1.160
36	16.618	33.139	36.123	2.028	3.900	-9.699	0.167	1.160
37	20.829	37.946	41.636	2.460	3.305	-3.010	0.167	0.340
38	24.393	42.015	47.664	3.761	9.854	3.679	0.167	1.629
44	14.351	30.550	33.427	1.991	2.114	-6.355	0.167	1.629
52	18.238	34.988	41.050	4.273	-1.459	13.712	-3.172	-1.067
63	14.027	30.180	31.630	0.903	0.030	-3.010	-3.172	-0.598
69	19.857	36.837	38.924	1.313	-3.543	0.334	-9.015	-2.004
70	24.069	41.645	46.857	3.464	-3.245	13.712	0.167	-1.653
71	20.505	37.577	35.199	-1.934	3.007	-3.010	3.506	1.043
81	15.322	31.659	35.948	3.042	3.007	-9.699	-3.172	1.512
88	23.097	40.535	44.566	2.654	1.816	-9.699	-7.346	0.105
90	23.421	40.905	45.170	2.812	-3.543	3.679	0.167	-2.004
91	16.294	32.769	28.994	-3.046	-1.161	-9.699	0.167	-1.418
92	16.618	33.139	15.782	-13.218	-4.436	0.334	-7.346	-2.708
95	17.590	34.248	37.820	2.447	4.793	-3.010	-4.841	1.512
97	19.534	36.467	52.454	11.482	4.495	-3.010	0.167	1.160
110	22.125	39.426	39.607	-0.079	1.816	-3.010	0.167	-0.012
111	14.027	30.180	35.828	4.121	0.030	-13.043	-3.172	-3.059
112	13.703	29.810	35.035	3.808	1.816	10.368	-4.007	-0.598
148	17.266	33.878	39.933	4.304	2.114	-13.043	0.167	-1.184
163	27.956	46.083	42.997	-2.316	4.793	-16.388	1.002	1.043
169	23.745	41.275	52.361	7.622	3.007	-3.010	0.167	-1.184
188	16.618	33.139	48.503	11.307	5.091	-6.355	-2.337	-0.246
218	15.970	32.399	35.815	2.366	4.793	3.679	-1.503	1.981
222	22.449	39.796	41.255	0.833	2.114	-13.043	1.836	-1.184
224	25.688	43.494	39.039	-3.307	7.472	3.679	-4.841	0.340
231	18.238	34.988	31.851	-2.528	4.793	17.057	-1.503	-0.129
232	3.661	39.056	31.737	-5.461	-0.268	3.679	3.506	0.223
233	14.998	31.290	31.805	0.183	3.900	7.023	0.167	1.629
238	37.026	56.438	68.808	7.682	0.327	13.712	0.167	1.160
253	12.407	28.331	33.124	3.519	4.793	23.746	-9.015	-0.246
266	13.379	29.440	39.283	7.379	2.411	-16.388	-11.519	-1.418

Table 7: The desirable selected plants from the F₂ generation which had higher threshold value for all the studied traits of the two cotton crosses

Traits Plant No.	BW g	SCY/P g	LY/P g	L%	FL mm	Mic	FS	UR %
Cross I ((Giza 71 x Giza 74) x Giza 71)								
Better parent	2.589	84.420	28.268	36.401	34.230	2.720	12.000	85.440
115	3.08	123.20	45.50	36.93	37.40	2.80	12.00	87.90
127	3.01	120.40	44.10	36.63	37.90	3.90	12.00	87.90
184	3.05	122.00	45.53	37.32	34.70	3.00	11.90	86.20
193	3.05	122.00	46.21	37.88	36.10	3.40	12.00	88.00
248	3.00	120.00	44.79	37.32	34.50	3.40	12.00	86.30
262	3.00	120.00	45.23	37.69	35.40	2.90	12.00	85.90
Cross II (Giza 92 x CB 58)								
Better parent	3.087	102.750	35.065	34.198	33.590	2.990	11.980	85.310
13	3.54	134.52	47.42	35.25	33.60	2.80	12.00	85.70
29	3.58	136.04	47.15	34.66	34.90	2.90	12.20	86.10
36	3.60	136.80	47.73	34.89	34.90	2.70	12.00	86.30
38	3.84	145.92	51.78	35.48	36.90	3.10	12.00	86.70
44	3.53	134.14	46.79	34.88	34.30	2.80	12.00	86.70
97	3.69	140.22	50.65	36.12	35.10	2.90	12.00	86.30
233	3.55	134.90	46.22	34.26	34.90	3.20	12.00	86.70
238	4.23	160.74	59.19	36.82	33.70	3.40	12.00	86.30

