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# GENETIC VARIABILITY AND CORRELATION STUDIES FOR SEED COTTON YIELD AND FIBRE QUALITY PARAMETERS IN DIVERSE COTTON GENOTYPES

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**ABSTRACT**

An experiment was executed at RARS, Lam, Guntur during the *kharif*, 2024 to determine variability and correlation studies across 50 cotton genotypes, including three check varieties (NDLH 2051-1, Sivanandhi, and CICR 23 Bt) for 14 traits in an Augmented Block Design. ANOVA revealed significant differences among the 53 cotton genotypes for all the 14 traits, indicating substantial variability within the experimental material,that could be used for further crop improvement. Genotypic coefficient of variation and phenotypic coefficient of variation were high for number of monopodia per plant,boll weight and seed cotton yield per plant. High heritability coupled with high genetic advance was observed for plant height, number of monopodia per plant, number of bolls per plant, boll weight, lint index, seed index and seed cotton yield per plant rendering the probability of selecting genotypes for these characters which would behave with fidelity being the additive gene action in the inheritance of these attributes. Correlation study demonstrated a significant positive relationship between seed cotton yield per plant and plant height, number of bolls per plant, boll weight, seed index and lint index, indicating direct selection could be preferable for improving the seed cotton yield per plant.The genotypes LHBT 2203, LHBT 9, L 2278 and L 2281 were identified as the best performers for lint index, seed index and seed cotton yield per plant; while Suvin, CCB 29, L 2275, L 2385 and L 2268 for fibre quality traits.

**Keywords:** Cotton, Correlation, GCV, Genetic Advance,Heritability and PCV

## INTRODUCTION

Cotton (*Gossypium* spp.) belongs to the group of oldest domesticated species and it is cultivated as the main source of raw materials for the textile industries. It is a vital commercial cash crop in India, contributing about 20.67% of global cotton production (AICRP on Cotton, 2024-25). Cotton is mainly cultivated in tropical as well as sub-tropical regions and is mainly grown for fibre and oil purpose. It is crucial for increasing the country's economy and is popularly known as "white gold"(Komala *et al*., 2018). It is classified under the genus *Gossypium* and the family Malvaceae.India is the only country that cultivates all four cultivated species of cotton that include

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*Gossypium arboreum* L.and *Gossypium herbaceum* L. which are diploid species (2n=26) and are known as old world cotton. *Gossypium barbadense* L. and *Gossypium hirsutum* L. which are tetraploid species (2n=52) and are known as new world cotton.

India holds the position of the second largest cotton producer across the globe after China. India ranks as the largest cultivating nation in the world with 11.8 million hectare and produces 25.00 million bales (170 kg/bale) with productivity of 461 kg per hectare (AICRP on Cotton, 2024–25). During 2024-25, the Cotton production in India amounted to produce 299.26 lakh bales from 113.6 lakh hectares with a productivity of 448 kg lint/ha. In comparison of present year (2024-25) to last year (2023-24) the imports were estimated to increase from 15.20 lakh bales (64.47%) to 25.00 lakh bales in 2024-25. Whereas the exports were estimated to decrease from 28.36 (36.53%) to 18.00 lakh bales (AICRP on Cotton, 2024–25). Hence, it becomes crucial to develop high yielding cotton genotypes coupled with superior fibre quality to meet textile industry demands. Climate change further complicates cotton productivity. While many high-yielding cultivars exist, they often lack the desired fibre quality. Over the past decade, a decline in both yield and quality has been observed, largely attributed to a loss of genetic diversity in current cotton genotypes (Sahar *et al.,* 2021).

Genetic variability depends upon numerous morphological and agronomical at tributes and their interaction with surrounding biotic influences and abiotic influences. The extent and nature of available genetic variation within germplasm offers significant potential for use in successful breeding programs. This could lead to improvements in various characteristics related to cotton yield alongside with fibre quality(Chapara *et al.,* 2022).To effectively select superior genotypes and understand the relationships among yield components and fibre characteristics, it is important to know information on the kind and degree of genetic variation, heritability and genetic advance.

