Genetic Analysis of Variation among the Biparental Progenies of Two Egyptian Cotton Crosses. (*Gossipum Barbadense* L.)

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Abstract: North Carolina designs are very effective in breaking undesirable linkage and lead to creating genetic variability in a population. F1 population was obtained by crossing the four varieties were used to produce two crosses (Giza 93 × Menofy) and (G.96× C.B58). The F_1 seeds for each cross were planted in order to obtain the seeds of F_2 generation through self-pollination. F_2 seeds were used as a material for this study. The analysis of variance was highly significant for all studied traits for genotypes for the two crosses. Also, the males were significant for all studied traits except position of ball node (PFN), boll weight (BW) g/plant, micronaire value and fiber strength for cross I, but in cross II males sets were significant for all studied traits, which exhibit difference between them except position of ball node (PFN), aboll weight (BW) g/plant and seed index (SI) which showed difference between them.Mean squares due to females within males were significant for all studied traits except duration of boll maturation, boll weight, micronaire value and fiber strength in cross I and position of ball node (PFN), boll weight (BW) g/plant and seed index in cross II. The contribution of male or female parents was more pronounced in the genetic variation. Additive components of variation were higher than dominance ones for most studied traits reflecting decreased ($\sqrt{D}$/A) values (less than unity). While the dominance portion of the genetic variation played a role for some traits reflecting higher ($\sqrt{D}$/A) values. In biparental progenies which confirmed by high mean genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values. The variation created on account of biparental mating was found to be heritable as seen from increases of discrepancy between (PCV) and (GCV) and reflected less influence of environmental factors.

Keywords: *Cotton, North Carolina, Biparental mating, PCV, GCV, Genetic variance*.

INTRODUCTION

Creation of variability using proper breeding procedures is pre-requisite either for development of varieties or inbred lines. Generally, the amount of variability generated is more noticeable in the early segregating generations as compared to later generations. In Egyptian cotton (G. barbadense L.), since selection within local materials has been going on for a long time, the genetic variability have been decreased. Further, breakthrough in productivity will have to come from controlled crosses designed to create new and wide variability. Conventional breeding methods like pedigree, bulk and back crossing methods with some modifications impose restrictions on the chances of better recombination's because of larger linkage blocks associated with the weakness of causing rapid homozygosity and low genetic variability (Rudra, *et al*., 2009). Further, negative association among yield components and genotype by environmental interaction prevent full exploitation of genetic variability for characters like yield. Biparental mating among the sergeant's in the F2 of a cross may provide more opportunity for the recombination to occur, mop up desirable genes as a result release concealed variability (Pradeep and Sumalini, 2003). Biparental mating, is a useful system of mating for generation of increased variability and may be applied where desired variation for traits of interest is lacking (Guddadamath, *et al*., 2010 and 2011). Very few

researches were applied by using biparental mating in cotton. Tyagi (1986) indicated that the biparental intermated was more amenable to improve through selection than F3 selfed. Abo Arab (2000), Soliman (2003) and Abd El-Salam (2005) cleared that biparental mating system was more effective in breaking undesirable linkages. On the other side, many researchers pointed out that several cycles intermating population may be useful for exploitation both type of gene effects, additive and non-additive. Such strategy will help to increase frequency of favorable alleles (EL-Mansy ,2005 ; EL-Mansy, *et al*., 2010 and Hamoud, *et al*., 2013). In view of the above facts, an attempt has been made in the present study to create and assess the different pattern of variability in the biparental progenies for its use in improving yield and fiber quality in cotton and to compare it with F3 selfed generation.

