

Genetic Potential for Seed Cotton Yield and Fiber Quality Improvement through Heterosis and Combining Ability Analysis in Cotton (*Gossypium hirsutum* L.)

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Abstract

Background:

Improvement of seed cotton yield and fiber quality in upland cotton (*Gossypium hirsutum* L.) requires identification of genetically diverse parents and superior cross combinations. The present study was undertaken to assess genetic variability, combining ability, heterosis and trait associations using a line × tester mating design to facilitate effective breeding strategies for yield and fiber quality enhancement.

Results:

Forty-five F_1 hybrids developed from nine lines and five testers were evaluated along with their fourteen parents in a randomized block design during *kharif* 2022–23. Analysis of variance revealed significant variability among genotypes for most traits. Mahalanobis D^2 analysis grouped the parents into six clusters, indicating substantial genetic divergence. Combining ability analysis showed the predominance of non-additive gene action ($\sigma^2_{sca} > \sigma^2_{gca}$) for most yield and fiber traits. Lines GJHV-548, GTHV-13/32 and GBHV-187, and testers GJHV-503 and GJHV-517 were identified as superior general combiners. Crosses such as GTHV-13/32 × GJHV-585, RAH-1047 × GJHV-517 and GJHV-522 × GJHV-503 exhibited high specific combining ability effects and significant mid-parent heterosis for seed cotton yield and related traits. Correlation and path analysis indicated that number of bolls per plant exerted the highest positive direct effect on seed cotton yield, followed by number of sympodia and boll weight.

Conclusions:

The predominance of non-additive gene action and the presence of high heterosis in specific crosses highlight the effectiveness of heterosis breeding in cotton. Selection based on boll number per plant, along with exploitation of genetically diverse superior combiners, can accelerate the development of high-yielding cotton hybrids with improved fiber quality.

Background

Cotton is one of the major fiber crops worldwide, and has extensive phenotypic diversity among the 50 representative species (Wendel and Cronn, 2003). Among these species, upland cotton (*Gossypium hirsutum* L.) is the leading fibre-producing crop and is grown in more than 80 countries worldwide. Currently, *G. hirsutum* is responsible for 95% of the annual cotton production in the world (Chen et al., 2007). Cotton plays a pivotal role in the global economy, particularly in developing countries, where it sustains millions of smallholder farmers and provides employment to nearly 150 million people worldwide. In addition to being a critical raw material for the textile industry, it also serves as a major source of rural income and economic stability (Jabran et al., 2019). India holds the distinction of being a pioneer in the world for the development of cotton hybrids for commercial cultivation. The release of the world's first commercial intra-hirsutum hybrid H-4 (Patel, 1971) and inter-specific hybrid, Varalaxmi (Katarki, 1971) during the seventies was an important milestone in the history of cotton improvement not only in India but also in the world. Since then, several hundreds of hybrids have been developed and released for cultivation. Therefore, development of superior quality cotton varieties is one of the most effective approaches to meet the growing demand of the textile sector.

The success of any plant breeding program critically depends on the selection of appropriate parental lines for generating new crosses. Effective parent selection necessitates a comprehensive understanding of combining ability, gene action, and the genetic variability of economically important traits during the early stages of the breeding process (Abdelghany et al., 2022; El-Sorady et al., 2022). Knowledge of gene action is particularly important for developing cultivars with higher yield potential and superior quality (Fasahat et al., 2016). In this context, combining ability studies serve as a fundamental tool in plant breeding, enabling the identification of parental lines capable of producing high-yielding and stress-resilient hybrids. The line × tester mating design is widely employed to assess both general combining ability (GCA) and specific combining ability (SCA), providing insights into the relative contributions of additive and non-additive gene effects for traits of economic importance (Singh & Chaudhary, 2021). Such analyses not only facilitate the efficient utilization of genetic resources but also support the selection of superior parental combinations and their hybrids, thereby contributing to the development of improved crop varieties with enhanced yield and adaptability. Hence, a line × tester mating design strategy was used in current study to assess the combining ability and performance of cotton in terms of seed cotton 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 experiment was conducted at Cotton Research Station, Junagadh Agricultural University, Junagadh, Gujarat, India. Forty-five hybrids were generated during *kharif* 2021-22 using nine lines as females and five testers as males through line x tester mating scheme. Thus, the 45 crosses and their 14 parents formed the experimental material for the present study. The list and source of parental materials used in the present study are given in Table 1. These genotypes were evaluated using Randomized Block Design with three replications during *kharif* 2022-23. Each entry was accommodated in single row of 6.3 m. length spaced at 120 cm apart with plant-to-plant spacing of 45 cm. Recommended agronomic practices and plant protection measures were adopted in a timely manner to raise the healthy crop.

Table 1
The list and source of fourteen parental genotypes under study

Sr. No.	Genotypes	Source
Female Parents (Lines)		
1.	GJHV-522	Genotype from CRS, JAU, Junagadh, India
2.	GJHV-548	Genotype from CRS, JAU, Junagadh, India
3.	GTHV-13/32	Genotype from CRS, SDAU, Talod, India
4.	GBHV-187	Genotype from RCRS, NAU, Bharuch, India
5.	GISV-360	Genotype from MCRS, NAU, Surat, India
6.	GISV-365	Genotype from MCRS, NAU, Surat, India
7.	TCH-1828	Genotype from TNAU, Coimbatore
8.	SIMA-5	Genotype from SIMA, CDRA, Coimbatore, India
9.	RAH-1047	Genotype from MARS, UAS, Raichur, India
Male Parents (Testers)		
1.	GJHV-503	Genotype from CRS, JAU, Junagadh, India
2.	GJHV-517	Genotype from CRS, JAU, Junagadh, India
3.	GJHV-534	Genotype from CRS, JAU, Junagadh, India
4.	GJHV-585	Genotype from CRS, JAU, Junagadh, India
5.	G.Cot-38	Released variety from CRS, JAU, Junagadh, India

Sampling and data recording

Five competitive plants from each entry in each replication were randomly selected before flowering and tagged for the purpose of recording observations on different characters and their average values were used in the statistical analysis. The observations were recorded for 12 characters viz., PH-plant height (cm), NM-number of monopodia per plant, NS-number of sympodia per plant, NB-number of bolls per plant, BW-boll weight (g), SCY-seed cotton yield per plant (g), GP-ginning percentage (%), SI-seed index (g), LI-lint index (g), SL-span length (mm), FS-fiber strength (g/tex) and FF-fiber fineness (mv). For the determination of fiber quality traits, lint samples from each plot were collected to estimate SL, FS and FF at Cotton Quality Evaluation Laboratory, Cotton Research Station, Junagadh Agricultural University, Junagadh, Gujarat, India.

Statistical analysis

All the recorded data were subjected to analysis of variance (Gomez *et al.*, 1984). The line $\times$ tester mating design was used to estimate the GCA effects of the parents and SCA of the crosses as described by Kempthorne (1958). Clustering of the genetic material using Tocher's method and Mahalanobis D^2 distance were performed to dissect the genetic relationship among the fourteen parents, and then used to construct the cluster diagram. To explore the relationship among all studied traits, Pearson correlation coefficients were estimated. Path coefficients analysis was used to partition the correlation coefficients among seed cotton yield and other trait components into direct and indirect effects. All statistical analyses were performed using the online statistical platform GRAPES (Gopinath, 2020) and Agri Analyze (Popat, 2024).

Results

Dissecting the relationship among parent genotypes (lines and testers)

The genetic relationship among fourteen parental genotypes (nine lines and five testers) was assessed using Mahalanobis D^2 statistics (Table 2) and Tocher's clustering method (Fig. 1). The divergence analysis grouped the parents into six distinct clusters (Table 3). Cluster I comprised the maximum number of parents (five), namely GJHV-517, GJHV-522, GJHV-534, RAH-1047, and TCH-1828, indicating close genetic similarity among these genotypes. Cluster II contained four parents (G.Cot-38, GISV-365, GJHV-503, and SIMA-5), while Cluster III consisted of two parents, GBHV-187 and GISV-360. In contrast, Clusters IV, V, and VI were solitary clusters, each represented by a single parent, namely GJHV-548, GTHV-13/32, and GJHV-585, respectively, reflecting their distinct genetic constitution. The formation of both multi-genotype and solitary clusters suggests the presence of considerable genetic diversity among the parental material.

