J. Farm Sci., 38(4): (363-369) 2025

RESEARCH PAPER

Unravelling the genetic variability, correlation and explore the structure of genetic divergence in the RIL population of cotton (*Gossypium hirsutum* L.) derived from the cross RHAP 12 x RHAP 15

K. SAINATH*, B. P. MARUTHI PRASAD, B. R. PATIL AND M. AKSHAYA

Department of Genetics and Plant Breeding, College of Agriculture, Dharwad
University of Agricultural Sciences, Dharwad - 580 005, India
*E-mail: maruthiprasad1996@gmail.com

(Received: August, 2025 ; Accepted: November, 2025)

DOI: 10.61475/JFS.2025.v38i4.07

Abstract: The nature and magnitude of genetic variability, correlation and principal component analysis were estimated in the 142 RIL populations of cotton developed by hybridization between RAHP 12 and RAHP 15 by considering 10 quantitative and 6 fibre quality traits to reveal the considerable amount of diversity among these RILs. The 142 RILs along the check variety (MCU 5, Sahana, DHH 263, Binds, RHAP 12 and HBS 144) were evaluated in augmented design at the University of Agricultural Sciences, Dharwad during *kharif* 2021. The variability studies indicated that a high estimate of phenotypic coefficient of variation (PCA) and genotypic coefficient of variation (GCV) was observed for sympodial branches per plant, whereas the character plant height, number of monopodia per plant, number of bolts per plant and boll Weight showed moderate GCV and PCV and also high heritability was evident in plant height, number of monopodia per plant, number of bolls per plant, seed cotton yield and ginning output. The correlation coefficient indicated that the number of bolls per plant, boll weight and lint yield per plant were significantly associated with seed cotton yield, suggesting that one or more yield traits can be used as selection criteria to improve the seed cotton yield. Five principal components showed an eigenvalue of more than one with an accumulated variability of 75.96%. The principal component with the highest variability was mostly related to boll weight and seed index.

Key words: Correlation, Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCA), Recombinant inbred lines

Introduction

Cotton is known as the “king of appraisal fibers,” as it meets mankind’s basic needs. It belongs to the Malvaceae family and the genus *Gossypium*. It is one of the most significant *kharif* fiber crops that is grown all over the world. It is a cornerstone of textile industries; 60 *per cent* of Indian textile industries depend on cotton, which provides raw material for various agro-based industries like ginning factories, oil mills and textile industries, which provide employment to over 60 million individuals. But in recent decades, progress in improving cotton yield and fiber quality traits has been stagnant, which fails to meet the basic demands of the modern textile industry. However, it is reported that in upland cotton yield is often negatively correlated with fiber quality (Yu *et al.,* 2013). It is tedious to break the linkage associated with negatively correlated traits through conventional breeding programs, (Bridge and Meredith, 1983). So, it is necessary to create the genetic variation in cotton through various means *viz.*, recombination, genetic transformation, mutation, *etc*.

The use of plant genetic resources (PGR) in crop improvement as a potential tool to conserve valuable genetic resources for the future breeding programs. The improved materials are probably one of the most sustainable ways to ‘conserve’ valuable genetic resources for the future. Incorporation, genetic enhancement or base broadening aim at increasing the genetic variation for quantitative traits in breeding material. Various methods of population improvement can be used. Cross-over genotype-environment interactions represent the situation where newly bred ‘widely adapted’ cultivars are inferior to local, indigenous varieties under extreme environmental conditions. Hence, the development of the RIL population is one of the classical forms of breeding strategy, where released varieties are crossed to create recombinants that are then inbred to isogeneity, resulting in a permanent resource for trait mapping and analysis. (Haussmann *et al.,* 2004)

Furthermore, variability is the key element in plant breeding, where selection acts to produce a desired genotype. Insight into the magnitude of variability present in a crop is of utmost importance as it provides the basis for selection. Genetic variability along with the heritability of a character, indicates the possibility and extent to which improvement can be achieved through selection on a phenotypic basis. High heritability coupled with a high genetic advance as a percent of the mean would bring out the progress expected from selection. Therefore, the present study was undertaken to elucidate the genetic variability, heritability and genetic advance over mean of various yield components andfibre quality parameters in the RIL population of cotton. Also, successful hybridization programs rely on utilizing genetic diversity based on various morphological and agronomic traits, necessitating meticulous selection due to the influence of environmental factors. Therefore, significant attention should be devoted to developing high-yielding cotton cultivars (Ahmad *et al.,* 2012). Future cotton production hinges on the development of varieties with enhanced yield potential, seed cotton quality and improved tolerance to biotic and abiotic stresses. Breeding efforts typically involve recording data on economically favorable traits; understanding the correlation of factors affecting yield is essential for designing effective plant-breeding programs.