The results of genotypic correlation through F₂ population for cross I ((Giza 71 x Giza 74) x Giza 71) showed that, there is a highly significant and positive correlation between yield traits (boll weight, seed cotton yield / plant, lint yield / plant and lint %) and between fiber quality traits (uniformity ratio % and both fiber strength and micronaire value). While, highly significant and positive correlation among yield and fiber quality traits was recorded between lint % with each of fiber length, fiber strength and uniformity ratio %. Cross II (Giza 92 x CB 58) has highly significant and positive correlation among yield traits. While, between yield and fiber quality traits showed highly significant, moreover positive correlation was between micronaire value with both lint yield / plant and lint % as well as between fiber strength with three yield traits (boll weight, seed cotton yield / plant and lint yield / plant). Also, positive association between fiber quality traits was observed.

On the other hand, the desirable selected plants had highly significant and positive correlation between boll weight and seed cotton yield / plant as well as between fiber length and uniformity ratio for cross I. While, cross II showed highly significant and positive correlation between seed cotton yield / plant with both boll weight and lint yield / plant and among lint yield / plant with both yield traits (boll weight and lint %). Also, highly significant and positive correlation recorded between seed cotton yield / plant and micronaire value. The lowest significant correlation through desirable selected F₂ plants may be related to the lowest number of desirable selected plants (8 plants) compared to the total number of F₂ population (280 plants). These results of genotypic correlation indicated that the highest yield is an indicator to fiber quality traits. So, indirect selection is a good tool to improve these traits. These findings agreed with AL-Hibbiny *et al.*, (2020) and El-Mansy *et al.*, (2020).

Table 8: Genotypic correlation coefficient among yield and fiber quality traits for F_2 population (above diagonal) and desirable selected plants (below diagonal) for the two crosses

Traits	BW g	SCY/P g	LY/P g	L%	FL mm	Mic	FS	UR %
Cross I ((Giza 71 x Giza 74) x Giza 71)								
BW		0.995**	0.896**	-0.03	-0.04	0.10	0.185**	0.03
SCY/P	1.000**		0.901**	-0.03	-0.03	0.11	0.185**	0.02
LY/P	0.628	0.628		0.404**	-0.01	0.169**	0.140*	0.03
L%	-0.070	-0.070	0.732		0.404**	-0.01	0.169**	0.140*
FL	0.305	0.305	-0.277	-0.621		0.04	0.02	0.609**
MIC	-0.458	-0.458	-0.572	-0.335	0.320		0.01	0.132*
FS	-0.271	-0.271	-0.206	-0.026	0.453	0.277		0.01
UR%	0.514	0.514	0.077	-0.353	0.832*	0.396	0.410	
Cross II (Giza 92 x CB 58)								
BW		0.995**	0.896**	-0.031	-0.037	0.102	0.185**	0.026
SCY/P	1.000**		0.901**	-0.030	-0.028	0.114	0.185**	0.023
LY/P	0.943**	0.943**		0.404**	-0.014	0.169**	0.140*	0.027
L%	0.539	0.539	0.788*		0.029	0.155**	-0.065	0.013
FL	-0.030	-0.030	-0.047	-0.039		0.044	0.023	0.609**
MIC	0.763*	0.763*	0.645	0.217	0.034		0.007	0.132*
FS	-0.194	-0.194	-0.251	-0.277	0.044	-0.128		0.009
UR%	0.085	0.085	0.004	-0.143	0.548	0.326	-0.288	
* and ** Significant at 0.05 and 0.01 probability levels, respectively.								

