Received: 13 Mar 2023 | Revised: 06 Jun 2023 | Accepted: 10 Jun 2023

Electronic Journal of Plant Breeding

Research Article

Study on interplay of yield-related characteristics and fibre quality traits in *arboreum* cotton (*Gossypium arboreum* L.)

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Abstract
The purpose of the study was to examine the genetic variability, heritability and genetic advance as a per cent of mean among the six parents selected through principal component analysis and 30 hybrids of desi cotton. The experiment was laid out in during *kharif*,2022, at the Department of Cotton, TNAU. Five fibre quality traits and 13 yield contributing traits were analysed as a part of genetic variability investigations. With the exception of the uniformity index, ANOVA demonstrated significance for all of the characteristics examined, suggesting that parents and hybrids have adequate amount of variation. An increased environmental influence on these traits is indicated by the fact that the phenotypic coefficient of variation was marginally greater than the genotypic coefficient of variance. Positive and significant correlation with seed cotton yield per plant was observed for plant height, number of sympodia per plant, number of bolls per plant, boll weight and number of seeds per boll which suggested that increase or improvement in these characters lead to improvement in seed cotton yield/ plant. The traits namely, fibre strength, lint index and number of bolls exerted a high direct effect on seed cotton yield while, boll weight and plant height exerted a moderate positive direct effect on seed cotton yield. The hybrids K12 × RG763 and CNA1007 × RG763 can be used for the better attainment of yield as they have highest boll weight along with seed cotton yield per plant and ginning outturn.

Keywords: *Arboreum*, *Desi* cotton, Genetic variability, Heritability, Path analysis

INTRODUCTION

The most valuable raw material for textile factories is provided by cotton, the king of fibre crops also known as "white gold". It is the principal economic and industrial crop of many nations. There are more than 50 species in the genus *Gossypium*, of which two tetraploids with AD genome *viz, G. hirsutum* and *G. barbadense* and two A-genome diploids, *G. arboreum* and *G. herbaceum*, are cultivars. Around 95% of today's cotton production is credited to *G. hirsutum*, although its vulnerability to biotic and abiotic stress is a serious negative. So, in this context, diploid cotton will be the most suitable to display favourable qualities including appropriateness for low input management approaches and resilience to harsh climatic circumstances. Although diploid cotton fibres do not meet the rigorous requirements of textile industry, the short fibre strands of diploids are suitable for surgical applications.

Due to its ease of hybridization and frequent cross-pollination, cotton exhibits extremely high genetic variation for several yield and quality parameters (Joshi and Patil, 2018). To meet the demands of farmers and the textile industry, improving yield and fibre quality is the primary goal of each plant breeder. The total of all the characteristics that make up seed cotton yield can be increased by leveraging the favourable impacts of the constituent parts of the yield. However, their combined improvement is constrained by the negative correlation between yield and fibre quality (Gapare *et al*., 2017). Effective cotton breeding and the creation of elite varieties and hybrids require knowledge of the degree of variability, combined with heritability and genetic advancement. Genetic diversity shows that both genotypic and phenotypic selection are possible. The current work therefore focuses on comprehending genetic variability in desi cotton parents and their hybrids for 18 yield and its component traits along with fibre quality parameters and provides a complete analysis of its heritable components for further selection in breeding programmes.

MATERIALS AND METHODS

The present study was carried out with 15 genotypes (**Table 1)** raised during summer 2022 at Department of cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. From the 15 genotypes studied, six were selected using principal component analysis (PCA) and crossed in full diallel fashion with during summer 2022. The 30 hybrids were evaluated along with the six parents in a Randomised Block Design (RBD) with two replications during *kharif*, 2022 at Department of cotton. Recommended crop management practices were followed for better crop stand.

Observations on 13 quantitative parameters namely, days to fifty percent flowering (days), plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, number of locules per boll, number of seeds per boll, days to boll bursting (days), boll weight(g), seed cotton yield per plant (g), seed index (g), lint index(g), ginning out turn (%) and five qualitative parameters such as upper half mean length (mm), fibre strength (g/tex), uniformity index, elongation percent (%) and fibre micronaire (µg/inch) were recorded by randomly selecting five plants from each replication of each cross. Days to fifty percent flowering was recorded on plot basis.

The collected data were subjected to Analysis of Variance (ANOVA) (Panse and Sukhatme,1961) and genetic parameters *viz.* phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance were estimated as per Lush (1940), Burton (1952), Allard (1960) and Johnson *et al.* (1955) using R software 4.1.2 version. The parental polymorphism was tested with 75 markers which are linked to particular traits. Principal component analysis (PCA) was analysed using GRAPES software developed by Kerala Agricultural University, Kerala, India.

RESULTS AND DISCUSSION

Principal Component Analysis: A dimensionality reduction technique, specifically Principal Component Analysis (PCA) based on correlation matrix, was employed to create a model that could discern measurable distinctions among different genotypes within a population of cotton. The analysis was conducted using the mean values of the cotton genotypes. The results revealed that the first five Principal Components (PCs) played a pivotal role in accurately classifying the cotton population. These five PCs were selected based on their Eigen values, which exceeded 1, and collectively accounted for 82.66% of the total variation observed in the data. (**Table 3, Fig. 1)**

An attempt has been made to observe the variation explained by eleven quantitative and five qualitative characters along one and two principal component vectors *i.e.,* Biplot (**Fig. 2 and Fig. 3**). From Biplot, 16 characters were grouped into five groups. Number of bolls per plant, seed cotton yield per plant, number of monopodia per plant and number of locules per boll were grouped in same cluster; Upper half mean length, elongation percent and fibre strength as single group; number of seeds per boll and lint index as one group; boll weight, seed index, number of sympodia per plant and plant height as single group and Ginning outturn, uniformity index and fibre micronaire as one group. Those genotypes nearer to each trait can be said as best suited for those traits respectively. From the biplot, the genotypes LD0995 was highly suitable for uniformity index whereas RG763 for number of seeds per boll. The genotypes CAN 1007 and RG8 were best suited for number of bolls per plant and

Table 1. List of 15 genotypes used for divergence study

S.No.	Genotypes	S.No.	Genotypes
1	RG 872	8	CNA1039
2	LDO995	9	FDX231
3	K11	10	DSV 1202
4	k12	11	PDB29
5	RG8	12	PAIG379
6	NDL 2679	13	RG763
7	AKA0262	14	CNA1007
		15	PA838