## MATERIAL AND METHODS

The study was executed at Regional RARS, Lam, Guntur, Andhra Pradesh during *kharif,* 2024-25. The trail comprised of 50 cotton genotypes and three checks (NDLH 2051-1, Sivanandhi and CICR 23 Bt), that were planted in an Augmented Block Design in six blocks. In first five blocks, 12 entries (nine genotypes + three checks) and in the last block eight entries (five genotypes + three checks) were planted randomly in the blocks. Each entry was sown in two rows with a row length of 6.3 m each with a spacing of 105 x 60 cm.

Data was recorded from ten randomly selected plants on various seed cotton yield contributing attributes like days to fifty percent flowering (plot basis), plant height (cm), number of sympodia per plant, number of monopodia per plant, number of bolls per plant, boll weight (g), seed index (g),lint index (g), ginning out turn (%), seed cotton yield per plant (g) and for fibre traits like Upper Half Mean Length (UHML) (mm), uniformity index (%), micronaire (µg/inch) and tenacity (g/tex) data was recorded on plot basis.

The means of 14 traits were assigned to Analysis of Variance (ANOVA). The genotypic, phenotypic and environmental coefficients of variation (GCV, PCV and ECV) along with magnitude of heritability ($h^2$) and genetic advance. All the analysis were performed using the 'augmented RCBD' package from R Studio software version R.4.4.2.Correlation between character pairs were computed at $p< 0.05$ and $p< 0.01$ in Microsoft Excel using trait averages.

## RESULTS AND DISCUSSION

ANOVA indicated notable differences among 50 cotton genotypes and three checks for all the 14 attributes suggesting substantial genetic variability among the materials (Table 1).As per the mean performance, the genotypes specifically NDLH 3104-4, L 2281, L 2278, LHBT 2203, L 2396, L 2381 and L 2386 exhibited superior characteristics particularly for seed index, lint index, boll weight and seed cotton yield per plant and forfibre quality attributes like Upper Half Mean Length (UHML), tenacity, uniformity index and micronaire the genotypes Suvin, CCB 29, L 2275, L 2385, LHBT 2395, LHBT 26 and Lam Bt 2208 recorded high mean values. Hence, the above genotypes could be suggested for future breeding programs to enhance seed cotton yield and fibre quality traits.

Across all traits analyzed, PCV estimates spanned from 1.83 to 31.27%, while the GCV estimates ranged from 1.61 to 29.67%, demonstrating a close relationship between the two for every trait. The findings also indicated higher heritability ($h^2$), ranged from 77.63 to 98.79, combined with considerable genetic advance estimates, from 0.71 to 58.49, for all traits examined.

The maximum GCV was observed for the number of monopodia per plant (29.67%), followed by seed cotton yield per plant (23.38%) and boll weight (20.31%).A similar pattern was observed for PCV respectively (Table 2). The environmental coefficients of variation were relatively low compared to the GCV, suggesting minimal environmental impact on these traits. These findings imply substantial genetic variability for these parameters, indicating their suitability for direct selection in breeding programs aimed at enhancing cotton yield and quality.Comparable results have been earlier documented by Sahar *et al.,*(2021),Chapara *et al.,* (2022), Mawblei *et al.,*(2022),Subalakhshmi *et al*., (2022), Keerthivarman *et al.,* (2023) and Harini *et al.,*(2025).

Plant height, number of sympodia per plant, number of bolls per plant, seed index and lint index exhibited moderate GCV and PCV values.Rigorous selection could be used for the enhancement of these attributes. These results were in agreement with those of Chapara *et al,.* (2022), Mawblei *et al.,* (2022) and Harini *et al*., (2025). Low estimates of GCV and PCV were recorded for days to fifty percent flowering, ginning outturn,upper half mean length, uniformity index, micronaire and tenacity, suggesting limited variation among the genotypes evaluated for these traits. Corresponding results were earlier noted by Chapara *et al*. (2022) and Harini *et al.* (2025) (Table 2).