Table 2
Mahalanobis D² distance matrix among fourteen parental genotypes (nine lines and five testers)

Genetic material	GJHV-522	GJHV-548	GTHV-13/32	GBHV-187	GISV-360	GISV-365	TCH-1828	SIMA-5	RAH-1047	GJHV-503	GJHV-517	G.Cot-38
GJHV-548	12523.75											
GTHV-13/32	4354.723	3698.261										
GBHV-187	5527.355	2217.878	1750.12									
GISV-360	7689.324	3117.893	4774.293	893.3844								
GISV-365	3016.988	25124.04	12207.61	13653.93	15700.23							
TCH-1828	1065.429	7025.033	2141.722	2602.675	4487.301	6777.002						
SIMA-5	1461.567	20078.59	8174.924	10104.58	12895.25	591.2639	4323.076					
RAH-1047	529.8153	10990.66	4516.874	4013.895	5180.938	3423.38	977.485	2113.226				
GJHV-503	3670.481	28766.64	13607.68	17132.2	20698	1010.134	7991.092	1118.22	5339.511			
GJHV-517	1258.372	6173.257	1250.468	2070.396	4141.218	6988.901	195.0986	4360.874	1254.467	8417.244		
GJHV-534	3954.551	2870.491	1263.616	1448.726	3186.599	13198.64	1273.534	9455.198	3777.784	14753.87	1108.676	
GJHV-585	8373.715	34914.8	22233.91	20920.11	20739.67	2582.697	12845.48	5183.189	7476.813	5045.861	13908.55	2113.226
G.Cot-38	2924.921	24159.25	10894.5	13151.17	15892.76	200.8529	6461.248	351.5517	3574.601	850.7575	6472.368	1108.676

Table 3
Distribution of parental genotypes into different clusters based on genetic divergence

Cluster	Total Genotypes	Parental Genotypes
Cluster 1	5	GJHV-517, GJHV-522, GJHV-534, RAH-1047, TCH-1828
Cluster 2	4	G.Cot-38, GISV-365, GJHV-503, SIMA-5
Cluster 3	2	GBHV-187, GISV-360
Cluster 4	1	GJHV-548
Cluster 5	1	GTHV-13/32
Cluster 6	1	GJHV-585

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

The ANOVA for line × tester analysis revealed significant differences among hybrids for most traits, indicating substantial genetic variability (Table 4). Mean squares due to hybrids were highly significant for all the traits except PH and LI. Lines showed highly significant effects for PH, NM, NB, BW, SCY, GP, SI, SL, FS and FF, while testers exhibited significant variation for NM, NB, BW, SCY, SI, LI, SL, FS and FF. The L × T interaction was significant for most traits, particularly NM, NS, NB, BW, SCY, SI, SL, FS and FF, suggesting differential cross performance. Variance component analysis indicated that σ^2_{sca} exceeded σ^2_{gca} for most traits, and the $\sigma^2_{gca}/\sigma^2_{sca}$ ratio was less than unity, confirming the predominance of non-additive gene action. The per cent contribution analysis showed a higher contribution of lines for PH, NB, BW, SCY, SL, FS and FF, whereas L × T interaction contributed substantially to NS, GP, SI and LI.

GCA effects

The estimates of general combining ability (gca) revealed considerable variation among lines and testers for yield, its component traits, and fiber quality characters (Table 5). For plant height (PH), three lines, viz., GJHV-548 (6.46), GTHV-13/32 (6.46) and GBHV-187 (6.46), along with the tester GJHV-585 (3.71), exhibited significant and positive gca effects, indicating their potential as good general combiners for increased plant height. For number of monopodia (NM), two lines, TCH-1828 (0.34) and RAH-1047 (0.20), and two testers, GJHV-503 (0.56) and GJHV-517 (0.13), recorded significant and positive gca effects. For number of sympodia (NS), only one line, GBHV-187 (0.66), and one tester, G.Cot-38 (0.47), showed significant and positive gca effects. Three lines, GJHV-548 (8.33), GTHV-13/32 (3.13) and RAH-1047 (4.40), and one tester, GJHV-503 (6.22), exhibited significant and positive gca effects for number of bolls per plant (NB). For boll weight (BW), two lines, GTHV-13/32 (0.20) and GISV-360 (0.37), and one tester, GJHV-517 (0.19), showed favorable gca effects. Notably,

four lines, GJHV-548 (13.93), GTHV-13/32 (20.40), GBHV-187 (9.60) and RAH-1047 (12.53), along with the tester GJHV-503 (15.60), exhibited significant and positive gca effects for seed cotton yield (SCY). For ginning percentage (GP), only one line, GISV-365 (0.62), emerged as a good general combiner. For seed index (SI), one line, GBHV-187 (0.48), and one tester, GJHV-517 (0.63), recorded significant positive gca effects, whereas for lint index (LI), only the tester GJHV-517 (0.43) exhibited a significant and positive gca effect. With respect to fiber quality traits, four lines, viz., GJHV-548 (1.48), GTHV-13/32 (0.73), TCH-1828 (0.61) and SIMA-5 (0.96), and two testers, GJHV-517 (0.94) and GJHV-534 (0.93), showed significant and positive gca effects for staple length (SL). For fiber strength (FS), three lines, GJHV-548 (1.48), GBHV-187 (1.54) and SIMA-5 (0.56), and one tester, GJHV-517 (0.99), were identified as good general combiners. Desirable significant and negative gca effects for fiber fineness (FF) were recorded in five lines, GJHV-548 (-0.18), GBHV-187 (-0.16), TCH-1828 (-0.10), SIMA-5 (-0.50) and RAH-1047 (-0.24), and two testers, GJHV-534 (-0.07) and G.Cot-38 (-0.10).

SCA effects

The analysis of specific combining ability (SCA) effects revealed significant variability among the crosses for yield and fiber quality traits, indicating the importance of non-additive gene action (Table 6). For yield components, TCH-1828 × GJHV-517 (0.69) exhibited the highest positive SCA effect for number of monopodia (NM), while GJHV-522 × GJHV-503 (1.83) showed maximum SCA for number of sympodia (NS). A remarkably high SCA effect for number of bolls per plant (NB) was recorded in RAH-1047 × GJHV-517 (11.64), followed by SIMA-5 × G.Cot-38 (7.24) and GTHV-13/32 × GJHV-585 (6.76). Positive SCA effects for boll weight (BW) were observed in SIMA-5 × GJHV-517 (0.32) and GISV-365 × G.Cot-38 (0.28). For seed cotton yield (SCY), the cross GTHV-13/32 × GJHV-585 (30.60) exhibited the highest positive SCA effect, followed by RAH-1047 × GJHV-517 (20.91), GBHV-187 × GJHV-585 (19.73), and TCH-1828 × GJHV-503 (18.87). Regarding fiber traits, positive SCA effects for ginning percentage (GP) were noted in TCH-1828 × GJHV-503 (1.73), while RAH-1047 × GJHV-503 showed maximum SCA for staple length (2.06) and fiber strength (1.59). Desirable negative SCA effects for fiber fineness (FF) were observed in RAH-1047 × GJHV-517 (-0.66) and SIMA-5 × GJHV-534 (-0.43).

