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Combining ability of Egyptian cotton (*Gossypium barbadense* L.) reveals genetic potential for improved yield and fiber quality

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Abstract

Background As the most widely cultivated fiber crop, cotton production depends on hybridization to unlock the yield potential of current varieties. A deep understanding of genetic dissection is crucial for the cultivation of enhanced hybrid plants with desired traits, such as high yield and fine fiber quality. In this study, the general combining ability (GCA) and specific combining ability (SCA) of yield and fiber quality of nine cotton parents (six lines and three testers) and eighteen F₁ crosses produced using a line × tester mating design were analyzed.

Results The results revealed significant effects of genotypes, parents, crosses, and interactions between parents and crosses for most of the studied traits. Moreover, the effects of both additive and non-additive gene actions played a notably significant role in the inheritance of most of the yield and fiber quality attributes. The F₁ hybrids of (Giza 90 × Aust) × Giza 86, Uzbekistan 1 × Giza 97, and Giza 96 × Giza 97 demonstrated superior performance due to their favorable integration of high yield attributes and premium fiber quality characteristics. Path analysis revealed that lint yield has the highest positive direct effect on seed cotton yield, while lint percentage showed the highest negative direct effect on seed cotton yield. Principal component analysis identified specific parents and hybrids associated with higher cotton yield, fiber quality, and other agronomic traits.

Conclusion This study provides insights into identifying potential single- and three-way cross hybrids with superior cotton yield and fiber quality characteristics, laying a foundation for future research on improving fiber quality in cotton.

Keywords *Gossypium barbadense* L., Combining ability, Seed cotton yield, Fiber quality, Cluster analysis, Path analysis

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Background

Cotton contributes substantially to the economy, especially of several developing nations, as well as in the livelihoods of millions of rural smallholder households worldwide. Furthermore, the cotton sector employs nearly 150 million people globally, making it a crucial source of income (Jabran et al., 2019). Cotton production faces numerous challenges because of the strong and rapidly increasing demand for man-made fibers. Properly addressing these challenges is crucial to bolster worldwide economic growth and development (Jabran et al., 2019). Thus, one of the primary goals of cotton breeding programs is to improve yield and fiber properties. In Egypt, extensive efforts have been undertaken to enhance both the yield and fiber quality traits of cotton. Therefore, it is crucial to evaluate the adaptability and productivity of promising cotton varieties through hybridization methods.

The effectiveness of selecting superior cotton lines can be achieved by the hybridization process, followed by early transgressive segregation and subsequent selection (Koide et al., 2019). Using cotton parent lines that have diverse genetic backgrounds and different geographical origins is important for achieving genetic gain and improvement in yield and fiber quality traits (Khokhar et al., 2018). It has been reported that a genetically heterozygous plant population has a higher probability of successfully adapting to diverse environments than a genetically homozygous one (Markert et al., 2010). The most significant aspect determining the success of breeding program is how parents are selected to generate new crosses. To complete this step, plant breeders must possess a solid understanding of combining ability, gene action, and genetic variation of economic characteristics throughout the early stages of the plant breeding program (Fasahat et al., 2016; Abdelghany et al., 2022; El-Sorady et al., 2022).

Understanding the influence of gene actions on economic traits is crucial for developing cultivars that achieve higher yields and superior quality (Fasahat et al., 2016). Evaluating the combining ability of candidate parents is essential in identifying superior combiner parents and determining the type of gene action that regulates the inheritance of traits (Moustafa et al., 2021; Mutimaamba et al., 2020). Combining ability is classified into the general combining ability (GCA) of parents and the specific combining ability (SCA) of their crosses, which are mainly associated with additive and non-additive gene actions, respectively (Böhm et al., 2014; Youssef et al., 2021; Lamlo et al., 2020). Analyzing GCA and SCA enables the identification of the best combining parents and crosses exhibiting strong hybrid vigor, respectively. There are several methods of determining

the GCA and SCA of genotypes based on mating designs among which include line \times tester. The significant advantage of the line (female) \times tester (male) method is that it requires fewer experimental materials for the mating process compared with other mating designs such as North Carolina and diallel (such as NCI and NCII). The line \times tester method has been widely used to investigate cotton yield, its components, and fiber quality characteristics (Elmardy et al., 2021; Karademir et al., 2016; Khokhar et al., 2018; Patel et al., 2018; Prakash et al., 2018). The line \times tester breeding method is a theoretical extension of the top cross method, which uses numerous testers to identify superior parental combinations (Saitwal, 2017; Ochar Kingsley et al., 2022). This method also aids in selecting promising parents and crosses for developing high-yielding hybrids (Basbag et al., 2007; Jain et al., 2012). Additionally, it helps identify the best heterotic crosses (Akaogu et al., 2013; Bradshaw, 2017; Salem et al., 2020). Furthermore, because of the fewer experimental materials required for the mating process, it reduces costs and simplifies resource management. Hence, a line \times tester mating design strategy was used in current study to assess the combining ability and performance of cotton in terms of yield, yield components, and fiber quality characteristics. In addition, the association between the studied traits and diversity among parental genotypes was determined.

Methods

Experimental site and plant materials

The study was conducted at the Sakha Experimental Research Station, Kafr EL-Sheik Governorate, Egypt. A collection of nine cotton genotypes was utilized in this study during three successful growing seasons (2019, 2020, and 2021). The nine cotton genotypes belong to *Gossypium barbadense* L., and are composed of six Egyptian cotton genotypes, including two crosses Giza 89 \times Giza 86 (G.89 \times G.86), Giza 90 \times Aust (G.90 \times Aust), and four cultivars Giza 96 (G.96), Giza 94 (G.94), Giza 86 (G.86), and Giza 97 (G.97). The remaining three genotypes were foreign: TNB and Australian 12 (Aust 12) from Australia, and Uzbekistan 1 from Uzbekistan, which have been adapted to Egyptian environmental conditions. Origin, pedigree, and year of release of these genotypes are presented in Table 1.

Pure homozygous seeds of all genotypes were obtained from the Cotton Research Institute, Agricultural Research Center, Egypt. In the 2019 season, pure seeds of the nine genotypes were sown on 24th April according to the line \times tester mating system design. Six of the cotton genotypes, including the four cultivars TNB, Aust 12, Uzbekistan 1, and G.96, and the two crosses G.89 \times G.86 and G.90 \times Aust were used as lines (females). The three

Table 1 Origin and pedigree of the nine cotton genotypes under study

No	Genotypes	Pedigree	Origin	Year of release
Lines				
1	TNB	Unknown	Australia	Unknown
2	Giza 89×Giza 86	(Giza 75×R102)×(Giza 75×Giza 81)	Egypt	2007
3	Giza 90×Aust	(Giza 83×Dandra)×Aust	Egypt	2003
4	Uzbekistan 1	Unknown	Uzbekistan	Unknown
5	Aust 12	Unknown	Australia	Unknown
6	Giza 96	[Giza 84×(Giza 70×Giza 51B)]×S106	Egypt	2016
Testers				
1	Giza 86	Giza 75×Giza 81	Egypt	1995
2	Giza 94	10229×Giza 86	Egypt	2015
3	Giza 97	[(Giza 89×R101)×Giza 86]×Giza 94	Egypt	2020

Egyptian cotton genotypes G.94, G.86, and G.97 were used as testers (males) to produce eighteen F₁ crosses. In the 2020 and 2021 seasons, parents and F₁ seeds were sown on 28th April. Seeds of all plant materials were sown in a randomized complete blocks design (RCBD) with three replicates. The experimental plots comprised five rows per genotype in each replicate, with ten plants in each row. Each row was 4.0 m long and 0.7 m wide, and hills were spaced 0.4 m apart to give ten hills/row, with one plant per hill. All normal cultural practices were adopted during the two growing seasons.