The estimates of heritability, when considered along side genetic advance, offer valuable insights into the nature of gene action governing the expression of polygenic traits, particularly quantitative ones and serve as a dependable criterion for making selection decisions. In the present study, all traits exhibited high heritability values. Notably, high heritability coupled with high genetic advance as a percentage of the mean was observed for plant height, number of monopodia per plant, number of bolls per plant, boll weight, seed index, lint index and seed cotton yield per plant, indicating the predominance of additive gene effects. This suggests that direct phenotypic or simple selection would be effective for improving these traits. Selecting traits that combine high heritability with high genetic advance as a percentage of the mean can therefore be highly beneficial. Comparable results have been reported by Chapara *et al.,* (2022), Mawblei *et al.,* (2022), Keerthivarman *et al.,* (2023) and Harini *et al.,* (2025).

Days to fifty percent flowering, number of sympodia per plant, ginning outturn, upper half mean length, and micronaire displayed high heritability coupled with moderate genetic advance as a percentage of the mean, suggesting the influence of both additive and non-additive gene actions. This indicates that these traits could be more effectively improved

**Table 1. Analysis of variance for seed cotton yield attributing traits and fibrequality traits in 53 cotton genotypes**

| Source | Mean Sum of Squares (MSS) | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | df | DFF | PH (cm) | NMP | NSP | NB | BW (g) | SI (g) | LI (g) | GOT (%) | SCY (g) | UHML (mm) | UI (%) | MIC (µg/ inch) | TEN (g/ tex) |
| **Blocks** | 5 | 14 | 2114.6** | 0.11** | 6.36** | 240.06** | 3.19** | 14.01** | 1.57** | 1.75* | 25 97.7** | 0.90* | 3.38** | 0.1** | 3** |
| **Treatments** | 52 | 12.85** | 656.86** | 0.15** | 10.98** | 64.11** | 0.64** | 3.73** | 0.90** | 5.12** | 491.55** | 2.77** | 2.45** | 0.32** | 1.29** |
| **Checks** | 2 | 3.39** | 217.62** | 0.12** | 121.94** | 531.12** | 0.07 | 37.53** | 3.62** | 19.31** | 105.27** | 0.62 | 13.17** | 0.07 | 4.41** |
| **Treatment: Testand Testvs. Check** | 50 | 13.23** | 674.43** | 0.15** | 6.54** | 45.43** | 0.66** | 2.38** | 0.79** | 4.55** | 507** | 2.85** | 2.03** | 0.33** | 1.17** |
| **Error** | 10 | 0.72 | 18.31 | 0.01 | 1.189 | 2.46 | 0.02 | 0.09 | 0.06 | 0.42 | 8.7 | 0.17 | 0.5 | 0.02 | 0.08 |

**DFF=** Days to fifty per cent Flowering**; PH=** Plant Height(cm**); NMP=**Number of Monopodia per Plant;
**NSP**= Number of Sympodia per Plant; **NB**= Number of Bolls per Plant; **BW**= Boll Weight (g); **SI**= Seed Index(g);
**LI**= Lint Index (g); **GOT**= Ginning Out Turn (%); **SCY**= Seed Cotton Yield per Plant (g); **UHML**= Upper Half Mean Length(mm);
**MIC**= Micronaire(µg/inch); **TEN**=Tenacity (g/tex); **UI**= Uniformity index (%)