The mid-parent heterosis

The mid-parent heterosis analysis revealed considerable variation among crosses for yield, yield components and fiber quality traits (Table 7). SCY exhibited high and significant positive heterosis in crosses such as GJHV-522 × GJHV-503 (67.19%), GTHV-13/32 × GJHV-585 (65.35%), GTHV-13/32 × GJHV-503 (55.07%), GTHV-13/32 × GJHV-534 (50.56%) and GISV-365 × GJHV-503 (46.11%), accompanied by significant heterosis for NB (up to 61.09%) and BW (up to 29.47%). Positive heterosis for ginning percentage was recorded in TCH-1828 × GJHV-517 (12.09%) and SIMA-5 × GJHV-585 (8.26%). For fiber traits, several crosses showed significant improvement in FS, notably GBHV-187 × GJHV-503 (27.41%) and GTHV-13/32 × GJHV-517 (12.66%). Importantly, desirable negative heterosis for FF was observed in crosses such as GBHV-187 × G.Cot-38 (-11.97%), GISV-360 × G.Cot-38 (-8.97%), RAH-1047 × GJHV-517 (-15.15%), RAH-1047 × GJHV-585 (-9.09%) and RAH-1047 × G.Cot-38 (-6.16%), indicating improvement towards finer fiber.

Correlation analysis

Correlation analysis (Fig. 2) revealed that SCY was strongly and positively associated with NB (0.888**), followed by PH (0.549**), NS (0.405**), FS (0.301*) and NM (0.291*), indicating the importance of these traits in yield improvement. PH showed significant positive correlations with NS (0.616**), SL (0.422**), FS (0.49**) and SI (0.372**). NB exhibited a significant negative association with BW (-0.399**) and SI (-0.262*). Among fiber quality traits, SL was strongly correlated with FS (0.658**), while LI showed strong positive association with SI (0.887**), BW (0.669**) and GP (0.539**). FF was positively correlated with BW (0.384**), LI (0.566**) and SCY (0.273*), while its associations with SL (-0.097) and FS (-0.006) were negative but non-significant.

Table 4
Analysis of variance and variance components of combining ability and per cent contribution in cotton

Source	DF	PH	NM	NS	NB	BW	SCY	GP	SI	LI	SL	FS	F
Replications	2	1911.12**	0.01	10.25**	10.69	0.84**	707.47	1.76	0.001	0.08	0.00	0.01	C
Hybrids	44	190.42	0.66**	3.40**	175.97**	0.21**	1531.72**	2.23*	1.86**	0.86	6.11**	6.06**	C
Lines	8	633.42**	0.51**	2.69	418.42***+	0.56***+	3637***+	4.70**	1.90*	1.05	14.94***+	16.47***+	1
Testers	4	246.79	3.48***+	3.54	416.72***+	0.36**	2720.1***	0.89	6.21***+	2.65**	14.03***+	10.87***+	C
Lines x testers	32	72.62	0.34**	3.56**	85.26**	0.10**	856.85**	1.77	1.31*	0.58	2.91**	2.86**	C
Error	88	148.24	0.04	1.65	27.98	0.05	260.29	1.25	0.81	0.6	0.73	0.96	C
Variance components													
σ^2_l		37.39	0.01	-0.06	22.21	0.03	185.34	0.20	0.04	0.03	0.80	0.91	C
σ^2_t		6.45	0.12	0.001	12.28	0.01	69.01	-0.03	0.18	0.08	0.41	0.30	C
σ^2_{lt}		-25.21	0.10	0.64	19.10	0.02	198.85	0.17	0.17	-0.01	0.73	0.64	C
σ^2_{gca}		17.50	0.08	-0.02	15.82	0.02	110.56	0.05	0.13	0.06	0.55	0.51	C
σ^2_{sca}		-25.21	0.10	0.64	19.10	0.02	198.85	0.17	0.17	-0.01	0.73	0.64	C
$\sigma^2_{gca}/\sigma^2_{sca}$		-0.69	0.77	-0.03	0.83	0.92	0.56	0.28	0.77	-8.74	0.76	0.81	C
Per cent contribution													
Lines		60.48	14.17	14.37	43.23	48.43	43.17	38.44	18.49	22.26	44.44	49.37	5
Testers		11.78	47.99	9.47	21.53	15.81	16.14	3.66	30.29	28.16	20.88	16.29	4
Lines x Testers		27.74	37.83	76.15	35.24	35.76	40.68	57.91	51.22	49.57	34.68	34.34	3
*, ** Significant at 5% and 1% levels of probability when tested against error mean square, respectively													

+, ++ Significant at 5% and 1% levels of probability when tested against mean square due to line x tester interaction, respectively

Table 5
General combining ability effect for lines and testers in cotton

Parents	PH	NM	NS	NB	BW	SCY	GP	SI	LI	SL	FS	FF
Lines												
GJHV-522	-11.61**	-0.09	-0.26	1.93	-0.13*	3.47	0.13	0.06	0.08	-0.68**	-1.2**	0.41**
GJHV-548	6.46*	0.07	0.46	8.33**	-0.29**	13.93**	0.07	-0.30	-0.17	1.48**	1.48**	-0.18**
GTHV-13/32	6.46*	-0.16**	0.14	3.13*	0.20**	20.40**	-0.04	0.10	0.06	0.73**	-0.11	0.17**
GBHV-187	6.46*	0.08	0.66*	1.40	0.04	9.60*	0.06	0.48*	0.30	0.06	1.54**	-0.16**
GISV-360	4.19	-0.21**	-0.05	-8.07**	0.37**	-15.47**	0.42	0.39	0.34	-1.02**	-1.45**	0.16**
GISV-365	-6.47*	-0.16**	-0.54	-1.80	0.02	-5.93	0.62*	0.17	0.26	-0.74**	-0.16	0.43**
TCH-1828	0.06	0.34**	-0.04	-2.80*	-0.11	-14.20**	-0.99**	-0.20	-0.36	0.61**	-0.08	-0.10**
SIMA-5	-4.01	-0.08	-0.59	-6.53**	-0.04	-24.33**	-0.81**	-0.02	-0.23	0.96**	0.56*	-0.50**
RAH-1047	-1.54	0.20**	0.23	4.40**	-0.06	12.53**	0.55	-0.68**	-0.26	-1.38**	-0.57*	-0.24**
SE_(gi)	3.14	0.05	0.33	1.37	0.06	4.17	0.29	0.23	0.20	0.22	0.25	0.04
Testers												
GJHV-503	0.38	0.56**	-0.19	6.22**	-0.10**	15.6**	0.17	-0.44**	-0.23	-0.28*	-0.01	0.03
GJHV-517	1.38	0.13**	0.19	-3.7**	0.19**	-5.51*	0.19	0.63**	0.43**	0.94**	0.99**	-0.01
GJHV-534	-1.03	-0.35**	-0.48*	-2.93**	0.01	-9.18**	-0.02	0.09	0.05	0.39**	-0.28	-0.07**
GJHV-585	3.71*	-0.18**	0.02	0.78	-0.01	4.27	-0.09	0.24	0.13	-0.07	0.04	0.15**
G.Cot-38	-4.44*	-0.16**	0.47*	-0.37	-0.09**	-5.18*	-0.25	-0.52**	-0.37**	-0.98**	-0.74**	-0.10**
SE_(gj)	2.34	0.04	0.25	1.02	0.04	3.10	0.21	0.17	0.15	0.16	0.19	0.03
*, ** Significant at 5% and 1% levels of probability, respectively												