Correlation studies in plant breeding offer crucial insights into the associations between highly heritable traits and economically important characteristics. Understanding these relationships helps breeders comprehend the individual contributions of traits to the genetic makeup of the crop. Given the complexity of seed cotton yield and fiber quality traits, which are influenced by environmental factors, direct selection alone may not be dependable. Hence, breeders must carefully examine both direct and indirect correlations among different traits when selecting plants for breeding purposes. This holistic approach ensures a more effective selection process and contributes to the development of superior crop varieties (Nikhil *et al.,* 2018).

In cotton crop breeding, the primary goal is to develop varieties that yield high quantities of seed cotton while maintaining acceptable fiber quality. However, the complexity of economic traits such as seed cotton yield, influenced by environmental factors and polygenic inheritance with low heritability, poses challenges to direct selection, so multivariate statistical techniques, such as principal component analysis (PCA) was employed by breeders to evaluate genetic diversity and understand the associations among different variables. The practical application of multivariate statistics involves various types of analyses to elucidate relationships among variables and their relevance to real-world problems (Bidri *et al.,* 2019).

Material and methods

Selection of parents

For development of the RIL population RHAP 12 and RHAP 15 were selected as parental lines. These parental lines were stabilized and segregating lines were developed at theUniversity of Agricultural Sciences, Dharwad. RHAP 12 was derived from hybridization between HGHV 99/300 and Pusa 1927 upland cotton lines, whereas RHAP 15 was drawn from crossing between Surabhi and GMR 5 of *Gossypium hirsutum*. The parent RHAP 12 is used as male as it exhibits tolerance to sucking pests, while the parent RHAP 15 is used as female as it has good fibre quality traits, *i.e.,*fibre strength up to 29.3 g/tex and it is an early maturing type, so we can go for early picking. These parents are considered for the development of the RIL population and we can also use the population as a mapping population.

Table 1. Characteristics of parental lines *viz.,*RHAP 12 and RHAP 15 of *G. hirsutum*

Traits	RHAP 12	RHAP 15
Plant height (cm)	124.70	131.10
Number of monopodia per plant	3.00	3.65
Number of sympodia per plant	10.60	12.90
Number of bolls per plant	25.40	18.50
Seed cotton yield per plant (g)	70.00	55.00
Seed index (g)	7.40	6.45
Boll weight (g)	3.35	2.64
Ginning outturn (%)	38.80	35.85
Lint index (g)	4.69	3.61
Fibre strength (g/tex)	29.30	22.20
Upper half mean length (mm)	27.50	25.10
Micronaire value (mg/inch)	3.83	3.54
Uniformity index (%)	88.80	84.50
Maturity ratio	0.47	0.55
Fibre elongation length (%)	6.40	6.90

Table 2. Characteristics of parents

Character	RAHP12	RAHP 15
Maturity	Early	Late
Fibre strength	29.3 g/tex	23.2 g/tex
Quality of Fibre	Good	Poor
Pubescence	Less	More
sucking pest incidence	susceptible	Tolerance

Development of RIL population

The Recombinant Inbred Lines (RIL) were derived from intraspecific hybridization between cotton (*Gossypium hirsutum* L) genotypes, *viz.,* RHAP 12 and RHAP 15, which are contrastingly different *w.r.t.* fiber strength, tolerance to sucking pests, early maturing and seed cotton yield, which is illustrated in Fig 1 and The salient features of the parents used in the present investigation are also provided in Tables 1 and 2. During *kharif* 2015 both the parents were crossed to develop the F_1 and further during 2016 F_1 generation was selfed to generate F_2 population and during *kharif* 2017, we forwarded 230 F_2 individuals using single seed descent method and further during *kharif* 2018, no evaluation carried out, forwarded all F_3 material. Again, during *kharif* 2019, evaluation and selection families for high yielding and conducted a genetic study and keep the remnant seed from line and forwarded 142 F_4 individuals. Again, during *kharif* 2020, no evaluation of the F_5 population was carried out and the material was forwarded and during *kharif* 2021, the F_6 population was evaluated and selected as the top-performing individual RIL's for fibre quality traits. The pedigree of mentioned parents along with their silent feature are

