



## Elucidating Genetic Variability and Association Among Yield and Fibre Quality Traits in American Cotton (*Gossypium hirsutum* L.)

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**ABSTRACT:** The present investigation was carried out to access genetic variability, heritability, genetic advancement and associations among yield and quality traits in 33 genotypes of upland cotton (*Gossypium hirsutum* L.) during Kharif 2020-21. Results unveiled considerable variation among genotypes for all the examined traits. The phenotypic coefficient of variance (PCV) slightly surpassed the genotypic coefficient of variance (GCV), implying a minimal environmental influence on trait expression. Notably, seed cotton yield exhibited a high level of GCV (24.40), PCV (26.41), high heritability (85.36), and substantial genetic advance (46.44). Whereas, number of bolls and boll weight exhibited high heritability along with moderate genetic advance indicating a contribution of both additive and non-additive gene actions to controlling these traits. Likewise, in case of quality traits, fibre length and fibre strength demonstrated high heritability (50.99 and 78.92, respectively) with low genetic advance (3.88 and 8.19), indicating their genetic control with limited scope for improvement. Furthermore, association studies revealed a highly positive significant correlation of seed cotton yield with lint yield (0.98), number of bolls (0.63), number of sympods (0.49), boll weight (0.42), number of monopods (0.38), ginning outturn (0.28) and plant height (0.25). Therefore, these attributes can be considered suitable selection criteria for increasing the yield of seed cotton.

**Keywords:** Cotton, correlation, GCV, heritability PCV, variability, yield.

### INTRODUCTION

Cotton holds significant economic importance in India, being regarded as one of the primary cash crops. Recognized as 'White Gold' due to its agricultural and industrial significance, the predominant species cultivated in India is *Gossypium hirsutum* L., covering over 90% of the total area. Worldwide, upland cotton, a prominent fibre-producing crop, is grown in over 80 countries (Dutt *et al.*, 2004). Despite its importance, the productivity of cotton, especially *Gossypium hirsutum*, has not seen substantial improvement.

Consequently, it is imperative to break the yield plateau by developing high-yielding cotton hybrids or varieties. This focus on research is crucial as these cultivars satisfy 90% of the world's cotton demand (Wendel *et al.*, 1992). To design effective crop improvement programs, it is essential to comprehend the nature and extent of genetic variability. Assessing genetic relationships among crop species provides insights into genetic diversity. The variability of a trait indicates the potential and scope for improvement through phenotypic selection. Studying the genetics of germplasm aids in estimating variability, correlations, path coefficient analysis, and quantifying the degree of divergence. This information is valuable for identifying

diverse genotypes and making recommendations for breeding programs to enhance both quality and quantity. While the primary goal for any breeder is to maximize yield, seed cotton yield is a complex quantitative trait influenced by polygenes. Relying solely on seed cotton yield for selection may not be effective. Breeders must understand the inter-relationships among different traits for efficient selection. Correlation coefficient analysis helps measure the magnitude of relationships between various plant characters, aiding in determining the component characters suitable for selection to enhance seed cotton yield. It quantifies the association among different traits and identifies the specific characteristics on which selection can effectively drive genetic improvement (Salahuddin *et al.*, 2010). It streamlines the selection process, empowering breeders to simultaneously choose a genotype based on two or more traits (Salahuddin *et al.*, 2010). So, keeping all these points, the aim of this study was to optimize the utilization of the variability and association present among the existing reference types of tetraploid cotton genotypes.

### MATERIALS AND METHODS

During Kharif 2020–21, thirty-three upland cotton genotypes were planted at the Cotton Section Research