The ultimate goal of cotton breeding program is to increase yielding capacity and improve fiber properties of stable commercial cotton varieties. Exploration of hybrid vigor and understanding of nature of gene action in cotton are considered the important application of the science of genetics in cotton breeding program. Choice of the most efficient methodology mainly depends upon the type of gene action controlling the genetic variation. Therefore, unambiguous testes of the genetic components help the breeder to the rightful

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decision making about the most effective breeding method to be applied. In its respect, North Caroline design III (Comstock and Robinson, 1948 and 1952) has been extensively applied to detect and estimate the components of the genetic variation, i.e. additive and dominance genetic variances, as well as, it's very effective in breaking undesirable linkage and leading to create genetic variability in a population by creating heterozygosity. Assessment and quantifying the components of genetic variance controlling yield and its attributes as well as fiber properties in cotton have been studied by several researchers. Tyagi, *et al*., (1988) indicated that the biparental intermitted population was more amenable for improvement through selection than the selfed F3. Abo-Arab ,(1999); Soliman, (2003) and Abd El–Salam, (2005) indicated that biparental system was more effective in breaking undesirable linkage.

In the light of the advantages N.C.D. II, the present investigation targeted to estimate additive and dominance genetic variance, heritability in broad and narrow sense to help the breeder to choose the

effective cotton breeding method and maximize breeding progress.

MATERIALS AND METHODS
The present study was done in the Agronomy Department, Faculty of Agriculture, Cairo University. The investigation was carried out at Sakha Agric. Res. Stat. Kafr EL-Sheikh, Agric. Res. Center Egypt, during 2016 and 2017 growing seasons.

Genetic Materials
The genetic materials used in this study included four cotton genotypes belonging to (*Gossypium barbadense* L.), named Giza 93,Menofy, Giza 96 and C.B58 Cotton Research Institute (CRI) (Table 1). The four varieties were used to produce two crosses (Giza 93 × Menofy) and (G.96× C.B58) as a part of a breeding program towards tolerant varieties for drought stress, (Cotton Research Institute, Agricultural Research Center). The F_1 seeds for each cross were planted in order to obtain the seeds of F_2 generation through self-pollination. F_2 seeds were used as a material for this study.

Table 1: The names, pedigree and the main characteristics of four cotton genotypes (*G. barbadense* L.)whichwas used as parents in the present study

Varieties	Pedigree	Characteristics
G.93	Giza 77 x pima S6	Extra fine long. Its color is creamy. High yielding variety and it is characterized by drought tolerance.
Menofy	Giza 12 x Sakha 3	Extra-long staple variety, characterized by micronaire value, and fiber strength and it is caracterized by drougth tolerance.
G.96	Giza 84 x (Giza 70 x Giza 51 B)) x S62	Extra-long staple variety, characterized by fiber length, high lint yield and high ginning out turn.
C.B58	American Egyptian variety	Long staple variety, characterized by earliness, fiber length and uniformity index and it is caracterized by drougth tolerance.

The F_1 seeds for each cross were planted in order to obtain the seeds of F_2 generations through self-pollination.

In 2016 growing season, the F_2 seeds of the two crosses (G.93 × Menofy) and (G.96× C.B58) were planted at Experimental And Research Station, Faculty Of Agriculture, Cairo University, Giza, Egypt to obtain F_2 plant populations. Biparental mating (North Carolina Design-1, **Singh and Pawar, 2002**) was applied. Thirty two individual plants were randomly selected from each of cross I and cross II and were used as females. For each cross, four F_2 plants were randomly selected and used as males (each male was crossed with eight females), to obtain 32 biparental progenies for each of the two crosses.

In 2017 growing season, the field trials were conducted in RCBD with three replications at Sakha Research Station –Kafr El Shikh, Egypt evaluate the biparental progenies of the two cotton crosses. Each experimental plot consists of one row with 4.0 m. long and 0.70 m. in width and comprised 14 plants spacing 30 cm apart and two plants / hill.

Biparental Mating (North Carolina Design- I).
This experiment was developed to the biparental mating system Design I. Thirty two progenies (BIP) from cross I and II were evaluated at randomized complete blocks design with three replicates. Each replicate consisted of thirty two plots. Each plot was one row with 4.0 m. long and

0.70 m. in width and comprised 10 plants spacing 30 cm apart and one plant / hill.

COLLECTION OF DATA AND RECORDING OF OBSERVATIONS:-

The following observations were recorded on five individual guarded plants in all the biparental F_1 progeny populations for each cross.