Table 6
Specific combining ability effect for hybrids in cotton

Sr. No.	Crosses	PH	NM	NS	NB	BW	SCY	GP	SI	LI	SL	FS	FF
1	GJHV-522 x GJHV-503	3.09	0.08	1.83*	6.51*	-0.14	15.2	0.24	-1.22*	-0.66	-2.11**	-1.32*	0.09
2	GJHV-522 x GJHV-517	4.42	-0.35**	1.48*	-10.56**	0.11	-30.02**	-0.18	-0.39	-0.28	0.41	1.02	-0.08
3	GJHV-522 x GJHV-534	-5.50	0.19	-2.14**	3.66	-0.01	6.64	0.42	0.88	0.63	0.96	-0.25	-0.01
4	GJHV-522 x GJHV-585	3.09	0.22*	-0.78	0.62	-0.09	1.20	0.00	0.10	0.05	-0.32	0.84	0.07
5	GJHV-522 x G.Cot-38	-5.10	-0.13	-0.39	-0.23	0.12	6.98	-0.48	0.63	0.25	1.06*	-0.28	-0.08
6	GJHV-548 x GJHV-503	-2.98	-0.02	-0.29	-6.56*	-0.11	-27.27**	-0.10	0.07	0.06	-1.17*	0.67	-0.08
7	GJHV-548 x GJHV-517	1.69	-0.51**	0.67	-1.30	0.07	2.84	-0.32	0.74	0.37	0.81	0.07	0.52**
8	GJHV-548 x GJHV-534	-1.90	0.63**	0.21	0.59	-0.08	-2.16	0.28	-0.93	-0.49	0.60	0.54	-0.42**
9	GJHV-548 x GJHV-585	0.02	-0.20	-1.39	3.56	0.07	12.40	-0.58	0.73	0.30	0.46	-0.31	0.00
10	GJHV-548 x G.Cot-38	3.17	0.11	0.79	3.70	0.05	14.18	0.71	-0.61	-0.23	-0.70	-0.96	-0.02
11	GTHV-13/32 x GJHV-503	-10.64	0.34**	-1.50*	-5.36	0.06	-21.07*	-0.63	-0.10	-0.20	0.32	-0.60	0.13
12	GTHV-13/32 x GJHV-517	-0.64	0.38**	-0.48	0.24	-0.16	-7.29	0.89	0.33	0.44	0.00	0.53	-0.04
13	GTHV-13/32 x GJHV-534	5.76	-0.95**	0.80	-1.87	0.16	5.38	0.59	-0.13	0.08	-0.81	0.30	0.13
14	GTHV-13/32 x GJHV-585	10.36	0.09	1.30	6.76*	0.11	30.60**	-0.97	0.42	-0.03	0.41	-0.45	-0.09
15	GTHV-13/32 x G.Cot-38	-4.83	0.14	-0.12	0.24	-0.18	-7.62	0.12	-0.52	-0.29	0.09	0.23	-0.14
16	GBHV-187 x GJHV-503	5.36	0.10	0.21	-3.29	0.16	-3.60	0.01	-0.81	-0.52	0.78	1.51**	-0.34**
17	GBHV-187 x GJHV-517	3.36	-0.06	-0.40	-3.03	0.00	-8.82	-0.65	0.63	0.19	-0.73	-2.02**	-0.04
18	GBHV-187 x GJHV-534	-2.57	-0.12	0.64	-3.81	-0.08	-15.82	0.39	0.66	0.54	-0.38	0.34	0.26**
19	GBHV-187 x GJHV-585	-6.31	0.25*	-1.06	5.49	0.01	19.73*	1.06	-0.28	0.09	-0.03	-0.57	0.34**
20	GBHV-187 x G.Cot-38	0.17	-0.17	0.62	4.64	-0.08	8.51	-0.81	-0.19	-0.31	0.36	0.74	-0.21*
21	GISV-360 x GJHV-503	5.96	-0.20	0.49	4.18	-0.07	15.47	-0.25	0.24	0.08	-0.30	0.03	-0.12
22	GISV-360 x GJHV-517	-2.04	-0.23*	-0.92	1.10	0.18	8.58	-0.47	0.48	0.16	1.65**	0.66	0.08
23	GISV-360 x GJHV-534	-1.97	0.24*	-0.65	-0.34	-0.11	-3.09	0.04	-0.82	-0.5	-1.63**	-1.14*	-0.06
24	GISV-360 x GJHV-585	-2.38	0.08	0.98	-3.71	0.01	-18.53*	-0.19	-0.36	-0.27	-0.01	0.68	0.23**
25	GISV-360 x G.Cot-38	0.44	0.12	0.10	-1.23	-0.01	-2.42	0.87	0.46	0.53	0.30	-0.24	-0.13
26	GISV-365 x GJHV-503	4.96	-0.32**	1.68*	-1.42	0.15	-1.73	0.02	0.16	0.10	-0.28	-1.66**	0.07
27	GISV-365 x GJHV-517	-4.38	0.05	-1.00	2.84	-0.07	8.71	-0.20	-0.50	-0.33	-0.67	1.01	-0.10
*, ** Significant at 5% and 1% levels of probability, respectively													

Sr. No.	Crosses	PH	NM	NS	NB	BW	SCY	GP	SI	LI	SL	FS	FF
28	GISV-365 x GJHV-534	4.36	0.12	0.51	2.73	-0.32*	-4.29	-0.06	0.47	0.25	-0.15	0.44	0.07
29	GISV-365 x GJHV-585	-5.38	0.16	-1.06	-5.31	-0.03	-16.07	0.08	-0.18	-0.09	0.68	0.03	-0.25**
30	GISV-365 x G.Cot-38	0.44	0.00	-0.14	1.17	0.28*	13.38	0.17	0.05	0.07	0.42	0.18	0.20*
31	TCH-1828 x GJHV-503	1.76	-0.15	-1.56*	5.24	0.07	18.87*	1.73**	0.23	0.51	0.34	0.50	-0.20*
32	TCH-1828 x GJHV-517	4.09	0.69**	0.96	-0.16	-0.02	-0.02	1.24	0.27	0.49	0.52	-0.04	0.17*
33	TCH-1828 x GJHV-534	-3.84	-0.04	-0.76	0.06	0.26*	8.64	-0.69	0.27	-0.04	0.87	0.66	0.00
34	TCH-1828 x GJHV-585	-1.91	-0.34**	1.14	2.02	-0.21	-2.47	-1.42*	-0.51	-0.61	-0.57	0.15	-0.31**
35	TCH-1828 x G.Cot-38	-0.10	-0.16	0.22	-7.16*	-0.10	-25.02*	-0.86	-0.25	-0.35	-1.16*	-1.27*	0.34**
36	SIMA-5 x GJHV-503	-1.18	0.20	-0.17	1.31	-0.27*	-5.00	-0.53	0.52	0.18	0.38	-0.71	0.31**
37	SIMA-5 x GJHV-517	-3.18	-0.37**	0.42	-0.76	0.32*	5.11	-0.18	-0.01	-0.07	-0.23	-0.71	0.14
38	SIMA-5 x GJHV-534	0.90	0.04	0.32	-4.54	0.13	-10.22	-0.78	-0.57	-0.53	0.12	-0.71	-0.43**
39	SIMA-5 x GJHV-585	-0.18	-0.06	-0.11	-3.24	0.05	-6.00	1.43*	0.22	0.49	-0.76	0.81	0.22*
40	SIMA-5 x G.Cot-38	3.64	0.19	-0.46	7.24*	-0.24	16.11	0.05	-0.16	-0.07	0.49	1.32*	-0.23**
41	RAH-1047 x GJHV-503	-6.31	-0.02	-0.69	-0.62	0.16	9.13	-0.48	0.91	0.45	2.06**	1.59**	0.14
42	RAH-1047 x GJHV-517	-3.31	0.42**	-0.74	11.64**	-0.43**	20.91*	-0.13	-1.55**	-0.97*	-1.76**	-0.51	-0.66**
43	RAH-1047 x GJHV-534	4.76	-0.11	1.07	3.53	0.05	14.91	-0.20	0.18	0.07	0.43	-0.18	0.47**
44	RAH-1047 x GJHV-585	2.69	-0.20	0.97	-6.18*	0.07	-20.87*	0.58	-0.13	0.06	0.15	-1.19*	-0.21*
45	RAH-1047 x G.Cot-38	2.17	-0.09	-0.61	-8.36**	0.15	-24.09*	0.23	0.60	0.39	-0.87	0.29	0.27**
Significant and desirable crosses		0	8	3	4	3	4	2	0	0	3	3	10
SE(S_{ij})±		7.03	0.11	0.74	3.05	0.13	9.31	0.64	0.52	0.45	0.49	0.56	0.09
*, ** Significant at 5% and 1% levels of probability, respectively													

