

Estimates of genetic parameters for cotton yield, its components, and fiber quality traits based on line x tester mating design and principal component analysis



Waleed M. B. Yehia¹ and Essam F. El-Hashash^{2*} 

Address:

¹ Cotton Breeding Department, Cotton Research Institute, Agricultural Research Center, Giza, Egypt

² Department of Agronomy, Faculty of Agriculture, Al-Azhar University, Cairo, Egypt

*Corresponding author: **Essam F. El-Hashash**, e-mail: dressamelhashash@yahoo.com

Received: 17-04-2022; Accepted: 16-05-2022; Published: 22-05-2022

doi: [10.21608/ejar.2022.134192.1228](https://doi.org/10.21608/ejar.2022.134192.1228)

ABSTRACT

The present study aimed at assessing the mid (MPH) and better (BPH) parents heterosis, potence ratio (PR) and genetic parameters for yield, its components and fiber traits in eighteen F₁ hybrids developed by crossing between six lines and three testers using line × tester mating design. Pearson correlation coefficient and principal component analysis (PCA) were used for a better understanding of the relationship during this study. The lines, testers and their F₁ hybrids were evaluated in a randomized complete block design (RCBD) with three replications at Sakha Agriculture Research Station, Kafr El- Sheikh Governorate, Egypt, during the 2020 cropping season. The variances due to the sources of variation in line x tester analysis exhibited significant differences for most measured traits. The proportional contribution of line × tester was higher than the individual contribution of lines and testers for most studied traits. The lines G.90x Aus.12 and Uzbekistan as well as the tester G.97 showed superior cotton yield and most studied traits based on mean performance compared to the other parents. The hybrid combinations TNB x G. 94, (G.90x Aus.12) x G.86 and G.96 x G.94 were identified as excellent based on mean performance, MPH, BPH and PCA analysis for cotton yield and most studied traits. Potence ratio exhibited that the hybrid combinations have positive or negative nature for studied traits. Genetic parameters indicated that non-additive gene action effects had a more important role compared to the additive in controlling all the studied traits, except the number of seeds/boll trait. Significant correlation coefficients were found between all possible pairs of mean performances, MPH, BPH (positive) and PR (negative) parameters for most investigated traits. PCA can be used as a suitable method for studying the studied traits and to determine the best hybrids across line x tester analysis. Finally, and based on the results of statistical methods used in this study, the parents and hybrids above are promising enhancement and improvement of cotton productivity and its fiber quality through use in cotton breeding programs in Egypt.

Keywords: Line x Testers Analysis, Heterosis, Potence Ratio, Genetic Parameters, Correlation, PCA, Cotton

INTRODUCTION

Cotton is the most important fiber crop in the world and the most important cash crop in Egypt. In the world, the total area harvested, yield and production of cotton were 32.65 Million hectares, 811 Kilograms per hectare and 121.57 Million 480 lb. bales in Dec 2021/2022, respectively. While, the total area harvested, yield and production of cotton were 0.1 Million hectares, 718 Kilograms per hectare and 0.33 Million 480 lb. bales in Egypt. Cotton production decreased in 2021/22 cropping season than last year with 8.83% in the world and with 53.49% in Egypt (USDA, 2022). The main goal of cotton breeders is to look and select the genotypes with high yield traits and take advantage of the permanent untapped genetic variation of Egyptian varieties, substantial work has been carried out to develop both yield and quality traits of cotton in Egypt (Yehia and El-Hashash, 2019).

Different methods have been applied to improve the selection of genes controlling the useful agronomic traits. The most used breeding designs are bi-parental, multiple hybrids, test hybrids, line × tester and diallel designs (Nduwumuremyi *et al.*, 2013). The major purpose of these designs is to determine the combining abilities of experimental hybrids and parental lines besides understanding the heredity of the evaluated traits (Sharma, 2006). The line x tester mating design is an extension (modified version) of the top cross method in which several testers are used. It is a common approach for assessing the expression of genetic aspects of traits (Kempthorne, 1957). which helps identify the best heterotic hybrids, it provides information regarding genetic mechanisms controlling quantitative traits. The most important merit of this approach is that it enables evaluation with fewer experimental materials compared to other mating designs. Many researchers have been used the line x tester design in cotton such as (Usharani *et al.*, 2016; Chinchane *et al.*, 2018; Khokhar *et al.*, 2018; Yehia and El-Hashash, 2019; Mariz *et al.*, 2021; and Mudhalvan *et al.*, 2021).

The term heterosis was coined by (Shull, 1914). it is the superiority of F₁ hybrid over the mid-parents or the better parent or the standard check with regard to agriculturally useful traits. The genetic causes involved in the expression of heterosis are dominance and nonallelic interactions (Hayes and Foster, 1976). The magnitude of heterosis can be maximized if the parents are genetically varied from each other. Exploiting heterosis is one of the methods to improve yield and fiber quality traits in cotton. (Kumar, 2008) stated that to maximize heterosis, there is a need for utilizing breeding programs aimed at constantly creating variability and increasing genetic diversity between populations that can further be exploited through selection for combining abilities between such diverse populations. Also heterosis can be enhanced by

increasing dominant gene action. It is difficult to precisely detect and manipulate the degree of dominant gene action while selecting, based on phenotypic measurements, for high heterosis. However, it is possible to create and improve heterotic populations against a tester or reciprocally develop diverse populations which differ for the alleles at a large number of yields influencing loci (showing dominance).

The breeding value of a line is a function of the additive gene action. The additive genes are directly transported from the parents to the offspring, are responsible for the resemblance between relatives and can be used to calculate heritability (Falconer, 1989). The development of high-yielding varieties requires detailed knowledge of the genetic variability present in the germplasm of the crop, the association among yield components, input requirements and culture practices (Dutta *et al.*, 2013). Genetic parameters, such as genotypic and phenotypic coefficients of variation are useful in detecting the amount of variability present in the germplasm. Moreover, knowledge of heritability is beneficial in the formulation of plant breeding procedures and in assessing the progress of selection, as it indicates the extent of transmissibility of a character into future generations and the quality of phenotype data in multilocation trials (Sabesan *et al.*, 2009; Falconer, 1989) stated that means and variances of generation of the related population are beneficial in estimating the broad and narrow sense heritability affecting the quantitative trait in a hybrid. Additionally, the potence ratio is useful to determine the nature of dominance and its direction. Selecting parents based on mean performance, adaption and genetic diversity does not lead necessarily to desirable results. This is due to the differential ability of the parents, which depended on the complex interactions among the genes and cannot be judged by the mean performance alone (Allard, 1960). Selection based on seed yield and its components should be based on genotypic variance and the proportion of the genetic gain and heritability for each trait (El-Hashash and Agwa, 2018). In this context, several researchers like (Khan *et al.*, 2009; El-Hashash, 2013; Anjum *et al.*, 2018; Hamed and Said, 2021; and Mariz *et al.*, 2021) have reported that the majority of genetic variances of yield, its components and fiber quality traits are under the control of non-additive nature of genes.

There is a need to use principal component analysis (PCA) to show the results of cotton breeding experiments. Thus, many researchers such as (Abasianyanga *et al.*, 2017; Nandhini *et al.*, 2018; Shah *et al.*, 2018; Vinodhana and Gunasekaran, 2019; Abdel-Monaem *et al.*, 2020; and Yehia and El-Hashash, 2021) have used the PCA to assess the relationship and diversity between several cotton germplasms, in addition to knowing the relationships between yield, its components and fiber quality traits. Here, the Pearson correlation coefficient and principal component analysis were used to assess the heterosis, potence ratio, genetic components, and associations between mean performances, heterosis, and potence ratio for cotton yield, its components, and fiber quality traits in a line tester mating design.

MATERIAL AND METHODS

Genetic Material and Field Procedure:

Two experiments were conducted at Sakha Agriculture Research Station, Kafr El- Sheikh Governorate, Egypt during cropping years 2019 and 2020. The experimental material comprised six lines (TNB, G.89 x G.86, G.90x Aus.12, Uzbekistan, Aus. 12 and G.96) and three testers (G.94, G.86 and G.97) of cotton belonging to *Gossypium barbadense* L. The lines and testers were crossed to produce eighteen F₁ hybrids as per the line x tester mating design developed by Kempthorne (1957) in the year 2019. Eighteen F₁ hybrids, three lines and six testers were evaluated in Randomized Complete Block Design (RCBD) with three replications during the year 2020. In each replication, parents (lines and testers) and F₁ hybrids were sown in a single row of 4 m long with a spacing of 70 cm between rows and 30 cm between plants. Recommended cultural practices were carried out and the crop was grown under uniform field conditions to minimize environmental variations to the maximum possible extent.

Data recording:

Data were recorded on 10 guarded plants for cotton yield and related traits i.e., seed cotton yield/plant (SCY/P) in gram, lint cotton yield/plant (LCY/P) in gram, seed index (SI) in gram, boll weight (BW) in gram, number of open bolls/plant (No. B/P), lint percentage (L %), lint index (LI) and number of seeds/boll (No. S/B), as well as for fiber quality traits i.e. fiber fineness (FF) micronair reading, fiber strength (FS) in Presley, upper half means (2.5%SL) in mm and uniformity ratio (UR%). The fiber quality traits were estimated at Cotton Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

Statistical Analysis:

Data recorded were subjected to analysis of variance according to (Steel and Torrie, 1980), to determine significant differences among genotypes. The CV% estimates were categorized as very high (CV \geq 21%), high (15% \leq CV \leq 21%), moderate (10% $<$ CV \leq 15%) and low (CV $<$ 10%) according to Pimentel-Gomes (2009). The gene action and heritability were estimated by the using of the line x tester analysis methods described by Kempthorn (1957) and adopted by (Singh and Chaudhary, 1979). According to (Robinson *et al.*, 1949) the heritability estimates were categorized as 0-30% = low; 31-60% = moderate and above 60% = high. Heterosis relative to mid-parents (MPH) and better parent (BPH) were calculated manually in MS Excel-2019 worksheet as per the formula given by (Liang *et al.*, 1972). The significance of MPH and BPH was determined using the least significant difference value (LSD) at 0.05 and 0.01 levels of probability given by (Steel and Torrie, 1980). The nature of dominance was determined by calculating the potence ratio (PR) according to (Mather, 1949; and Smith, 1952). Genotypic (GCV%) and phenotypic (PCV%) coefficients of variation were calculated according to Burton (1952). Pearson's correlation coefficient and principal component analysis (PCA) were applied for a better understanding of the relationship among studied traits across mean performances, MPH, BPH and PR, using the computer software program PAST version 4.03.