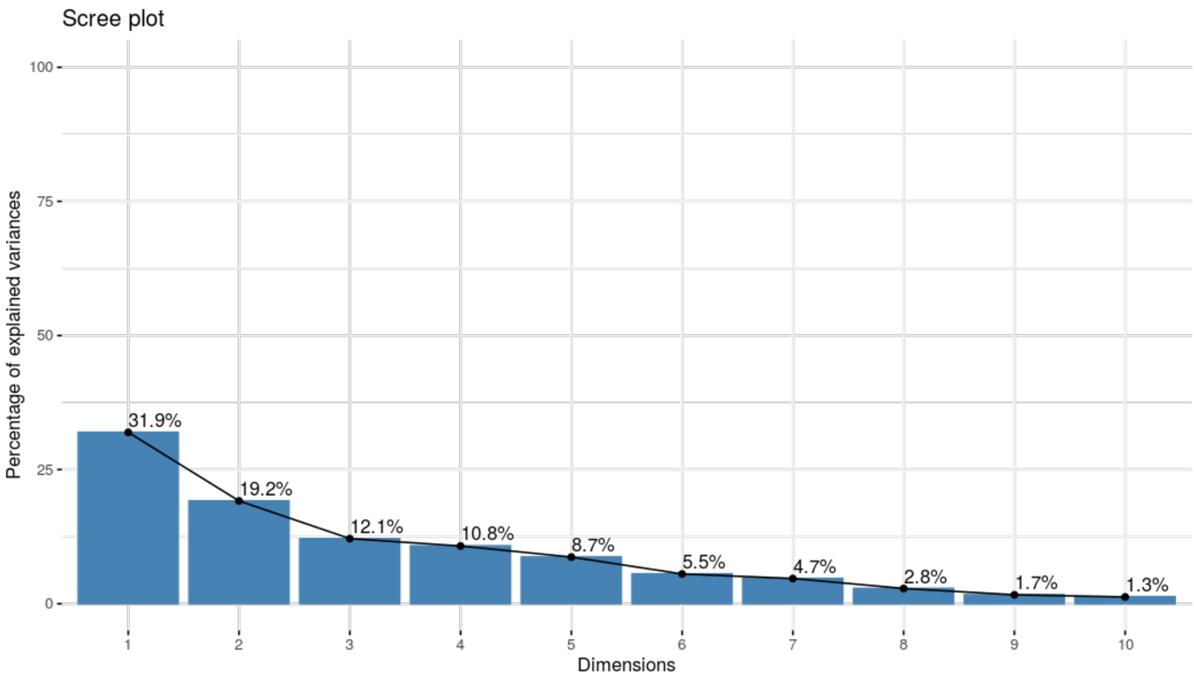

Fig. 1. Scree plot for variation explained by principal components

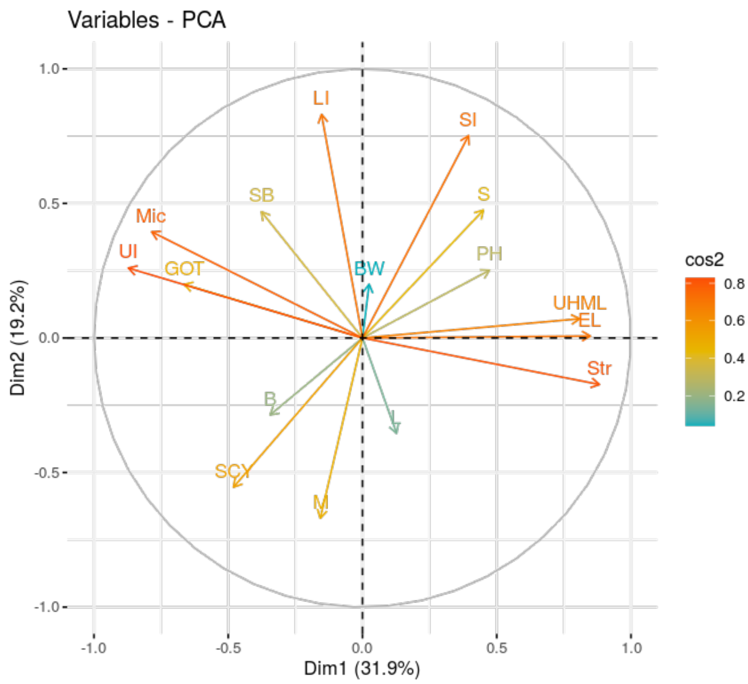

Fig. 2. PCA biplot showing variation among the traits

https://doi.org/10.37992/2023.1402.064

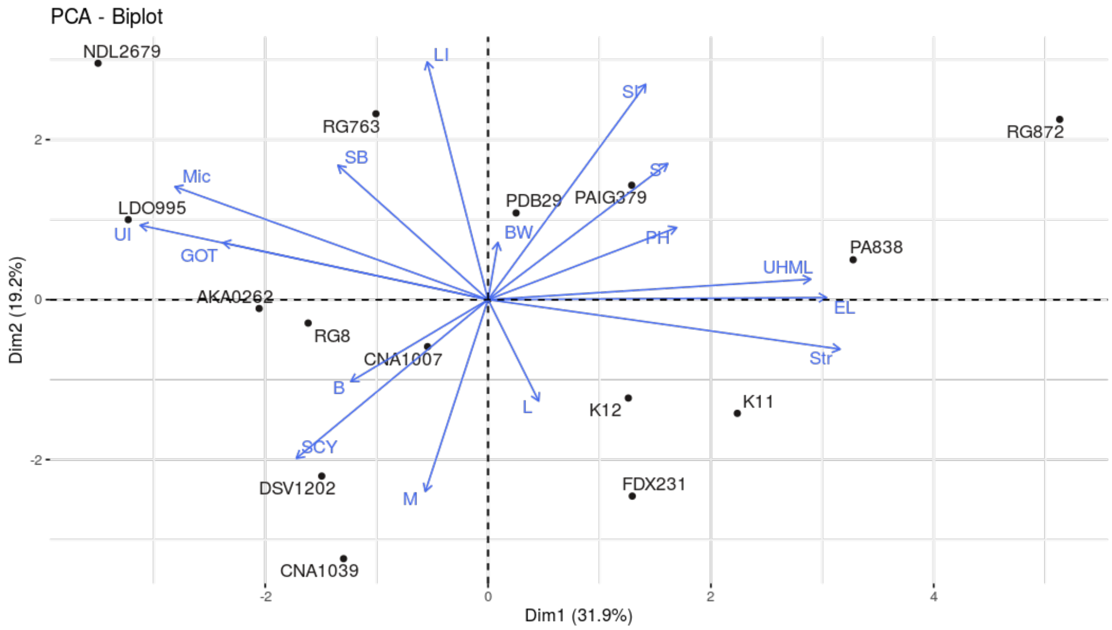

Fig. 3. Genotype by trait Biplot showing distribution of genotypes across first two PCs