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

Crosses	PH	NM	NS	NB	BW	SCY	GP	SI	LI	SL	FS	FF
GJHV-522 x GJHV-503	18.72 *	53.85 **	20.24 **	61.09 **	2.62	67.19 **	0.67	-2.33	-0.65	-2.57	3.05	23.51 **
GJHV-522 x GJHV-517	13.25	3.03	11.18 *	-18.49	20.63 **	4.45	4.57 *	11.59	20.52	5.85 *	10.50 **	17.32 **
GJHV-522 x GJHV-534	0.31	63.64 **	-7.50	19.83 *	12.90 *	33.52 **	4.61 *	22.22 **	31.37 **	6.38 **	-2.43	12.45 **
GJHV-522 x GJHV-585	5.08	147.06 **	-2.50	9.92	11.48 *	26.71 **	2.52	13.71	18.85	-3.09	3.68	14.49 **
GJHV-522 x G.Cot-38	1.13	-3.03	7.37	12.65	12.77 *	30.80 **	-2.48	13.86	9.26	0.25	-0.28	3.55
GJHV-548 x GJHV-503	17.58 *	10.71	6.96	17.47 *	-4.08	14.62	-0.66	6.90	6.33	7.08 **	14.17 **	11.39 **
GJHV-548 x GJHV-517	15.55 *	-32.00 **	5.24	0.70	11.34 *	15.53 *	3.72	18.21 **	25.88 *	12.83 **	11.40 **	24.17 **
GJHV-548 x GJHV-534	9.17	38.46 **	2.09	6.67	2.62	11.34	3.77	-3.28	2.56	10.57 **	4.35 *	-5.18 *
GJHV-548 x GJHV-585	7.67	0.00	-6.78	10.97	8.51	19.92 **	0.50	14.95 *	16.61	5.22 *	4.21	5.34 *
GJHV-548 x G.Cot-38	14.29	-12.00	10.85 *	15.36 *	2.59	20.39 **	0.27	-5.54	-6.06	-0.54	1.94	-2.99
GTHV-13/32 x GJHV-503	16.99 *	20.00 **	3.14	53.68 **	5.56	55.07 **	-0.99	8.33	7.05	13.94 **	9.51 **	18.25 **
GTHV-13/32 x GJHV-517	19.70 *	10.20	1.96	28.50 *	8.41	40.36 **	8.35 **	16.96 *	33.33 **	10.82 **	12.66 **	12.16 **
GTHV-13/32 x GJHV-534	21.84 **	-100.00 **	6.98	25.24 *	13.74 **	50.56 **	5.83 **	8.66	19.48	6.19 **	2.97	9.77 **
GTHV-13/32 x GJHV-585	21.67 **	9.09	7.31	43.72 **	13.46 **	65.35 **	0.56	14.80 *	16.19	5.82 *	3.13	5.42 *
GTHV-13/32 x G.Cot-38	13.23	-22.45 **	8.79	33.64 **	0.47	36.20 **	-0.22	-1.09	-1.84	2.99	5.23 *	-3.18
GBHV-187 x GJHV-503	29.26 **	10.00	12.43 **	15.75	9.80 *	26.41 **	-0.66	5.75	4.10	19.35 **	27.41 **	-1.19
GBHV-187 x GJHV-517	20.59 **	-11.11	3.01	-12.92	14.85 **	3.42	2.50	25.36 **	31.21 **	10.98 **	13.58 **	3.91
GBHV-187 x GJHV-534	11.92	-25.58 **	6.86	-12.59	8.54	-2.24	3.76	22.63 **	30.99 **	10.77 **	12.26 **	4.87 *
GBHV-187 x GJHV-585	5.58	26.32 *	-2.80	6.44	12.24 *	20.29 **	4.69 *	12.43	21.25 *	6.89 **	12.00 **	7.19 **
GBHV-187 x G.Cot-38	15.19	-33.33 **	12.96 **	8.63	4.48	12.38	-4.06	7.75	0.91	6.68 **	16.60 **	-11.97 **
GISV-360 x GJHV-503	20.00 *	-12.73	13.28 **	44.62 **	-1.71	44.02 **	-1.31	2.52	0.00	3.43	0.61	4.44
GISV-360 x GJHV-517	7.35	-30.61 **	-0.24	-3.77	12.93 **	14.95	2.98	8.69	12.88	9.41 **	2.29	6.96 **
GISV-360 x GJHV-534	4.25	-10.53	-0.08	-5.21	2.18	4.85	2.77	-6.92	-3.85	-4.45	-11.24 **	-1.41
GISV-360 x GJHV-585	1.29	3.03	5.82	-14.41	6.19	-6.19	1.26	-2.23	-0.81	-3.04	-3.32	5.08 *
GISV-360 x G.Cot-38	6.80	-26.53 **	9.85 *	-4.11	1.30	3.76	0.39	0.49	1.05	-3.64	-6.57 **	-8.97 **
GISV-365 x GJHV-503	22.30 *	-17.86 *	16.68 **	44.44 **	5.71	46.11 **	0.84	11.91	13.04	7.32 **	-0.72	29.17 **
GISV-365 x GJHV-517	6.91	-12.00	-3.08	17.21	8.65	29.43 **	5.28 *	8.64	18.50	4.28	7.50 **	22.63 **
GISV-365 x GJHV-534	11.38	-17.95	2.99	19.63	-2.44	17.89	4.04	15.68 *	22.64 *	4.68 *	-2.45	19.69 **

Crosses	PH	NM	NS	NB	BW	SCY	GP	SI	LI	SL	FS	FF
GISV-365 x GJHV-585	-0.28	11.76	-6.12	-3.77	6.93	7.77	3.51	8.90	15.08	2.86	-1.35	12.45 **
GISV-365 x G.Cot-38	8.49	-32.00 **	6.07	18.02	11.11 *	29.63 **	0.00	5.65	5.36	0.19	-1.17	14.39 **
TCH-1828 x GJHV-503	15.71 *	8.20	-1.88	28.00 **	2.94	29.22 **	7.76 **	5.71	18.12	11.10 **	7.98 **	14.41 **
TCH-1828 x GJHV-517	11.81	41.82 **	4.17	-14.61	9.90 *	-3.85	12.09 **	10.15	32.20 **	10.04 **	5.65 *	21.55 **
TCH-1828 x GJHV-534	1.83	-4.55	-4.87	-12.03	14.57 **	1.04	4.61	6.85	14.29	9.85 **	-0.41	10.29 **
TCH-1828 x GJHV-585	0.79	-2.56	2.16	-7.90	1.02	-5.71	1.51	-1.04	1.66	-0.24	0.42	3.15
TCH-1828 x G.Cot-38	5.52	-20.00 **	5.65	-24.82 **	-0.50	-22.57 **	-0.85	-4.09	-6.41	-4.09	-4.39	10.00 **
SIMA-5 x GJHV-503	14.74	14.29	11.01 *	35.64 **	1.04	36.63 **	0.05	14.02	14.09	8.90 **	12.36 **	34.67 **
SIMA-5 x GJHV-517	6.85	-32.00 **	7.04	-7.76	29.47 **	19.07	6.32 **	12.01	23.39 *	5.13 *	11.55 **	26.73 **
SIMA-5 x GJHV-534	7.06	-17.95	5.52	-15.60	19.79 **	4.45	2.88	2.53	6.80	4.92 *	2.61	2.35
SIMA-5 x GJHV-585	3.16	0.00	1.44	-11.93	18.48 **	7.86	8.26 **	11.23	26.25 *	-2.74	10.29 **	20.54 **
SIMA-5 x G.Cot-38	10.20	-16.00	8.07	19.47	3.70	24.96 *	0.37	1.46	1.28	0.00	12.00 **	-0.87
RAH-1047 x GJHV-503	2.91	6.45	5.67	15.49	14.14 **	34.01 **	-0.88	19.11 *	18.00	13.15 **	17.89 **	4.98 *
RAH-1047 x GJHV-517	0.41	17.86 *	-0.62	13.62	5.82	22.20 **	5.04 *	-5.28	3.70	-3.23	9.61 **	-15.15 **
RAH-1047 x GJHV-534	3.93	-20.00 *	6.77	-0.67	17.20 **	17.60 *	3.25	10.81	17.57	3.50	1.76	4.73 *
RAH-1047 x GJHV-585	-0.26	-5.00	4.39	-19.38 **	19.13 **	-5.04	4.45 *	7.43	16.17	-2.34	1.01	-9.09 **
RAH-1047 x G.Cot-38	2.24	-25.00 **	4.88	-21.43 **	15.96 **	-8.84	-0.22	9.77	8.92	-7.96 **	5.84 *	-6.16 **
S.E.Difference	8.61	0.14	0.91	3.74	0.15	11.41	0.79	0.64	0.55	0.61	0.69	0.11