Sampling and data recording

At full maturity, six plants in the middle of the total ten plants in each row of all entries were used to determine yield and yield-related traits (El-Aty et al., 2012). The number of bolls per plant (NBP) was counted as the total number of bolls divided by the number of selected plants. The number of seeds per boll (NSB) was calculated by assuming the number of seeds collected from twelve random bolls from each replicate. Fully opened bolls were selected from each of the six plants and weighed to determine boll weight (BW, g). The seed cotton was manually harvested from the individual selected plants and then dried and weighed to determine seed cotton yield per plant (SCY, g). Lint percentage (LP, %) was calculated as follows: (lint cotton yield/seed cotton yield)×100% (Shahzad et al., 2019). Lint cotton yield per plant (LCY, g) was determined after ginning the seed cotton for each sample. The seed index (SI, g) was calculated by counting and weighing 100 cotton seeds. The lint index (LI, g) was calculated according to the weight of lint produced by 100 seeds in grams. For the determination of fiber quality traits, lint samples from each plot were collected to estimate micronaire (MIC), fiber strength (FS, g·tex⁻¹), fiber uniformity ratio (FUR, %), and fiber length (FL, mm) using HVI (High Volume Instrument) at Cotton

Technology Laboratory, Cotton Research Institute, Agricultural Research Center, Giza, Egypt.

Statistical analysis

All the recorded data were subjected to analysis the variance (Gomez et al., 1984). The line×tester mating design was used to estimate the GCA effects of the parents and SCA of the crosses as described by Kempthorne (1958). Dissimilarity coefficients based on Euclidean distance were performed to dissect the genetic diversity among the nine parents, and then used to conduct cluster dendrogram based on yield and fiber quality traits using Ward's method. To explore the relationship among all studied traits, Pearson correlation coefficients were estimated. A principal component analysis (PCA) was carried out to find out the relative importance of different traits in capturing genetic variation and to identify the superiority of cotton genotypes with respect to each of the studied traits. Path coefficients analysis was used to partition the correlation coefficients among SCY and other trait components into direct and indirect effects. All statistical analyses were performed with RStudio v.3.5.1 software (R Core Team, 2013), where correlation diagram was performed using the *corrplot* package, cluster dendrogram and PCA biplot were conducted using the *factoextra* package, and path analysis was performed with the *lavaan* package (Rosseel, 2012).

Results

Dissecting the relationship among parent genotypes (lines and testers)

The dissimilarity coefficient matrix data, which ranged from 4.76 to 49.78, was used to determine the genetic distance among the nine parental genotypes, as presented in Table 2. The dendrogram (Fig. 1) based on the dissimilarity coefficients classified the nine parental genotypes into three clusters. Cluster I included three parents and was

Table 2 Dissimilarity coefficient between nine parental genotypes (6 lines and 3 testers) based on Euclidean distance

Genotypes	Aust 12	G.86	G.89×G.86	G.90×Aust	G.94	G.96	G.97	TNB	TNB
G.86	5.80								
G.89×G.86	5.87	8.40							
G.90×Aust	17.00	13.19	20.98						
G.94	22.12	18.33	25.53	8.83					
G.96	11.45	14.26	8.63	26.79	32.52				
G.97	39.14	35.61	42.56	24.57	17.34	49.78			
TNB	7.76	9.10	6.06	21.18	27.09	6.56	44.35		
Uzbekistan 1	4.76	5.65	9.31	14.07	20.10	14.14	36.96	10.03	

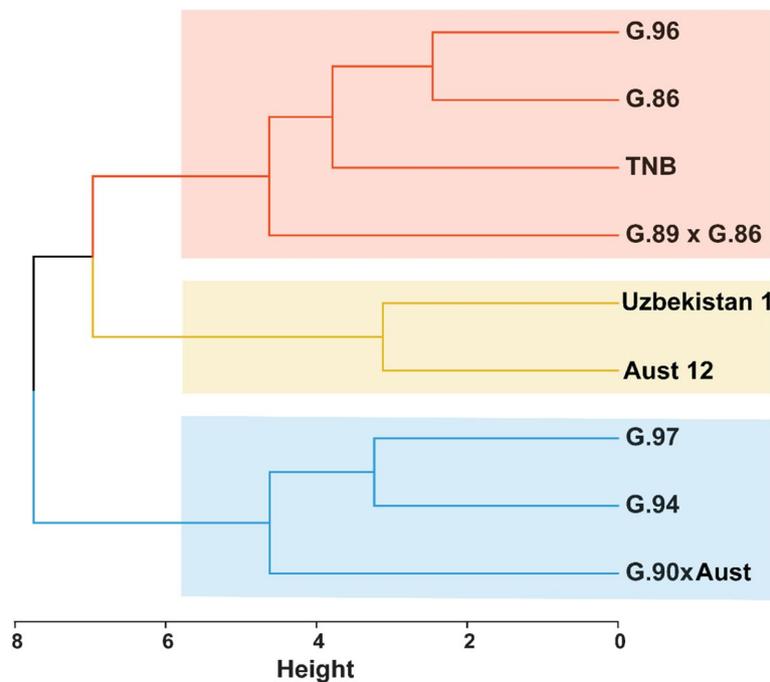


Fig. 1 Dendrogram based on dissimilarity coefficients for yield, yield components, and fiber quality traits measured on nine parental cotton genotypes over two years of the study

further subdivided into two sub-clusters, one with two parents (G.97 and G.94) and the other with one parent (G.90×Aust). Cluster II contained the two closest parents, Aust 12 and Uzbekistan 1. Cluster III consisted of four parents, which were divided into two sub-clusters, one with three parents (TNB, G.86, and G.96) and the other with one parent (G.89×G.86).

Analysis of variance (ANOVA) and performance of genotypes for target traits

The data presented in Table 3 indicated that a highly significant difference ($P \leq 0.001$) was observed among the

27 genotypes (9 parents and 18 F_1 hybrids) for yield, yield components, and fiber quality traits, except for BW which showed a non-significant difference. Also, highly significant differences ($P \leq 0.001$) were noticed among the parents, crosses, and parents vs. crosses for LCY, SCY, SI, NBP, LP, FS, and FUR; while there were no significant differences among parents, crosses, and parents vs. crosses for FL. The GCA effects of the lines were significant for all studied traits. GCA effects of the testers were significant for almost all measured traits except for SI, BW, LP, and LI, which showed non-significant effects. In addition, the SCA effect of line×tester was significant for all studied traits except for FS (Table 3).