Table 2. List of parents and their hybrids (F_1s)

Parents	Hybrids	Parents	Hybrids
PDB29	PDB29 × PAIG379	CNA1007	CNA1007 × PDB29
	PDB29 × RG763		CNA1007 × PAIG379
	PDB29 × CNA1007		CNA1007 × RG763
	PDB29 × PA838		CNA1007 × PA838
	PDB29 × K12		CNA1007 × K12
PAIG379	PAIG379 × PDB29	PA838	PA838 × PDB29
	PAIG379 × RG763		PA838 × PAIG379
	PAIG379 × CNA1007		PA838 × RG763
	PAIG379 × PA838		PA838 × CNA1007
	PAIG379 × K12		PA838 × K12
RG763	RG763 × PDB29	K12	K12 × PDB29
	RG763 × PAIG379		K12 × PAIG379
	RG763 × CNA1007		K12 × RG763
	RG763 × PA838		K12 × CNA1007
	RG763 × K12		K12 × PA838

DSV1202 for seed cotton yield per plant. The genotype PA838 was highly suitable for the traits upper half mean length and elongation percentage. Likewise, PDB29 for Boll weight and PAIG379 for number of sympodia per plant.

The present study was carried out with six parents selected and analysed statistically. Analysis of variance revealed highly significant differences for all the quantitative and qualitative characters studied indicating sufficient variability except for uniformity index at 1% (**Table 4**).

Mean performance for yield and fibre quality characters observed among the parents and their hybrids are presented in **Table 5**. It indicated that hybrids recorded maximum range for most of the yield and fibre quality traits over parents. Among the parents, K12 recorded higher boll weight (2.61grams), while among the hybrids, K12 × RG763 recorded highest boll weight (2.69 grams). The hybrid K12 × PDB29 recorded highest seed cotton yield per plant of 74.5 g followed by RG763 × PDB29 (72.39g), K12 × RG763 (71.6g) and CNA1007 × RG763 (71.3g). Ginning outturn is the most important trait in

https://doi.org/10.37992/2023.1402.064

Table 3. Eigen values and proportion of variance for different principal components

Principal components	Eigenvalue	Percentage of variance	cumulative percentage of variance
PC1	5.111	31.941	31.941
PC2	3.065	19.155	51.096
PC3	1.941	12.128	63.225
PC4	1.721	10.754	73.979
PC5	1.39	8.687	82.665
PC6	0.886	5.538	88.204
PC7	0.751	4.691	92.895
PC8	0.454	2.834	95.729
PC9	0.264	1.65	97.38
PC10	0.201	1.258	98.637
PC11	0.088	0.55	99.187
PC12	0.067	0.42	99
PC13	0.057	0.353	99.96
PC14	0.006	0.04	100
PC15	0	0	100

Table 4. Analysis of variance for yield and fibre quality traits in *arboreum* cotton

S.No.	Characte	Mean Sum of Squares		
		Replications	Genotypes	Error
		df : 1	df:35	df:35
1	Days to 50% Flowering	2.723	18.958**	1.791
2	Plant Height	10.83	942.15**	10.11
3	Number of Monopodia per plant	0.0019	0.655**	0.0018
4	Number of Sympodia per plant	0.108	17.016**	0.33
5	Number of Bolls per plant	0.212	27.985**	0.462
6	Number of Locules per Boll	0.015	0.0927**	0.0066
7	Days to Boll Bursting	0.247	26.535**	5.718
8	Boll Weight	0.0005	0.188**	0.0015
9	Number of Seeds per Boll	0.0652	28.675**	0.31
10	Seed Cotton Yield per plant	5.819	180.836**	2.242
11	Ginning Outturn	0.071	67.03**	1.903
12	Seed Index	0.0003	2.541**	0.061
13	Lint Index	0.0014	0.247**	0.0126
14	Upper Half Mean Length	0.292	4.034**	0.523
15	Uniformity Index	0.07	1.842	1.528
16	Fibre Strength	1.578	5.514**	0.302
17	Elongation Percentage	0.0209	0.086**	0.0108
18	Fibre Micronaire	0.0029	0.537**	0.013

** Significant at 1%

cotton and the highest GOT has been recorded by CNA1007 × RG763 (40.68%) followed by PDB29 × K12 (40.14%) and PAIG379 × K12 (39.87%). Lint index was higher in CNA1007 × RG763 (4.9g) followed by PAIG379 × K12 (4.37g). Among the fibre quality parameters, upper half mean length (UHML) is the most important trait as it determines the length of the lint or fibre which will be used in textile industries or surgical industries. As *arboreum* cotton produces short fibres, these will be used mostly in surgical industries. UHML value was observed to range from 24.22 mm to 29 mm in our study. Fibre micronaire is the most important trait in case of

Table 5. ***Per se*** **performance of six parents and thirty hybrids of** ***arboreum*** **cotton for yield and fibre quality traits**