Earliness Traits:
➢ **Days to First Flower**: recorded on 5 guarded plants as number of days from sowing to opening of the 1st flower.
➢ **Position of First Sympodium**: determined on 5 guarded plants by counting the number of nodes below the 1st fruiting branch discounting the cotyledonary node.
➢ **Duration of the Boll Maturation**: recorded on 5 guarded plants as number of days from opening the flower to the boll mature.

Yield and Yield Components:
➢ **Seed Cotton Yield/ Plant (gm):** measured as average weight of seed cotton yield picked from 5 guarded plants.
➢ **Lint Cotton Yield/ Plant (gm):** measured as average weight of lint cotton yield of 5 guarded plants.
➢ **Boll Weight (gm)**: estimated as the average weight of 5 bolls per plant as average of 10 guarded plants.
➢ **Lint Percentage**: estimated as (lint weight in a sample/ seed cotton weight in the same sample) x 100.

Fiber Quality Properties:

Fiber property tests were made according to the American society for testing materials (ASTM).
➢ **Fiber Length:** measured as 2.5% span length by fibrograph.
➢ **Fiber Strength:** measured by pressly instrument at zero gauge.
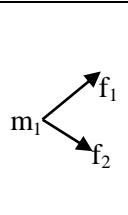➢ **Fiber Fineness:** measured by micronaire equivalent (units).

Testing was performed according to the standard method of A.S.T.M.(1986).

Statistical and Genetic Analysis.

The obtained data were subjected to two different statistical and biometrical techniques according to their mating system as follows:

Biparental Mating System Design I:-

The data by individual of all studied traits were subjected to statistical and biometrical analysis of variance assuming that all genetic components to be random according to the procedure out line by **Comstock and Robinson (1952),** and developed by **Kearsy and pooni (1996),** and **Singh and pawar (2002),** In this design each male plant is crossed to a different set of female plants (independent sample) to produce F_1 progenies. Thus the genetic structure of the progenies includes full-sib that have both parents in common and half-sibs, that have a male parent in common. In total the experimental consists of m x f x r individual progeny. Therefore, expected mean squares can be expressed in covariance of relatives.

		Parents	Progenies		Genetic structure			
m_1	f_1	m_1 x f_1	mf_{11}	x	x		X	
	f_2	m_1 x f_2	mf_{12}	x	Fs	x	Hs	X

Individuals within each P_{ij} progeny are full-sibs. The P_{ij} ,P_{ik} progenies are half-sibs. The linear model is

$$Y_{ijk} = u + m_i + f_{ij} + r_k + e_{iik}$$

Where u is the mean, m_i is the effect of the i male , f_{ij} is the effect of the j female mated to the i male,

r_k is the replication effect and e_{iik} is the experimental error (environmental and remainder of genetic variance among plots. The expected mean squares can be expressed in the more useful covariance of relatives (Table 2).

Table 2: Analysis of variance of the design I mating design

S.V	Df	MS	EMS
Replication	r- 1		
Genotypes	g-1		
Males	m- 1	M_3	$\sigma^2 e + k_2 \sigma^2 f + k_2 \sigma^2 m$
Females/Males	m(f- 1)	M_2	$\sigma^2 e + k_1 \sigma^2 f$
Error	(r- 1)(mf- 1)	M_1	$\sigma^2 e$

R= number of replications.

g= number of genotypes.

M= number of paternal plants (males).

F= number of maternal plants (females)/ paternal plant.

K= k_2= number of plats / maternal plants.

K_3= number of plats / paternal plants = r x f/m.

M_1= $\sigma^2 e$ is the sum of intra plat environmental variance.

M_2= $\sigma^2 f/m$ is the variance of females/males.

M_3= $\sigma^2 m$ is the variance of male effects.

Estimation of variance components:

The variance components can be estimated from appropriate mean squares as follows:

$$\sigma^2 m = \frac{M_3 - M_2}{FK}$$

$$\sigma^2 f/m = \frac{M_2 - M1}{K}$$

$$\sigma^2 e = MS_e$$

f :number of female / male .

K: number of progeny / female.

MS_e: environmental variance.