These findings revealed that the parents differed in their genetic background and using hybridization method will develop new recombination that create large amount of genetic variability for yield and fiber quality in most of the individual progenies. The transgressive segregant may be arising in F_2 population due to dominance and dominance interaction. The desirable selected plants are the good methods to obtain effective transgressive segregants by obtain new genetic recombination between both linked and unlinked alleles. Therefore, the desirable selected plants could be used to improve extra-long staple breeding program after breaking negative linkage between yield and fiber quality traits. Similar results were also reported by Anupama and Mehetre, (2012) and Kumar *et al.*, (2018).

CONCLUSION

The output of the present investigation revealed that the parents involved in this study differed in many genes which creating differ of genetic variability for all the studied traits in F_2 population over the two crosses. The diverse parents having highly combining ability may be having higher change to give the highest ratio of transgressive segregants. The parents carrying different alleles or genes for any trait which could be bring into a single genotype through rigorous selection and evaluation in later generations. The most promising transgressive segregant plants need for more evaluation during further generations. The breeders could be select the most promising families or plants under multi-location evaluation to release as a new variety or may be used

as a parent in future breeding programme.

REFERENCES

Abdalla, A. M. A. (2015). Data quality for expanding genetic base of cotton lint quality traits. Egypt. J. Plant Breed. 19(1): 139-158.

Abd El-Moghny, A. M., Mariz, S. Max and M. H. M. Orabi (2016). Genetic variability in segregating generations of some cotton crosses. Egyptian J. Plant Breeding, 20 (3): 507-527.

AL-Hibbiny, Y. I. M., A. H. Mabrouk and Reham H. A. O. Gibely (2020). The role of non-allelic interaction in inheritance of some economic traits in *G. barbadense*. Menoufia J. Plant Prod., 5: 399-410.

Anupama, H. and S. S. Mehetre (2012). Detection of transgressive segregants for quantitative characters in F_3 generation of in-ovulo cultured interspecific triple cross of cotton viz; colchicide *(G. arboreum x G. anomalum) x G. barbandense*. Ann. Agric. Res. New Series, 33 (3):157-162.

Anusha, G., P. N. Rasal, M. R. Patil, B. Lavanya, B. Nitya Menora and K. Shankaraiah (2019). Studies on transgressive segregation in F_2 generation in Deshi cotton (*Gossypium arboreum* L.). Int. J. Pure App. Biosci. 7(1): 172-176.

Baloch, M. J., M. S. Kakar, W. A. Jatoi and N. F. Veesar (2010). Identification of potential F_2 populations from intraspecific crosses in Upland cotton. Pak. J. Sci. Ind. Res., 53: 151-157.

Baloch, M. J., R. Lochi, W. A. Jatoi, A. W. Baloch and M. A. Arain (2018). Genetic variability, heritability and correlation studies in F_2 populations of Upland cotton. Pak. J. Sci. Ind. Res. Ser. B: Biol. Sci. 61b (3):136-144.

Burton, G. W. and E. M. Devane, (1953). Estimating heritability in tall fescue (*Festuca circunclinaceae*) from replicated clonal material. Agron. J., 45: 478-481.

De Carlo, L. T. (1997). On the meaning and use of kurtosis. Psychological methods 2: 292-307.

EL-Mansy, Y. M., A. M. Abdelmoghny, Reham H. A. O. Gibely and A. H. Mabrouk (2020). Relationship between combining ability, genetic components and genetic diversity using triple test cross in cotton. 16th Int. Conf. Crop Sci. Al-Azher Univ. 13-14 October 53-78.

Falconar, D. S. (1981). Introduction to Quantitative Genetics. The Ronald Press Company, New York.

Hanson, G. H., H. F. Robinson and R. E. Comstock (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. Agron. J., 48: 267-282.

Johnson, H. W., H. F. Robinson and R. E. Comstock (1955). Estimates of genetic and environmental variability in soybeans. Agron. J. 47:314-308.

Kumar, M. N. V., I. S. Katageri, G. S. Kumar and S. A. Gowda (2018). Transgressive segregation for fiber quality, seed cotton yield and its component traits in *Gossypium barbadense* L. cotton. Int. J. Curr. Microbiol. App. Sci. 7(01): 1040-1051.

Panse, V. G. and P. V. Sukhatme (1967). Statistical Methods for Agricultural Workers. ICAR, New Delhi.