Table 3 Mean squares of line × tester analysis for yield, yield components, and fiber traits (combined analysis of two growing seasons)

Source of variation	DF	LCY	SCY	SI	BW	NBP	LP	LI	NSB	FS	FL	MIC	FUR
Replications	2	2.24	0.93	0.11	0.03	1.02	1.07	0.25	5.69	0.07	0.34	0.04	0.54
Genotypes	26	1 651.82***	251.23***	2.37***	0.28	236.32***	8.83***	1.14***	4.13***	0.18***	2.78***	0.19***	2.01***
Parents	8	821.09***	150.33***	2.69***	0.11***	84.86***	14.57***	1.51***	1.08	0.27***	4.98	0.22***	2.98***
Crosses	17	2 001.05***	298.14***	1.99***	0.19	261.57***	5.88***	1.02***	4.74***	0.11***	1.89	0.14***	1.09***
Parents vs. crosses	1	2 360.76***	261.03 ***	6.31***	2.89***	1 018.81***	12.94***	0.31	18.22***	0.52***	0.31	0.79	9.58***
Lines (GCA)	5	2 489.79***	400.58***	3.48***	0.32**	453.61***	6.81**	0.91**	10.01***	0.24**	1.16**	0.30***	1.06**
Testers (GCA)	2	5 560.90***	875.06***	0.32	0.14	446.25***	0.31	0.05	3.23***	0.15***	1.05***	0.09**	1.29**
Lines × testers (SCA)	10	1 044.72***	131.53***	1.57***	0.14***	128.61***	6.54***	1.26***	2.42**	0.036	2.43***	0.07***	1.07***
Error	52	3.52	1.36	0.35	0.08	3.39	1.74	0.18	1.26	0.06	0.21	0.04	0.34

DF degree of freedom, LCY lint cotton yield per plant, SCY seed cotton yield per plant, SI seed index, BW boll weight, NBP number of bolls per plant, LP lint percentage, LI lint index, NSB number of seeds per boll, MIC micronaire, FS fiber strength, FL fiber length, FUR fiber uniformity ratio

* Significant at $P \leq 0.05$; **Significant at $P \leq 0.01$; ***Significant at $P \leq 0.001$

The mean performance among the lines showed that Uzbekistan 1 recorded the highest SCY, NSB, and FL, while the maximum mean values of LCY, NBP, LP, and LI were recorded by G.90 × Aust (Table 4). The highest mean values of traits such as SI, BW, MIC, and FUR were recorded by G.96. For FS, the genotype Aust 12 recorded the highest mean value.

For the tester genotypes, G.94 recorded the highest mean values for LCY, SI, LI, and NSB, whereas G.86 had the highest mean values for BW, MIC, FL, and FUR. G.97 recorded the highest means of SCY, NBP, LP, and FS. Among the F_1 hybrids, [(G.90 × Aust) × G.86] had the highest mean performance for SCY, whereas (Uzbekistan 1 × G.97) had the maximum value of LCY, which is higher than both parents G.97 and Uzbekistan 1 for such trait. For other traits, the following hybrids exhibited notable mean performance: (TNB × G.97) for SI, [(G.90 × Aust) × G.94] for BW, (G.96 × G.97) for NBP, (Uzbekistan 1 × G.94) for LP and LI, (TNB × G.94) for NSB, (Aust 12 × G.94) for FS, (Uzbekistan 1 × G.97) for FL, [(G.90 × Aust) × G.86] for MIC, and (Uzbekistan 1 × G.97) for FUR (Table 4).

GCA effects

The average performance of line × tester crosses was used to assume the effects of GCA (Table 5). For LCY, the genotypes G.96 (15.44), G.90 × Aust (13.86), and Uzbekistan 1 (12.44) exhibited highly significant and positive GCA effects, which were the highest among all the traits evaluated in this study. Among the three testers, G.94 recorded the highest positive and significant GCA effect for LCY (7.72), while G.86 had a negative GCA effect (−7.11). For SCY, the effect of GCA for female lines ranged from −9.46 for (G.89 × G.86) to 6.62 for Uzbekistan 1. For

testers, GCA estimates of SCY ranged from −2.43 (G.86) to 2.48 (G.94).

For GCA estimates of SI and BW, the maximum positive GCA effect was recorded by G.90 × Aust (0.53 and 0.29, respectively), while the maximum negative effects of GCA were recorded by Aust 12 (−0.50) and TNB (−0.18) for SI and BW, respectively. Among the testers, the highest positive effect of GCA for SI and BW was obtained by G.86 (0.21) and G.97 (0.03), respectively, whereas the maximum negative GCA effect was recorded by G.94 (−0.35) and G.86 (−0.02) for SI and BW, respectively. For NBP, the highest positive and significant GCA effect among female lines was recorded by G.96 (5.87), while G.89 × G.86 (−8.84) and Aust 12 (−4.97) recorded the highest negative and significant GCA effects. Among the testers, G.94 and G.86 had GCA of 2.91 and −2.60, respectively, for NBP. Two female lines had positive and relatively higher GCA for LP, namely Uzbekistan 1 (1.99) and Aust 12 (0.71), while TNB (−1.63) and G.89 × G.86 (−0.72) showed a negative GCA effect for LP. As regards the GCA effect of LI, Aust 12 (0.34) and Uzbekistan 1 (0.30) among lines, and G.86 (0.16) among testers, were the top general combiners. For NSB, G.90 × Aust (0.81) and G.94 (0.51) showed highly significant and positive GCA effects as good combiners among female lines and testers, respectively. For fiber quality traits, the female line G.89 × G.86 had a GCA effect of 0.12 and 0.57 for FS and FUR, respectively, while G.94 (0.16) and G.97 (0.17) showed a preferable GCA effect among testers for FS and FUR, respectively. Among the six lines Uzbekistan 1 had the best GCA effect for FL (0.62) and MIC (0.14), whereas tester genotypes G.97 (0.25) and G.86 (0.23) showed favorable GCA for FL and MIC, respectively.

Table 4 Mean performances for yield, yield components, and fiber traits of lines, testers, and F₁ hybrids (combined analysis of two growing seasons)