Genetical interpretations:

According to **Comstock and Robinson, (1952); and kearsy and pooni (1996),** its clearly that:-

$\sigma^2 m = Cov\ H.s \implies$ the covariance between half sibs means is entirely due to the additive effects, where F = zero

$\sigma^2 m = Cov\ Hs = \frac{1}{4} \sigma^2 A$ $\sigma^2 A = 4 \sigma^2 m$ (additive genetic variance)

$\sigma^2 f/m$ is obtained from differences between maternal plants within paternal plants, so that

$\sigma^2 f/m = CovFs - CovHs = \frac{1}{4} \sigma^2 A + \frac{1}{4} \sigma^2 D$ for F = zero

$\sigma^2 D = 4 (\sigma^2 f/m - \sigma^2 m) = 4 (CovFs - CovHs) - CovHs$

             $= 4 (\frac{1}{4} \sigma^2 A + \frac{1}{4} \sigma^2 D) - \frac{1}{4} \sigma^2 A = \sigma^2 D$

        (*It refers to non-additive genetic variance*).

$\sigma^2 G = 4 \sigma^2 f/m = \sigma^2 A + \sigma^2 D$

$\sigma^2 G - CovFs = \frac{1}{2} \sigma^2 A + \frac{3}{4} \sigma^2 D$

The average degree of dominance d = $\sqrt{\dfrac{\sigma^2 D}{\sigma^2 A}}$

Estimates of heritability:

Estimates of heritability in broad sense (h^2_b) and narrow sense (h^2_n) were calculated according to **Kearsy and Pooni (1996),** as follows:

Heritability in broad sense (h^2_b) = $\dfrac{\sigma^2 g}{\sigma^2 P} x100$ = $\dfrac{\sigma^2 A + \sigma^2 D}{\sigma^2 A + \sigma^2 D + \sigma^2 E} x100$

Phenotypic variance on an individual basis

$\sigma^2 P = \sigma^2 m + \sigma^2 f/m + \sigma^2 E$ (**Kearsy and Pooni 1996**)

Heritability in narrow sense $h^2_n = \dfrac{\sigma^2 A}{\sigma^2 P} x100$ = $\dfrac{4\sigma^2 m}{\sigma^2 m + \sigma^2 f / m + \sigma^2 E} x100$

The standard error was calculated according to formula: $\sqrt{\dfrac{EMS(n_1 + n_2)}{r(n_1 n_2)}}$

According to Steel and Torrie (1980).

Where
EMS: The mean squares of experimental error from the analysis of variance.
r = Number of replications.
n_1 = Number of the F_1 means.
n_2 = Number of parent means.

The phenotypic and genotypic coefficients of variation were estimated using the formula developed by Burton (1952)

1. Phenotypic coefficient of variation (PCV %) = $\dfrac{\sigma p}{\bar{x}}$. 100
2. Genotypic coefficient of variation (GCV %) = $\dfrac{\sigma g}{\bar{x}}$. 100

Where
σp = Phenotypic standard deviation.
σg = Genotypic standard deviation.
$\overline{X}$ = Population mean.

RESULTS AND DISCUSSION

Breeders very often use the segregating populations as a source of variability to obtain homozygous recombinant lines with better performance which developed into varieties.

Biparental mating among the sergeant's in the F_2 of a cross may provide more opportunity for the recombination to occur, mop up desirable genes as a result release concealed variability (Pradeep and Sumalini, 2003)

Table 2: Analysis of variance for the studied characters in biparental progenies of two cotton crosses (G.93 × Suvin) and (G.96 × S.B58)