RESULTS

Analysis of variance:

The analysis of variance showed a significant difference ($p < 0.05$ or 0.01) between genotypes, parents (P), hybrids (C) and interaction P x C for most investigated traits Table (1). The variance due to hybrids is partitioned into lines, testers and their interaction. The variance due to the lines (L), testers (T) and interaction L x T were significant ($p < 0.05$ or 0.01) for cotton yield and most measured traits. In Table 1, the coefficient of variation (CV%) was higher in seed cotton yield/plant, lint cotton yield/plant and the number of bolls/plant traits ($CV > 15\%$) than in other studied traits ($CV < 10\%$).

Table 1. ANOVA of line x tester analysis for investigated traits in cotton.

S.O.V.	df	SCY/P	LCY/P	SI	BW	No.B/P	L %	LI	No.S/B	FF	FS	2.5%SL	UR%
Replications	2	763.80*	77.05	0.646*	0.015 ^{ns}	100.41*	1.788 ^{ns}	0.547*	1.67 ^{ns}	0.03 ^{ns}	0.08 ^{ns}	0.34 ^{ns}	0.35 ^{ns}
Genotypes	26	2062.90**	248.88**	2.85**	0.11**	219.90**	6.91**	1.62**	7.84**	0.13**	0.20**	2.79**	1.75**
Parents (P)	8	539.01**	83.80**	5.37**	0.03 ^{ns}	40.86	3.17 ^{ns}	2.67**	17.64**	0.21**	0.37**	4.98**	2.99**
Hybrids (C)	17	2412.30**	310.00**	1.29**	0.12**	280.04**	6.11**	0.54**	2.45 ^{ns}	0.09*	0.12**	1.90**	0.82 ^{ns}
P. vs. C.	1	8313.60**	1466.50**	9.18**	0.47**	629.93**	50.27**	11.52**	21.02**	0.21*	0.29**	0.32 ^{ns}	7.65**
Lines (L)	5	3028.10**	399.80**	1.77**	0.21**	315.02**	14.20**	0.30**	3.70 ^{ns}	0.02 ^{ns}	0.10*	0.91**	0.84 ^{ns}
Testers (T)	2	3563.70**	458.53**	0.19 ^{ns}	0.09 ^{ns}	509.48**	0.56 ^{ns}	0.19**	1.41 ^{ns}	0.32**	0.42**	2.10**	0.99 ^{ns}
L x T	10	1874.10**	235.40**	1.27**	0.08 ^{ns}	216.66**	3.18 ^{ns}	0.74**	2.03 ^{ns}	0.08 ^{ns}	0.07 ^{ns}	2.35**	0.77 ^{ns}
Error	52	183.39	27.35	0.20	0.04	26.42	2.05	0.18	2.25	0.05	0.04	0.20	0.49
C.V. %		15.81	16.95	4.27	6.81	18.52	3.99	7.05	7.93	5.26	1.94	1.30	0.81

Statistically significant differences at * $p \leq 0.05$ and ** $p \leq 0.01$; ns: indicate the non-significant difference. SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

Mean Performance:

Tables (2) and 3 described the detailed results of mean performances of parents (six lines and three testers) and their eighteen hybrids for yield, yield components and fiber quality traits, respectively. When compared the means and the L.S.D., the lines, testers and their hybrids showed highly significant effects for all evaluated traits ($P < 0.01$), except boll weight in lines and testers had significant ($P < 0.05$). Some lines, testers and their hybrids exhibited higher values than the grand mean for all traits measured. Compared with that of other lines, the best mean performances were recorded by the line G.90x Aus.12 for seed cotton yield/plant, lint cotton yield/plant and number of bolls/plant traits, by the line Uzbekistan for boll weight, number of seeds/boll and 2.5% span length traits, as well as by the line G.96 for other traits investigated. The G.97 tester recorded the highest mean performances for all studied traits, except seed and lint indexes traits (G.94) as well as 2.5% span length and uniformity ratio traits (G.86). Among lines and testers, the best parents are G.97 tester for most studied traits as well as Uzbekistan and G.96 lines for fiber quality traits. These parents might be reliably useful in a breeding program for improving cotton yield and fiber quality in Egypt.

Table 2. Mean performances values of lines and testers for investigated traits.

Parents	SCY/P	LCY/P	SI	BW	No. B/P	L %	LI	No. S/B	FF	FS	2.5% SL	UR%
Lines												
TNB	65.80	22.95	9.23	3.02	21.77	34.87	4.94	21.33	4.51	9.97	32.92	85.10
G.89 x G.86	68.46	22.91	8.93	2.99	22.87	33.46	4.49	22.30	4.45	10.10	33.65	85.55
G.90x Aus.12	82.35	28.27	9.13	2.94	28.04	34.33	4.77	21.12	4.50	9.93	34.05	86.15
Uzbekistan	71.94	25.47	8.68	3.03	23.77	35.40	4.76	22.53	4.17	10.06	37.25	87.30
Aus. 12	70.24	24.05	9.42	2.94	23.92	34.24	4.91	20.50	4.05	9.75	35.25	87.40
G.96	61.47	21.81	9.51	2.89	21.29	35.49	5.23	19.58	3.78	10.40	34.60	87.60
G. mean	70.04	24.24	9.15	2.97	23.61	34.63	4.85	21.23	4.24	10.04	34.62	86.52
Testers												
G.94	89.27	32.10	12.04	3.12	28.58	35.96	6.76	16.62	4.40	10.35	33.90	85.35
G.86	73.79	26.69	11.81	2.98	24.79	36.17	6.69	16.09	4.40	10.50	34.10	86.55
G.97	104.21	38.16	11.45	3.21	32.50	36.62	6.61	17.75	4.00	10.90	33.30	85.25
G. mean	89.09	32.32	11.77	3.10	28.62	36.25	6.69	16.82	4.27	10.58	33.77	85.72
LSD at												
0.05	22.19*	7.42*	0.64*	0.30*	7.29*	2.03*	0.59*	2.13*	0.32*	0.28*	0.63*	0.99*
0.01	29.56**	9.89**	0.85**	0.40 ^{ns}	9.72**	2.71**	0.79**	2.83**	0.43**	0.38**	0.85**	1.32**

Statistically significant differences at * $p \leq 0.05$ and ** $p \leq 0.01$; ns: indicate the non-significant difference. SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

The mean performances of some hybrids were significantly higher than the highest lines and testers for all studied traits, and except number of seeds/boll, fiber fineness, 2.5% span strength and fiber strength traits [Table \(3\)](#). Also, some F₁ hybrids were superior to grand means for all studied traits. Thus, relatively large differences in all genotypes for these measured traits were found in our study. The superior hybrids with high mean values were the cross TNB x G. 94 for seed cotton yield/plant and number of bolls/plant traits, the cross (G.90x Aus.12) x G.94 for boll weight and number of seed/boll traits and the cross Uzbekistan x G.94 for lint % and lint index traits. The best lint cotton yield/plant, seed index, fiber fineness, fiber strength, 2.5% span length and uniformity ratio% were produced by the hybrids (G.90x Aus.12) x G.86, TNB x G.97, G.96 x G.94, Aus.12 x G.94, Uzbekistan x G.97 and (G.89 x G.86) x G.94, respectively.

Table 3. Mean performances values of F₁ hybrids for investigated traits.

F ₁ Hybrids	SCY/P	LCY/P	SI	BW	No. B/P	L %	LI	No. S/B	FF	FS	2.5%SL	UR%
TNB x G. 94	144.98	48.29	10.43	3.11	46.62	33.31	5.21	19.89	4.25	10.25	34.00	86.85
TNB x G. 86	69.66	25.47	11.27	3.14	22.16	36.57	6.50	17.69	4.48	10.25	33.90	86.95
TNB x G.97	123.33	44.11	12.17	3.22	38.30	35.77	6.78	16.99	4.15	10.35	35.20	86.80
(G.89 x G.86) x G.94	103.05	37.14	10.82	3.32	31.01	36.04	6.10	19.64	4.45	10.60	36.00	87.75
(G.89 x G.86) x G.86	48.29	17.46	10.57	3.01	16.04	36.16	5.99	18.18	4.42	10.30	33.90	87.25
(G.89 x G.86) x G.97	66.49	24.05	11.11	3.24	20.54	36.17	6.30	18.59	4.20	10.57	33.65	87.40
(G.90x Aus.12) x G.94	82.33	30.99	10.83	3.52	23.37	37.64	6.54	20.28	4.35	10.42	33.45	86.10
(G.90x Aus.12) x G.86	131.19	48.60	10.95	3.37	38.97	37.05	6.44	19.36	4.47	10.41	34.77	87.03
(G.90x Aus.12) x G.97	114.08	41.36	11.36	3.50	32.56	36.25	6.46	19.65	4.35	10.35	34.55	86.75
Uzbekistan x G.94	106.79	42.68	10.56	3.25	32.89	39.97	7.03	18.46	4.45	10.55	35.20	86.30
Uzbekistan x G.86	87.14	33.59	10.74	3.27	26.65	38.55	6.74	18.72	4.42	9.95	33.80	87.50
Uzbekistan x G.97	121.97	46.32	9.42	2.83	43.05	37.98	5.77	18.65	4.32	10.10	36.25	87.20
Aus.12 x G.94	54.26	19.79	10.80	3.14	17.28	36.47	6.20	18.47	4.40	10.65	34.10	86.50
Aus.12 x G.86	66.12	25.12	10.18	3.22	20.56	37.99	6.24	19.59	4.40	10.30	34.40	86.05
Aus.12 x G.97	108.59	41.49	9.56	2.89	37.57	38.21	5.91	18.69	4.15	10.25	34.55	87.65
G.96 x G.94	117.18	42.96	11.06	2.97	39.45	36.66	6.40	17.01	4.07	10.55	34.90	86.30
G.96 x G.86	91.86	32.96	11.28	3.25	28.24	35.88	6.31	18.49	4.85	10.00	33.70	87.25
G.96 x G.97	124.57	45.49	10.13	2.87	43.40	36.52	5.83	17.99	4.30	10.35	34.10	86.60
G. mean	97.88	35.99	10.74	3.17	31.04	36.84	6.26	18.69	4.36	10.34	34.47	86.90
LSD at												
0.05	22.19*	7.42*	0.64*	0.30*	7.29*	2.03*	0.59*	2.13*	0.32*	0.28*	0.63*	0.99*
0.01	29.56**	9.89**	0.85**	0.40**	9.72**	2.71**	0.79**	2.83**	0.43**	0.38**	0.85**	1.32**

Statistically significant differences at * $p \leq 0.05$ and ** $p \leq 0.01$; ns: indicate the non-significant difference. SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

Heterosis:

Through the influence of the heterosis, it is possible to identify the extent of the ability of the hybrid to outperform its parents. The experimental results pertaining to the mid-parents heterosis (MPH) and better parent heterosis (BPH) of eighteen hybrids for measured traits under study have been presented in [Tables \(4 and 5\)](#) respectively.