Preetha, S. and T. S. Raveendra (2008). Genetic appraisal of yield and fiber quality traits in cotton using interspecific F_2, F_3 and F_4 population. Int. J. Integrative Bio. 3(2): 136-142.

Ranganatha, H. M., Shreekanth S. Patil, S. M. Manjula and B. N. Arvindkumar (2013). Genetic Variability Studies in Segregating Generation of Upland Cotton (*Gossypium hirsutum* L.).

Molecular Plant Breeding, 4 (10): 84-88.

Reyes, B. G. (2019). Genomic and epigenomic bases of transgressive segregation – new breeding paradigm for novel plant phenotypes. Plant Science, 288:110-213.

Roy, U., M. C. Paloti, A. Tigga and R. S. Patil (2019). Genetic variability studies in the F_2 populations of interspecific cotton (*G. hirsutum* L. x *G. barbadense* L.) hybrids. Inter. J. Gene. 11 (10): 660-663.

Sharma, J. R. (1988). Statistical and Biometrical Techniques in Plant Breeding. New Delhi, New Age International.

Singh, R. K. and B. D. Chaudhary (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, India.

Singh, P. and S. S. Narayanan (2013). Biometrical Techniques in Quantitative Genetics in Plant Breeding. Kalyani Publ., 5th Ed. New Delhi.

Vrinda, J. and B. R. Patil (2018). Genetic variability and heritability study in F_2 population for yield, yield attributes and Fiber quality traits in cotton (*Gossypium hirsutum* L.). J. Pharmacognosy and Phytochemistry, 7(4): 2816-2818.

تقدير مكونات التباين الوراثى وتحديد الانعزال فائق الحدود لاثنين من الهجن الصنفية لطبقة الأقطان فائقة الطول

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الملخص العربى

تكونت مواد الدراسة من الجيل الأول والثانى بالاضافة الى كلا الابوين لهجينين من القطن ينتميان إلى جوسييم باربادنس, وهما **((جيزة ٧١x جيزة ٧٤) x جيزة ٧١)** و **(جيزة ٩٢x CB58)،وذلك** لتقدير درجة التوريث على النطاق الواسع ودرجة التحسين الوراثي كنسبة مئوية من المتوسط والانعزال فائق الحدود لصفات المحصول ومكوناته وصفات التيلة.

كان تباين الاباء أقل لجميع الصفات المدروسة ، مما يشير إلى التجانس داخل هذة الاباء. لكنة زاد بشكل مفاجئ في الجيل الثانى بسبب الانعزال فائق الحدود.

أظهرت معظم الصفات المدروسة قيم مرتفعة لدرجة التوريث على النطاق الواسع مقترنًا بانخفاض درجة التقدم الوراثى كنسبة مئوية من المتوسط مما يشير إلى الدور الغالب للفعل الجيني الغير مضيف في التعبير عن هذه الصفات.

كان كلا من معاملى الالتواء والتفرطح لهما قيم أقل ويختلفان بين الهجينين للصفات المدروسة. أظهر محصول الشعر / النبات والنسبة المئوية للتصافى إشارة التواء سالبة وقيمة التفرطح لقراءة الميكرونير كانت موجبة للهجينين تحت الدراسة.

أعطى الهجينين عددًا كبيرًا من الانعزال فائق الحدود مقارنة بالاب الافضل لصفة وزن اللوزة متبوعًا بطول التيلة والمتانة. بينما تم الحصول على عدد أقل من الانعزال فائق الحدود **لصفة نسبة الانتظام** فى كلا الهجينين.

تم انتخاب افضل النباتات والتى تحتوى على اعلى قيم threshold value من نباتات الجيل الثانى والتى تعد الاعلى فى صفات المحصول وجودة التيلة معا بالنسبة لطبقة الاقطان فائقة الطول والتى تظهر كسر الارتباط السالب بين صفات المحصول والتيلة.

توصى الدراسة باستخدام شدة انتخاب عالية للوصول الى هذة النباتات ومتابعتها فى الاجيال المتقدمة وتقييمها فى مناطق مختلفة للوصول الى درجة السلالة النقية لانتاجها كصنف جديد