Path coefficient analysis

Path coefficient analysis (Fig. 3) revealed that NB exerted the highest positive direct effect on SCY (1.0888), confirming its major contribution to yield improvement. NS (0.0255), BW (0.4478), SI (0.0853), GP (0.021) and FS (0.0018) showed positive direct effects on SCY, although the magnitude varied. In contrast PH (-0.013), NM (-0.0258), LI (-0.0369), SL (-0.0103) and FF (-0.0221) exhibited negative direct effects. Despite negative direct effects, traits such as PH, NM and FF showed significant positive correlations with SCY due to strong positive indirect effects, mainly via NB and BW. The low residual effect (2.247%) indicated that 97.753% of the total variation in SCY was explained by the studied traits.

Discussion

In the current study, a line × tester mating design was utilized to create 45 F₁ hybrids by crossing nine lines with five testers. The clustering pattern of the fourteen parents revealed substantial genetic divergence, as indicated by their distribution into six clusters with varying cluster sizes. These findings were consistent with previous studies (such as Zafar et al., 2021). The grouping of several parents in Clusters I and II suggests a relatively narrow genetic base among these genotypes, whereas the presence of solitary clusters (IV, V, and VI) highlights the existence of genetically unique parents. Such genetically divergent parents are valuable in hybrid breeding programmes, as crosses between parents belonging to widely separated clusters are expected to result in higher heterosis and greater recombination potential. The clustering pattern did not correspond strictly to the classification of parents as lines or testers, indicating that genetic diversity was independent of their breeding role. Therefore, the genetically distant parents identified in solitary clusters, particularly those exhibiting superior performance for yield and fiber quality traits, can be effectively utilized as potential parents in future cotton improvement programmes (Akter et al., 2019; Geng et al., 2021; Geng et al., 2020; Vasconcelos et al., 2020).

The significant effects of lines, testers and L × T interactions indicate the involvement of both additive and non-additive gene actions in the inheritance of the studied traits. However, the predominance of σ^2_{sca} over σ^2_{gca} and $\sigma^2_{gca}/\sigma^2_{sca} < 1$ for most traits suggests that non-additive gene action is more important, particularly for NM, NB, BW, SCY, SI, SL, FS and FF. As observed in the present study, the predominant role of non-additive gene action in the inheritance of

seed cotton yield was reported by many workers including Gnanasekaran et al. (2019), Thiyagu et al. (2019), Bankar et al. (2020), Rani et al. (2020), Chakholoma et al. (2022) and Kanasagra et al. (2022). The significant $L \times T$ interaction highlights the importance of specific cross combinations for trait improvement. The higher per cent contribution of lines for PH, NB, BW, SCY, SL, FS and FF emphasizes the role of superior female parents, whereas the greater contribution of $L \times T$ interaction for NS, GP, SI and LI indicates the influence of dominance effects. Overall, the results suggest that heterosis breeding would be effective for improving yield and fiber quality traits in cotton.

The presence of significant and positive gca effects for most yield and fiber traits among a few selected parents suggests the predominance of additive gene action in the inheritance of these characters, indicating the effectiveness of selection-based breeding approaches. Lines such as GJHV-548, GTHV-13/32 and GBHV-187 consistently exhibited favorable gca effects for multiple yield-contributing traits, particularly SCY, NB, PH and important fiber properties, highlighting their broad genetic potential. Similarly, testers like GJHV-503 and GJHV-517 emerged as strong general combiners for yield and fiber quality traits, suggesting their suitability for use in hybridization programmes aimed at simultaneous improvement of productivity and fiber quality. The identification of parents with desirable negative gca effects for fiber fineness further emphasizes the scope for improving fiber quality without compromising yield. Overall, the results underscore the importance of selecting parents with superior general combining ability to develop high-yielding and quality cotton hybrids and varieties through judicious exploitation of additive genetic variance. The high gca effects for seed cotton yield and its different components traits were also reported by Rathava et al. (2018), Gnanasekaran et al. (2019) and Thiyagu et al. (2019).

The predominance of high and positive SCA effects for seed cotton yield and its component traits suggests that non-additive gene action, including dominance and epistatic effects, plays a major role in their inheritance. Crosses such as GTHV-13/32 $\times$ GJHV-585 and RAH-1047 $\times$ GJHV-517, which exhibited high SCA effects for seed cotton yield along with favourable effects for yield components, indicate the presence of complementary gene interactions and strong heterotic potential. Similarly, RAH-1047 $\times$ GJHV-503 demonstrated superiority for staple length and fiber strength, highlighting the possibility of simultaneous improvement of yield and fiber quality through appropriate cross combinations. The occurrence of desirable negative SCA effects for fiber fineness further supports the role of dominance effects in quality trait improvement. Overall, the results emphasize the utility of exploiting specific cross combinations in hybrid breeding programmes and suggest that selection in later segregating generations or heterosis breeding approaches may be effective strategies for genetic improvement in cotton. The significant SCA effects for seed cotton yield and different component traits were also recorded by several workers viz., Monicashree et al. (2017), Rathava et al. (2018), Gnanasekaran et al. (2019) and Chakholoma et al. (2022).

The occurrence of high and significant mid-parent heterosis for seed cotton yield and its contributing traits suggests the predominance of non-additive gene action, emphasizing the potential of heterosis breeding in cotton. Crosses such as GJHV-522 $\times$ GJHV-503 and GTHV-13/32 $\times$ GJHV-585 combined superior heterosis for SCY, NB and BW, reflecting effective parental complementation. The presence of significant positive heterosis for FS along with desirable negative heterosis for FF in several crosses indicates the possibility of simultaneous improvement of yield and fiber quality. Crosses involving G.Cot-38 and RAH-1047 contributed notably to reduced FF values, highlighting their role in developing finer fiber types. Overall, the identified crosses with high yield potential and improved fiber quality parameters can be effectively utilized in hybrid development and future cotton improvement programmes. High heterosis for seed cotton yield has been reported by Shashibhushan and Patel (2019), Vavadiya et al. (2019), Sudha Rani et al. (2020), Gnanasekaran and Thiyagu (2021) and Kanasagra et al. (2022).

The correlation patterns unearthed in this study correspond with those identified in earlier research. The strong positive association of SCY with NB, PH and NS indicates that improvement in boll number and plant architecture would effectively enhance cotton productivity ((Shavkiev et al., 2021 and Song et al., 2018;)). The negative correlation of NB with BW and SI suggests a compensatory relationship between boll number and boll size, emphasizing the need for balanced selection. Significant positive interrelationships among fiber quality traits such as SL, FS, SI and LI suggest simultaneous improvement of these traits is feasible. Although fiber fineness exhibited positive correlation with yield and certain yield components, its weak and negative association with SL and FS indicates scope for selecting genotypes with finer fiber without adversely affecting fiber strength and length. Overall, the correlation pattern highlights NB, PH and NS as key selection criteria for yield improvement, while coordinated selection among fiber quality traits can aid in developing high-yielding cotton genotypes with acceptable fiber quality.