The estimates of MPH and BPH showed that none of the eighteen hybrids had consistently proved to be superior in all evaluated traits. Among eighteen hybrids, four hybrids for seed index, boll weight and fiber strength, five hybrids for lint %, six hybrids for 2.5% span length, seven hybrids for number of bolls/plant, eight hybrids for lint index and uniformity ratio %, eleven hybrids for seed cotton yield/plant and twelve hybrids for lint cotton yield/plant were exhibited positive and significant values of MPH ($P < 0.05$ or 0.01). While, two hybrids for boll weight, lint % and 2.5% span length, three hybrids for seed cotton yield/plant, four hybrids for uniformity ratio % and five hybrids for seed cotton yield/plant and number of bolls/plant traits showed significant positive values for BPH ($P < 0.05$ or 0.01). On the other hand, the other hybrids have undesirable MPH and BPH for these evaluated traits. There are some hybrids for seed index, lint index, number of seeds/boll, fiber strength (positive) and fiber fineness (negative) displayed desirable values of MPH and BPH.

TNB x G. 94 hybrid exhibited significant and positive MPH and BPH for seed cotton yield/plant, lint cotton yield/plant, number of bolls/plant, uniformity ratio % and it had the best fiber fineness. The hybrid (G.90x Aus.12) x G.86 presented the highest MPH and BPH for seed cotton yield/plant and boll weight traits, accompanied with significant and positive MPH and BPH for seed cotton yield/plant and the number of bolls/plant traits, and with positive MPH and BPH for lint percentage, 2.5% span length and uniformity ratio% traits. Besides, MPH and BPH for seed and lint cotton yields/plant traits, G.96 x G.94 hybrid expressed significant MPH and BPH for the number of bolls/plant, and positive MPH and BPH for lint percentage, fiber strength and uniformity ratio % traits.

Table 4. Mid-parents heterosis estimates for the investigated traits in eighteen F₁s cotton genotypes.

F ₁ Hybrids	SCY/P	LCY/P	SI	BW	No. B/P	L %	LI	No. S/B	FF	FS	2.5%SL	UR%
TNB x G. 94	86.98**	75.46**	-1.91	1.19	85.19**	-5.94*	-10.95*	4.80	-4.64	0.90	1.77	1.91**
TNB x G. 86	-0.19	2.64	7.13*	4.78	-4.79	2.95	11.68*	-5.44	0.60	0.16	1.17	1.31*
TNB x G.97	45.09**	44.37**	17.75**	3.37	41.18**	0.05	17.30**	-13.06*	-2.51	-0.80	6.32**	1.91**
(G.89 x G.86) x G.94	30.66*	35.04*	3.24	8.66	20.53	3.84	8.45	0.91	0.56	3.67**	6.59**	2.69**
(G.89 x G.86) x G.86	-32.10*	-29.60	1.93	0.84	-32.67*	3.84	7.04	-5.29	-0.19	0.00	0.07	1.39*
(G.89 x G.86) x G.97	-22.98*	-21.24	9.08**	4.41	-25.79	3.22	13.41*	-7.18	-0.59	0.63	0.52	2.34**
(G.90x Aus.12) x G.94	-4.06	2.67	2.36	16.28**	-17.47	7.11*	13.43*	7.47	-2.25	2.78*	-1.55	0.41
(G.90x Aus.12) x G.86	68.04**	76.86**	4.55	13.87**	47.52**	5.10	12.37*	4.06	0.37	1.86	2.03*	0.79
(G.90x Aus.12) x G.97	22.30*	24.50*	10.45**	14.05**	7.58	2.18	13.49*	1.11	2.35	-0.61	2.60**	1.23*
Uzbekistan x G.94	32.48**	48.28**	1.93	5.58	25.66	12.01**	22.09**	-5.68	3.81	3.40*	-1.05	-0.03
Uzbekistanx G.86	19.59	28.80*	4.82	8.94	9.76	7.72**	17.67**	-3.08	3.03	-3.19*	-5.26**	0.66
Uzbekistanx G.97	38.48**	45.59**	-6.38*	-9.09	53.01**	5.46	1.47	-7.39	5.63	-3.61**	2.76**	1.07
Aus.12 x G.94	-31.97*	-29.52*	0.67	3.63	-34.17	3.90	6.31	-0.47	4.14	5.97**	-1.37	0.14
Aus.12 x G.86	-8.18	-0.99	-4.10	8.79	-15.59	7.90**	7.54	7.11	4.14	1.73	-0.79	-1.06
Aus.12 x G.97	24.50*	33.37**	-8.40**	-5.91	33.21**	7.83**	2.58	-2.30	3.11	-0.73	0.80	1.53**
G.96 x G.94	55.47**	59.38**	2.65	-1.16	58.21**	2.64	6.79	-6.02	-0.57	1.69	1.90*	-0.20
G.96 x G.86	35.83*	35.92*	5.83	10.97*	22.55	0.15	5.90	3.68	18.58**	-4.31**	-1.89*	0.20
G.96 x G.97	50.38**	51.70**	-3.37	-5.80	61.38**	1.29	-1.65	-3.61	10.54*	-2.82*	0.44	0.20
LSD at												
0.05	19.22	7.42	0.64	0.30	7.29	2.03	0.59	2.13	0.32	0.28	0.63	0.99
0.01	25.60	9.89	0.85	0.40	9.72	2.71	0.79	2.83	0.43	0.38	0.85	1.32

Statistically significant differences at *p ≤ 0.05 and **p ≤ 0.01; SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

Table 5. Better parent heterosis estimates for the investigated traits in eighteen F₁s cotton genotypes.

F ₁ Hybrids	SCY/P	LCY/P	SI	BW	No. B/P	L %	LI	No. S/B	FF	FS	2.5%SL	UR%
TNB x G. 94	62.40**	50.45**	-13.35**	-0.43	63.10**	-7.36*	-22.91**	-6.78	-3.41	-0.97	0.29	1.76*
TNB x G. 86	-5.59	-4.56	-4.57	3.97	-10.60	1.10	-2.92	-17.07**	1.89	-2.38	-0.59	0.46
TNB x G.97	18.35	15.59	6.35	0.42	17.86	-2.34	2.48	-20.35**	3.75	-5.05**	5.71**	1.82**
(G.89 x G.86) x G.94	15.43	15.71	-10.08**	6.40	8.48	0.24	-9.74	-11.95*	1.14	2.42	6.19**	2.57**
(G.89 x G.86) x G.86	-34.55*	-34.58*	-10.50**	0.56	-35.28*	-0.05	-10.56*	-18.48**	0.38	-1.90	-0.59	0.81
(G.89 x G.86) x G.97	-36.19**	-36.98**	-2.91	0.94	-36.78**	-1.24	-4.79	-16.65**	5.00	-3.06*	0.01	2.16**
(G.90x Aus.12) x G.94	-7.78	-3.46	-10.00**	12.81*	-18.25	4.69	-3.23	-3.98	-1.14	0.71	-1.76	0.88
(G.90x Aus.12) x G.86	59.31**	71.92**	-7.31*	13.10*	38.96*	2.42	-3.74	-8.34	1.52	-0.89	1.96	0.56
(G.90x Aus.12) x G.97	9.47	8.37	-0.73	9.25	0.20	-1.01	-2.30	-6.95	8.75	-5.02**	1.47	0.70
Uzbekistanx G.94	19.62	32.96*	-12.30**	3.95	15.08	11.15**	4.00	-18.06**	6.63	1.93	-5.50**	1.11
Uzbekistanx G.86	18.10	25.86	-9.09**	8.04	7.50	6.57*	0.63	-16.94**	5.83	-5.24**	-9.26**	0.23
Uzbekistanx G.97	17.04	21.38*	-17.71**	-11.64*	32.47*	3.70	-12.79*	-17.21**	7.92	-7.34**	-2.68**	-0.11
Aus.12 x G.94	-39.22**	-38.36**	-10.27**	0.53	-39.55**	1.43	-8.26	-9.90	8.64	2.90	-3.26**	-1.03
Aus.12 x G.86	-10.39	-5.89	-13.80**	8.06	-17.07	5.02	-6.82	-4.42	8.64	-1.90	-2.41*	-1.54*
Aus.12 x G.97	4.21	8.71	-16.51**	-9.88	15.62	4.32	-10.67*	-8.84	3.75	-5.96**	-1.99	0.29
G.96 x G.94	31.26*	33.84*	-8.11**	-4.91	38.04*	1.97	-5.26	-13.12*	7.58	1.44	0.87	-1.48*
G.96 x G.86	24.49	23.50	-4.46	9.29	13.91	-0.80	-5.65	-5.56	28.31**	-4.76**	-2.60*	-0.40
G.96 x G.97	19.54	19.20	-11.53**	-10.50*	33.56*	-0.28	-11.92*	-8.10	13.76**	-5.05**	-1.45	-1.14
LSD at												
0.05	22.19	7.42	0.64	0.30	7.29	2.03	0.59	2.13	0.32	0.28	0.63	0.99
0.01	29.56	9.89	0.85	0.40	9.72	2.71	0.79	2.83	0.43	0.38	0.85	1.32

Statistically significant differences at *p ≤ 0.05 and **p ≤ 0.01; SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

Potence ratio:

Out of eighteen hybrids in Table (6), one hybrid for lint %, two hybrids for lint index, three hybrids for uniformity ratio %, four hybrids for lint cotton yield/plant and boll weight, five hybrids for seed index, six hybrids for seed cotton yield/plant, number of bolls/plant, fiber fineness and 2.5% span length traits, seven hybrids for fiber strength and eleven hybrids for number of seeds/boll exhibited a positive potence ratio of more than one. These results indicated that these hybrids showed the role of over dominance for these traits which would emphasize the major role of over dominance effect in the inheritance of these traits. While, the potence ratio estimates were less than unity (negative) by the other hybrids for

the same previously traits, this result reflected partial dominance effect in these hybrids towards these traits. On the contrary, the (G.89 x G.86) x G.86 only displayed an absence of dominance effect for fiber strength.

Table 6. Potence ratio estimates for the investigated traits in eighteen F₁ scotton genotypes.