	S.V	d.f	DFF	PFN	DBM	BW (g)	SCY/P (g)	LY/P (g)	L%	seed index	Micronaire value	Fiber length (mm)	Fiber strength (g/tex)
cross I	Reps	2	0.97	0.14	0.17	0.04	1.87	0.87	0.45	0.45	0.03	1.43	0.2
	genotypes	31	6.7**	1.68*	1.69*	0.25	437.19**	67.2**	3.21*	1.85*	2.11**	1.94**	2.37**
	males	3	21.26**	2.62	8.15**	0.5	2454.11**	341.39**	4.76**	2.92*	0.27	2.88*	1.16
	Female/male	28	5.14**	1.72*	1.00	0.23	221.09**	34.51**	3.04**	1.1	0.1	0.96	2.28**
	Error	62	1.33	0.14	0.35	0.02	13.95	2.13	0.33	0.2	0.01	0.38	0.05
cross II	Reps	2	2.375	0.0104	0.5938	0.00002	0.51	0.52	0.46	0.13	0.003	0.166	0.115
	genotypes	31	10.29**	0.4731	7.073**	2.05**	35.66**	7.82*	2.67**	2.24**	1.913*	1.87*	2.46*
	males	3	19.8715**	0.4167	18.5278**	0.35	94.77**	36.19**	16.26**	0.72	3.044*	2.80*	4.313**

Female/ male	2 8	9.263 4**	0.47 92	5.848 2**	2.04 **	29.32 **	4.77* *	1.22	1.72 *	0.009	9.11 4**	2.258 **
error	6 2	0.611 6	0.35 6	0.862 6	0.00 4	0.48	0.19	0.19	0.99	0.005	0.29 3	0.072

DFF, PFN, DBM, BW, SCY, LY, L%, and SI: days to first flower, position of first node, duration of boll maturation, boll weight, seed cotton yield, lint yield, lint percentage and seed index, respectively.

Data in (table 2) showed analysis of variance of biparental sets of families and results revealed significant or highly significant mean squares among crosses (biparental progenies) for most traits over two crosses indicating presence of high segregations in F_2, this variation further transmitted to biparental progenies. Biparental crosses were partitioned into mean square of male and female within male.

Mean squares due to males in cross I were significant for seed index and fiber length and highly significant for days to first flower, duration of ball maturation, seed cotton yield, lint yield and lint percentage while reveled not significant for position of first node, ball weight, Micronaire value and fiber strength.

In cross II Mean squares due to males were significant for Micronaire value and fiber length and highly significant for days to first flower, duration of ball maturation, seed cotton yield, lint yield, lint percentage and fiber strength while reveled not significant for position of first node, ball weight, and seed index.

Mean squares due to females within males in cross I were significant for position of first node and

highly significant for days to first flower, seed cotton yield, lint yield, lint percentage, and fiber strength while reveled not significant for duration of boll maturation, ball weight, seed index, Micronaire value and fiber length.

In cross II Mean squares due to females within males were significant for seed index and highly significant for days to first flower, duration of ball maturation, ball weight, seed cotton yield, lint yield, lint fiber length and fiber strength while reveled not significant for position of first node, lint percentage, Micronaire value.

In most studied traits mean squares due to males are large in magnitude than female within male, which revealed over all differences between F2 male parents. However, female within male were also significant for most characters, indicating significant genetic variation. Genetic variation composed of additive and / or non-additive, dominance or epistasis, would be necessary to make further improvements in such characters.

These findings were in agreement with Soliman, *et al*., (2007) and El-Mansy, *et al*., (2008). Similar results were in agreement with Khedr, (2002) and EL-Mansy, (2005) for earliness characters, Tyagi, (1987); Pradeep and Sumalini, (2003); for yield characters and May and Cynthia, (1994); Zeina, (2002) and Hassan, (2012) for fiber quality characters.

Table 3: Means, standered error, genotypic (GCV%) and Phenotypic (PCV%) for the two cotton crosses (G.93 × Suvin) and (G.96 × S.B58) for all study traits

characters	means		standered error		G.C.V		P.C.V	
	Cross I	cross II	Cross I	cross II	Cross I	cross II	Cross I	cross II
DFF	66.00	68.66	1.41	0.96	2.71	4.70	3.38	5.00
PFN	6.95	6.08	0.46	0.73	1.53	0.64	2.18	2.59
DBM	56.07	56.25	0.72	1.14	0.80	3.68	1.01	4.19
BW(g)	3.45	3.18	0.17	0.08	2.25	0.52	2.44	0.56
SCY/P(g)	84.48	74.58	4.57	0.85	67.00	15.72	72.50	15.94
LY/P(g)	32.43	27.04	1.79	0.53	66.89	9.40	69.08	9.63
L%	38.41	36.24	0.70	0.53	2.50	2.29	2.78	2.46
Seed index	10.45	10.68	0.55	1.22	2.92	2.32	3.55	0.76
Micronaire value	3.41	3.18	0.12	0.09	0.97	0.08	1.11	0.13
fiber length (mm)	35.14	35.33	0.75	0.66	0.63	0.92	0.99	1.20