farm area of the Department of Genetics and Plant Breeding, CCS HAU, Hisar in randomized block design with plant geometry of 60 cm distance between plant to plant and 90 cm between row to row in three replications. From each replication, five competitive plants were chosen at random from every entry and data were collected for various traits *viz.*, plant height (PH), number of monopods (NOM), number of sympods (NOS), boll number (BN), boll weight (BW) in grams, seed index (SI) in grams, lint yield (LY) in grams, ginning out turn (GOT) in percentage, seed cotton yield (SCY) in kilograms per hectare, and fibre quality traits such as fibre length (FL) in millimetres, bundle/fibre strength (BS) in grams per tex, and fibre fineness/micronaire (FF) in micrograms per inch. Five competitive plants were randomly selected from each entry in every replication and data were recorded for various traits, including boll number (BN), boll weight (BW) (g), plant height (PH) (cm), number of monopods (NOM), number of sympods (NOS), seed index (SI) (g), lint yield (LY) (g), ginning out turn (GOT) (%), seed cotton yield (SCY) (kg/ha) and fibre quality traits, namely fibre length (FL) (mm), bundle/fibre strength (BS) (g/tex), and fibre fineness/micronaire (FF) ( $\mu\text{g}/\text{inch}$ ). The statistical method outlined by Johnson *et al.* (1955) was employed for calculating the mean, range, heritability, genetic advance, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and correlation coefficients based on the obtained data. The

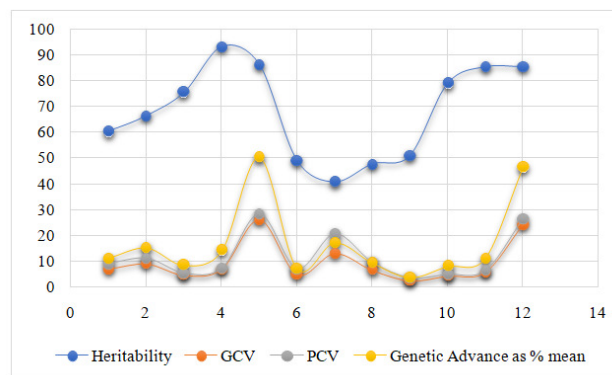
methodology proposed by Deway and Lu (1959) was employed to conduct path analysis.

## RESULTS AND DISCUSSION

According to Table 1 and Graph 1, the current study's findings demonstrated that for every trait, the phenotypic coefficient of variance (PCV) slightly surpassed the genotypic coefficient of variance (GCV), implying a minimal environmental influence on trait expression. There was a range of 3.70 to 28.38 percent for the phenotypic coefficient of variance. Lint yield (28.38%) and seed cotton yield (26.41%) had the greatest PCVs. The range of GCV for different yield and its related traits varied from 4.79 to 26.36 percent. The yield of lint (26.36%) and seed cotton (24.40%) had the greatest GCV values. For every character, phenotypic and genotypic variance showed a strong and parallel link. The yield of lint (26.36%) and seed cotton (24.40%) had the greatest GCV values. For every character, phenotypic and genotypic variance showed a strong and parallel link. Seed cotton and lint yield had highest PCV and GCV values. Similar conclusions were reached by Preetha and Raveendran (2007); Dheva and Potdukhe (2002); Dhivya *et al.* (2014). Boll weight, GOT, seed index, plant height, number of sympods, fibre length/2.5 span length, fibre/bundle strength, and fibre fineness/micronaire were shown to have low PCV and low GCV, whereas boll number and number of monopods showed moderate PCV and GCV.

**Table 1: Variability parameters in extant tetraploid cotton genotypes for fibre yield and its attributing traits.**

Parameters	Mean	Heritability	GCV	PCV	Genetic Advance as % mean
<b>Boll Weight (g)</b>	3.61	60.13	7.11	9.17	11.36
<b>Number of bolls</b>	34.93	66.45	9.19	11.27	15.43
<b>Ginning out turn (%)</b>	37.14	75.47	4.79	5.52	8.58
<b>Seed index</b>	6.75	93.23	7.14	7.39	14.20
<b>Lint Yield (kg/ha)</b>	1006.11	86.26	26.36	28.38	50.43
<b>Plant height (cm)</b>	198.31	49.05	5.08	7.26	7.34
<b>Number of monopods</b>	2.26	40.77	13.23	20.72	17.41
<b>Number of sympods</b>	15.73	47.72	6.73	9.74	9.58
<b>Fibre Length (mm)</b>	27.22	50.99	2.64	3.70	3.88
<b>Bundle/Fibre Strength (g/tex)</b>	29.36	78.92	4.48	5.04	8.19
<b>Micronaire (<math>\mu\text{g}/\text{inch}</math>)</b>	4.06	85.33	5.92	6.41	11.27
<b>Seed Cotton Yield (Kg/ha)</b>	2700.52	85.36	24.40	26.41	46.44