F ₁ Hybrids	SCY/P	LCY/P	SI	BW	No. B/P	L %	LI	No. S/B	FF	FS	2.5%SL	UR%
TNB x G. 94	-5.75	-4.54	0.14	-0.73	-6.29	3.89	0.71	-0.39	3.65	-0.48	-1.20	-13.00
TNB x G. 86	0.03	-0.35	-0.58	-6.14	0.74	-1.61	-0.78	0.39	-0.47	-0.06	-0.66	-1.55
TNB x G.97	-2.00	-1.78	-1.66	-1.15	-2.08	-0.02	-1.20	1.43	0.42	0.18	-10.91	-21.67
(G.89 x G.86) x G.94	-2.32	-2.10	-0.22	-4.08	-1.85	-1.07	-0.42	-0.06	-1.00	-3.00	-17.80	-23.00
(G.89 x G.86) x G.86	8.57	3.88	-0.14	-3.00	8.12	-0.99	-0.36	0.33	0.33	0.00	-0.11	-2.40
(G.89 x G.86) x G.97	1.11	0.85	-0.74	-1.28	1.48	-0.71	-0.70	0.63	0.11	-0.17	-1.00	-13.33
(G.90x Aus.12) x G.94	1.01	-0.42	-0.17	-5.29	18.25	-3.08	-0.78	-0.63	2.00	-1.35	7.00	-0.88
(G.90x Aus.12) x G.86	-12.41	-26.72	-0.36	-20.50	-7.72	-1.95	-0.74	-0.30	-0.33	-0.67	-27.67	-3.42
(G.90x Aus.12) x G.97	-1.90	-1.65	-0.93	-3.20	-1.03	-0.68	-0.83	-0.13	-0.40	0.13	-2.33	-2.33
Uzbekistan x G.94	-3.02	-4.19	-0.12	-3.55	-2.79	-15.49	-1.27	0.38	-1.44	-2.36	0.22	0.03
Uzbekistan x G.86	-15.46	-12.30	-0.31	-10.73	-4.65	-7.17	-1.04	0.18	-1.15	1.48	1.19	-1.53
Uzbekistan x G.97	-2.10	-2.29	0.46	3.15	-3.42	-3.22	-0.09	0.62	-2.65	0.90	-0.49	-0.90
Aus.12 x G.94	2.68	2.06	-0.05	-1.18	3.85	-1.60	-0.40	0.05	-1.00	-2.00	0.70	-0.12
Aus.12 x G.86	3.32	0.19	0.36	-13.00	8.71	-2.88	-0.49	-0.59	-1.00	-0.47	0.48	2.18
Aus.12 x G.97	-1.26	-1.47	0.87	1.35	-2.18	-2.33	-0.17	0.32	-5.00	0.13	-0.28	-1.23
G.96 x G.94	-3.01	-3.11	-0.23	0.30	-3.98	-4.01	-0.53	0.74	0.08	-7.00	-1.86	0.16
G.96 x G.86	-3.93	-3.57	-0.54	-7.15	-2.97	-0.16	-0.48	-0.38	-2.45	9.00	2.60	-0.33
G.96 x G.97	-1.95	-1.90	0.37	1.10	-2.95	-0.82	0.14	0.74	-3.73	1.20	-0.23	-0.15
Dominance Absence	-	-	-	-	-	-	-	-	-	1	-	-
Partial Dominance	12	14	13	14	12	17	16	7	12	10	12	15
Over Dominance	6	4	5	4	6	1	2	11	6	7	6	3

SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

Proportional contributions %

The highest contribution of lines, testers and lines x tester interaction were recorded for lint %, fiber fineness and lint index traits, respectively Fig. (1). The proportional contribution of lines had higher than the proportional contribution of testers for cotton yield and all studied traits, except fiber fineness and fiber strength traits. Additionally, the contribution of line x tester was higher in magnitude as compared to those of lines and testers for all the traits under study, except boll weight, lint % and fiber strength traits.

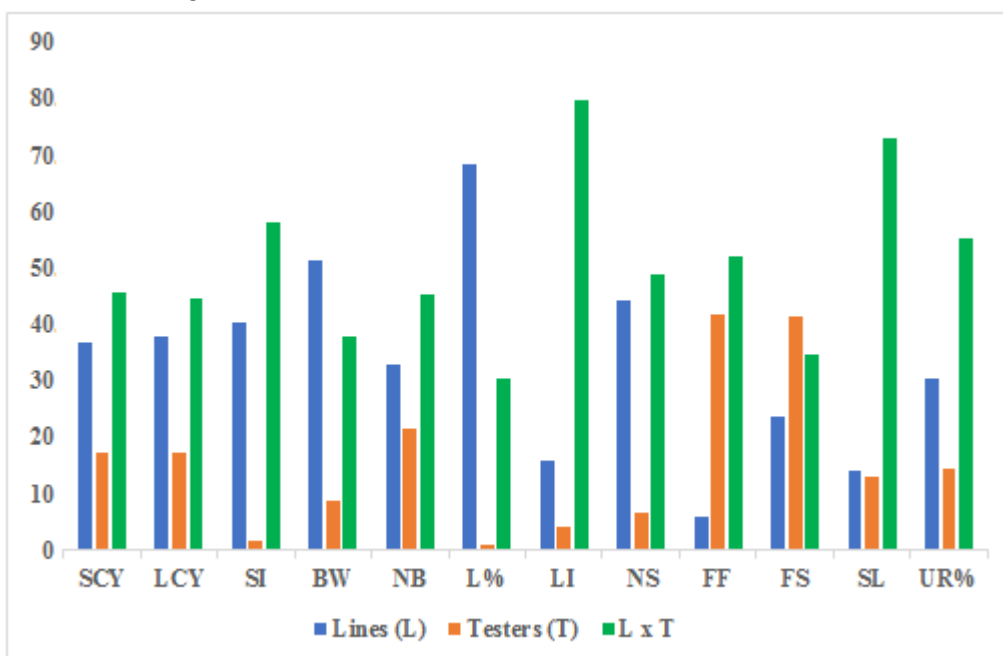


Fig.(1) Proportional contribution (%) of lines, testers and their interactions to total variance for cotton investigated traits. SCY and LCY: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; NB: number of open bolls/plant, L % and LI: lint percentage and index, respectively; NS: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

Genetic parameters:

The estimates of the different genetic parameters of hybrids from linextester analysis for studied traits are presented in Table (7). Both the additive (σ_A^2) and dominance (σ_D^2) genetic variances were observed for seed cotton yield/plant, lint cotton yield/plant, number of bolls/plant and lint % traits. The values of σ_A^2 were negative and estimated to zero for boll weight, seed and lint indexes as well as all studied fiber quality traits. While, the σ_D^2 had negative and equivalent to zero for number of seeds/boll. The estimates of σ_D^2 were greater in magnitude as compared to σ_A^2 for all investigated traits except the number of seeds/boll trait.

(According to Robinson *et al.*, 1949) the results of broad-sense heritability estimates exhibited the highest values ($H^2 > 60\%$) for seed and lint cotton yields/plant, seed and lint indexes, number of bolls/plant and 2.5% span length traits, while were moderate ($30\% < H^2 < 60\%$) for other studied traits, except only the number of seed/boll had low ($H^2 < 30\%$). Narrow sense heritability estimates for all registered traits were low ($h^2 < 30\%$) and ranged from 0 to 16.85%. The h^2 was estimated to zero because of the negative values of additive genetic variances. Simultaneously, equal values of H^2 and h^2 were observed for the number of seeds/boll, due to the additive genetic variance values being negative, which may be considered as zero. The values of H^2 were higher compared to the values of h^2 for all studied traits.

The highest values of genotypic (GCV%) and phenotypic (PCV%) coefficients of variation were recorded for seed cotton yield/plant, lint cotton yield and number of bolls/plant, while were low for other traits. These results indicate that the least variability for GCV% and PCV% corresponded to high heritability. The values for PCV% were higher than the values of GCV% for all studied traits. It is interesting to observe that the differences between PCV% and GCV% (DPG) were low (<10%) volatility of the measured traits.

Table 7. Genetic parameters estimate for the investigated traits by line x tester analysis in cotton.

Parameters	SCY/P	LCY/P	SI	BW	No. B/P	L %	LI	No. S/B	FF	FS	2.5%SL	UR%
σ_A^2	42.94	5.87	0.00	0.00	4.90	0.22	0.00	0.03	0.00	0.00	0.00	0.00
σ_D^2	563.58	69.35	0.36	0.01	63.41	0.38	0.19	0.00	0.01	0.01	0.72	0.09
σ_E^2	61.13	9.12	0.07	0.02	8.81	0.68	0.06	0.75	0.02	0.01	0.07	0.16
σ_G^2	606.52	75.22	0.36	0.01	68.31	0.59	0.19	0.03	0.01	0.01	0.72	0.09
σ_{PR}^2	667.65	84.34	0.42	0.03	77.12	1.28	0.25	0.78	0.03	0.02	0.79	0.26
H^2	90.84	89.19	83.96	46.43	88.58	46.39	76.42	3.60	37.04	43.48	91.46	35.94
h^2	6.43	6.96	0.00	0.00	6.35	16.85	0.00	3.60	0.00	0.00	0.00	0.00
GCV%	28.75	28.11	5.69	3.25	29.78	2.14	7.35	0.92	2.33	0.97	2.47	0.35
PCV%	30.16	29.77	6.14	5.62	31.64	3.15	8.43	4.67	4.04	1.37	2.59	0.59
DPG	1.41	1.66	0.45	2.37	1.86	1.01	1.08	3.75	1.71	0.40	0.12	0.24

σ_A^2 , σ_D^2 , σ_E^2 , σ_G^2 and σ_{PR}^2 : additive, dominance, error, genetic and phenotypic variances, respectively; H^2 and h^2 : broad and narrow senses heritability, GCV% and PCV%: Genotypic and phenotypic coefficients of variation, respectively; DPG: differences between PCV% and GCV%; SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

Pearson Correlation:

As can be observed in Table (8), Pearson’s correlation coefficient is performed for an evident understanding of relationships between cotton studied traits across the mean performances, mid-parents heterosis (MPH), better parent heterosis (BPH) and potence ratio (PR). The statistical evaluation showed hybrids *per se* performance, MPH and BPH highly significantly positively correlated with each other for all measured traits ($P < 0.01$), except with BPH for uniformity ratio had positive and significant ($P < 0.05$), and for fiber fineness and 2.5% span length had not significant. While, PR with hybrids *per se* performance, MPH and BPH showed a significant negative correlation ($p < 0.05$ or 0.01) for all evaluated traits, except with hybrids *per se* performance for fiber fineness and uniformity ratio traits.