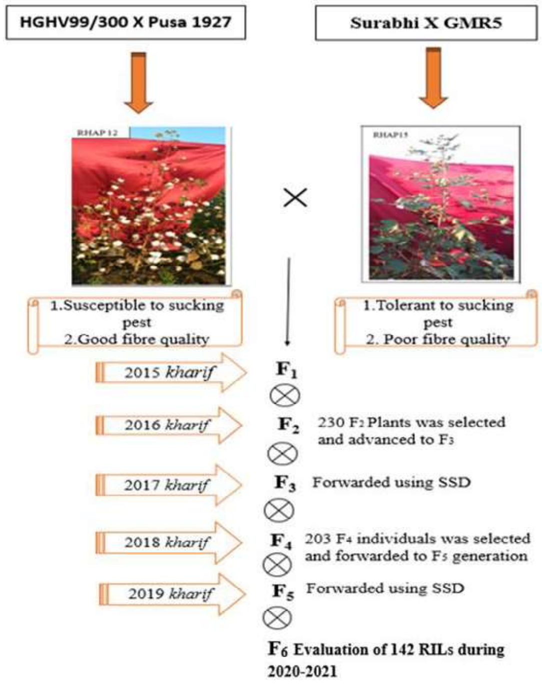

Fig 1. The schematic representation of development of RIL population by crossing RAHP 12 and RAHP 15

mentioned in Table and developmental process of these RIL population is illustrated Table 1 and Table 2.

Evaluation of RIL population

The RILs and check variety (MCU 5, Sahana, DHH 263, Binds, RHAP 12, and HBS 144) were evaluated in augmented design at the University of Agricultural Sciences, Dharwad, during *kharif* 2021. The spacing between and within the rows was maintained at 90 and 30 cm, respectively. The randomly selected five plants from each line were used for observing the following parameters: plant height (cm), number of sympodial branches, number of monopodial branches, number of bolls per plant, seed cotton yield per plant (g), seed index (g), boll weight (g), lint index (g), lint yield per plant (g), ginning out turn (%), fiber strength (g/text), fiber length (mm), Micronaire value (µg/inch), maturity coefficient (%), fiber elongation (%) and fiber uniformity ratio (%). Analysis and estimates of genotypic and phenotypic coefficients of variation, broad sense heritability, genetic advance over mean and principal components analysis (PCA) performed by the R package, Excel (2013), and SPSS (22.0).

Results and discussion

The analysis of variance for all yield and yield-attributing traits showed highly significant phenotypic mean sum of squares. The results clearly showed wide genetic differences between yield and yield-attributing traits (Table 3) and Fig 2 depicts the distribution of phenotypic values in box plot form for each yield attribute considered for study. The level of variability in various genotypes concerning 16 traits were measured in terms of range, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), broad sense heritability (h^2bs)and genetic advance over mean (GAM), as shown in Table 4 and also illustrated in graphical form in Fig 3 and 4.

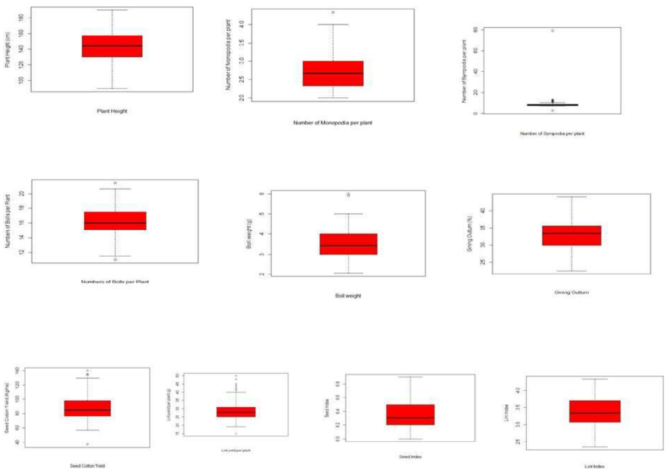

Fig 2. Box plot showing phenotypic distribution of yield and its components

In population RHAP 12 X RHAP 15, only one character registered high GCV and PCV for yield-related traits, *viz.,* sympodial branches per plant (20.4; 27.42), whereas the character plant height (13.52; 14.5), number of monopodia per plant (13.74; 16.69), number of bolts per plant (10.94; 13.14), and boll weight (14.23; 18.72) showed moderate GCV and PCV. The present findings confirm the results of Choudki *et al.* (2012), Deyi *et al.* (2016) and Ramesh *et al.* (2018). The results indicated that sufficient availability of variability is presentfor these traits, moderate to high GCV and PCV for these characteristics suggested ample opportunity for yield improvement in cotton through selection. The character *viz.,* seed index (3.95; 5.73)

Tables 3. Analysis of variance for yield, yield attributes and fibre quality traits in RIL population of cotton (*Gossypium hirsutum* L).