Genotypes	DFF	PH	M	S	B	L	DBB	BW	SB	SCY	GOT	SI	LI	UHML	UI	Str	EL	Mic
PDB29	58.64	109.11	1.69	19.01	33.36	3.28	100.51	2.17	26.53	55.18	34.90	10.24	3.57	26.13	48.10	22.06	5.49	5.57
PDB29 × PAIG379	52.91	78.98	1.99	12.71	26.98	3.02	99.71	2.21	21.58	47.78	36.56	9.67	3.54	27.35	48.88	23.86	6.11	5.56
PDB29 × RG763	54.48	126.07	2.86	18.90	28.97	2.94	103.40	1.43	18.11	43.22	38.34	10.54	4.04	26.86	48.16	24.02	6.01	5.88
PDB29 × CNA1007	56.39	97.85	1.98	15.53	27.19	3.17	97.02	1.75	21.41	47.90	37.35	10.31	3.85	26.35	47.42	21.90	5.65	5.26
PDB29 × PA838	65.90	141.35	3.01	22.30	28.15	3.01	103.34	1.55	17.46	44.67	35.30	10.74	3.79	28.20	47.42	24.77	6.18	5.77
PDB29 × K12	64.22	103.13	1.86	18.60	31.96	2.93	101.91	2.22	26.85	61.08	40.14	10.21	4.10	25.57	48.31	21.07	5.61	5.42
PAIG379	58.88	123.12	1.80	19.60	30.33	3.04	104.55	1.94	24.24	55.39	34.42	10.51	3.62	28.08	49.50	22.29	5.76	5.75
PAIG379 × PDB29	64.94	120.27	2.17	19.92	25.71	3.02	101.87	1.84	21.80	42.51	34.32	10.63	3.65	27.13	47.97	24.73	5.89	4.87
PAIG379 × RG763	66.17	87.67	1.63	15.48	25.85	3.03	106.42	1.89	23.25	41.67	34.80	10.50	3.66	25.68	48.87	20.54	5.77	6.29
PAIG379 × CNA1007	57.84	98.75	1.00	17.56	26.29	3.01	103.40	1.99	20.82	47.70	33.70	8.91	3.00	27.93	46.58	24.22	6.06	5.68
PAIG379 × PA838	56.93	120.11	1.00	18.26	28.92	3.14	104.03	2.04	21.93	52.22	35.99	10.18	3.66	26.67	47.19	22.43	5.80	5.39
PAIG379 × K12	57.91	123.56	1.60	19.91	30.22	3.01	105.50	2.17	26.16	53.07	39.87	10.97	4.37	26.21	48.38	21.84	5.71	5.88
RG763	59.21	93.71	0.84	15.02	29.66	3.01	95.78	2.16	26.23	55.58	38.04	10.32	3.93	26.51	48.74	20.84	5.59	5.97
RG763 × PDB29	57.09	108.15	2.19	17.05	38.21	3.02	106.17	2.11	29.22	72.39	36.49	9.83	3.59	26.98	47.74	21.64	5.80	5.81
RG763 × PAIG379	59.88	108.75	2.15	18.74	33.61	3.15	94.32	2.21	27.70	60.36	37.93	11.31	4.29	26.82	47.16	21.42	5.58	5.83
RG763 × CNA1007	55.19	125.95	2.18	19.78	29.97	3.15	101.84	2.01	21.63	54.59	36.20	10.34	3.74	24.48	49.83	19.32	5.28	6.31
RG763 × PA838	55.37	144.29	2.17	23.09	35.59	2.99	96.85	2.36	27.31	67.64	35.70	10.36	3.70	28.37	47.59	23.82	5.74	5.46
RG763 × K12	57.59	129.03	1.99	22.21	33.16	3.23	101.82	2.43	28.96	66.83	36.30	11.11	4.03	24.22	49.29	20.46	5.65	6.73
CNA1007	58.25	110.54	2.36	18.22	27.85	2.99	100.60	2.00	22.40	51.00	37.38	8.98	3.36	25.42	48.51	20.26	5.40	5.60
CNA1007 × PDB29	59.90	66.05	1.00	13.46	26.39	3.02	101.53	1.79	20.22	46.60	39.08	10.29	4.02	26.86	48.10	21.51	5.84	5.97
CNA1007 × PAIG379	57.93	115.40	1.70	19.19	29.25	3.00	98.83	2.01	26.41	54.19	35.91	11.86	4.26	29.97	46.04	24.50	5.72	4.67
CNA1007 × RG763	58.09	136.64	2.02	22.25	33.73	3.60	104.85	2.33	29.57	71.30	40.68	12.06	4.90	25.35	48.98	20.21	5.51	5.40
CNA1007 × PA838	56.65	174.63	3.02	24.70	32.65	2.99	102.10	2.11	26.49	55.50	34.52	9.79	3.38	27.87	46.74	20.61	5.44	5.58
CNA1007 × K12	59.38	90.90	2.00	14.91	27.02	3.01	106.38	1.56	18.01	37.73	36.52	10.28	3.76	26.30	46.77	18.17	5.39	4.98

Table 5. Continued..

Genotypes	DFF	PH	M	S	B	L	DBB	BW	SB	SCY	GOT	SI	LI	UHML	UI	Str	EL	Mic
PA838	56.06	128.85	2.32	20.79	29.30	3.30	104.31	2.20	24.99	50.80	34.85	10.15	3.54	29.61	46.42	23.88	5.95	4.90
PA838 × PDB29	55.88	113.25	1.53	20.56	35.61	3.00	100.91	2.27	25.93	59.67	37.29	9.40	3.50	27.71	47.13	23.76	5.74	4.69
PA838 × PAIG379	57.75	122.14	2.66	20.38	39.02	3.04	106.58	2.25	21.69	64.34	28.91	4.85	1.39	29.40	47.12	24.18	5.96	4.81
PA838 × RG763	57.04	90.34	1.66	16.30	32.84	3.02	99.69	1.89	25.09	50.33	38.59	10.17	3.92	29.81	46.98	22.24	5.64	4.92
PA838 × CNA1007	57.65	95.60	1.32	22.86	30.74	3.31	102.50	1.91	22.00	51.30	37.85	9.80	3.71	26.73	47.81	21.45	5.52	5.18
PA838 × K12	58.78	129.42	1.91	21.16	28.27	3.21	104.73	2.04	22.97	53.26	37.74	10.03	3.78	26.54	46.60	20.55	5.51	5.22
K12	62.74	134.09	2.99	17.70	27.58	4.07	95.17	2.61	25.03	55.56	35.87	9.33	3.35	26.40	47.76	21.53	5.63	5.67
K12 × PDB29	62.10	129.65	2.04	21.93	37.86	3.09	105.61	2.43	29.71	74.50	37.84	10.76	4.07	26.73	47.07	21.60	5.62	5.46
K12 × PAIG379	59.14	144.08	2.01	21.12	35.81	2.94	96.13	2.24	29.05	66.73	37.99	10.76	4.09	28.39	46.32	23.31	5.75	5.86
K12 × RG763	57.02	145.64	2.49	24.08	34.45	2.95	93.57	2.69	30.39	71.60	35.42	10.46	3.71	24.93	48.29	21.46	5.67	5.44
K12 × CNA1007	57.80	119.39	1.16	18.21	28.03	3.28	103.73	2.30	23.20	51.39	38.12	10.51	4.01	27.55	46.90	21.30	5.66	6.08
K12 × PA838	56.10	115.09	2.49	16.88	27.77	3.15	101.68	1.28	15.41	43.73	35.28	10.45	3.69	25.76	47.00	19.79	5.48	5.48
Mean	58.55	116.71	1.97	19.12	30.79	3.11	101.59	2.07	24.16	54.98	37.70	10.18	3.79	26.97	47.71	21.99	5.70	5.55
Max	66.17	174.63	3.02	24.70	39.02	4.07	106.58	2.69	30.39	74.50	40.68	12.06	4.90	29.97	49.83	24.77	6.18	6.73
Min	52.91	66.05	0.84	12.71	25.71	2.93	93.57	1.28	15.41	37.73	33.70	4.85	3.00	24.22	46.04	18.17	5.28	4.67
SD	3.08	21.54	0.572	2.917	3.741	0.215	3.643	0.306	3.786	9.51	5.787	1.128	0.351	1.42	0.959	1.66	0.209	0.504
SE	0.40	1.994	0.408	0.667	0.674	0.122	0.361	0.213	0.77	1.283	0.943	0.353	0.18	0.273	0.139	0.354	0.088	0.214
CD 5%	2.71	6.45	0.08	1.167	1.38	0.166	4.85	0.08	1.13	3.03	2.8	0.5	0.22	1.46	2.5	1.11	0.21	0.23
CD 1%	3.64	8.659	0.116	1.56	1.85	0.22	6.51	0.1	1.51	4.07	3.75	0.67	0.3	1.97	3.36	1.49	0.28	0.31