| fiber strength (g/tex) | 11.09 | 11.00 | 0.27 | 0.33 | 0.94 | 1.17 | 1.10 | 1.39 |

DFF, PFN, DBM, BW, SCY, LY, L%, and SI: days to first flower, position of first node, duration of boll maturation, boll weight, seed cotton yield, lint yield, lint percentage and seed index, respectively.

The estimates of phenotypic and genotypic coefficients of variation PCV were higher than GCV.

In general, there were relatively distinct differences between phenotypic and genotypic coefficients of variation for earliness, indicating that environmental effects had important effects on these characters under the conditions of this study.

In cross I and cross II the estimates of phenotypic and genotypic coefficients of variation PCV% were higher for yield and its component traits than GCV% except seed index in cross I the GCV% was higher than PCV%. In general, there were relatively distinct differences between phenotypic and genotypic coefficients of variation for most yield and its component traits, indicating that environmental effects had their important effects on these characters under the conditions of this study.

In cross I and cross II the estimates of phenotypic and genotypic coefficients of variation PCV% were higher for all traits under the study than GCV%. In general, there were relatively distinct differences between phenotypic and genotypic coefficients of variation for most fiber quality traits, indicating that environmental effects had their important effects on these characters under the conditions of this study.

Partitioning of genetic variance.
The knowledge about the nature and magnitude of genetic effects prevailing in the breeding material is necessary to decide the kind of breeding procedure to be chosen. Although gene action of the characters in cotton is reported by many researchers, but the genetics of a particular characters may vary in plant material and environments. So it is necessary to study gene action of quantitative characters before starting any breeding program.

Assessment of component of genetic variation, which included additive ($\sigma^2 A$) and non-additive ($\sigma^2 D$) in addition to heritability in broad (H_b^2 %) and narrow (H_n^2 %) sense as well as dominance degree ratio $\sqrt{\dfrac{\sigma^2 D}{\sigma^2 A}}$.

Table 4: Assessment of additive (A), dominance (D), Phenotypic (PCV %), genotypic (GCV %) coefficients of variation, heritability in broad (H²b %) and narrow sense (H²n %) and degree of dominance √D/A for the two cotton crosses (G.93 × Suvin and (G.96 × S.B58) for earliness traits.

	cross I			cross II		
	DFF	**PFN**	**DBM**	**DFF**	**PFN**	**DBM**
σ^2_A	2.69	0.07	1.19	1.33	0	1.58
σ^2_D	2.39	0.31	0	7.33	0.13	3.4
H_n^2%	47.39	15.42	85.26	14.974	3.23	30.057
H_b^2%	89.54	86.11	84.84	97.698	50.937	94.547
$\sqrt{D/A}$	0.94	2.14	0	2.35	0	1.465

DFF, PFN and DBM: days to first flower, position of first node and duration of boll maturation, respectively.
Information about Partitioning of genetic variance, heritability, degree of dominance phenotypic and genotypic coefficients of variation, heritability in broad and narrow sense for earliness traits are showed in Table 4. According to cross I the relative magnitude of additive (A) and dominance (D) components estimates of additive variance were higher than those of dominance variance for

DFF and DBM resulting in (√D/A) values less than unity and explaining that, the additive component was the predominant type in the inheritance of such traits. This was confirmed by high narrow sense heritability estimates. This agrees with Abd El Bary (2003) , El-Mansy, (2005) and El-Mansy, *et al*., (2008) .While, the magnitude of dominance component was larger than corresponding additive ones for PFN reflecting higher (√D/A) values. These findings showed the importance of over dominance gene

effects in the control of these traits and indicated that non-fixable genes could be exploited efficiently through hybrid breeding method for improving these traits. These reselts were in the same line with Abou El-yazied, (2014), Dawwam, *et al*., (2016), El-Mansy, *et al*., (2020), Said, *et al*., (2021) and Amer, (2022).