Source	Df	PH	MP	SP	NBP	BW	SCY	LYP	SI	GOT	LI
Treatment (ignoring Blocks)	142	482.17**	0.2**	11.94*	4.49**	0.55*	388.56**	41.64**	0.17*	15.05**	0.19*
Treatment: Check	5	794.4**	0.21*	5.34*	5.47*	0.43**	257.95**	22.11**	0.04*	3.72*	0.06*
Treatment: Test vs. Check	1	5506.84**	0.44*	18.17**	3.53*	1.25*	3968.71**	462.29**	1.73**	29.63*	1.54**
Treatment: Test	136	433.74**	0.19**	12.14*	4.46**	0.55*	367.03**	39.27**	0.17*	15.36**	0.19*
Block (eliminating Treatments)	4	103.76	0.25*	6.13	1.01	1.09**	101.08	6.53	0.09	1.43	0.08
Residuals	20	56.79	0.06	5.37	1.37	0.23	117.5	14.81	0.09	5.4	0.08

Source	Df	EL	Mic	MR	STR	UHML	UI
Treatment (ignoring Blocks)	142	0.02*	0.11 **	0.0034 *	2.11 **	0.79 **	17.16**
Treatment: Check	5	0.04*	0.33 **	0.01 **	13.25 **	2.42 **	45.9**
Treatment: Test vs. Check	1	0.38**	0.0016	0.00042	0.15	4.92 **	306.88**
Treatment: Test	136	0.01	0.09 **	0.0025	0.74 *	0.47 *	6.05**
Block (eliminating Treatments)	4	0.03*	0.00053	0.00003	0.02	0.00083	0.44*
Residuals	20	0.004	0.00091	0.00074	0.09	0.08	0.04

*P <= 0.05; **P <= 0.01

PH-Plant Height in cm, NMP- Number of Monopodia per Plant, NSP- Number of Sympodia per Plant, NBP- Number of Bolls per Plant, BW-Boll Weight, GOT- Ginning Outturn in per cent, SI- Seed Index, LI- Lint Index, SCY- Seed Cotton Yield (g), UHML- Upper Half Mean Length in mm, UI- Uniformity index, STR- Fibre Strength in g tex^{-1}, EL-Fibre Elongation in per cent, MR- Maturity Ratio and MIC- Micronaire value in µg inch^{-1}.

Table 4. Mean, range and component of variance of yield and its component traits and fibre quality traits in recombinant inbred lines of cotton (*Gossypium hirsutum* L).

Traits	Mean	Range	PCV		GCV	h^2	GAM
			Min	Max			
PH	143.62	85.1	188.38	14.5	13.52	86.91	26
MP	2.64	1.67	4.47	16.69	13.74	67.83	23.35
SP	12.71	4.4	19.57	27.42	20.47	55.74	31.53
NBP	16.08	10.64	21.06	13.14	10.94	69.41	18.81
BW	3.97	2.31	7	18.72	14.23	57.79	22.32
SCY	89.03	35.33	139.5	21.52	17.74	67.99	30.18
SI	7.13	6.44	8.09	5.73	3.95	47.41	5.61
LYP	29.49	14.47	49.3	21.25	16.77	62.28	27.31
LI	3.66	2.51	4.62	11.83	9.05	58.6	14.3
GOT	32.85	22.65	40.73	11.93	9.61	64.85	15.96
UHML	27.64	26.09	30.2	2.49	2.28	83.78	4.3
STR	25.7	21.35	29.1	3.34	3.12	87.13	6.01
Mic	3.64	3.06	4.32	8.17	8.12	98.96	16.67
UI	84.71	72.7	91.39	2.9	2.89	99.26	5.95
MR	0.6	0.51	0.73	8.27	6.93	70.33	11.99
EL	5.59	5.35	6	1.75	1.34	58.26	2.11

PH-Plant Height in cm, NMP- Number of Monopodia per Plant, NSP- Number of Sympodia per Plant, NBP- Number of Bolls per Plant, BW-Boll Weight, GOT- Ginning Outturn in per cent, SI- Seed Index, LI- Lint Index, SCY- Seed Cotton Yield (g), UHML- Upper Half Mean Length in mm, UI- Uniformity index, STR- Fibre Strength in g tex^{-1}, EL-Fibre Elongation in per cent, MR- Maturity Ratio and MIC- Micronaire value in µg inch^{-1}.

followed by fiber quality parameters registered a low GCV and PCV, hence it indicated that presence of lesser amount of variability for these traits. These results are in agreement with the observations of Nagaraju (2016), Muhammad *et al.,* 2015 and Deyi *et al.* (2016).

High heritability was evident for plant height (86.91%), number of monopodia per plant (67.83 %), number of bolls per plant (69.41%*),* seed cotton yield (67.99 %*)* and ginning outturn (64.85 %). High heritability coupled with high genetic advance over a mean for character, *viz.,* plant height, number of monopodia per plant, number of sympodial branches, seed cotton yield and lint yield per plant. It reveals the preponderance of additive gene action in the expression of these traits in cotton.