Although correlation coefficients may be significant, they do not establish cause-and-effect relationships, as the association between two traits may be influenced by other variables. Correlation analysis also fails to distinguish between direct and indirect effects. Therefore, path coefficient analysis was used in the present study to better understand these relationships. The predominance of a high positive direct effect of NB on SCY highlights it as the most reliable selection criterion for yield improvement in cotton. These results were in alignment with previous research (Pujer et al., 2014). Traits such as NS and BW contributed indirectly to yield enhancement by reinforcing boll formation and boll size, emphasizing their supportive role in productivity. The negative direct effects of PH, NM and FF, despite their positive correlations with SCY, suggest that their contribution to yield is largely mediated through other yield components, particularly NB and BW, rather than through direct influence. This indicates that direct selection for these traits may not be effective unless accompanied by improvement in key yield attributes. The high proportion of explained variation confirms the adequacy of the path model and underscores the importance of focusing on NB, NS and BW for effective yield enhancement while maintaining acceptable fiber quality in cotton breeding programmes.

Conclusion

The present investigation demonstrated substantial genetic variability among the parental lines, with clear evidence of both additive and non-additive gene actions governing yield and fiber quality traits in cotton. The predominance of non-additive gene action for most economic traits, coupled with significant heterosis and high SCA effects in specific cross combinations, highlights the strong potential of heterosis breeding for improving seed cotton yield and fiber attributes. Parents such as GJHV-548, GTHV-13/32, GBHV-187, GJHV-503 and GJHV-517 were identified as superior general combiners, while crosses like GTHV-13/32 $\times$ GJHV-585, RAH-1047 $\times$ GJHV-517 and GJHV-522 $\times$ GJHV-503 exhibited promising specific combining ability and heterotic performance. These genotypes and hybrids can be effectively utilized in future hybrid development and cotton improvement programmes. Correlation and path coefficient

analyses further revealed that boll number per plant (NB) is the most reliable selection criterion for enhancing seed cotton yield, with supportive contributions from number of sympodia (NS) and boll weight (BW). The findings emphasize that strategic exploitation of genetically diverse parents, superior combiners and high-performing cross combinations will facilitate the development of high-yielding cotton hybrids with improved fiber quality.

Abbreviations

ANOVA Analysis of variance

GCA General combining ability

SCA Specific combining ability

PH Plant height (cm)

NM Number of monopodia per plant

NS Number of sympodia per plant

NB Number of bolls per plant

BW Boll weight (g)

SCY Seed cotton yield per plant (g)

GP Ginning percentage (%)

SI Seed index (g)

LI Lint index (g)

SL Span length (mm)

FS Fiber strength (g/tex)

FF Fiber fineness (mv)

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

All authors have read and approved the manuscript for publication.

Availability of data and materials

The datasets generated and analyzed during the current study are available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

Dr. C. J. Rajani carried out the major research work, data collection, statistical analysis, interpretation of results and manuscript preparation.

Dr. D. M. Vekaria assisted in recording observations and data analysis.

Dr. M. G. Valu served as the major guide and provided overall supervision, technical guidance and critical review of the research work and manuscript.

Dr. R. M. Madariya served as the minor guide and contributed to the planning and execution of the research work.

All authors read and approved the final manuscript.

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Figures

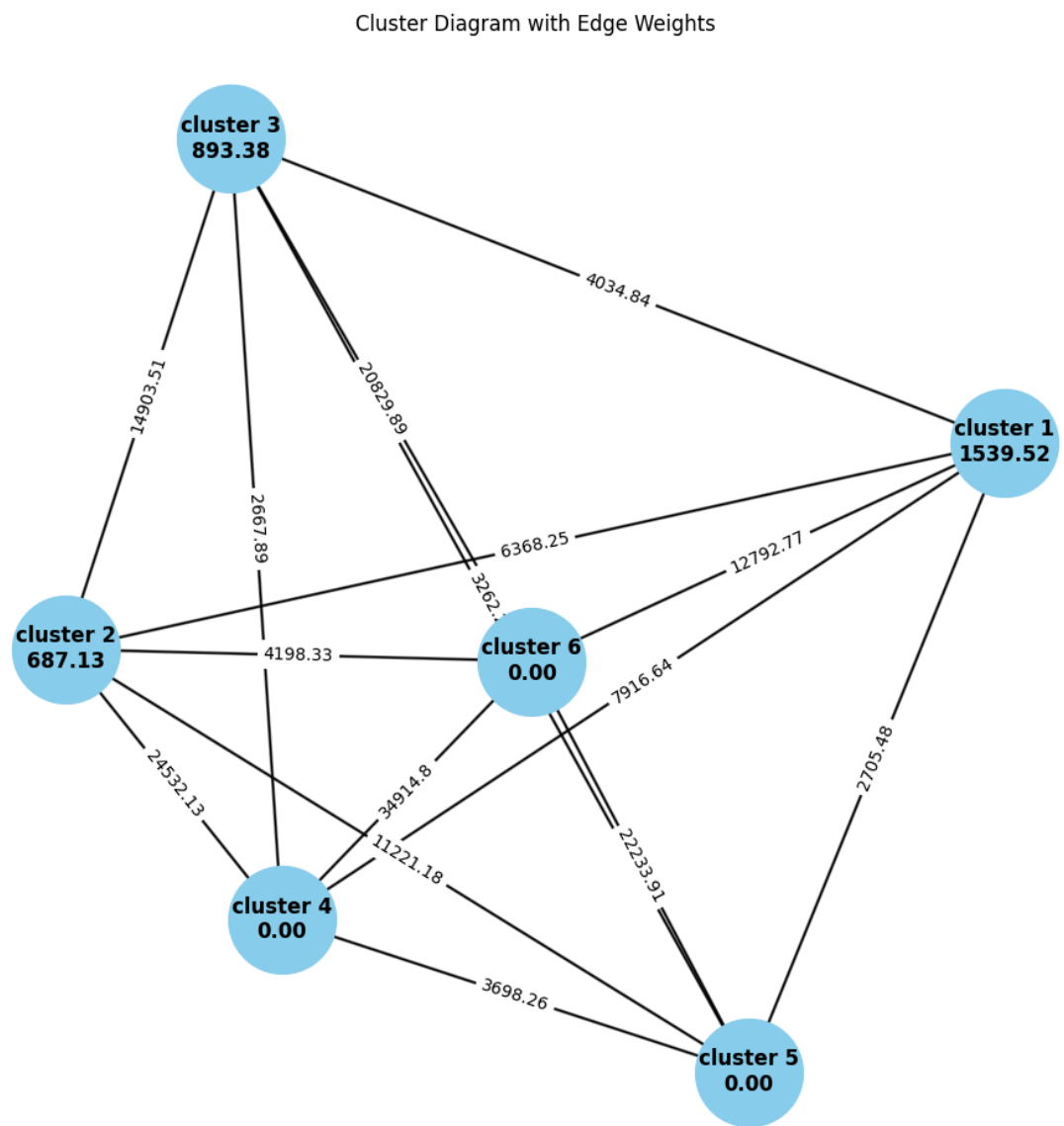


Figure 1

Cluster diagram showing inter-cluster distances among parental genotypes based on Mahalanobis D² analysis