Genotypes	SCY /g	LCY /g	SI /g	BW /g	NBP	LP /%	LI /g	NSB	FS /(g.tex ⁻¹)	FL /mm	MIC	FUR /%	
Lines (females)													
TNB	67.44	24.90	11.76	3.60	19.30	36.61	6.80	19.41	10.66	32.9	3.96	85.10	
G.89×G.86	68.45	22.33	10.49	3.63	19.08	32.61	5.10	20.39	10.10	33.7	4.45	85.55	
G.90×Aust	79.62	36.72	10.33	3.33	27.06	40.81	7.14	19.10	10.00	34.1	4.50	86.15	
Uzbekistan 1	80.58	30.38	9.44	3.23	25.17	36.93	5.61	20.65	10.70	37.3	3.95	87.30	
Aust 12	73.54	25.49	10.20	3.16	20.57	34.62	5.40	19.76	10.75	35.3	4.05	87.40	
G.96	49.29	17.41	11.96	3.67	13.15	34.95	6.41	20.03	10.40	34.6	4.65	87.60	
Lines average	69.82	26.20	10.70	3.44	20.72	36.09	6.08	19.89	10.43	34.6	4.26	86.51	
Tester (pollinators)													
G.94	100.49	37.09	12.03	3.51	25.31	35.95	6.78	19.50	10.35	33.9	4.40	85.35	
G.86	67.27	25.06	11.81	3.67	20.01	35.98	6.64	19.24	10.50	34.1	4.40	86.55	
G.97	101.13	36.32	11.44	3.37	30.96	36.01	6.44	18.86	10.90	33.3	4.00	85.25	
Tester average	89.63	32.82	11.76	3.51	25.42	35.98	6.62	19.20	10.58	33.8	4.26	85.71	
F₁ hybrids													
G.94	TNB	117.66	39.21	8.49	2.74	41.05	33.31	4.24	20.51	10.25	34.0	4.25	86.85
	G.89×G.86	100.34	35.32	10.69	3.19	35.55	36.04	6.03	19.54	10.60	36.0	4.45	87.75
	G.90×Aust	92.93	37.00	10.83	3.52	26.49	37.64	6.54	20.28	10.25	33.5	4.35	86.10
	Uzbekistan 1	103.71	41.39	10.34	3.25	32.82	39.96	6.88	18.84	10.55	35.2	4.45	86.56
	Aust 12	47.36	17.69	10.13	2.80	23.67	36.47	5.82	18.22	10.65	34.1	4.40	86.50
	G.96	98.34	36.48	9.49	2.82	35.50	37.23	5.62	18.66	10.55	34.9	4.25	86.30
G.86	TNB	66.27	24.54	11.27	2.69	27.71	36.57	6.50	15.14	10.25	33.9	4.75	86.95
	G.89×G.86	46.83	17.38	10.57	2.92	16.55	37.32	6.29	17.37	10.30	33.9	4.65	87.25
	G.90×Aust	122.41	43.86	10.94	3.05	39.59	37.05	6.45	18.47	10.36	34.8	4.80	87.03
	Uzbekistan 1	87.14	33.58	10.44	3.27	32.46	38.55	6.55	19.04	9.95	33.8	4.75	87.50
	Aust 12	67.31	25.07	10.18	3.11	21.34	37.30	6.06	19.52	10.30	34.4	4.40	86.05
	G.96	85.05	31.37	10.95	3.25	25.57	35.88	6.13	19.07	10.00	33.7	4.85	87.25
G.97	TNB	57.38	20.32	12.17	3.22	14.57	35.76	6.78	17.40	10.35	35.2	4.25	86.80
	G.89×G.86	53.26	14.46	10.78	3.23	14.48	36.17	6.10	19.76	10.40	33.7	4.30	87.40
	G.90×Aust	97.56	35.38	11.36	3.50	28.95	36.25	6.46	19.65	10.20	34.6	4.35	86.75
	Uzbekistan 1	121.30	46.97	9.64	2.83	41.78	37.98	5.91	18.24	10.10	36.3	4.65	88.33
	Aust 12	96.07	36.69	9.89	2.89	33.36	38.20	6.10	18.03	10.25	34.6	4.15	87.65
	G.96	120.85	43.26	10.12	2.87	45.19	36.52	5.82	18.02	10.35	34.1	4.45	86.60
Crosses average	87.87	32.22	10.46	3.06	29.81	36.90	6.12	18.65	10.31	34.5	4.47	86.97	
Overall average	84.06	30.95	10.66	3.19	27.30	36.61	6.17	18.99	10.37	34.4	4.41	86.73	
LSD_{0.05}	3.07	1.91	0.97	0.46	3.01	2.16	0.70	1.84	0.39	0.7	0.33	0.96	

SCY seed cotton yield per plant, LCY lint cotton yield per plant, SI seed index, BW boll weight, NBP number of bolls per plant, LP lint percentage, LI lint index, NSB number of seeds per boll; MIC micronaire, FS fiber strength, FL fiber length, FUR fiber uniformity ratio. LSD least significant difference

SCA effects

The SCA mean squares were significant ($P \leq 0.01$) for all agronomic and fiber quality characteristics except for FS, as indicated in Table 3. Table 6 presents the SCA effects, with the F₁ hybrid of TNB×G.94 exhibiting the highest positive SCA value for SCY (47.85), LCY (14.92), NBP (19.2), and NSB (2.45) among all the 18 F₁ hybrids. The F₁ hybrid of TNB×G.97 showed the highest positive SCA values of 1.39 and 0.31 for SI and BW, respectively. The F₁ hybrids of Uzbekistan

1×G.94 (1.30) and TNB×G.97 (0.89) showed the highest SCA values for LP and LI, respectively. The F₁ hybrids of (G.90×Aust)×G.86, (G.89×G.86)×G.94, Aust 12×G.94, and Aust 12×G.97 recorded the highest positive SCA for FS, FL, MIC, and FUR, respectively.

The mid-parent heterosis

In this study, the estimation of mid-parent heterosis was conducted to assess the performance of F₁ hybrids compared with their mid-parents. The presence of heterosis

Table 5 General combining ability (GCA) effects of 6 cotton female lines and 3 testers based on 12 measured traits (combined analysis of two growing seasons)

Genotypes	LCY	SCY	SI	BW	NBP	LP	LI	NSB	FS	FL	MIC	FUR
Lines												
TNB	-0.07	-1.93	0.13	-0.18	2.67	-1.63	-0.31	-0.81	-0.03	-0.10	-0.06	-0.04
G.89×G.86	-24.33	-9.46	0.16	0.05	-8.84	-0.72	-0.11	0.18	0.12	0.05	-0.01	0.57
G.90×Aust	13.86	5.31	0.53	0.29	1.82	0.14	0.34	0.81	-0.04	-0.21	0.03	-0.27
Uzbekistan 1	12.44	6.62	-0.38	0.05	3.46	1.99	0.30	0.21	-0.12	0.62	0.14	0.10
Aust 12	-17.34	-5.78	-0.50	-0.13	-4.97	0.71	-0.12	-0.10	0.09	-0.12	-0.16	-0.17
G.96	15.44	5.23	0.07	-0.08	5.87	-0.49	-0.10	-0.29	-0.02	-0.23	0.04	-0.19
Testers												
G.94	7.72	2.48	-0.35	-0.01	2.91	-0.16	-0.21	0.51	0.16	0.14	-0.11	-0.27
G.86	-7.11	-2.43	0.21	-0.02	-2.60	0.19	0.16	-0.52	-0.12	-0.39	0.23	0.10
G.97	-0.60	-0.06	0.14	0.03	-0.31	-0.03	0.04	0.01	-0.04	0.25	-0.11	0.17
LSD _{0.05}	4.40	1.78	0.22	0.09	2.01	0.52	0.17	0.55	0.08	0.14	0.06	0.23

LCY lint cotton yield per plant, SCY seed cotton yield per plant, SI seed index, BW boll weight, NBP number of bolls per plant, LP lint percentage, LI lint index, NSB number of seeds per boll, MIC micronaire, FS fiber strength, FL fiber length, FUR fiber uniformity ratio. LSD least significant difference

Table 6 Specific combining ability (SCA) effects of 18 cotton hybrids based on 12 measured traits (combined analysis of two growing seasons)