Identification of top performing superior RILs for fibre quality traits

With all the above results, an attempt was made to identify the top-performing superior RILs drawn from the crosses, *viz*., RHAP 12 × RHAP 15, which are represented in Table 5

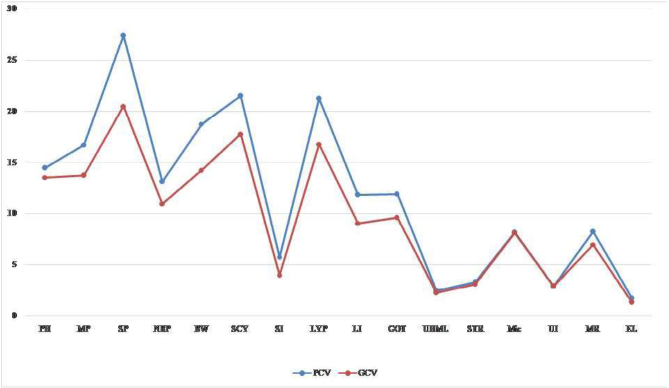

Fig 3. Depicting the phenotypic and genotypic coefficient of variation for yield, yield contributing character and fibre quality traits in RIL population of cotton (*Gossypium hirsutum* L)

PH-Plant Height in cm, **NMP**- Number of Monopodia per Plant, **NSP**- Number of Sympodia per Plant, **NBP**- Number of Bolls per Plant, **BW**- Boll Weight, **GOT**- Ginning Outturn in per cent, **SI**- Seed Index, **LI**- Lint Index, **SCY**- Seed Cotton Yield (g), **UHML**- Upper Half Mean Length in mm, **UI**- Uniformity index, **STR**- Fibre Strength in g tex^{-1}, **EL**-Fibre Elongation in per cent, **MR**- Maturity Ratio and **MIC**- Micronaire value in µg inch^{-1}.

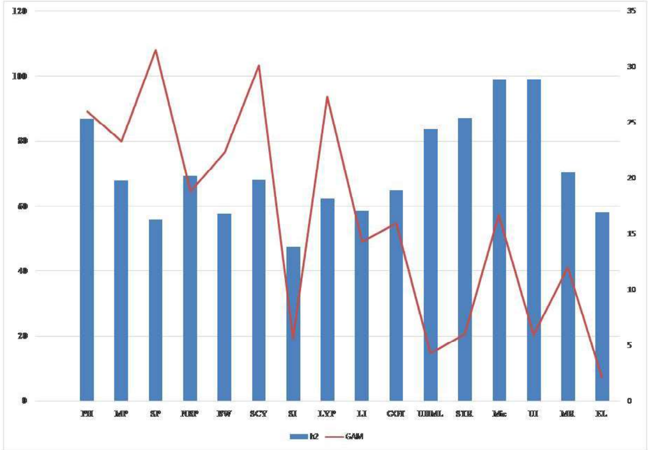

Fig 4 . Depiction of heritability and genetic advance over a mean for yield, yield contributing character and fibre quality traits in RIL population of cotton

PH-Plant Height in cm, NMP- Number of Monopodia per Plant, NSP- Number of Sympodia per Plant, NBP- Number of Bolls per Plant, BW- Boll Weight, GOT- Ginning Outturn in per cent, SI- Seed Index, LI- Lint Index, SCY- Seed Cotton Yield (g), UHML- Upper Half Mean Length in mm, UI- Uniformity index, STR- Fibre Strength in g tex^{-1}, EL-Fibre Elongation in per cent, MR- Maturity Ratio and MIC- Micronaire value in µg inch^{-1}

Table 5. Top five superior RIL'S identified from the cross RHAP 12 × RHAP 15

RILs	UHML (mm)	FS (g/tex)
RIL 48-2	29.1	27.6
RIL 19-2	28.7	27.1
RIL 83-2	28.5	26.9
RIL 148-2	28.4	26.8
RIL 58-2	28.3	26.6
Mean ± SD	28.1	26.3

Correlation analysis

Correlation coefficient analysis is a valuable tool for assessing the relationships between different plant characteristics. Phenotypic correlations between traits are crucial for initiating breeding programs. When two traits exhibit a positive and significant correlation, improvements in one trait will have a notable effect on the other. Therefore, selecting one characteristic will also positively affect other associated traits. The correlation coefficient serves as a reliable indicator of these relationships, helping breeders distinguish between essential traits and those that are less critical for breeding purposes.The phenotypic correlation coefficient between yield and yield components is shown in Table 6 and also depicted in graphical form in Fig 6. (Ahsan *et al.,* 2015).