**df** = Degree of Freedom

*** Significant at 5% level, ** Significant at 1% level**

**Table 2. Estimates of genetic parameters for seed cotton yield attributing traits and fibre quality traits in 53 cotton genotypes**

| Traits | GCV (%) | PCV (%) | ECV (%) | $h^2_{bs}$ (%) | GA | GAM (%) |
|---|---|---|---|---|---|---|
| Days to fifty per cent flowering | 6.18 | 6.34 | 1.4 | 95.15 | 7.57 | 12.44 |
| Plant height (cm) | 19.27 | 19.48 | 2.88 | 97.82 | 58.49 | 39.32 |
| Number of monopodia per plant | 29.67 | 31.27 | 9.87 | 90.04 | 0.71 | 58.09 |
| Number of sympodia per plant | 10.39 | 11.79 | 5.58 | 77.63 | 3.67 | 18.88 |
| Number of bolls per plant | 17.44 | 17.77 | 3.37 | 96.4 | 16.44 | 35.34 |
| Boll weight (g) | 20.31 | 20.57 | 3.28 | 97.46 | 1.91 | 41.36 |
| Seed index (g) | 18.61 | 18.82 | 2.83 | 97.75 | 3.95 | 37.95 |
| Lint index (%) | 15.95 | 16.61 | 4.64 | 92.2 | 1.64 | 31.6 |
| Ginning out turn (%) | 5.79 | 6.07 | 1.84 | 90.85 | 4 | 11.38 |
| Seed cotton yield per plant (g) | 23.38 | 23.52 | 2.59 | 98.79 | 54.64 | 47.94 |
| Upper half mean length (mm) | 5.49 | 5.67 | 1.41 | 93.79 | 3.16 | 10.97 |
| Uniformity index (%) | 1.61 | 1.83 | 0.86 | 77.93 | 2.42 | 2.94 |
| Micronaire | 9.49 | 9.9 | 2.8 | 91.99 | 0.86 | 18.78 |
| Tenacity (g/tex) | 4.1 | 4.22 | 1 | 94.39 | 2.35 | 8.21 |

**GCV**= Genotypic Coefficient of Variation; **PCV**= Phenotypic Coefficient of Variation;
**ECV**= Environmental Coefficient of Variation; **GA**= Genetic Advance;
**GAM**= Genetic Advance Mean: $\mathbf{h}^2_{bs}$ = Heritability in broad sense

**Table 3. Correlation matrix of seed cotton yield attributing and fibre quality traits in 53 cotton genotypes**

| Traits | DFF | PH (cm) | NMP | NSP | NB | BW (g) | SI (g) | LI (g) | GOT (%) | SCY (g) | UHML (mm) | MIC (µg/inch) | TEN (g/tex) | UI (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | 1 | | | | | | | | | | | | | |
| PH (cm) | -0.245 | 1 | | | | | | | | | | | | |
| NMP | 0.395** | 0.041 | 1 | | | | | | | | | | | |
| NSP | -0.055 | 0.189 | 0.179 | 1 | | | | | | | | | | |
| NB | -0.310** | 0.387** | -0.119 | 0.218 | 1 | | | | | | | | | |
| BW (g) | -0.202 | -0.087 | -0.387** | 0.180 | 0.160 | 1 | | | | | | | | |
| SI (g) | -0.057 | 0.43** | -0.111 | 0.222 | 0.569** | 0.412** | 1 | | | | | | | |
| LI (g) | -0.044 | -0.234 | -0.262 | 0.147 | 0.463** | 0.457** | 0.714** | 1 | | | | | | |
| GOT (%) | -0.208 | 0.028 | -0.339* | -0.012 | -0.02 | 0.140 | -0.231 | 0.229 | 1 | | | | | |
| SCY (g) | -0.234 | 0.500** | -0.230 | 0.174 | 0.648** | 0.519** | 0.616** | 0.523** | 0.065 | 1 | | | | |
| UHML (mm) | 0.594** | -0.015 | 0.228 | 0.192 | -0.303* | 0.087 | 0.089 | 0.015 | -0.098 | -0.049 | 1 | | | |
| MIC (µg/inch) | -0.615** | 0.155 | -0.240 | -0.219 | 0.301* | -0.095 | -0.107 | -0.09 | -0.03 | 0.003 | -0.704** | 1 | | |
| TEN (g/tex) | 0.259 | 0.013 | 0.169 | 0.031 | -0.300* | 0.198 | 0.173 | 0.088 | 0.006 | 0.009 | 0.649** | -0.460** | 1 | |
| UI(%) | 0.553** | -0.045 | 0.339* | 0.200 | -0.224 | 0.077 | 0.041 | -0.134 | -0.254 | -0.030 | 0.569** | -0.389** | 0.382** | 1 |