Regarding to cross II the relative magnitude of additive (A) and dominance (D) components estimates of dominance variance were higher than those of additive variance for all earliness traits resulting in ($\sqrt{D/A}$) values more than unity and explaining that, These findings showed the importance of over dominance gene effects in the

control of these traits and indicated that non-fixable genes could be exploited efficiently through hybrid breeding method for improving these traits.

A successful selection mainly depends on heritability, which is an index for the transmission of a character from one generation to the next generation (Larik, *et al*., 1999), and efficient selection is possible with high heritability and genetic advance (Kumar, *et al*., 2019). It was defined as low when broad-sense heritability was below 30, medium 30-60 and high above 60 by Srivinias, *et al*., (2014).

Table 5: Assessment of additive (A), dominance (D), Phenotypic (PCV %), genotypic (GCV %) coefficients of variation, heritability in broad (H²b %) and narrow sense (H²n %) and degree of dominance $\sqrt{D/A}$ for the two cotton crosses (G.93 × Suvin and(G.96 × S.B58) for yield and its components

	cross I					cross II				
	BW	**SCY/P**	**LY/P**	**L%**	**SI**	**bw**	**scy**	**ly**	**lp%**	**si**
$\sigma^2 A$	0.05	372.17	51.15	0.29	0.02	0.04	8.18	3.93	1.88	0.07
$\sigma^2 D$	0.23	0.00	0.00	3.33	1.19	0.00	20.66	0.66	0.00	0.00
H²n %	16.17	31.79	15.96	7.63	1.60	24.52	28.21	84.50	72.11	14.06
H²b %	96.88	97.80	97.85	96.13	93.26	93.63	99.45	98.63	94.27	99.66
$\sqrt{D/A}$	2.23	0.00	0.00	3.41	7.58	0.00	1.59	0.41	0.00	0.00

BW , SCY, LY, L%, and SI: boll weight, seed cotton yield, lint yield, lint percentage and seed index, respectively

In cross I the results revealed that the magnitude of dominance genetic variance ($\sigma^2 D$) were larger than those of additive genetic variance ($\sigma^2 A$) for boll weight, lint percentage and seed index. These indicated that predominate of dominance genetic variance in the inheritance of these traits. These results were in harmony with those were obtained by Dva, *et al*., (1982) abd disagreed with those obtained by Valienko, *et al*., (1983). The magnitude of additive genetic variances ($\sigma^2 A$) were larger than those of dominance genetic variance ($\sigma^2 D$) for seed and lint cotton yield. These indicated that predominate of additive genetic variance in the inheritance of these traits. In cross II The magnitude of additive genetic variances ($\sigma^2 A$) were larger than those of dominance genetic variance ($\sigma^2 D$) for boll weight, lint cotton yield, lint percentage and seed index. These indicated that predominate of additive genetic variance in the inheritance of these traits. And the magnitude of dominance genetic variance ($\sigma^2 D$) was larger than those of additive genetic variance ($\sigma^2 A$) for seed cotton yield. This

indicated that predominate of dominance genetic variance in the inheritance of this trait.

The ratio of additive/dominance indicated that the dominance play a major role in inheritance for seed trait. These findings were in harmony with those recorded by El –Hoseiny, *et al*., (2012), Abou El-yazied, (2014); Dawwam, *et al*., (2016); AL-Hibbiny, *et al*., (2020) and ElMansy, *et al*., (2020).