In the present study, plant height exhibited a positive and non-significant correlation with the number of monopodia per plant, seed index, lint yield per plant, number of sympodia per plant, and seed cotton yield. However, plant height showed a negative but non-significant relationship with the number of bolls per plant, boll weight, lint index, and GOT. The number of monopodia per plant showed a positive and non-significant association with boll weight and seed index, while there was a negative and non-significant association with the number of sympodial per plant, the number of bolls per plant, the lint yield per plant, the lint index, and GOT, but no correlation with seed cotton yield. The number of sympodia per plant exhibited a positive and non-significant correlation with seed cotton yield, followed by the number of bolls per plant and boll weight lint yield per plant. The number of bolls per plant showed a positive and significant association with seed cotton yield, followed by lint yield per plant, while character boll weight exhibited a negative and significant correlation, while seed index, lint index, and GOT showed a negative and non-significant correlation with boll weight. The boll weight exhibited a positive and significant correlation with seed cotton yield, followed by lint yield pre-plant, but a positive and non-significant correlation with seed index and a negative and non-significant correlation with lint index and GOT. The seed index showed a positive and significant correlation with the lint index but a positive and non-significant correlation with seed cotton yield, lint yield per plant and GOT. The lint yield per plant showed a positive and significant correlation with seed cotton yield, followed by GOT, and a negative and non-significant correlation with the lint index. The lint index exhibited a positive and significant correlation with GOT but a negative and significant correlation with seed cotton yield, while GOT showed a negative and significant association with seed cotton yield. Similar results are reported by Deyi *et al.* (2016), Fakhar *et al.,* 2015, Hafiz *et al.,* 2013, Rehman *et al.,* 2020 and Ramesh *et al.* (2018).

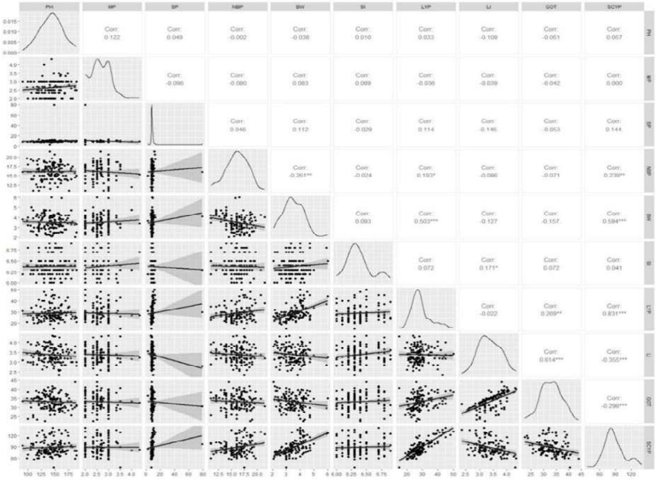

Fig 5. Schematic model of plot showing characters correlation with each other

PH-Plant Height in cm, **NMP**- Number of Monopodia per Plant, **NSP**- Number of Sympodia per Plant, **NBP**- Number of Bolls per Plant, **BW**- Boll Weight, **GOT**- Ginning Outturn in per cent, **SI**- Seed Index, **LI**- Lint Index, **SCY**- Seed Cotton Yield (g)

Principal component analysis

Principal component analysis was carried out to explore the structure of genetic divergence among cotton RIL's based on multiple traits. The eigenvalues represent the amount of variance explained by each principal component (PC). PC1 had an eigenvalue of 2.47, indicating that it accounts for the most variability in the dataset, followed by PC2 (1.71), PC3 (1.29), PC4 (1.11), and PC5 (1.00). The percentage of variance explained

Table 6. Phenotypic correlation for yield and yield contributing characters in RIL population of cotton

PH	MP	SP	NBP	BW	SI	LYP	LI	GOT	SCYP	
PH	1.000	0.122	0.049	-0.020	-0.038	0.010	0.033	-0.108	-0.051	0.057
MP		1.000	-0.096	-0.080	0.083	0.089	-0.036	-0.039	-0.042	0.000
SP			1.000	0.046	0.112	-0.029	0.114	-0.146	-0.053	0.144
NBP				1.000	-0.261**	-0.024	0.193*	-0.086	-0.071	0.239**
BW					1.000	0.093	0.503**	-0.127	-0.157	0.594**
SI						1.000	0.072	0.171*	0.072	0.041
LYP							1.000	-0.022	0.269**	0.831**
LI								1.000	0.614**	-0.355**
GOT									1.000	-0.298**

Table 7. Principal factor matrix after varimax rotation for 10 characters in RIL population of cotton (*Gossypium hirsutum* L)