Table 8. Pearson’s correlation coefficient among the mean performances (F₁), mid-parents heterosis (MPH), better parent heterosis (BPH) and potence ratio (PR).

Correlation	SCY/P	LCY/P	SI	BW	No. B/P	L %	LI	No. S/B	FF	FS	2.5%SL	UR%
r (F ₁ , MPH)	0.95**	0.95**	0.96**	0.96**	0.97**	0.96**	0.96**	0.82**	0.64**	0.84**	0.67**	0.71**
r (F ₁ , BPH)	0.89**	0.86**	0.94**	0.92**	0.95**	0.98**	0.99**	0.64**	0.52 ^{ns}	0.75**	0.37 ^{ns}	0.46*
r (F ₁ , PR)	-0.57*	-0.51*	-0.95**	-0.57*	-0.68**	-0.87**	-0.98**	-0.84**	-0.14 ^{ns}	-0.72**	-0.49*	-0.41 ^{ns}
r (MPH, BPH)	0.97**	0.96**	0.97**	0.98**	0.99**	0.96**	0.96**	0.89**	0.93**	0.90**	0.91**	0.85**
r (MPH, PR)	-0.65**	-0.61**	-0.99**	-0.71**	-0.73**	-0.82**	-0.99**	-0.97**	-0.69*	-0.70**	-0.61**	-0.80**
r (BPH, PR)	-0.74**	-0.76**	-0.96**	-0.78**	-0.72**	-0.90**	-0.98**	-0.77**	-0.54*	-0.63**	-0.62**	-0.79**

Statistically significant differences at * $p \leq 0.05$ and ** $p \leq 0.01$; ns: indicate the non-significant difference. SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

Principal component analysis (PC):

The data of PCs for all cotton traits based on eighteen *F₁per se* performance, MPH, HMP and PR are shown in Table 9. Out of all PCs, the first five main PCs extracted had eigenvalues larger than one (Eigenvalue >1). While the rest of the other PCs had eigenvalues less than one (Eigenvalue <1). The highest eigenvalues had recorded by PC1 in *F₁per se* performance, MPH, HMP and PR, followed by PC2, PC3, PC4 and PC5. The first five PCs contributed 85% of the total variation existing among cotton yield and other studied traits regarding *F₁per se* performance, MPH, HMP and PR parameters. The contributions of PC1 and PC2 to the total variance were higher than that of the other five PCs, that PC1 and PC2 explain more than 46% of the data total variability of all investigated variables in *F₁per se* performance, MPH, HMP and PR parameters. Based on the data of hybrids in *F₁per se* performance, MPH, HMP and PR parameters (Table 9), the PC1 had a high positive correlation with seed and lint cotton yields/plant, the number of bolls/plant, 2.5% span length and uniformity ratio traits. As for PC2, the highest positive correlations were found for seed and lint indexes, boll weight in *F₁per se* performance, seed index, 2.5% span length and uniformity ratio traits in MPH and BPH parameters as well as for lint %, number of seeds/boll and fiber fineness traits in PR parameter. While, positive or negative correlations were recorded among of studied traits by the other PCs under measured parameters as shown in Table (9) Based on the hybrids loadings, the five PCs have positive correlations with most hybrids in this study (Fig. 2). In PC1, the higher positive correlations with the hybrid Uzbekistan x G.97 in *F₁per se* performance parameter, with the hybrid TNB x G. 94 in MPH and BPH parameters, and with the hybrid (G.89 x G.86) x G.86 in PR parameter. Regarding PC2, the hybrid TNB x G.97 recorded the highest positive correlation in *F₁per se* performance, MPH, BPH and PR parameters.

Table 9. Results of principal component analysis (PCs) in the first five PCs for the investigated traits during the mean performance, MPH, BPH and PR parameters.

Traits	Mean Performance					Mid-parents Heterosis (MPH)					Better Parent Heterosis (BPH)					Potence Ratio (PR)				
	PC1	PC2	PC3	PC4	PC5	PC1	PC2	PC3	PC4	PC5	PC1	PC2	PC3	PC4	PC5	PC1	PC2	PC3	PC4	PC5
SCY/P	0.46	0.23	0.22	0.01	0.04	0.45	-0.02	0.31	0.11	0.12	0.53	0.04	0.24	0.02	-0.03	0.46	0.15	-0.14	0.08	-0.01
LCY/P	0.46	0.26	0.16	0.12	0.05	0.42	-0.04	0.33	0.16	0.23	0.49	-0.01	0.33	0.06	-0.08	0.51	0.18	-0.06	-0.06	0.10
SI	-0.21	0.44	0.18	-0.37	0.35	-0.10	0.47	0.20	0.36	-0.27	-0.11	0.45	0.24	-0.42	0.15	0.20	-0.45	0.31	0.02	-0.38
BW	-0.27	0.38	0.46	0.10	-0.13	-0.25	0.12	0.60	0.04	-0.24	-0.12	0.21	0.46	0.23	0.39	0.38	0.23	0.27	-0.30	-0.06
No. B/P	0.49	0.13	0.11	0.00	0.06	0.48	-0.05	0.14	0.09	0.17	0.55	-0.03	0.09	-0.05	-0.14	0.33	-0.03	-0.44	0.28	-0.02
L %	-0.07	0.11	-0.35	0.68	-0.04	-0.29	-0.18	0.02	0.18	0.60	-0.18	-0.34	0.40	0.24	-0.30	0.07	0.28	0.37	0.45	0.21
LI	-0.25	0.50	-0.14	0.27	0.26	-0.31	0.24	0.20	0.46	0.27	-0.26	0.10	0.58	-0.15	-0.14	0.20	-0.07	0.59	0.28	-0.18
No. S/P	-0.04	-0.10	0.52	0.25	-0.55	-0.07	-0.28	0.49	-0.40	-0.26	0.16	-0.17	-0.02	0.19	0.68	0.04	0.34	0.10	-0.57	0.05
FF	-0.23	-0.12	0.37	0.32	0.26	-0.01	-0.42	-0.06	0.37	-0.32	-0.01	-0.30	0.16	-0.50	0.34	-0.04	0.32	-0.24	0.44	-0.23
FS	-0.07	0.32	-0.25	-0.28	-0.49	-0.20	0.16	0.21	-0.49	0.37	-0.09	0.12	0.07	0.61	0.17	-0.02	-0.18	0.16	0.12	0.82
SL	0.30	0.19	-0.17	0.24	0.01	0.25	0.42	-0.03	-0.14	0.10	0.13	0.50	-0.17	-0.05	0.15	0.42	-0.20	-0.13	-0.06	0.20
UR%	0.08	-0.31	0.16	0.03	0.42	0.13	0.46	-0.19	-0.13	-0.18	0.01	0.50	-0.03	0.14	-0.25	0.13	-0.56	-0.14	-0.07	0.01
Eigenvalues	3.76	2.04	1.68	1.52	1.31	3.87	2.48	1.72	1.53	1.22	3.14	2.47	1.94	1.56	1.46	3.29	2.24	1.89	1.84	1.22
Variance %	31.32	16.98	14.01	12.68	10.94	32.27	20.69	14.36	12.72	10.13	26.19	20.54	16.14	12.97	12.17	27.43	18.66	15.71	15.33	10.18
Cumulative%	31.32	48.30	62.31	74.99	85.93	32.27	52.96	67.31	80.04	90.17	26.19	46.73	62.87	75.83	88.00	27.43	46.09	61.79	77.13	87.30

SCY/P and LCY/P: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; No. S/B: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio.

In biplot analysis Fig. (2), the sharp angle (below 90 degrees) and the obtuse angle (above 90 degrees) between the variables indicate the positive and negative correlation between variables, respectively. Strong correlations were observed among seed cotton yield/plant, lint cotton yield/plant, the number of bolls/plant and 2.5% span length traits, among seed index, boll weight, lint % and lint index traits, between the number of seeds/boll and fiber fineness traits, and between 2.5% span length and uniformity ratio traits across *F₁per se* performance, MPH, HMP and PR parameters.

Moreover, the PC1 and PC2 had mainly distributed and distinguished the hybrids into two groups according to their phenotypic similarities. The first group was related to PC1 and includes the genotypes classified as best performance with the highest mean and positive values of MPH, BPH and PR parameters for cotton yield and fiber quality traits. While, the second group is related to PC2 and includes the other hybrids classified as lower mean and negative values of MPH, BPH and PR parameters for most traits in this study. The hybrids i.e., TNB x G. 94, TNB x G.97, (G.89 x G.86) x G.94, (G.90x Aus.12) x G.86, G.96 x G.94 and G.96 x G.97 had the best mean and positive values of MPH and BPH for cotton yield and its related traits as well as most fiber quality traits. While the Uzbekistanx G.94 hybrid showed the best performance with the high mean and positive MPH and BPH values for lint % and lint index traits and most fiber quality traits. In our research, the PCA had good in the identification of genotypes and their relation to studied traits, where the results obtained from *F₁per se* performance Table (3), MPH Table (4), HMP Table (5) and PR Table (6) were very similar to those from PCA analysis.