Hybrids	LCY	SCY	SI	BW	NBP	LP	LI	NSB	FS	FL	MIC	FUR
TNB×G.94	14.92	47.85	-1.81	-0.13	19.02	-1.74	-1.39	2.45	-0.19	-0.51	-0.05	0.25
(G.89×G.86)×G.94	11.19	30.17	0.36	0.08	8.76	0.08	0.20	-0.36	0.01	1.34	0.10	0.55
(G.90×Aust)×G.94	-9.66	-28.74	0.13	0.18	-11.05	0.82	0.27	0.61	-0.18	-0.95	-0.04	-0.26
Uzbekistan 1×G.94	-1.95	-9.37	0.55	0.14	-5.21	1.30	0.64	-0.23	0.19	-0.02	-0.05	-0.43
Aust 12×G.94	-9.90	-25.61	0.33	-0.12	-7.98	-0.92	-0.08	-1.00	0.09	-0.39	0.20	0.04
G.96×G.94	-4.61	-14.30	0.44	-0.15	-3.54	0.47	0.36	-1.46	0.09	0.53	-0.15	-0.15
TNB×G.86	-3.14	-12.65	0.42	-0.18	-3.72	1.17	0.49	-1.88	0.09	-0.08	0.11	-0.02
(G.89×G.86)×G.86	-3.68	-9.76	-0.32	-0.17	-1.79	-0.16	-0.21	-0.33	-0.01	-0.23	-0.04	-0.32
(G.90×Aust)×G.86	12.86	34.95	-0.31	-0.30	14.68	-0.12	-0.20	-1.08	0.22	0.90	0.07	0.30
Uzbekistan 1×G.86	-3.56	-7.68	0.10	0.17	-3.63	-0.47	-0.06	0.56	-0.13	-0.89	-0.09	0.40
Aust 12×G.86	0.32	1.08	-0.05	0.19	-0.87	0.25	0.06	1.21	0.02	0.44	-0.14	-0.79
G.96×G.86	-2.80	-5.95	0.16	0.29	-4.67	-0.66	-0.09	1.52	-0.18	-0.14	0.11	0.43
TNB×G.97	-11.78	-35.19	1.39	0.31	-15.30	0.58	0.89	-0.57	0.11	0.58	-0.05	-0.23
(G.89×G.86)×G.97	-7.50	-20.41	-0.04	0.09	-6.97	0.08	0.01	0.69	0.01	-1.12	-0.05	-0.23
(G.90×Aust)×G.97	-3.20	-6.22	0.18	0.12	-3.64	-0.70	-0.07	0.48	-0.03	0.05	-0.04	-0.04
Uzbekistan 1×G.97	5.51	17.05	-0.65	-0.31	8.84	-0.82	-0.58	-0.33	-0.06	0.92	0.15	0.04
Aust 12×G.97	9.57	24.53	-0.28	-0.07	8.85	0.68	0.02	-0.20	-0.11	-0.05	-0.05	0.75
G.96×G.97	7.40	20.25	-0.60	-0.14	8.21	0.19	-0.28	-0.07	0.09	-0.38	0.05	-0.28
LSD _{0.05}	3.08	7.69	0.39	0.16	3.48	0.91	0.31	0.96	0.14	0.25	0.12	0.41

LCY lint cotton yield per plant, SCY seed cotton yield per plant, SI seed index, BW boll weight, NBP number of bolls per plant, LP lint percentage, LI lint index, NSB number of seeds per boll, MIC micronaire, FS fiber strength, FL fiber length, FUR fiber uniformity ratio. LSD least significant difference

is attributed to the genetic diversity and the origin of parents, which enables the creation of new recombination and leads to improved adaptation in the F₁ hybrids. All eighteen hybrids included in the study exhibited either positive or negative heterosis for the twelve measured traits, as shown in Table 7. Among the traits, SCY

and LCY showed the highest significant positive heterosis for Uzbekistan 1×G.86 with values of 68.58% and 50.82% in the growing seasons, respectively. For SI and BW, G.96×G.94 displayed the highest significant heterosis values of 17.83% and 22.99%, respectively. In terms of NBP, LI, and LP, Uzbekistan 1×G.86 exhibited the

Table 7 Heterosis relative to mid-parent (MP) for yield and fiber traits using line x tester hybrids of cotton

Hybrids	SCY /%	LCY /%	SI /%	BW /%	NBP /%	LP /%	LI /%	NSB /%	MIC /%	FS /%	FL /%	FUR /%
G.94 TNB	-35.96**	-38.66**	17.16**	18.08**	-46.76**	-4.31	5.36	9.18	-15.74**	6.37**	-6.02**	-2.58**
G.89xG.86	-25.27*	-36.44**	2.21	17.86**	-37.4**	-15.03**	11.19	-20.05**	0.00	0.00	-1.54	-2.31**
G.90x Aust	-22.21*	-16.14	0.45	8.58	-30.08*	7.00*	5.49	12.85*	-2.17	-1.48	0.29	-1.03
Uzbekistan 1	-22.02*	-23.74*	-4.78	9.04	-29.28*	-2.76	11.09	-8.85	-12.71**	4.90**	5.45**	0.78
Aust 12	-13.39	-21.18	1.71	5.56	-18.18	-9.13**	3.48	-12.54*	-5.26	4.62**	2.25*	0.63
G.96	-35.53**	-38.50**	17.83**	22.99**	-48.21**	-6.18*	8.41	14.63*	5.08	0.73	1.02	1.48*
G.86 TNB	-15.07	-17.11	16.92**	15.33*	-26.29*	-2.64	-0.17	12.59*	-7.37*	2.99	-3.07**	-2.15**
G.89xG.86	-21.48*	-24.05*	13.34**	19.48**	-35.19*	-2.87	3.63	8.58	-2.22	3.70*	-0.07	-1.03
G.90x Aust	-3.70	-4.32	8.62	10.18	-14.04	-0.55	1.70	7.67	-13.98**	0.24	-1.77	-1.93**
Uzbekistan 1	68.58**	50.82**	-22.10**	-9.36	85.47**	7.80*	16.39*	-33.12**	-4.49	7.13**	-4.83**	-0.17
Aust 12	37.67**	33.02*	-3.07	4.42	29.86	-2.55	6.62	-6.34	5.95	2.91	3.23**	0.60
G.96	-7.60	-3.93	-2.84	15.71	-22.32	4.15	15.88*	3.83	0.00	-0.97	-3.46**	-0.69
G.97 TNB	23.39*	31.57*	1.34	6.97	11.59	-9.66	0.52	6.10	-0.56	2.93	0.72	-1.15*
G.89xG.86	-22.61	-24.90	-3.18	-8.38	-16.03	-1.93	-4.75	-5.76	4.14	3.15	0.00	-1.17*
G.90x Aust	16.58	17.33	2.20	-7.53	22.36	0.88	-8.09	4.11	-2.86	1.69	3.03**	-0.80
Uzbekistan 1	-35.17**	-36.37**	7.32	-15.10*	-24.7*	-1.47	-20.11**	5.01	5.56	0.99	-4.24**	-0.03
Aust 12	-49.86**	-51.5**	-0.53	-8.45	-45.75**	-2.88	-6.27	-4.51	9.41**	0.73	-1.88*	0.06
G.96	18.67*	20.92*	1.88	-4.50	22.68	1.82	-6.80	5.05	9.09**	0.89	1.29	0.41

LCY lint cotton yield per plant, SCY seed cotton yield per plant, SI seed index, BW boll weight, NBP number of bolls per plant, LP lint percentage, LI lint index, NSB number of seeds per boll, MIC micronaire, FS fiber strength, FL fiber length, FUR fiber uniformity ratio. *Significant at $P \leq 0.05$; **Significant at $P \leq 0.01$; ***Significant at $P \leq 0.001$

highest significant positive heterosis values of 85.47%, 16.39%, and 7.80%, respectively. For NSB, G.96xG.94 demonstrated the highest significant positive heterosis of 14.63%. G.96xG.94 also achieved the highest significant heterosis value of 1.48% for FUR. In terms of MIC, Aust 12xG.97 and G.96xG.97 achieved the top two significant positive heterosis values of 9.41% and 9.09%, respectively. For FS, Uzbekistan 1xG.86 showed the highest significant heterosis value of 7.13%. Lastly, for FL, Uzbekistan 1xG.94 demonstrated the best performance with the highest significant and positive heterosis value of 5.45%. These results indicate that certain F₁ hybrids, such as from Uzbekistan 1xG.86, G.96xG.94, Aust 12xG.97, G.96xG.97, and Uzbekistan 1xG.94 exhibited superior performance in specific fiber quality traits, displaying significant positive heterosis compared with their mid-parents.