DFF-days to fifty per cent flowering (number of days), PH-plant height (cm), M-number of monopodia per plant, S-number of sympodia per plant, B-number of bolls per plant, L-number of locules per boll, DBB-days to first boll bursting (number of days), BW-boll weight (g), SB- number of seeds per boll, SCY-seed cotton yield per plant (g), SI-seed index (g), LI-lint index (g), GOT-ginning out turn (%), UHML-upper half mean length (mm), Str-fibre strength (g/tex), UI-uniformity index, and EL-elongation percentage (%), Mic-fibre fineness (µg/inch)

Table 6. Mean, Range, Coefficient of variation, Heritability and genetic advance as percent of mean for yield and fibre quality traits in cotton

Traits	Mean	Range		Variance		Coefficient of variation (CV) %		Heritability (broad sense) (h^2)	Genetic Advance	Genetic advance as percent of mean
		Maximum	Minimum	Phenotypic	Genotypic	PCV	GCV			
DFF	58.55	66.17	52.91	10.38	8.59	5.50	5.00	82.75	5.49	9.38
PH	116.64	174.63	66.04	476.11	466.00	18.71	18.51	97.88	44.00	37.72
M	1.97	3.02	0.84	0.33	0.33	29.14	29.06	99.44	1.17	59.70
S	19.12	25.31	12.70	8.67	8.34	15.40	15.11	96.20	5.84	30.52
B	30.79	39.03	25.71	14.22	13.76	12.25	12.05	96.74	7.52	24.41
L	3.11	4.11	2.93	0.05	0.04	7.18	6.68	86.41	0.40	12.78
DBB	101.59	106.58	93.57	16.13	10.41	3.95	3.18	64.57	5.34	5.26
BW	2.07	2.69	1.28	0.10	0.09	14.91	14.79	98.32	0.62	30.20
SB	24.16	30.39	15.41	14.49	14.18	15.76	15.59	97.87	7.67	31.77
SCY	54.98	74.50	37.73	91.54	89.30	17.40	17.19	97.55	19.23	34.97
GOT	37.71	69.91	33.70	34.47	32.56	15.57	15.13	94.47	11.43	30.30
SI	10.18	12.10	4.85	1.30	1.24	11.21	10.94	95.26	2.24	21.99
LI	3.79	4.94	3.00	0.13	0.12	9.50	9.03	90.33	0.67	17.68
UHML	26.97	29.97	24.22	2.28	1.76	5.60	4.91	77.06	2.40	8.88
UI	47.71	49.83	46.04	1.69	0.16	2.72	0.83	9.27	0.25	0.52
Str	21.99	24.77	18.17	2.91	2.61	7.76	7.34	89.62	3.15	14.32
EL	5.70	6.18	5.27	0.05	0.04	3.86	3.41	77.76	0.35	6.19
Mic	5.53	6.73	4.65	0.27	0.25	9.30	9.06	94.98	1.03	18.19

DFF-days to fifty per cent flowering (number of days), PH-plant height (cm), M-number of monopodia per plant, S-number of sympodia per plant, B-number of bolls per plant, L-number of locules per boll, DBB-days to first boll bursting (number of days), BW-boll weight (g), SB- number of seeds per boll, SCY-seed cotton yield per plant (g), SI-seed index (g), LI-lint index (g), GOT-ginning out turn (%), UHML-upper half mean length (mm), Str-fibre strength (g/tex), UI-uniformity index, and EL-elongation percentage (%), Mic-fibre fineness (μg/inch)

surgical cotton. Micronaire value more than 6 is usually preferred for surgical purposes (MSME,2010). RG763 × K12 has recorded highest micronaire value of 6.73 μg/inch followed by RG763× CNA1007 (6.31 μg/inch). The combinations PAIG379 × RG763 and K12 × CNA1007 have also shown micronaire value of more than 6.

An increased environmental influence on these traits is indicated by the fact that the phenotypic coefficient of variation was marginally larger than the genotypic coefficient of variance (**Table 6**). Similar findings were reported by Reddy *et al*. (2014), Santosh kumar *et al.* (2014) and Deshmukh *et al.* (2019). The traits namely, plant height (PCV:18.71%, GCV:18.51%), number of monopodia per plant (PCV: 29.14, GCV:29.06) exhibited high PCV and GCV which indicates that selection could be effective for improvement of these traits. The results were in accordance with Erande *et al*. (2014), Deshmukh *et al*. (2019), Kumar *et al*. (2019) and Mankar *et al*. (2021). High PCV for number of monopodia per plant was reported by Jogender *et al*. (2023). Other traits such as number of sympodia per plant (PCV:15.4, GCV:15.11), number of bolls per plant (PCV:12.25, GCV:12.05), boll weight (PCV:14.91, GCV:14.79), number of seeds per boll (PCV:15.76, GCV:15.59), seed cotton yield per plant (PCV:17.40, GCV:17.19), ginning out turn (PCV:15.57, GCV:15.13) and seed index (PCV:11.21, GCV:10.94) exhibited moderate variability. Similar report for boll weight was shown by Kumar *et al*. (2019), Shruti *et al*. (2019) and Kolhe *et al*. (2022). Moderate genetic variability for seed cotton yield per plant was reported by Ahsan *et al*. (2015) and Jogender *et al*. (2023). Lint index (PCV: 9.50, GCV: 9.03), Upper Half Mean Length (PCV:5.60, GCV: 4.91), uniformity index (PCV:2.72, GCV:0.83), fibre strength (PCV:7.76, GCV:7.34), elongation percentage (PCV:3.86, GCV: 3.41) and fibre micronaire (PCV:9.30, GCV: 9.06) recorded low variability. The results were in accordance with Erande *et al*. (2014), Devidas *et al*. (2017), Joshi and Patil (2018), Shruti *et al*. (2019) and Kolhe *et al*. (2022).