	PC 1	PC 2	PC 3	PC 4	PC5	Communalities
PH	0.090	-0.152	0.154	0.626	0.589	0.793
MP	0.023	-0.051	0.577	0.503	-0.100	0.600
SP	0.272	-0.094	-0.215	-0.209	0.697	0.659
NBP	0.181	-0.086	-0.741	0.480	-0.262	0.889
BW	0.708	0.231	0.438	-0.303	0	0.839
SI	0.031	0.349	0.299	0.290	-0.176	0.327
LYP	0.772	0.545	-0.174	0.091	0.011	0.932
LI	-0.474	0.734	-0.015	0.016	0.032	0.765
GOT	-0.343	0.809	-0.151	0.054	0.209	0.841
SCYP	0.959	0.090	-0.082	0.067	-0.114	0.953

PH-Plant Height in cm, NMP- Number of Monopodia per Plant, NSP- Number of Sympodia per Plant, NBP- Number of Bolls per Plant, BW- Boll Weight, GOT- Ginning Outturn in per cent, SI- Seed Index, LI- Lint Index, SCY- Seed Cotton Yield (g)

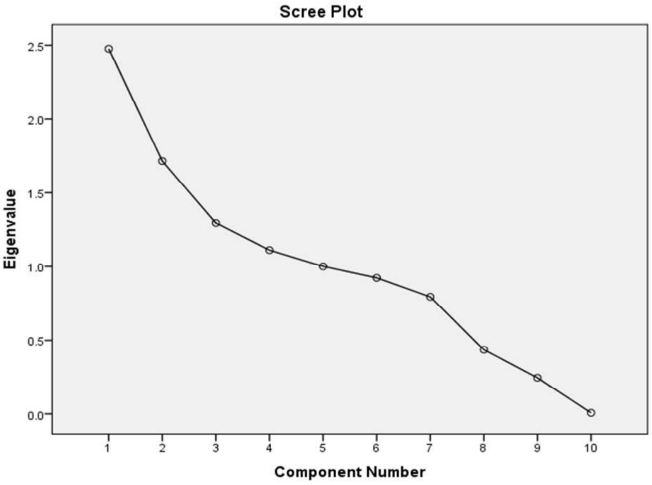

Fig 6. Scree plot showing eigenvalues in response to number of components for the estimated variables of cotton

by each PC provides insights into the proportion of total variability captured by the PCs. PC1 explained 24.76% of the total variance, PC2 explained 17.14%, PC3 explained 12.93%, PC4 explained 11.10%, and PC5 explained 10%. Together, these five components accounted for a cumulative total of 75.96% of the variance in the dataset (Table 8).

Table 8. Total variance explained for each component

Components	Eigen values	% of Variance	Cumulative %
1	2.48	24.76	24.76
2	1.72	17.15	41.91
3	1.29	12.93	54.85
4	1.11	11.11	65.95
5	1.00	10.01	75.96

In the first component, the number of sympodia per plant (0.272), boll weight (0.708) and lint yield per plant (0.772) have positive and high effects. In the second component, boll weight (0.231), seed index (0.349), lint yield per plant (0.545), lint index (0.734) and ginning outturn (0.090)has the highest and most positive effects. In the third component number of monopodia per plant (0.577), boll weight (0.438) and seed index outturn (0.299) have the highest and most positive effects. In the fourth component, plant height(0.626), number of monopodia per plant (0.503), number of bolls per plant (0.480) and seed index (0.290) have the highest and most positive effect.In the fifth component, plant height (0.589), number of sympodia per plant (0.697) and ginning outturn (0.209) have the highest and most positive effect (Table 7). A comparison of five components reveals that the number of bolls per plant and seed index exist in PC1, PC2, PC3 and PC2, PC3 and PC4 components, respectively, and have a positive and highest effect. The number of bolls per plant and seed index in cotton are important components of yield because they directly affect yield. Similar results are reported in the reports of Latif *et al.* (2015), Diaa *et al.* (2015) and Mohsen and Amein (2016).

Scree plot

A scree plot explained the percentage variance associated with each principal component obtained. By drawing a graph between eigenvalue and principal component number (Fig 6), PC1 showed 24.76% variability with eigen values 2.48, PC2 showed 17.15% variability with eigen values 1.72, PC3 showed 12.93% variability with eigen values 1.29, PC4 showed 11.11% variability with eigen values 1.11, and PC5 showed 10.01% variability with eigen values 1. (Table 8)

By examining the scree plot, it was evident that the first five PCs have considerable variability, while from PC6 to PC10, variability is reduced.

Conclusion

Success in cotton breeding is predominantly based on the selection and use of promising genotypes for hybridization, followed by assortment for favourable genes and gene complexes. The observed phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for the traits *viz.,* number of sympodia per plant indicating the lesser influence of environment. High heritability coupled with high genetic advance over a mean for character, *viz.,* plant height, number of monopodia per plant, number of sympodial branches, seed cotton yield, and lint yield per plant. It reveals the preponderance of additive gene action in the expression of these traits in cotton. Principal component analysis unveiled distinct patterns of divergence among the RILs, offering valuable insights that can be harnessed to identify and prioritize the selection of high-performing RILs for subsequent crop improvement endeavours.