Correlation analysis

The correlation analysis among different traits is illustrated in Fig. 2. SCY was found to have a strong positive correlation with LCY ($r=0.99, P<0.001$) and NBP ($r=0.97, P<0.001$), and a significant negative correlation with SI ($r=-0.38, P<0.05$). In addition, LCY had a highly significant positive correlation with the NBP ($r=0.94, P<0.001$). SI showed positive and significant correlations with LI ($r=0.72, P<0.01$) and BW ($r=0.59, P<0.01$), and a negative and significant correlation with

NBP ($r=-0.51, P<0.01$). LP was significantly positively correlated with LI ($r=0.64, P<0.001$), while MIC had a highly significant negative correlation with FS ($r=-0.66, P<0.001$).

Path coefficient analysis

The results of direct and indirect correlation coefficients among the measured traits and SCY are depicted in Fig. 3. In this regard, LCY displayed the most significant positive direct effect on SCY ($r=0.91$). Significant positive direct effects on SCY were also observed for LI and NBP ($r=0.33$ and 0.11 , respectively). The direct effects of NSB, FS, and FUR on SCY were positive but not statistically significant ($r=0.05, r=0.002$, and $r=0.01$, respectively). The most significant negative direct effect on SCY was exhibited by LP ($r=-0.36$), followed by SI ($r=-0.22$), while BW, MIC, and FL showed non-significant negative direct effects on SCY ($r=-0.04, r=-0.008$, and $r=-0.01$, respectively). Path coefficient analysis of direct and indirect effects of associated traits with SCY showed that NBP ($r=0.86$) had the highest indirect contribution to SCY via LCY, followed by SI via LI ($r=0.24$), LP via LI ($r=0.21$), and LP via LCY ($r=0.20$).

Variability of yield and fiber quality among parents and hybrids

PCA was performed based on yield, yield components, and fiber quality traits to investigate the variability

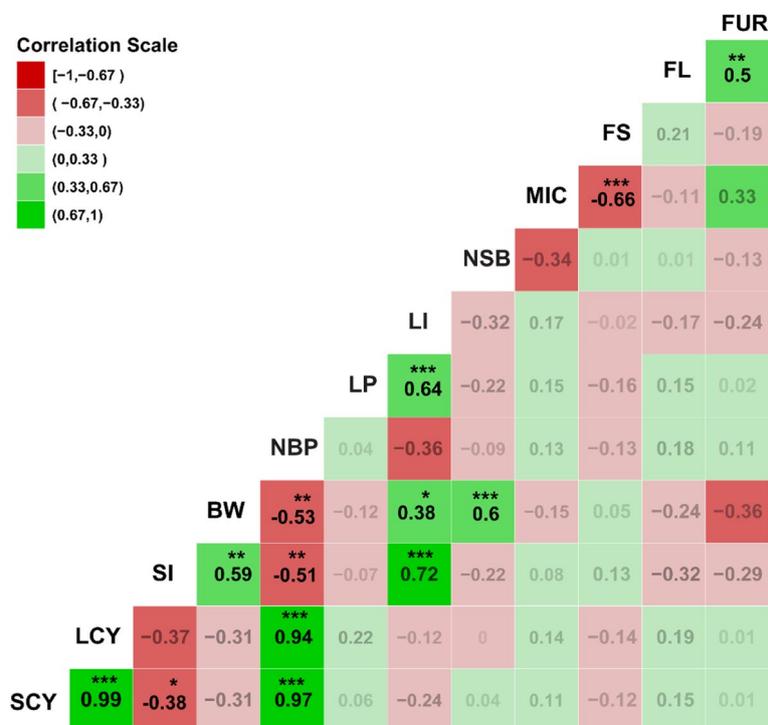


Fig. 2 Correlation coefficients among cotton yield, yield components, and fiber quality traits evaluated for parents and F₁ hybrids. Positive correlations are marked in green and negative correlations are marked in red. The intensity of the color is proportional to the correlation coefficients. The color gradient legends represent correlation coefficients (r) values ranging from +1.0 (dark green) to -1.0 (dark red). *, **, and *** indicate significant correlations at P ≤ 0.05, P ≤ 0.01, and P ≤ 0.001, respectively. LCY, lint cotton yield per plant; SCY, seed cotton yield per plant; SI, seed index; BW, boll weight; NBP, number of bolls per plant; LP, lint percentage; LI, lint index; NSB, number of seeds per boll; MIC, micronaire; FS, fiber strength; FL, fiber length; FUR, fiber uniformity ratio

among all the genotypes (Fig. 4). The first two principal components (PCs), PC1 and PC2, captured 32.3% and 18.8% of the total variance of all evaluated variables. The PCA technique enables us to group the genotypes by using the weights of the traits on PCs, as genotypes positioned closer to the tail end of a vector have higher values for the corresponding trait, and vice versa. G.86, [(G.90 × Aust) × G.86] F₁, and G.89 × G.86 were scattered around SCY, LCY, and NBP. Based on the PCA, these genotypes, which comprise parents and hybrids, can be selected for their potential for high cotton yield. Also, (G.96 × G.97) F₁ and G.90 × Aust were scattered around LP, while (TNB × G.94) F₁ was close to the MIC vector, indicating that these hybrids and parents had higher values of those studied parameters. Other genotypes such as (TNB × G.97) F₁, (Uzbekistan 1 × G.97) F₁, G.96, and [(G.89 × G.86) × G.97] F₁ clustered around BW, FS, NSB, and FL, respectively. (TNB × G.86) F₁ showed distinct character as it dispersed far from the center of vectors and loadings since it recorded low values for the majority of the studied cotton traits. Noteworthy, the genotypes located close to the origin or center of the biplot indicate

that they showed average performances in all parameters among all parents and hybrids.

Discussion

In the current study, a line × tester mating design was utilized to create 18 F₁ hybrids by crossing six lines with three testers. The results of cluster analysis indicated substantial phenotypic diversity among the parents, which encouraged their crossing into hybridization breeding programs. These findings were consistent with previous studies (such as Zafar et al., 2021). The three testers were placed into two different clusters, possibly due to the variation in their GCA for most of the measured traits. The two imported female parent genotypes, Aust 12 and Uzbekistan 1, were clustered together, indicating their close relationship and similar performance. TNB, G.89 × G.86, G.96, and G.86 were grouped together, and they had poor performances as general combiners for most of the studied yield and fiber quality traits. Previous studies have used cotton phenotypic performance to categorize cotton genotypes into different clusters that can be crossed to generate transgressive segregants in