**Graph 1.** Heritability, GCV, PCV and Genetic advance as % of mean for fibre, yield and yield attributing.

For nearly all of the characteristics, including boll weight, seed cotton yield, boll number, ginning out turn, seed index, lint yield and fibre fineness/micronaire, high estimates of heritability (over 60%) were noted. For plant height, number of monopods, number of sympods, and fibre length/2.5 % span length, moderate level estimates of heritability (30–60%) were noted. However, the heritability predictions will be more accurate when combined with the anticipated genetic advancement. According to Johnson *et al.* (1955), in order to get a more trustworthy result, high heritability should be paired with high genetic advance. All quantitative traits had genetic advances ranging from 3.88 (fibre length/2.5%) to 50.43 (lint yield). For both seed cotton yield and lint yield, considerable genetic advance and high heritability were noted. Boll weight and number, seed index, and fibre fineness/microware were shown to have high heritability with moderate genetic advance, suggesting that both additive and non-additive types of gene action affect these traits. It has been shown that for ginning out turn and bundle strength, there is high heritability but low genetic advance.

A trustworthy way to assess the relationship between the characters and identify important associates is through the correlation coefficient (Falconer, 1981). Table 2 displays the correlation coefficients of the characters linked to seed cotton yield/plant that were estimated. Plant height (0.25), number of monopods (0.38), number of sympods (0.49), number of bolls (0.63), ginning out turn (0.28), lint yield (0.98), and fibre fitness/micronaire (0.51) were found to have a highly significant and positive correlation with seed cotton yield; therefore, these traits can be regarded as

appropriate selection criteria for increasing seed cotton yield. This suggested that an increase in the above traits might be the cause of the observed rise in seed cotton yield per plant. Previous studies (Alkuddsi *et al.*, 2013); bolls and boll weight (Farooq *et al.*, 2014); and number of bolls (Ekinci *et al.*, 2010) found positive association between seed cotton yield and boll weight. The selection strategy will take advantage of the close association between yield and qualities that contribute to seed cotton yield, which could aid in the development of genotypes that yield at high levels. In terms of intercorrelation, plant height is positively and significantly correlated with the following: GOT (0.40), seed index (0.27), lint yield (0.31), number of monopods (0.38), number of sympods (0.48), fibre fitness/micronaire (0.52), and seed cotton yield (0.25). Number of monopods have positive significant inter correlation with seed index (0.51), lint yield (0.38), plant height (0.57), micronaire/ fibre fitness (0.21) and seed cotton yield (0.37). Number of sympods has positive significant inter correlation with boll weight (0.56), boll number (0.32), lint yield (0.48), micronaire/fibre fitness (0.48) and seed cotton yield (0.49). Boll weight has positive and significant correlation with GOT (0.33), lint yield (0.45), number of sympods (0.56), micronaire/ fibre fitness (0.26) and seed cotton yield (0.41). Number of bolls /plants has positive significant inter correlation with lint yield (0.57), number of sympods (0.32), micronaire/fibre fitness (0.31) and seed cotton yield (0.63). Ginning out turn has positive association with boll weight (0.33), lint yield (0.45), plant height (0.40), micronaire/fibre fitness (0.21) and seed cotton yield (0.28).

**Table 2: Genotypic correlation coefficients of American cotton genotypes with seed cotton yield for fibre and yield component traits.**

Parameters	BW	NOB	GOT	SI	LY	PH	NOM	NOS	FL	BS	FF
<b>BW</b>											
<b>NOB</b>	0.194										
<b>GOT</b>	0.332**	-0.072									
<b>SI</b>	-0.037	-0.135	0.149								
<b>LY</b>	0.459**	0.573**	0.457**	0.067							
<b>PH</b>	0.049	-0.038	0.406**	0.272**	0.310**						
<b>NOM</b>	-0.028	-0.004	0.142	0.518**	0.389**	0.578**					
<b>NOS</b>	0.560**	0.322**	-0.101	0.042	0.486**	0.066	-0.008				
<b>FL</b>	-0.216*	-0.169	-0.218*	0.011	-0.150	-0.037	-0.139	0.031			
<b>BS</b>	0.036	0.007	0.062	0.096	-0.006	0.284**	0.145	0.165	0.558**		
<b>FF</b>	0.261**	0.315**	0.212*	0.144	0.528**	0.437**	0.210*	0.485**	-0.022	0.419**	
<b>SCY</b>	0.419**	0.637**	0.282**	0.030	0.981**	0.251*	0.379**	0.494**	-0.107	-0.020	0.510**