References

Ahmad M Q, Khan S H and Azhar F M, 2012, Decreasing level of genetic diversity in germplasm and cultivars of upland cotton (*Gossypium hirsutum* L.) in Pakistan. *Journal of Agriculture and Social Sciences*, 8: 92-96.

Ahsan M Z, Majidano M S, Bhutto H, Soomro A W, PanhwarF H, Channa A R and Karim B S, 2015, Genetic variability coefficient of variance heritability and genetic advance of some *Gossypium hirsutum* L accessions. *Journal of Agriculture Science,* 7(2): 1-7.

Badri A M, Talat F and Fayyaz M A, 2019. Yield components analyses in cotton: *G. hirsutum* cultivars with multivariate statistical methods. *Genetika*, 51(2): 595-606.

Choudki V M, Katageri I S, Patil R S and Vamadevaiah H M, 2012, Evaluation of F_{11} recombinant lines of *G herbaceum* × *G anomalum and G herbaceum* × *G barbadense* crosses for fibre traits in cotton. *Karnataka Journal of Agricultural Sciences,* 25(4): 414-417.

Deyi S, Tao W, Haiping Z, Jianmei Z and Feiyu T, 2016, Variation heritability and association of yield fiber and morphological traits in a near long staple upland cotton population. *Pakistan Journal of Botany,* 48(5): 1945-1949.

Diaa A E, Ashraf A A, Hashem M A, 2015, Evaluating Bivariate and Multivariate statistical analysis of yield and agronomic characters in Egyptian cotton. *Scientia Agriculturae*, 9(3): 150-164

Fakhar Z K, Shoaib U R, Muhammad A A, Waqas M, Chaudhry M H, Muhammad B, Ghulam Q, Asif L, Javaria A and Umar F, 2015, Exploitation of germplasm for plant yield improvement in cotton (*Gossypium hirsutum* L*). Journal of Green Physiology, Genetics and Genomics,*11: 1-10.

Hafiz G A, Abid M and Qurban A, 2013, Genetic variability heritability genetic advance and correlation studies in cotton (*Gossypium hirsutum* L). *International Journal of Microbiology,* 4 (6): 156-161.

Haussmann B I G, Parzies H K, Presterl T, Susic Z and Miedaner T, 2004. Plant genetic resources in crop improvement. *Plant Genetic Resources*, 2(1): pp.3-21.

Latif A, Bilal M, Hussain S B and Ahmad F, 2015, Estimation of genetic divergence, association, direct and indirect effects of yield with other attributes in cotton (*Gossypium hirsutum* L.) using biplot correlation and path coefficient analysis. *Tropical Plant Research*, 2(2): 120-126.

Meredith W R Jr and Bridge R R, 1983, The relationship between F_2 and selected F_3 progenies in cotton *Gossypium hirsutum* L. *Crop Sciences,* 13: 354-356.

Mohsen A M, Amein, 2016, Study the relationships between seed cotton yield and yield component traits by different statistical techniques, *Bangladesh Journal of Agricultural Research*, 2225-3610.

Muhammad A K, Tanwir A M, Nida F, Aamir S, Ihsan K, Muhammad A, Sabah M and Plosha K, 2015, Correlation for economic traits in upland cotton, *Acta Scientific Agriculture,* 2(10): 59-62.

Nagaraju C H, 2016, Studies on genetics of QTLs for yield, yield component and fibre quality traits in cotton. *Ph D Thesis,* University of Agricultural Sciences, Dharwad, India.

Nikhil P G, Nidagundi J M and Hugar A, 2018. Correlation and path analysis studies of yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(5): 2596-2599.

Ramesh U M, Katageri I S and Mohan Kumar N V, 2018, Genetic variability and transgressive segregation studies in inter specific cotton (*Gossypium hirsutum* × *G. barbadense*) recombinant inbred lines population. *Journal of Farm Sciences*, 31(4): 373-377.

Rehman A, Mustafa N, Du X and Azhar M T, 2020, Heritability and correlation analysis of morphological and yield traits in genetically modified cotton. *Journal of Cotton Research*, 3: 1-9.

Yu J, Yu S, Gore M, Wu M, Zhai H, Li X, Fan S, Song M and Zhang J, 2013, Identification of quantitative trait loci across interspecific F_2, $F_{2:3}$ and test cross populations for agronomic and fibre traits in tetraploid cotton. *Euphytica*, 191(3): 375-389.