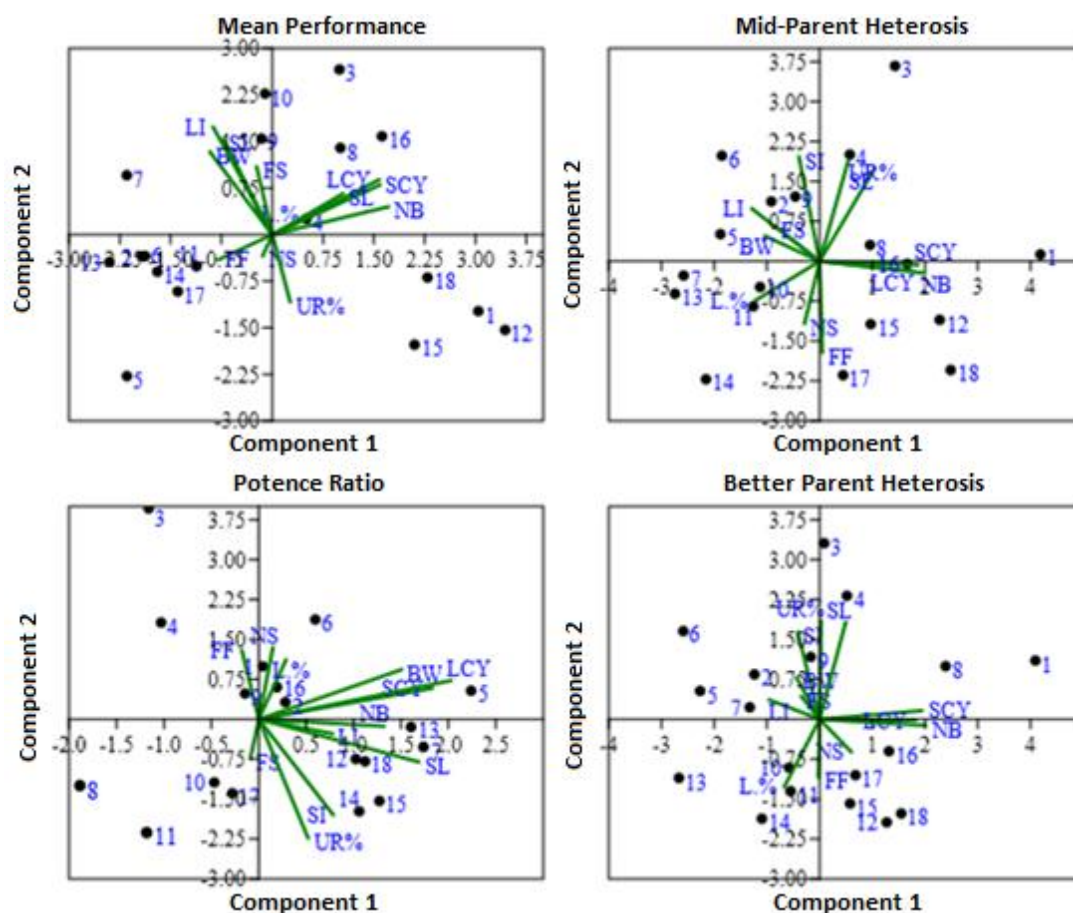


Fig 2. Biplot diagram between PC1 and PC2 shows similarities and dissimilarities relationships between the studied traits in the eighteen hybrids during F_1 *per se* performance, MPH, HMP and PR. SCY and LCY: seed and lint cotton yields/plant, respectively; SI: seed index; BW: boll weight; No. B/P: number of open bolls/plant, L % and LI: lint percentage and index, respectively; NS: number of seeds/boll; FF: fiber fineness; FS: fiber strength; 2.5% SL: upper half means; UR% uniformity ratio. 1: TNB x G. 94; 2: TNB x G. 86; 3: TNB x G.97; 4: (G.89 x G.86) x G.94; 5: (G.89 x G.86) x G.86; 6: (G.89 x G.86) x G.97; 7: (G.90x Aus.12) x G.94; 8: (G.90x Aus.12) x G.86; 9: (G.90x Aus.12) x G.97; 10: Uzbekistanx G.94; 11: Uzbekistanx G.86; 12: Uzbekistanx G.97; 13: Aus.12 x G.94; 14: Aus.12 x G.86; 15: Aus.12 x G.97; 16: G.96 x G.94; 17: G.96 x G.86; 18: G.96 x G.97

DISCUSSION

The ANOVA findings indicate the presence of considerable genetic variability between genotypes. These differences could be attributed to large differences between the parental lines of different studies. The significance of lines, testers and their interaction provides evidence of the presence of sufficient genetic variability among lines, testers, and hybrids, as well as indicating the importance of both additive and non-additive gene actions in controlling these studied traits. The results indicated that the pattern of appropriate line combinations may be varying depending on the tester mode. A higher magnitude of the mean square of testers indicates greater diversity among the testers and these testers can be pursued for developing plant heterotic groups with high combining ability (Chandel and Mankotta, 2014). Therefore, the choice of the appropriate tester is crucial in developing the cotton yield and fiber quality of hybrid cotton. Several previous studies reported similar conclusions to our results, for example, (Usharani *et al.*, 2016; Chinchane *et al.*, 2018; and Khokhar *et al.*, 2018; Yehia and El-Hashash, 2019; Mariz *et al.*, 2021; and Mudhalvan *et al.*, 2021) mentioned that the genotypes, parents, hybrids, parent vs cross, lines, testers and line x tester had significant effects on most yield, its components and fiber quality traits in cotton, it showed that there is significant variability for the traits under study.

The results of CV% indicated the environmental influence was high for seed and lint cotton yields/plant and the number of bolls/plant traits, and low for other traits, so this trial would be considered to have moderate to high precision. The magnitude of CV% indicated that the genotypes had exploitable genetic variability during the selection of cotton yield and fiber quality. In cotton, other studies by (Raza *et al.*, 2016; and Li *et al.*, 2020) manifested that the CV% values were more than 10%, on the contrary, (Yehia and El-Hashash, 2021; and El-Hashash and Yehia, 2021) mentioned that the CV% values for studied traits were low (CV%<10%).

The *per se* performance was considered as the first important selection index in the choice of parents and the parents with high mean performance will result in superior hybrids. These data showed that heterotic effects emerged highly in point for studied traits in these hybrids. These viewpoints were kept in mind while selecting these single crosses as diverse F_1 base populations for initiating reciprocal selection for combining ability. The highest combinations indicate the importance of low and average parents in the exploitation of heterosis for studied traits (Yehia and El-Hashash, 2019).

Consequently, the parents involved in the TNB x G. 94, (G.90x Aus.12) x G.86 and G.96 x G.94 combinations should be used in improving yield, its components and fiber quality traits, and the best crosses should be used in initiating the breeding program in Egypt.

Some F_1 hybrids reflected desirable (positive/negative) heterotic effects for cotton yield, its components, and fiber quality traits when estimated, especially, with the higher parents. The obtained results are consistent with previous findings of (Yehia *et al.*, 2009; and El-Hashash, 2013; Patel and Patel, 2018; Yehia and El-Hashash, 2019; and Mariz *et al.*, 2021) they reported significant heterosis in desired sign and direction for all studied traits in cotton. Based on MPH and BPH, the crosses TNB x G. 94, (G.90x Aus.12) x G.86 and G.96 x G.94 were identified as the best hybrids chosen in the best combination for yield, yield components and fiber quality traits. The preponderance of dominance type of gene actions clearly indicated that the selection of superior plants should be postponed to the next generations. The significant negative heterosis suggested the importance of additive genetic components (Muhammed *et al.*, 2003; El-Hashash, 2013). These results indicate the importance of low x medium, medium x medium, low x high and high x high parent combinations in the development of hybrids exhibiting a high level of hybrid vigour for yield and yield-related traits. Thus it can be concluded that the parents possessing only high values need not necessarily produce high-yielding hybrids as indicated by the present study (Kumar, 2008). Useful and significant MPH and BPH parameters were observed for yield, its related and fiber quality traits by (Babu *et al.*, 2018; and Bilwal *et al.*, 2018).

Potency ratio results emphasize the major role of over and partial dominance effects in the inheritance of traits studied in most cotton crosses. These findings were consistent with (Hussain *et al.*, 2008 and 2009; and Patel *et al.*, 2014). The results of proportional contributions % showed that lines, testers and the interaction lines x testers brought many variations in the expression of the studied traits. These findings were consistent with (Anjum *et al.*, 2018; and Yehia and El-Hashash, 2019; and different from Hamed and Said, 2021; and Mariz *et al.*, 2021).

The σ_A^2 and σ_D^2 expressions were equally important for seed cotton yield/plant, lint cotton yield/plant, number of bolls/plant and lint % traits. The results of gene action studies suggested the preponderance of dominant genes for most studied traits which revealed that the variation in these parameters was controlled by genes having non-additive gene effects at most of the loci, and manipulation of the parents by hybridization method may be useful through the exploitation of heterosis for genetic improvement of yield and quality traits. Similar results have also been reported earlier by (Khan *et al.*, 2009; El-Hashash, 2013; Anjum *et al.*, 2018; Hamed and Said, 2021) they mentioned that additive and dominance genetic effects were involved in the inheritance of cotton yield, its components and fiber quality traits, also the dominance effects being greater than additive effects on these traits. High to moderate values of H^2 , while low values of h^2 were observed for most studied traits. High H^2 estimates for yield, its components and fiber quality traits were reported by (El-Hashash, 2013; Mahrous, 2018; and El-Hashash and Yehia, 2021). The h^2 estimates for yield and fiber quality traits were lower than the described values by (Mahrous, 2018; and El-Hashash and Yehia, 2021). Higher H^2 than h^2 indicates the preponderance of dominance variance in governing the studied traits. When H^2 values are high, the genetic gain of the cotton yield and fiber quality can be achieved through the practice of individual plant selection in the early generations. Lower values of the estimates of H^2 and h^2 indicate that the effects of environmental variance were greater than the effects of the genetic components (Khan *et al.*, 2007), and environmental factors strongly influence traits, thus breeding for improving such traits is difficult (El-Hashash and Yehia, 2021). Low DPG for seed cotton yield/plant, its components and fiber traits indicate their variation was genotypic, the phenotype was close to the genotype, low environmental effect and the involvement of genes with non-additive genetic effects in the expression of these investigated traits. Thus, the varieties can be improved and selected for these characters under SA rates and irrigation conditions for the improvement of drought tolerance. Since the broad sense heritability was high for most traits, hence this also means that a greater proportion of variability was due to genetic factors. These results are in harmony with the findings of various researchers such as (Farooq *et al.*, 2015; Meena and Meena, 2017; and Sahar *et al.*, 2021).