**DFF=** Days to fifty percent Flowering**; PH=** Plant Height (cm**); NMP=**Number of monopodia per plant;
**NSP**= Number of sympodia per plant; **NB**= Number of bolls per plant; **BW**= Boll Weight (g); **SI**= Seed Index (g);
**LI**= Lint Index (g); **GOT**= Ginning Out Turn (%); **SCY**= Seed Cotton Yield per Plant (g);
**UHML**= Upper Half Mean Length(mm); **MIC**= Micronaire(µg/inch); **TEN**=Tenacity (g/tex) and **UI**= Uniformity index (%).
*** Significant at 5% level, ** Significant at 1% level**

through hybridization followed by selection.The present results concur with the findings of Chapara *et al.,* (2022), Keerthivarman *et al.,* (2023) and Harini *et al.,* (2025). High heritability combined with low genetic advance as a percent of the mean was recorded for uniformity index and tenacity. The heritability is being exhibited due to favourable influence of environment rather than genotype and implying that these traits could be improved through heterosis breeding as simple selection is ineffective. These results were in consonance with Chapara *et al.,* (2022) and Harini *et al.,* (2025) (Table 2).

Computation of correlation between yield attributing and fibre quality parameters is of considerable importance in plant selection. The correlation coefficients between yield contributing and fibre quality traits were presented in Table 3. Among 14 parameters studied, five traits namely, plant height (0.500**), number of bolls per plant (0.648**), boll weight (0.519**), seed index (0.616**) and lint index (0.523**)exhibited a significant positive correlation with seed cotton yield per plant; therefore, selecting for these traits would facilitate the identification of genotypes with superior seed cotton yield per plant. These results were in consonance with Arunkumar and Murthy (2020), Gnanasekaran *et al*., (2020), Gauswami Jyoti *et al.,* (2021), Chaudhry *et al.,* (2022), Mawblei *et al*., (2022) and Chapara *et al.,* (2024).

The principal fibre quality traits demonstrated positive inter-correlations. Upper half mean length, tenacity and uniformity index were positively and significantly associated with one another, while exhibiting a negative correlation with micronaire. Similar trends were reported by Gnanasekaran *et al.,* (2020), Chapara *et al.,* (2022), Gurmessa *et al.,* (2022) and Harini *et al.,* (2025). Therefore, simultaneous selection for plant height, number of bolls per plant, boll weight, seed index and lint index, along with fibre quality parameters such as upper half mean length, tenacity and uniformity index, could lead to substantial improvement in both cotton yield and fibre quality.

## CONCLUSION

In this investigation, analysis of variance indicated highly significant variation among 50 cotton genotypes and three checks for the 14 yield and fibre parameters indicating the existence of substantial genetic variation. Therefore, a combination of high heritability and high genetic advance was observed for the attributes *viz.*, plant height, number of monopodia per plant, number of bolls per plant, boll weight, seed index, lint index and seed cotton yield per plant rendering the probability of selecting the genotypes for these traits. The genotypes LHBT 2203, LHBT 9, L 2278 and L 2281 were identified to be the best performers for seed index, lint index and seed cotton yield per plant; Suvin, CCB 29, L 2275, L 2385 and L 2268 showed good for fibre quality traits. Association studies indicated that seed cotton yield was positively and significantly correlated with plant height, number of bolls per plant, boll weight, seed index and lint index and would help in direct selection and improving the seed yield of cotton genotypes.

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