Heritability in broad sense ranged from 9.27 per cent for uniformity index to 99.44 per cent for number of monopodia per plant. High heritability coupled with high genetic advance as percent of mean was recorded for plant height (H- 97.88%; GAM- 37.72), number of monopodia per plant (H-99.44%; GAM-59.70), number of sympodia per plant (H- 96.20% ; GAM - 30.52), number of bolls per plant (H- 96.74% ; GAM- 24.41), boll weight (H- 98.32% ; GAM- 30.20), number of seeds per boll (H- 97.87% ; GAM- 31.77), seed cotton yield per plant (H- 97.55% ; GAM- 34.97), ginning out turn (H- 94.47% ; GAM- 30.30) and seed index(H- 95.26% ; GAM- 21.99), which indicates that these traits are under the control of additive gene action . These results for plant height are in accordance with Erande *et al*. (2014), Ranjan *et al*. (2014), Joshi and Patil (2018), Deshmukh *et al*. (2019), Gnanasekaran *et al.* (2020), Mankar *et al*. (2021) and Kolhe *et al.* (2022). Similar findings for number of monopodia per plant, number of sympodia per plant were shown by Erande *et al*. (2014) and Deshmukh *et al*. (2019). High heritability coupled with moderate GAM was recorded for the parameters namely, number of locules per boll (H-86.41%; GAM-12.78), lint index (H- 90.33%; GAM-17.68), fibre strength (H-89.62%; GAM – 14.32) and fibre micronaire (H- 94.98%; GAM- 18.19). Similar report for lint index was reported by Ranjan *et al*. (2014) and Kolhe *et al.* (2022) for fibre micronaire. High heritability associated with moderate genetic advance as percent of mean for fibre strength was reported by Chaudhari *et al*. (2017), Devidas *et al*. (2017), Joshi and Patil (2018), Kumar *et al*. (2019), Shruti *et al*. (2019), Mankar *et al.* (2021) and Kolhe *et al*. (2022). High heritability and low GAM were recorded for days to fifty percent flowering (H-82.75%; GAM-9.38), days to boll bursting (H-64.57%; GAM-5.26), upper half mean length (H-77.06%; GAM-8.88) and elongation percentage (H-94.98; GAM-6.19) and high heritability coupled with low genetic advance as percent of mean was observed by Joshi and Patil (2018). Similar findings for days to fifty percent flowering were observed by Erande *et al*. (2014), Deshmukh *et al*. (2019), Mankar *et al*. (2021) and Kolhe *et al*. (2022). Low heritability (9.27%) coupled with low GAM (0.52) was noticed for uniformity index suggesting the environmental influence on the trait and selection is highly ineffective.

Correlation: Correlation research uncovers the relationships between trait pairs, providing knowledge to the breeder that aids in the directional/anti-directional improvement of the multitude of traits at a time. In the present study, seed cotton yield per plant showed positive and significant correlation with plant height (r=0.44), number of sympodia per plant (r=0.524), number of bolls per plant (r=0.863), boll weight (r=0.758) and number of seeds per boll (r=0.843) (**Table 7**). which suggested that increase or improvement in these characters could lead to improvement in seed cotton yield/ plant. This finding is in line with the results of Pooja *et al*. (2021) and Mahesh *et al*. (2021). Positive and non-significant correlation with seed cotton yield per plant was recorded for number of monopodia per plant, number of locules per boll, Ginning outturn, seed index, lint index, uniformity index and fibre micronaire which were in accordance with Narisireddy and Ratnakumari (2004), Anjaneyulu (2004) and Sambamurthy *et al.* (2006) and Nikhil *et al*. (2018).

Path analysis: To gain a better understanding of the precise relationships between yield component features and their impacts on closely related variables, path coefficient analysis can be employed. Path analysis allows for the identification of causal variables that best account for the variability observed in the dependent variable, with the residual effect being particularly informative in this regard (in this case, with a value of 0.0918). The traits under investigation in this study is considered to be significant based on its residual effect. Additionally, the direct effect on seed cotton output can be determined by examining the diagonal values in the path coefficient analysis.

The traits namely, fibre strength (1.317), lint index (1.148) and number of bolls exerted a high direct effect on seed cotton yield while, boll weight (0.54) and plant height (0.449) exerted a moderate positive direct effect on seed cotton yield. Days to fifty percent flowering (0.183), days to boll bursting (0.178), uniformity index (0.139), fibre micronaire (0.056) exerted low direct effect on seed cotton yield per plant. Number of monopodia (-0.008), number of sympodia (-0.541), number of locules per boll (-0.159), number of seeds per boll (-0.292), ginning out turn (-1.118), seed index (-1.383), upper half mean length (-0.216) and elongation percentage (-1.09) had a negative direct effect on seed cotton yield per plant (**Table 8**).

Plant height exerted positive direct effect on seed cotton yield per plant (0.449) while the correlation of plant height with seed cotton yield was positive and significant (0.43). The correlation between plant height and seed cotton yield was positive and significant due to the positive indirect effect contribution through number of bolls per plant (0.285), boll weight (0.173), ginning out turn (0.026), lint index (0.035), fibre strength (0.109) and elongation percentage (0.116). The positive direct effect of plant height with seed cotton yield per plant has been reported by Erande *et al*. (2014), Gnanasekharan *et al*. (2020) and Pooja *et al*. (2020).

Number of bolls per plant exerted positive direct effect on seed cotton yield per plant (0.781) while the correlation of number of bolls with seed cotton yield was positive and significant (0.876). The correlation between number of bolls and seed cotton yield was positive and significant due to the positive indirect effect contribution through plant height (0.164), number of locules (0.017), boll weight (0.285), seed index (0.284), lint index (0.19), fibre strength (0.099) and elongation percentage (0.139). Similar findings were reported by Pujer *et al*. (2014), Nikhil *et al*. (2018), Gnanasekharan *et al*. (2020), Pooja *et al*. (2020), Mahesh *et al*. (2021) and Jangid *et al*. (2022).