For the majority of the traits studied, significant correlation coefficients were found between all possible pairs of mean performances, MPH, BPH (positive), and PR (negative) parameters. The present findings are in line with those of (El-Hashash, 2013; Shang *et al.*, 2015; and Yehia and El-Hashash, 2019) who had also reported a high correlation between all possible pairs of F_1 *per se* performance, HMP and HBP were observed for all investigated traits in cotton, indicating the predominance of dominance over additive effects, which suggests the possibility of predicting these traits in F_1 hybrids from parent values. In cotton, (Shang *et al.*, 2015; and De Vienne and Fiévet, 2020) cleared that the relationship between PR and both heterosis (MPH and BPH) is very wide if found. The value of PR cannot correspond to a wide range of MPH or BPH values, and vice versa. This result means that the normalized differences between the parents markedly affect MPH and BPH parameters (De Vienne and Fiévet, 2020). The heterosis can be explained by divergence and also by the effect of the dominance of the alleles that control the trait in question (Falconer, 1989). These correlations among the traits should provide cotton breeders with insights on possible impacts of selection for one trait into the others (Lu and Myers, 2011). Based on PCA, the first two PCs in F_1 *per se* performance, MPH, HMP and PR were kept for the final analysis, in that, these PCs explain variance more than an individual trait and it expresses more variability and support to select the trait with a positive loading factor. Earlier, workers like (Abasianyanga *et al.*, 2017; Shah *et al.*, 2018; Abdel-Monaem *et al.*, 2020) reported the eigenvalues of the first five PCAs had higher than one and contributed more than 70% of the accumulative variation of the original variables under examination in cotton. The results of the PC1 and PC2 indicates may be used to summarize the original variables in any further analysis of the data, as well as to explain the total variance and the collection of the PCs. It is evident that the PC1 and PC2 can be interpreted as a response related to the hybrids and the evaluated traits, and which possess positive and negative contributions to the F_1 *per se* performance, MPH, HMP and PR parameters. Thus, the PC1 and PC2 were employed to draw a biplot Fig. (2). (Earlier researchers, namely Nandhini *et al.*,

2018; and Yehia and El-Hashash, 2021) had also reported the importance of PC1 and PC2 in cotton. The PC1 and PC2 are considered very important to increase cotton yield and fiber quality across these hybrids. Similar results were reported by (Abasianyanga *et al.*, 2017; Nandhini *et al.*, 2018; Vinodhana and Gunasekaran, 2019; and Yehia and El-Hashash, 2021) who explained that the highest variability by the first two PCs were related to yield, yield components and fiber quality traits in cotton. The PCA analysis could be used as a good predictor for separating genotypes into groups based on their performance, this result is in accordance with the findings of (Kahrman *et al.*, 2016; in corn and Grzesiak *et al.*, 2019) in wheat. Similarly, in studies by (El-Hashash and EL-Agoury, 2019; and Yehia and El-Hashash, 2021) the data of variables studied displayed a positive correlation among most studied traits, but they differed in their degree and consistency in quantity. (Kahrman *et al.*, 2016) stated that the PCA biplot has an important advantage because it can simultaneously present the means and heterosis of the genotypes and measured traits. Thus, we can say that the PCA biplot is a good choice to represent graphically the heterosis analysis results (Kahrman *et al.*, 2016). During the biplot diagram of the first two PCAs, the extent of variation in each trait between genotypes showed greater divergence (Rathinavel, 2019) and most traits contributed to more variance (Nandhini *et al.*, 2018), thus these traits could be considered essential for selection in large populations as well as which may be useful for an effective program to improve the cotton yield and fiber quality in Egypt (Yehia and El-Hashash, 2021).

CONCLUSION

The variances of all source variation by line x tester analysis revealed that there were significant differences in most measured traits. The interaction lines x testers contributed more to the variances of the expression for most studied traits. The lines G.90x Aus.12 and Uzbekistanas well as the tester G.97 remarkably increased cotton yield and most investigated traits compared to the other lines and testers. The hybrids TNB x G. 94, (G.90x Aus.12) x G.86 and G.96 x G.94 were found outstanding based on mean performance, MPH, BPH and PCA analysis for yield, most of its components and fiber quality traits. The results of genetic parameters indicated the preponderance of non-additive type of gene effects in advocating all the studied traits, except the number of seeds/boll trait. Significant correlation coefficients were found between all possible pairs of mean performances, MPH, BPH (positive) and PR (negative) parameters for most studied traits. PCA can be used as a suitable method for studying the studied traits and to determine the best hybrids across line x tester analysis. Finally, the three hybrids above are considered promising to be best exploited and used in breeding programs to produce hybrid cotton and improvement for yield, its components and fiber quality traits.

REFERENCES

- Abasianyanga, I., Balu, P. A., & Ramakrishnan, P. (2017). Association and principal component analysis of yield and its components in cultivated cotton. *Electronic Journal of Plant Breeding*, 8(3), 857-864.
- Abdel-Monaem, M. A., Abido, W. A. E., Hadházy, Á., Ghoneima, M. H., EL-Mansy, Y. M., and EL-Shazly, M. W. (2020). Genetic divergence among Egyptian cotton genotypes under water deficit conditions. *Acta Ecologica Sinica*. 42(2), 11-18.
- Allard, R. W. (1960). Principles of plant breeding. John Willey and Sons. Inc. New York, 485.
- Anjum, R., Baloch, M. J., Baloch, G. M., & Chachar, Q. (2018). Combining ability estimates for yield and fibre quality traits in Bt and non-Bt upland cotton genotypes. *Pure and Applied Biology (PAB)*, 7(1), 389-399.
- Babu, B. J., Satish, Y., Ahamed, M. L. & Rao, V. S. (2018). Studies on heterosis in cotton (*Gossypium hirsutum* L.) for yield and fibre quality traits. *International Journal of Chemical Studies*, 6(4), 1013-1018.
- Bilwal, B. B., Vadodariya, K. V., Lahane, G. R., & Rajkumar, B. K. (2018). Heterosis study for seed cotton yield and its yield attributing traits in upland cotton (*Gossypium hirsutum* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(1), 1963-1967.
- Burton, G. W. (1952, August). Qualitative inheritance in grasses. Vol. 1. In *Proceedings of the 6th International Grassland Congress, Pennsylvania State College* (pp. 17-23).
- Chandel, U., & Mankotta, B. S. (2014). Combining ability in tropical and CIMMYT inbred lines of maize for grain yield and yield components using line x tester analysis. *Sabrao Journal Breeding and Genetics*, 46(2), 256-264.
- Chinchane, V.N., Patil, V.S. & Ingole, D.G. (2018). Combining Ability Studies for Yield and Its Components in Desi Cotton (*Gossypium arboreum* L.). *International Journal Current Microbiology Applied Science*, Special Issue-6, 1368-1372.
- De Vienne, D., & Fiévet, J. B. (2020). The pitfalls of heterosis coefficients. *Plants*, 9(7), 875.
- Dutta, P., Dutta, P. N., & Borua, P. K. (2013). Morphological traits as selection indices in rice: A statistical view. *Universal Journal of Agricultural Research*, 1(3), 85-96.
- El-Hashash, E. F. (2013). Heterosis and gene action among single and double-cross hybrids performances in cotton. *American-Eurasian Journal of Agricultural and Environmental Sciences*, 13(4), 505-516.
- El-Hashash, E.F., & Agwa, M.A. (2018). Genetic Parameters and Stress Tolerance Index for Quantitative Traits in Barley under Different Drought Stress Severities. *Asian Journal of Research in Crop Science*, 1(1), 1-16.
- El-Hashash, E. F., & EL-Agoury, R. Y. A. (2019). Comparison of grain yield-based drought tolerance indices under normal and stress conditions of rice in Egypt. *Scholars Journal of Agriculture and Veterinary Sciences*, 6(1), 41-54
- El-Hashash, E. F., & Yehia, W. M. B. (2021). Estimation of Heritability, Genes Number and Multivariate Analysis Using Non-segregation and Segregation Generations in Two Cotton Crosses. *Asian Journal of Biochemistry, Genetics and Molecular Biology*, 9(3), 45-62.

- Falconer, D.S. (1989). Introduction to quantitative genetics, 2nd edition. Longman New York, USA, p 438 .
- Farooq, J., Anwar, M., Rizwan, M., Riaz, M., Mahmood, K., & Mahpara, S. (2015). Estimation of correlation and path analysis of various yield and related parameters in cotton (*Gossypium hirsutum* L.). *Cotton Genomics and Genetics*, 6(10), 1-6.
- Grzesiak, S., Hordyńska, N., Szczyrek, P., Grzesiak, M. T., Noga, A. & Szechyńska-Hebda, M. (2019). Variation among wheat (*Triticum easativum* L.) genotypes in response to the drought stress: I–selection approaches. *Journal of Plant Interactions*, 14(1), 30-44.
- Hamed, H. H. E., & Said S. R. N. (2021). Estimation of heterosis and combining ability for yield and fiber quality traits by using line x tester analysis in cotton (*Gossypium barbadense* L.). *Menoufia Journal of Plant Production*, 6, 35-51.
- Hayes, J. D., & Foster, C. A. (1976, June). Heterosis in self pollinated crops with particular reference to barley, Heterosis in plant breeding. In *Proc of 7th Congress EUCARPIA* (pp. 239-256).
- Hussain, M. A. N. Z. O. O. R., Azhar, F. M., & Khan, A. A. (2008). Genetic basis of variation in leaf area, petiole length and seed cotton yield in some cotton (*Gossypium hirsutum*) genotypes. *International Journal of Agriculture and Biology*, 10(6), 705-708.
- Hussain M., Azhar F. M., & Khan, A. A. (2009). Genetics of inheritance and correlations of some morphological and yield contributing traits in upland cotton. *Pakistan Journal Botany*, 41(6), 2975-2986.
- Kahriman, F., Egesel, C. Ö., Orhun, G. E., Alaca, B., and Avci, F. (2016). Comparison of graphical analyses for maize genetic experiments: Application of biplots and polar plot to line x tester design. *Chilean journal of agricultural research*, 76(3), 285-293.
- Kemphorne, O. (1957). An Introduction to Genetic Statistics, John Wiley & Sons, New York, NY, USA.
- Khan, A. A., Azhar, F. M., Khan, I. A., Riaz, A. H., & Athar, M. (2009). Genetic basis of variation for lint color, yield, and quality in cotton (*Gossypium hirsutum* L.). *Plant Biosystems-An International Journal Dealing with all Aspects of Plant Biology*, 143(sup1), S17-S24.
- Khan, A. I., Hussain, M., Rauf, S., & Khan, T. M. (2007). Inheritance of resistance to Cotton leaf curl virus in cotton (*Gossypium hirsutum* L.). *Plant Protection Science*, 43(1), 5-9.
- Khokhar, E. S., Shakeel, A., Maqbool, M. A., Abuzar, M. K., Zareen, S., Syeda, S. A., & Asadullah, M. (2018). Studying combining ability and heterosis in different cotton (*Gossypium hirsutum* L.) genotypes for yield and yield contributing traits. *Pakistan Journal of Agricultural Research*, 31(1), 55-68.
- Kumar, K.J.Y. (2008). Combining ability and heterosis studies in experimental hybrids of cotton (*Gossypium hirsutum* L.). M. Sci., Thesis, Dep. of Genetics and Plant Breed. College of Agric., Dharwad Univ. of Agric. Sci.
- Li, B., Tian, Q., Wang, X., Han, B., Liu, L., Kong, X., Si, A., Wang, J., Lin, Z., Zhang, X., Yu, Y., & Yang, X. (2020). Phenotypic plasticity and genetic variation of cotton yield and its related traits under water-limited conditions. *The Crop Journal*, 8(6), 966-976.
- Liang, G. H., Reddy, C. R., & Dayton, A. D. (1972). Heterosis, inbreeding depression, and heritability estimates in a systematic series of grain sorghum genotypes. *Crop Science*, 12(4), 409-411.
- Lu, H., & Myers, G. O. (2011). Combining abilities and inheritance of yield components in influential upland cotton varieties. *Australian Journal of Crop Science*, 5(4), 384-390.
- Mahrous, H. (2018). Line× Tester analysis for yield and fiber quality traits in Egyptian cotton under heat conditions. *Journal of Plant Production*, 9(6), 573-578.
- Mariz, M. S., Gibely, R. H. A. O., & Abdelmoghny A. M. (2021). Combining ability in relation to heterosis effects and genetic diversity in cotton using line x tester mating design. *Plant Archives*, 21(1), 1-9.
- Mather K, (1949). Biometrical Genetics. Dover Press, New York
- Meena, K. P., and Harphool, M. (2017). Heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.) genotypes. *Trends in Biosciences*, 10(25), 5332-5334.
- Mudhalvan, S., Rajeswari, S., Mahalingam, L., Jeyakumar, P., Muthuswami, M., and Premalatha, N. (2021). Combining ability estimates and heterosis analysis on major yield attributing traits and lint quality in American cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*, 12(4), 1111-1119.
- Muhammed, I., Chang, M. A., Iqbal, M. Z., Mahmood U., & Khalid, M. (2003). Genetic analysis of earliness and agronomic character in upland cotton. *Sarhad Journal of Agriculture*, 19(3), 353-357.
- Nandhini, K., Balu, P. A., & Isong, A. (2018). Genetic analysis and inheritance studies in f2 population of upland cotton (*G. hirsutum* L.). *International Journal Pure App. Biosci*, 6(2), 1499-1505.
- Nduwumuremyi, A., Tongoona, P., & Habimana, S. (2013). Mating designs: helpful tool for quantitative plant breeding analysis. *Journal of Plant Breeding and Genetics*, 1(3), 117-129.
- Patel, B. N., Jaiwar, S. S., Patel, N. A., Akbari, V. R., & Dave, P. B. (2014). Estimation of heterosis and dominance deviation for seed cotton yield, its components characters in upland cotton. *Electronic Journal of Plant Breeding*, 5(4), 862-868.
- Patel, H. R., & Patel, D. H. (2018). Heterotic analysis of GMS based hybrids of seed cotton yield and fiber quality traits in cotton (*Gossypium hirsutum*, L.). *International Journal of Chemical Studies*, 6(5), 1910-1914.
- Pimentel-Gomes, F. (2009). Curso de estatística experimental. 15. ed. Piracicaba: Fealq, 451 p.