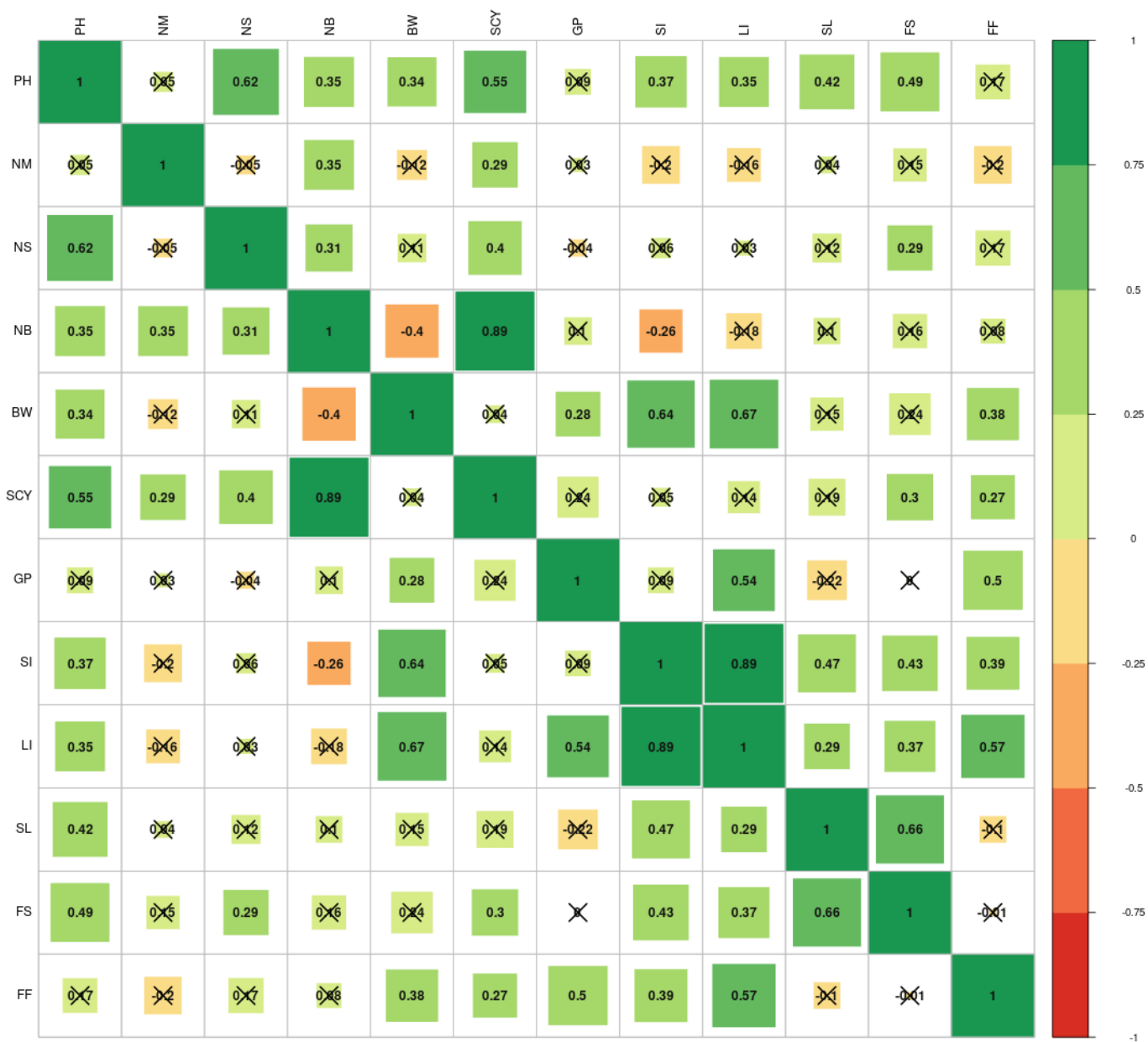


Figure 2

Correlation coefficients among cotton yield, yield components and fiber quality traits evaluated for parents and F_1 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). Cross mark (x) over value indicate non-significant correlations in the plot.

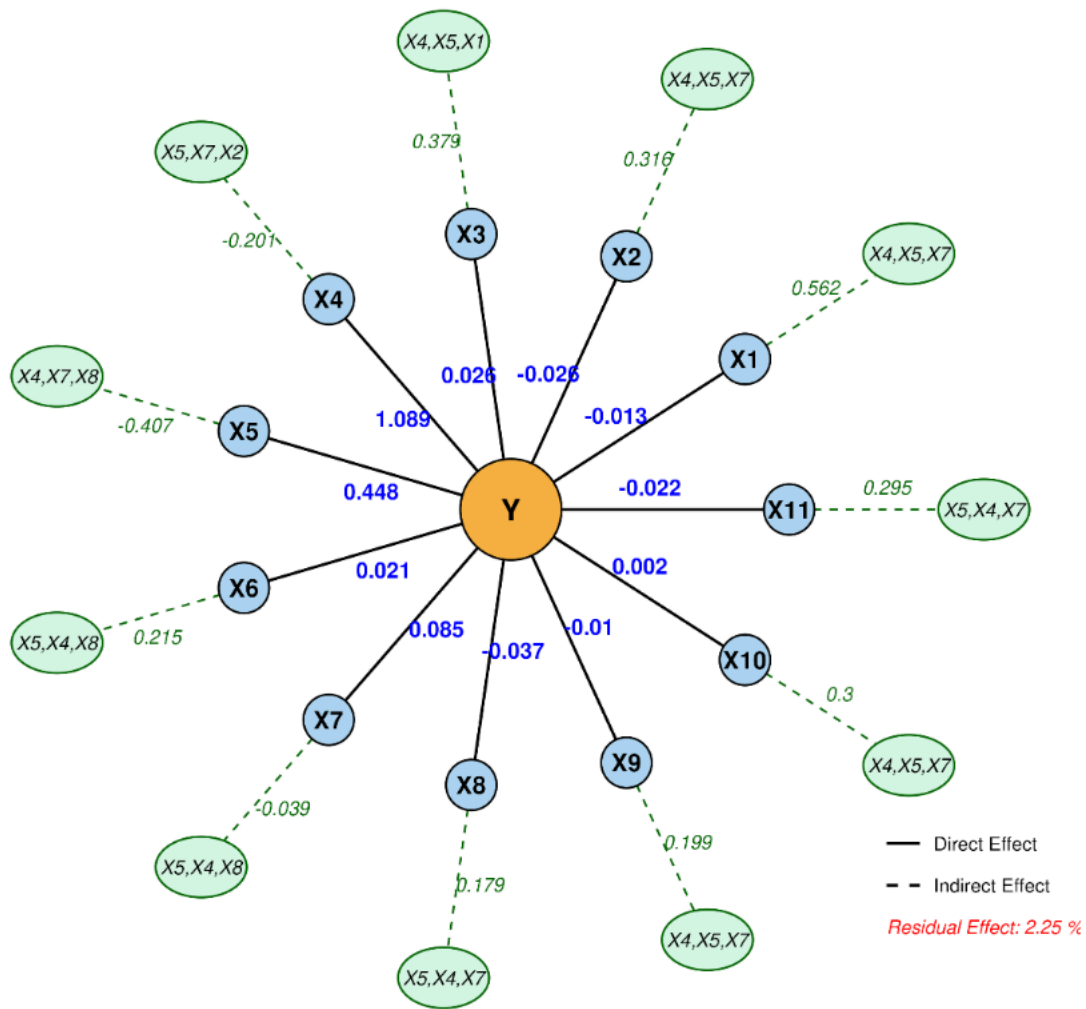


Figure 3

Path diagram showing the direct and indirect effect of the 11 explanatory variables on seed cotton yield assessed for parents and F₁ crosses across. X1 = Plant height (PH), X2 = Number of monopodia per plant (NM), X3 = Number of sympodia per plant (NS), X4 = Number of bolls per plant (NB), X5 = Boll weight (BW), X6 = Ginning percentage (GP), X7 = Seed index (SI), X8 = Lint index (LI), X9 = Staple length (SL), X10 = Fiber strength (FS), X11 = Fiber fineness (FF) and Y = Seed cotton yield per plant (SCY).