Concerning heritability values, the results revealed that for cross I the estimates in broad sense were 96.88, 94.46, 97.80, 97.85, 96.13 and 93.26 for boll weight, seed cotton yield, lint cotton yield, lint percentage and seed index, respectively. However, the data indicated that narrow sense heritability value (<30) were obtained for boll weight, , lint cotton yield, lint percentage and seed index and moderate narrow sense heritability value (50-30) was obtained for seed cotton yield. In cross II the heritability values, the results revealed that the estimates in broad sense were 93.63, 99.45, 98.63, 94.27, 96.13 and 99.66 for boll weight, seed cotton yield, lint cotton yield, lint percentage and seed index, respectively. However, the data indicated that high narrow sense heritability values (>50)

were obtained for lint percentage, and lint cotton yield, narrow sense heritability value (<30) were obtained for boll weight, seed cotton yield, and seed index. These results agree with those reported by Aripov and Ioelovich, (2020), Brown and Khan, (2022), Ahmad, *et al*., (2022), Imtiyaz, *et al*., (2020).

Table 6: Assessment of additive (A), dominance (D), Phenotypic (PCV %), genotypic (GCV %) coefficients of variation, heritability in broad (H²b %) and narrow sense (H²n %) and degree of dominance √D/A for the two cotton crosses (G.93 × Suvin and(G.96 × S.B58) for fiber quality.

	cross I			cross II		
	Micronaire value	**Fiber length (mm)**	**Fiber strength (g/tex)**	**Micronaire value**	**Fiber length (mm)**	**Fiber strength (g/tex)**
$\sigma^2 A$	0.03	0.15	0.15	0.00	0.20	0.26
$\sigma^2 D$	0.08	0.62	0.16	0.00	0.62	0.00
H²n %	25.72	16.42	44.83	68.47	21.60	62.25
H²b %	94.53	82.08	92.70	74.72	89.39	88.57
√D/A	1.64	2.00	1.03	0.30	1.77	0.00

In cross I the results revealed that the magnitude of dominance genetic variance ($\sigma^2 D$) were larger than those of additive genetic variance ($\sigma^2 A$) for all traits under the study. These indicated that predominate of dominance genetic variance in the inheritance of these traits. In cross II The magnitude of additive genetic variances ($\sigma^2 A$) were larger than those of dominance genetic variance ($\sigma^2 D$) for fiber strength. These indicated that predominate of additive genetic variance in the inheritance of this trait. And the magnitude of dominance genetic variance ($\sigma^2 D$) was larger than those of additive genetic variance ($\sigma^2 A$) for fiber length. This indicated that predominate of dominance genetic variance in the inheritance of this trait.

The ratio of additive/dominance indicated that the dominance play a major role in inheritance for seed trait. Hassan, *et al*., 2022) found that Additive component was extremely higher than dominance component for all traits.

Concerning heritability values, the results revealed that for cross I the estimates in broad sense were 94.53, 82.08, and 92.70 for micronaire value, fiber length and fiber strength, respectively. However, the data indicated that high narrow sense heritability values (>50) were obtained for fiber strength and low narrow sense heritability value (<30) were obtained for micronaire value and fiber length. In cross II the heritability values, the results revealed that the estimates in broad sense were 74.72, 899.39 and 88.57 for micronaire value, fiber length and fiber strength, respectively. However, the data indicated that high narrow sense

heritability values (>50) were obtained for micronaire value and fiber strength and narrow sense heritability value (<30) were obtained for fiber length. (SAHAR, *et al*., 2021).

CONCLUSIONS

In this study analysis of variance of biparental sets of families and results revealed significant or highly significant mean squares among crosses In most studied traits mean squares due to males are large in magnitude than female within male, which revealed over all differences between F_2 male parents. However, female within male were also significant for most characters, indicating significant genetic variation. Genetic variation composed of additive and / or non-additive, dominance or epistasis, would be necessary to make further improvements in such characters.

In cross I and cross II the estimates of phenotypic and genotypic coefficients of variation PCV% were higher for all traits under the study than GCV%. In general, there were relatively distinct differences between phenotypic and genotypic coefficients of variation for most traits under the study, indicating that environmental effects had their important effects on these characters under the conditions of this study.

The additive component was the predominant type in the inheritance of earliness traits. This was confirmed by high narrow sense heritability estimates.

The ratio of additive/dominance indicated that the dominance play a major role in inheritance for yield and its component trait.

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