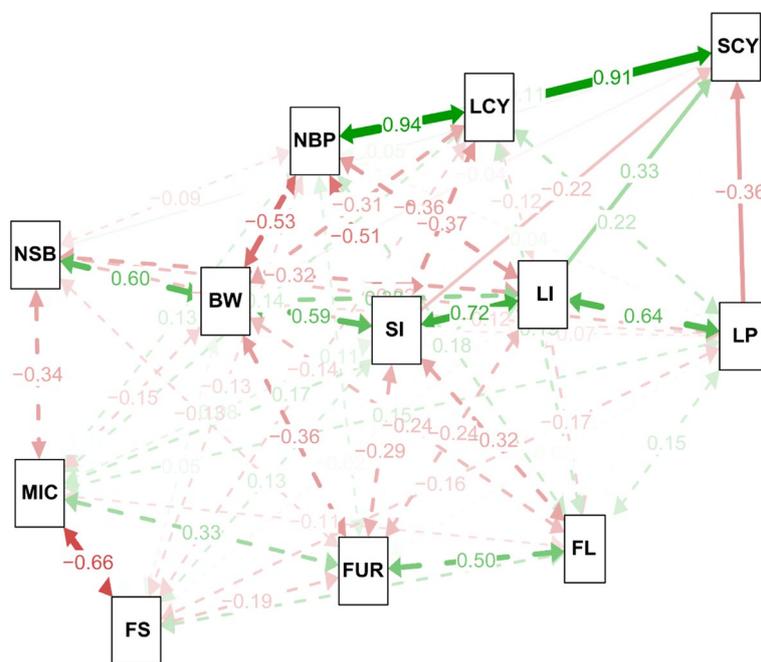


Fig. 3 Path diagram showing the direct effect of the 11 explanatory variables on seed cotton yield assessed for parents and F₁ crosses across the 2019 and 2020 growing seasons. Bidirectional arrows show the correlation between the variables, and unidirectional arrows indicate a direct effect on the direction of the arrow. Green and red arrows represent positive and negative effects, respectively. The color intensity and width of the arrows represent the standardized path coefficients values. Solid arrows indicate $P \leq 0.05$ and dashed arrows indicate $P > 0.05$. LCY, lint cotton yield per plant; SCY, seed cotton yield per plant; SI, seed index; BW, boll weight; NBP, number of bolls per plant; LP, lint percentage; LI, lint index; NSB, number of seeds per boll; MIC, micronaire; FS, fiber strength; FL, fiber length; FUR, fiber uniformity ratio

the early generations (Akter et al., 2019; Geng et al., 2021; Geng et al., 2020; Vasconcelos et al., 2020).

The highly significant genetic differences ($P \leq 0.01$) reported in this study for all the traits except BW indicate the existence of considerable genetic variability among all genotypes. The assessment of such genetic variation between lines and testers is crucial for the effective exploitation of heterosis in breeding, encouraging to conduct a subsequent analysis to assess combining ability (Karademir et al., 2016; Koebernick et al., 2019). The combining ability of genotypes is dissected to identify genotypes with a high genetic potential for developing cross-combinations with desirable traits and to investigate the activity of genes involved in trait expression (Constable et al., 2015). Thus, the line \times tester mating design was used in the current investigation, as it provides a more accurate estimation and valuable prediction of critical quantitative characters, as has been demonstrated in prior studies on various species, including wheat (Jain et al., 2012; Osaf, 2009), cotton (Karademir et al., 2016; Borzan et al., 2021), rice (El-Mowafi et al., 2021), and maize (Abdulhamed et al., 2021).

This study unveiled significant positive or negative GCA effects of the parents, indicating their strong or

weak combining abilities for specific traits, respectively. These findings are consistent with those of previous investigations (El-Aty et al., 2012; Mangi et al., 2021; Queiroz et al., 2021). Parents with a desirable significant GCA have a strong capacity to influence desired traits in their offspring and can be utilized as key materials for improving the traits of interest (Han et al., 2020). The significant GCA effects revealed in this study are consistent with those observed in previous research (El-Aty et al., 2012; Mangi et al., 2021; Queiroz et al., 2021). Both lines and testers with positive and significant GCA effects identified in this study are vital, as crossing them might lead to advantageous hybrid combinations in subsequent segregating populations. This, in turn, strengthens the selection process for specific characteristics. Highly significant GCA for lines and testers for LCY observed in this study further reveals the key role of additive gene action in the inheritance of this trait (Khokhar et al., 2018; Shaibu et al., 2021). It is noteworthy that parents with good GCA for LCY were also observed to have good GCA for the majority of yield components (Koebernick et al., 2019; Richika et al., 2021). Lint yield is significantly important for fiber crops (Koebernick et al., 2019). Among the female parents, G.96 exhibited the best GCA

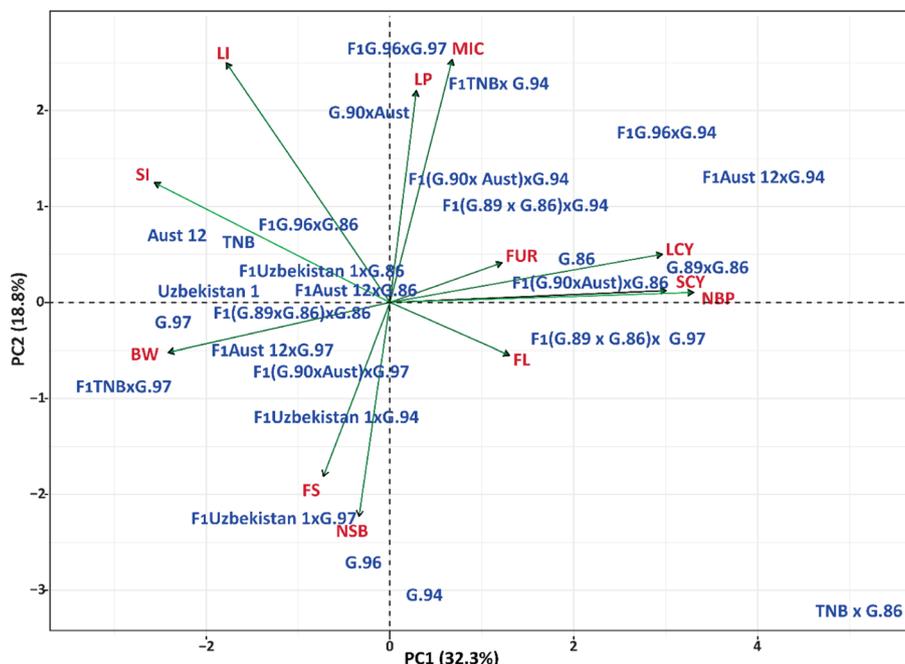


Fig. 4 Principal component analysis (PCA) showing biplot (score and loading) of the parents (lines and testers) and hybrids based on yield, yield components and fiber quality traits. LCY, lint cotton yield per plant; SCY, seed cotton yield per plant; SI, seed index; BW, boll weight; NBP, number of bolls per plant; LP, lint percentage; LI, lint index; NSB, number of seeds per boll; MIC, micronaire; FS, fiber strength; FL, fiber length; FUR, fiber uniformity ratio. The total variation was divided into 12 principal components (PCs). The loadings for 12 studied cotton traits on PC1 and PC2 are represented by the green arrows. Score plot for the 27 cotton genotypes (parents and hybrids) are shown on the plot in blue color

for LCY, indicating its superiority as the most favorable genotype in terms of lint yield.

Along with lint yield, promising genotypes with excellent fiber quality are vitally needed due to rising worldwide textile demand and competition from modern synthetic fibers (Fang et al., 2014). Thus, our study provided such favorable crossing materials characterized by high positive GCA effects recorded by both lines and testers for different fiber quality traits, such as line G.89 × G.86, and testers G.94 and G.97 for FS and FUR, and line Uzbekistan 1 and testers G.97 and G.86 for FL and MIC. Generally, lint yield is negatively correlated with cotton fiber quality, constituting an unfavorable association which has impeded cotton breeding efforts to enhance multiple fiber properties simultaneously (Yu et al., 2013; Clement et al., 2012). Hence, it is vital to employ a good general combiner for both high yield and prominent fiber quality traits as parents in crossing to improve them concurrently and to minimize their unfavorable interrelationship (Clement et al., 2012).