- Rathinavel, K. (2019). Agro-morphological characterization and genetic diversity analysis of cotton germplasm (*Gossypium hirsutum* L.). *International Journal of Current Microbiology and Applied Sciences*, 8(2), 2039-2057.
- Raza, H., Khan, N. U., Khan, S. A., Gul, S., Latif, A., Hussain, I., & Baloch, M. (2016). Genetic variability and correlation studies in F4 populations of upland cotton. *JAPS: Journal of Animal & Plant Sciences*, 26(4).
- Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimates of heritability and degree of dominance in corn. *Agronomy Journal*, 41, 353-359.
- Sabesan, T., Suresh, R., & Saravanan, K. (2009). Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. *Electronic Journal of Plant Breeding*, 1(1), 56-59.
- SAHAR, A., ZAFAR, M. M., RAZZAQ, A., MANAN, A., HAROON, M., SAJID, S., & Youlu, Y. U. A. N. (2021). Genetic variability for yield and fiber related traits in genetically modified cotton. *Journal of Cotton Research*, 4(1), 1-10.
- Shah, S. A. I., Khan, S. J., Ullahand, K., & Sayal, O. U. (2018). Genetic diversity in cotton germplasm using multivariate analysis. *Sarhad Journal of Agriculture*, 34, 130-135.
- Shang, L., Wang, Y., Cai, S., Wang, X., Li, Y., Abduweli, A., & Hua, J. (2015). Partial dominance, overdominance, epistasis and QTL by environment interactions contribute to heterosis in two upland cotton hybrids. *G3 (Bethesda, Md.)*, 6(3), 499-507.
- Sharma, J. R. (2006). *Statistical and biometrical techniques in plant breeding*. 432 p. New Age International, New Delhi, Delhi, India.
- Shull, G.H. (1914). *Methods of Plant Breeding*, McGraw Hill Book Company, New York, p.53.
- Singh, R. K., & Chaudhary, B. D. (1979). *Biometrical method in quantitative genetic analysis*. 2nd Ed., Kalyani. Publishers. Daryangai., New York, USA.
- Smith, H. H. (1952). Fixing transgressive vigor in *Nicotiana rustica*. *Heterosis. Iowa State College Press, Ames, IA*, 161-174.
- Steel, R. G. D., & Torrie J. H. (1980). *Principles and procedures of statistics*. 2nd edition. McGraw Hill Book Company Inc., New York.
- USDA, United States Department of Agriculture (2022). Cotton: World Markets and Trade. Available online: <https://apps.fas.usda.gov/psdonline/circulars/cotton.pdf> (accessed on 4 Jan 2022).
- Usharani, C. V., Manjula, S. M., & Patil, S. S. (2016). Estimating combining ability through line x tester analysis in upland cotton. *Research in Environment and Life Sciences*, 9(5), 628-633.
- Vinodhana, N. K., & Gunasekaran, P. (2019). Evaluation of genetic diversity in cotton (*Gossypium barbadense* L.) germplasm for yield and fibre attributes by principle component analysis. *International Journal Current Microbiology Applied Science*, 8(4), 2614-2621.
- Yehia. W. M. B., Hamoud, H. M. E., EL-Akhader, A. A. A., & Abd EL-Gelil, M. A. (2009). Yield and fiber quality potential for triallel hybrids in cotton .2- Superiority Journal Agric. Science Mansoura Univ., 34(6), 6145-6162.
- Yehia, W. M. B., & El-Hashash, E .F. (2019). Combining ability effects and heterosis estimates through line x tester analysis for yield, yield components and fiber traits in Egyptian cotton. *Elixir Agriculture*, 131, 53238-53246.
- Yehia, W. M. B., & El-Hashash, E. F. (2021). Correlation and multivariate analysis across non-segregation and segregation generations in two cotton crosses. *Egyptian Journal of Agricultural Research*, 99(4), 380-390.



Copyright: © 2022 by the authors. Licensee EJAR, EKB, Egypt. EJAR offers immediate open access to its material on the grounds that making research accessible freely to the public facilitates a more global knowledge exchange. Users can read, download, copy, distribute, print or share a link to the complete text of the application under [Creative Commons BY-NC-SA 4.0 International License](https://creativecommons.org/licenses/by-nc-sa/4.0/).



تقديرات المقاييس الوراثية لصفات محصول القطن ومكوناته وجودة الألياف بناءً على تصميم التزاوج السلالة x الكشاف وتحليل المكون الرئيسي

وليد محمد يحي¹ وعصام فتحى الحشاش^{2*}

¹ قسم بحوث تربية القطن، معهد بحوث القطن، مركز البحوث الزراعية، الجيزة، مصر

² قسم المحاصيل، كلية الزراعة، جامعة الأزهر، القاهرة، مصر

* بريد المؤلف المرسل: dressamelhashash@yahoo.com

هدفت الدراسة الحالية إلى تقييم قوة الهجين لمتوسط الأباء (MPH) وأفضل الأباء (BPH)، ودرجة السيادة (PR) والمقاييس الوراثية لصفات المحصول ومكوناتها وجودة الألياف في ثمانية عشر هجين فردى تم الحصول عليها عن طريق التهجين بين ستة سلالات و ثلاثة كشافات باستخدام تصميم السلالة x الكشاف. ولفهم العلاقات بشكل افضل خلال هذه الدراسة تم استخدام معامل ارتباط بيرسون و تحليل المكون الرئيسي (PCA). تم تقييم السلالات و الكشافات والهجن الفردية من خلال تصميم القطاعات الكاملة العشوائية في ثلاث مكررات بمحطة البحوث الزراعية بسخا، محافظة كفر الشيخ، مصر، خلال موسم النمو 2020. أظهرت التباينات الناتجة عن مصادر الاختلاف في تحليل السلالة x الكشاف فروق معنوية لمعظم الصفات المقاسة. أوضحت النتائج أن المساهمة النسبية للسلالة x الكشاف كانت أعلى من المساهمة الفردية للسلالات والكشافات لمعظم الصفات المدروسة. بناءً على متوسطات الأداء، كانت الأباء متمثلة في السلالتين G.90 x Aus و Uzbekistan والكشاف G.97 متفوقة في محصول القطن ومعظم الصفات المدروسة مقارنة بالآباء الأخرى. تم تحديد الهجين TNB x G. 94 والهجين G.86 x G.90x Aus.12) والهجين TNB x G. 94 على أنها الأفضل لمحصول القطن ومعظم الصفات الأخرى بناءً على متوسط الأداء و MPH و BPH و PCA. كما أظهرت درجة السيادة أن توليفات الهجن الفردية لها طبيعة موجبة أو سلبية للصفات المدروسة. كما أشارت المقاييس الوراثية إلى أن تأثيرات عمل الجينات غير المضيفة (السائدة) كان لها دور أكثر أهمية مقارنة بالعوامل المضيفة في التحكم في جميع الصفات المدروسة، باستثناء صفة عدد البذور/لوزة. تم العثور على معاملات ارتباط معنوية بين جميع الأزواج الممكنة لمتوسط الأداء و MPH و BPH (إيجابية) و PR (سلبية) لمعظم الصفات التي تم فحصها. يمكن استخدام تحليل PCA كطريقة مناسبة لدراسة الصفات المدروسة ولتحديد أفضل الهجن الفردية عبر تحليل السلالة x الكشاف. أخيراً، وبناءً على نتائج الأساليب الإحصائية المستخدمة في هذه الدراسة، فإن الأباء والهجن الفردية المذكورة أعلاه واعدة لتعزيز و تحسين إنتاجية القطن وجودة أليافه من خلال استخدامها في برامج تربية القطن في مصر.

الكلمات المفتاحية: تحليل السلالة x الكشاف، قوة الهجين، درجة السيادة، المقاييس الوراثية، الأرتباط، PCA، القطن