Table 7. Correlation analysis for yield and fibre quality traits in *arboreum* cotton

Traits	DFF	PH	M	S	B	L	DBB	BW	SB	SCY	GOT	SI	LI	UHML	UI	Str	EL	Mic
DFF	1	-0.041^{NS}	0.045^{NS}	-0.000^{NS}	-0.186^{NS}	0.090^{NS}	0.115^{NS}	-0.038^{NS}	0.007^{NS}	-0.121^{NS}	-0.056^{NS}	0.124^{NS}	0.086^{NS}	-0.104^{NS}	0.037^{NS}	-0.023^{NS}	0.078^{NS}	0.103^{NS}
PH	-0.041^{NS}	1	0.600**	0.839**	0.386*	0.145^{NS}	-0.069^{NS}	0.332*	0.343*	0.444**	-0.022^{NS}	0.086^{NS}	0.033^{NS}	0.050^{NS}	-0.148^{NS}	0.100^{NS}	-0.096^{NS}	0.020^{NS}
M	0.045^{NS}	0.600**	1	0.388*	0.189^{NS}	0.145^{NS}	-0.072^{NS}	-0.035^{NS}	-0.057^{NS}	0.104^{NS}	0.130^{NS}	-0.151^{NS}	-0.139^{NS}	0.004^{NS}	-0.031^{NS}	0.062^{NS}	0.029^{NS}	-0.063^{NS}
S	-0.000^{NS}	0.839**	0.388*	1	0.505**	0.058^{NS}	0.004^{NS}	0.373*	0.423*	0.524**	0.039^{NS}	0.075^{NS}	0.093^{NS}	0.029^{NS}	-0.103^{NS}	0.132^{NS}	-0.122^{NS}	-0.109^{NS}
B	-0.186^{NS}	0.386*	0.189^{NS}	0.505**	1	-0.109^{NS}	-0.048^{NS}	0.522**	0.672**	0.863**	0.421*	-0.197^{NS}	0.160^{NS}	0.142^{NS}	-0.085^{NS}	0.082^{NS}	-0.102^{NS}	-0.110^{NS}
L	0.090^{NS}	0.145^{NS}	0.145^{NS}	0.058^{NS}	-0.109^{NS}	1	-0.100^{NS}	0.319^{NS}	0.098^{NS}	0.093^{NS}	-0.044^{NS}	0.050^{NS}	0.049^{NS}	-0.198^{NS}	0.069^{NS}	-0.219^{NS}	-0.235^{NS}	0.022^{NS}
DBB	0.115^{NS}	-0.069^{NS}	-0.072^{NS}	0.004^{NS}	-0.048^{NS}	-0.100^{NS}	1	-0.316^{NS}	-0.292^{NS}	-0.188^{NS}	0.224^{NS}	-0.186^{NS}	-0.036^{NS}	0.028^{NS}	0.018^{NS}	-0.095^{NS}	0.132^{NS}	-0.006^{NS}
BW	-0.038^{NS}	0.332*	-0.035^{NS}	0.373*	0.522**	0.319^{NS}	-0.316^{NS}	1	0.820**	0.758**	0.130^{NS}	-0.075^{NS}	0.053^{NS}	-0.075^{NS}	0.107^{NS}	0.025^{NS}	-0.093^{NS}	0.029^{NS}
SB	0.007^{NS}	0.343*	-0.057^{NS}	0.423*	0.672**	0.098^{NS}	-0.292^{NS}	0.820**	1	0.843**	-0.044^{NS}	0.255^{NS}	0.330*	-0.046^{NS}	0.081^{NS}	-0.039^{NS}	-0.211^{NS}	0.066^{NS}
SCY	**-0.121^{NS}**	**0.444****	**0.104^{NS}**	**0.524****	**0.863****	**0.093^{NS}**	**-0.188^{NS}**	**0.758****	**0.843****	1	0.233^{NS}	0.005^{NS}	0.265^{NS}	-0.083^{NS}	0.079^{NS}	-0.021^{NS}	-0.155^{NS}	0.045^{NS}
GOT	-0.056^{NS}	-0.022^{NS}	0.130^{NS}	0.039^{NS}	0.421*	-0.044^{NS}	0.224^{NS}	0.130^{NS}	-0.044^{NS}	**0.233^{NS}**	1	-0.722**	0.027^{NS}	0.226^{NS}	-0.068^{NS}	0.141^{NS}	0.140^{NS}	-0.282^{NS}
SI	0.124^{NS}	0.086^{NS}	-0.151^{NS}	0.075^{NS}	-0.197^{NS}	0.050^{NS}	-0.186^{NS}	-0.075^{NS}	0.255^{NS}	**0.005^{NS}**	-0.722**	1	0.655**	-0.251^{NS}	0.131^{NS}	-0.193^{NS}	-0.207^{NS}	0.289^{NS}
LI	0.086^{NS}	0.033^{NS}	-0.139^{NS}	0.093^{NS}	0.160^{NS}	0.049^{NS}	-0.036^{NS}	0.053^{NS}	0.330*	**0.265^{NS}**	0.027^{NS}	0.655**	1	-0.169^{NS}	0.133^{NS}	-0.189^{NS}	-0.192^{NS}	0.129^{NS}
UHML	-0.104^{NS}	0.050^{NS}	0.004^{NS}	0.029^{NS}	0.142^{NS}	-0.198^{NS}	0.028^{NS}	-0.075^{NS}	-0.046^{NS}	**-0.083^{NS}**	0.226^{NS}	-0.251^{NS}	-0.169^{NS}	1	-0.633**	0.692**	0.498**	-0.548**
UI	0.037^{NS}	-0.148^{NS}	-0.031^{NS}	-0.103^{NS}	-0.085^{NS}	0.069^{NS}	0.018^{NS}	0.107^{NS}	0.081^{NS}	**0.079^{NS}**	-0.068^{NS}	0.131^{NS}	0.133^{NS}	-0.633**	1	-0.304^{NS}	-0.129^{NS}	0.532**
Str	-0.023^{NS}	0.100^{NS}	0.062^{NS}	0.132^{NS}	0.082^{NS}	-0.219^{NS}	-0.095^{NS}	0.025^{NS}	-0.039^{NS}	**-0.021^{NS}**	0.141^{NS}	-0.193^{NS}	-0.189^{NS}	0.692**	-0.304^{NS}	1	0.825**	-0.372*
EL	0.078^{NS}	-0.096^{NS}	0.029^{NS}	-0.122^{NS}	-0.102^{NS}	-0.235^{NS}	0.132^{NS}	-0.093^{NS}	-0.211^{NS}	**-0.155^{NS}**	0.140^{NS}	-0.207^{NS}	-0.192^{NS}	0.498**	-0.129^{NS}	0.825**	1	-0.097^{NS}
Mic	0.103^{NS}	0.020^{NS}	-0.063^{NS}	-0.109^{NS}	-0.110^{NS}	0.022^{NS}	-0.006^{NS}	0.029^{NS}	0.066^{NS}	**0.045^{NS}**	-0.282^{NS}	0.289^{NS}	0.129^{NS}	-0.548**	0.532**	-0.372*	-0.097^{NS}	1

DFF-days to fifty per cent flowering (number of days), PH-plant height (cm), M-number of monopodia per plant, S-number of sympodia per plant, B-number of bolls per plant, L-number of locules per boll, DBB-days to first boll bursting (number of days), BW-boll weight (g), SB- number of seeds per boll, SCY-seed cotton yield per plant (g), SI-seed index (g), LI-lint index (g), GOT-ginning out turn (%), UHML-upper half mean length (mm), Str-fibre strength (g/tex), UI-uniformity index, and EL-elongation percentage (%), Mic-fibre fineness (µg/inch).
** significant at 1%, * significant at 5 %