The findings of this study indicate that non-additive gene action is a crucial factor in the inheritance of both yield and fiber quality traits. This conclusion is supported by the substantial and statistically significant effect of SCA. Among the most promising combinations,

TNB × G.94 showed strong SCA for LCY, SCY, NBP, and NSB, while (G.90 × Aust) × G.86, (G.89 × G.86) × G.94, Aust 12 × G.94, and Aust 12 × G.97 were identified as elite crosses for FS, FL, MIC, and FUR, respectively, based on their fiber quality attributes. These promising hybrids have the potential to be selected for subsequent recombination breeding programs based on their performance and SCA, facilitating the improvement of various quality and yield attributes (Koebernick et al., 2019). The variances of GCA and SCA provide useful information on the magnitude of gene action and can aid in developing effective breeding strategies for future breeding programs. Understanding the relative importance of additive and non-additive gene effects is crucial in selecting appropriate parents and designing successful breeding programs. Therefore, analyzing GCA and SCA variances can guide breeders in making informed decisions and optimizing breeding efforts (Kaushik et al., 2018). The variances attributed to GCA effects (mean squares due to lines and testers) were found to be lower than those attributed to SCA (mean squares due to lines × testers) for certain traits, including LCY, SCY, SI, NBP, MIC, and FUR. These findings imply that non-additive gene actions, such as dominance or epistasis, had a more prominent influence on the inheritance of these traits. In contrast,

the variances of GCA outweighed the variances of SCA for traits such as BW, LP, LI, NSB, FS, and FL. This suggests that additive gene action plays a crucial role in the inheritance of these traits. These findings are consistent with previous studies (Yehia et al., 2019; El-Mowafi et al., 2021; Khokhar et al., 2018; Zafar et al., 2021).

The correlation patterns unearthed in this study correspond with those identified in earlier research. For instance, significant and strongly positive correlations were observed between SCY and NBP, as well as between SCY and LCY. These outcomes imply that incorporating either SCY or NBP into a yield enhancement initiative can result in heightened lint yield (Shavkiev et al., 2021; Song et al., 2018; Memon et al., 2017; Morab et al., 2021). Additionally, this research identified a noteworthy positive association between BW and NSB. This correlation is advantageous because increased BW may enhance NSB, leading to a larger surface area and ultimately enhancing the maximum LP. This study revealed a negative relationship between BW and NBP, aligning with previous studies (Kumar et al., 2021). However, previous literature reported a positive and significant correlation between BW and NBP (Rehman et al., 2020). Also, non-significant correlations were observed between SCY and LCY with fiber quality attributes, which is in line with earlier findings (Mangi et al., 2021; Desalegn et al., 2009).

Although the correlation coefficient holds significance, it does not provide an accurate measure of causation. This occurs because the relationship between two traits might result from the influence of a third attribute or a group of attributes on those characteristics. For example, the correlation between BW and LCY could be impacted by other factors like soil moisture levels, ambient temperature, or plant nutrition status. Similarly, the correlation between FS and MIC may be affected by additional attributes such as irrigation timing, boll maturation rates, and/or in-season climatic variability. Thus, when interpreting significant correlations, it is important to consider the potential effect of external variables outside the two parameters directly correlated with each other. This doesn't necessarily indicate the relative importance of the direct and indirect effects of the traits (Alwin et al., 1975; Lande et al., 1983). Because of this factor, the current study also applied path coefficient analysis. Interestingly, the study revealed a prominent positive direct effect of LCY on SCY. This implies that enhancing LCY would lead to a direct selection process that results in an increase in SCY. These outcomes align with findings from recent studies (Rasheed et al., 2020; Mahdy et al., 2021). In addition, this study found that NBP had the highest positive indirect contribution to SCY through LCY, followed by SI through LI, LP via LI, and LP through LCY.

These results were in alignment with previous research (Pujer et al., 2014). These results emphasize the importance of these traits and their indirect role in improving SCY and underscore the significance of considering multiple traits, such as LCY and NBP, when making selections to improve cotton yield.

The utilization of PCA has proven to be a valuable multivariate technique for identifying superior genotypes, inbred lines, and hybrids in cotton (Malik et al., 2013; Munir et al., 2020; Rathinavel, 2018). The results of the biplot in this study provided a clear-cut grouping of hybrids for the multi-trait selection procedure. In essence, the biplot analysis revealed that genotypes placed close together exhibited similar characteristics, while genotypes that were farther apart demonstrated distinct performance variations. The results obtained from the PCA in this study demonstrate that the eighteen F_1 crosses were located in closer proximity to most of the yield, yield components, and fiber traits vectors. This indicates the potential for SCA among the plant materials used in the study (Zafar et al., 2021).

Conclusions

The study revealed substantial genetic variability among parental lines, indicating high heterotic potential in hybrids. Non-additive gene action was the predominant gene action influencing lint yield, seed cotton yield, seed index, the number of bolls per plant, and fiber micronaire, while the inheritance of other traits was mainly controlled by additive genes. Analyzing genetic mechanisms influencing hybrid vigor and fiber traits could provide more targeted breeding efforts. Among the F_1 hybrids, [(G.90×Aust)×G.86] had the highest mean performance for SCY, whereas (Uzbekistan 1×G.97) had the maximum value of LCY, which is higher than both parents G.97 and Uzbekistan 1 for such trait. For other traits, the following F_1 hybrids exhibited notable mean performance: (TNB×G.97) for SI, [(G.90×Aust)×G.94] for BW, (G.96×G.97) for NBP, (Uzbekistan 1×G.94) for LP and LI, (TNB×G.94) for NSB, (Aust 12×G.94) for FS, (Uzbekistan 1×G.97) for FL, [(G.90×Aust)×G.86] for MIC, and (Uzbekistan 1×G.97) for FUR. These findings provide valuable insights into the genetic potential of different genotypes and hybrids for various economically important traits, which can guide future breeding strategies and hybrid development in cotton. Further evaluation of top-performing hybrids across diverse environments is warranted to confirm the performance and suitability for commercial cultivation. The use of molecular tools can be applied to further elucidating genetic mechanisms influencing heterosis and key fiber traits which would enable more targeted cotton breeding.

Abbreviations

ANOVA	Analysis of variance
BW	Boll weight
FL	Fiber length
FS	Fiber strength
FUR	Fiber uniformity ratio
GCA	General combining ability
LCY	Lint cotton yield
LI	Lint index
LP	Lint percentage
MIC	Micronaire
NBP	Number of bolls per plant
NSB	Number of seeds per boll
PCA	Principal component analysis
RCBD	Randomized complete block design
SCA	Specific combining ability
SCY	Seed cotton yield
SI	Seed index

Authors' contributions

Abdelghany MA performed experiments, analyzed data, and wrote the manuscript. Elbana AAA assisted in planning experiments. Lamlom SF did grammar editing and proofread of manuscript. El-Sorady GA provided cotton germplasm. Salama EAA assisted during hybridizing and data collection. Ren H provided the experiment place at his station. Shaibu AS managed the crop husbandry. Yehia W provided cotton germplasm, assisted in planning of experiments, and provided the experiment place at his station. The authors read and approved the final manuscript.

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Availability of data and materials

All the data are available in the manuscript and with Correspondence authors.

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Ethics approval and consent to participate

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Consent for publication

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The authors declare that they have no competing interests.

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