Table 8. Direct (diagonal bold) and Indirect effects of component characters on seed cotton yield/ plant

	DFF	PH	M	S	B	L	DBB	BW	SB	GOT	SI	LI	UHML	UI	Str	EL	Mic	gen_corr with SCY
DFF	**0.183**	-0.018	0	0.005	-0.146	-0.017	0.029	-0.023	-0.002	0.079	-0.191	0.096	0.029	0.023	-0.037	-0.14	0.003	-0.128
PH	-0.007	**0.449**	-0.005	-0.455	0.285	-0.032	-0.012	0.173	-0.093	0.026	-0.11	0.035	-0.009	-0.039	0.109	0.116	0	0.43**
M	0.009	0.276	**-0.008**	-0.213	0.149	-0.024	-0.015	-0.021	0.017	-0.145	0.212	-0.167	-0.001	-0.007	0.087	-0.039	-0.008	0.103
S	-0.002	0.378	-0.003	**-0.541**	0.402	-0.012	0.007	0.204	-0.125	-0.042	-0.105	0.11	-0.008	-0.038	0.184	0.13	-0.005	0.534**
B	-0.034	0.164	-0.001	-0.279	**0.781**	0.017	-0.008	0.285	-0.199	-0.484	0.284	0.19	-0.034	-0.039	0.099	0.139	-0.004	0.876**
L	0.019	0.09	-0.001	-0.042	-0.081	**-0.159**	-0.024	0.178	-0.03	0.047	-0.074	0.073	0.049	0.045	-0.287	0.303	-0.01	0.096
DBB	0.03	-0.031	0.001	-0.02	-0.036	0.022	**0.178**	-0.191	0.099	-0.306	0.311	-0.029	-0.007	0.028	-0.124	-0.145	0.004	-0.216
BW	-0.008	0.144	0	-0.205	0.412	-0.053	-0.063	**0.54**	-0.242	-0.149	0.1	0.072	0.017	0.042	0.039	0.117	-0.002	0.762**
SB	0.001	0.143	0	-0.231	0.531	-0.016	-0.06	0.447	**-0.292**	0.045	-0.355	0.396	0.011	0.033	-0.057	0.256	0.004	0.856**
GOT	-0.013	-0.011	-0.001	-0.021	0.338	0.007	0.049	0.072	0.012	**-1.118**	1.004	-0.001	-0.05	-0.024	0.184	-0.18	-0.015	0.234
SI	0.025	0.036	0.001	-0.041	-0.16	-0.009	-0.04	-0.039	-0.075	0.811	**-1.383**	0.78	0.055	0.039	-0.263	0.251	0.018	0.006
LI	0.015	0.014	0.001	-0.052	0.129	-0.01	-0.004	0.034	-0.101	0.001	-0.94	**1.148**	0.04	0.035	-0.27	0.22	0.01	0.271
UHML	-0.024	0.019	0	-0.02	0.122	0.036	0.005	-0.042	0.015	-0.261	0.354	-0.213	**-0.216**	-0.22	0.979	-0.609	-0.032	-0.106
UI	0.03	-0.126	0	0.15	-0.22	-0.052	0.036	0.163	-0.07	0.192	-0.386	0.288	0.343	**0.139**	-0.95	0.609	0.075	0.22
Str	-0.005	0.037	-0.001	-0.075	0.059	0.035	-0.017	0.016	0.013	-0.157	0.276	-0.235	-0.161	-0.1	**1.317**	-1.005	-0.021	-0.024
EL	0.023	-0.048	0	0.065	-0.099	0.044	0.024	-0.058	0.069	-0.184	0.319	-0.232	-0.121	-0.077	1.214	**-1.09**	-0.005	-0.157
Mic	0.009	0.001	0.001	0.045	-0.053	0.028	0.012	-0.021	-0.018	0.294	-0.433	0.211	0.121	0.184	-0.485	0.092	**0.056**	0.043

Residual effect square = 0.0918

DFF-days to fifty per cent flowering (number of days), PH-plant height (cm), M-number of monopodia per plant, S-number of sympodia per plant, B-number of bolls per plant, L-number of locules per boll, DBB-days to first boll bursting (number of days), BW-boll weight (g), SB- number of seeds per boll, SCY-seed cotton yield per plant (g), SI-seed index (g), LI-lint index (g), GOT-ginning out turn (%), UHML-upper half mean length (mm), Str-fibre strength (g/tex), UI-uniformity index, and EL-elongation percentage (%), Mic-fibre fineness (µg/inch)

Boll weight exerted positive direct effect on seed cotton yield per plant (0.54) while the correlation of boll weight with seed cotton yield was positive and significant (0.762). The correlation between boll weight and seed cotton yield was positive and significant due to the positive indirect effect contribution through plant height (0.144), number of bolls per plant (0.412), seed index (0.1), lint index (0.072) and all fibre quality parameters except micronaire. These findings are in line with Pujer *et al*. (2014), Nikhil *et al*. (2018), Pooja *et al*. (2020) and Jangid *et al*. (2022).

Fibre micronaire exerted positive direct effect on seed cotton yield per plant (0.056) while the correlation of boll weight with seed cotton yield was positive. This is in line with the report of Deshmukh *et al.* (2019), Gnanasekharan *et al*. (2020) and Mahesh *et al*. (2021).

Days to fifty percent flowering showed negative indirect effect to plant height, number of bolls, number of locules per boll, boll weight, seed index and elongation percentage while negligible effect to number of seeds per boll and micronaire. Ginning out turn showed negative direct effect on seed cotton yield per plant (-1.12) due to the indirect effect contribution by plant height, number of monopodia, number of sympodia per plant, lint index and all fibre quality parameters except fibre strength. Number of monopodia per plant showed negligible indirect effect for all the traits under study.

The present study concluded that hybrids performed superior to parents based on *per se* performance. The hybrids K12 × RG763 and CNA1007 × RG763 can be used for the better attainment of yield as they have highest boll weight along with seed cotton yield per plant and ginning outturn. Regarding surgical purpose, RG763 × K12, RG763× CNA1007, PAIG379 × RG763 and K12 × CNA1007 hybrids can be used as they have high micronaire value. The path analysis revealed that fibre strength, lint index, number of bolls, boll weight and plant height can be considered as most important characters which can be used as selection criteria for the improvement of seed cotton yield per plant.

ACKNOWLEDGEMENT

The authors are thankful to the Department of cotton, Centre for Plant Breeding and Genetics (CPBG), TNAU, Coimbatore for providing resources for research and helping in breeding aspects.

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