The correlation between bundle strength and fibre length was notably positive and significant at 0.55. Fibre length (0.55) and Plant height (0.28) were positively and substantially correlated with bundle strength. Boll weight (0.26), number of bolls (0.31), ginning out turn (0.21), lint yield (0.52), plant height (0.43), number of monopods (0.21), number of sympods (0.48), bundle strength (0.41), and seed cotton yield (0.51) were all positively and significant correlated with fibre fitness/micronaire. These findings demonstrated unequivocally that selecting for any one of these characteristics simultaneously improves other qualities and seed cotton yield. The relationship

between the number of bolls and monopods/plants and the seed cotton yield was also verified by Saraswat *et al.* (2023). According to the findings of Dutt *et al.* (2004); Basbag and Gencer (2007); Thiyagu *et al.* (2010), the fibre quality attributes showed significant positive correlation among themselves. The number of bolls, sympods and seed index exhibited a notably positive and significant correlation with fibre quality parameters including length, strength, fineness, and uniformity (Altaher and Singh 2003; Sakthi *et al.*, 2007; Thiyagu *et al.*, 2010).

Additionally, negative and significant correlations were found between fibre length and boll weight (0.21) and

ginning out turn (0.21). It was discovered that the main reason for the inverse relationship between yield and fibre quality characteristics was linking. Inter-mating has been suggested by Meredith and Bridge (1971) as a way to break this link. Because correlation studies compare one characteristic with another without accounting for the background effect influenced by other traits, they are unable to provide a clear picture. In order to separate direct impacts from indirect effects through other traits and use the most impacting traits as a selection criterion in cotton breeding programmes, path coefficient analysis is a crucial statistical tool. The direct and indirect effects of each component character on the dependent variable, seed cotton yield, were examined using path co-efficient analysis. Focusing on the variable that has a strong direct impact on seed cotton yield is made possible by research on

path coefficient. In the end, this leads to selection for one or a small number of critical traits (Dewey and Lu 1959). The genotypic correlation values between seed cotton yield and other yield and fibre quality traits were dissected to discern both direct and indirect effects (Table 3).

In terms of yield and fibre quality traits, the residual effect of the path analysis component was 0.0017. It was evident from the less residual effect that the traits selected for path analysis were suitable and sufficient. Lint yield showed a very strong positive direct influence (1.058). For direct effects, Thiyagu *et al.* (2010) also noted comparable outcomes. Additionally, according to Altaher and Singh (2003), the traits of lint yield, bolls/plant, and boll weight have a strong positive direct impact on the yield of seed cotton.

**Table 3: Direct and indirect effects of yield and fibre quality traits of extant tetraploid cotton genotypes.**

	BW	NOB	GOT	SI	LY	PH	NOM	NOS	SL	BS	FF	GC*
<b>BW</b>	<b>-0.006</b>	0.004	-0.065	0.001	0.486	0.001	-0.001	0.010	-0.005	0.000	-0.006	<b>0.419</b>
<b>NOB</b>	-0.001	<b>0.023</b>	0.014	0.002	0.606	-0.001	0.000	0.005	-0.004	0.000	-0.007	<b>0.637</b>
<b>GOT</b>	-0.002	-0.002	<b>-0.195</b>	-0.002	0.484	0.006	0.001	0.002	-0.005	-0.001	-0.005	<b>0.282</b>
<b>SI</b>	0.000	-0.003	-0.029	<b>-0.016</b>	0.071	0.004	0.005	0.001	0.000	-0.001	-0.003	<b>0.030</b>
<b>LY</b>	-0.003	0.013	-0.089	-0.001	<b>1.058</b>	0.005	0.004	0.010	-0.004	0.000	-0.012	<b>0.981</b>
<b>PH</b>	0.000	-0.001	-0.079	-0.004	0.328	<b>0.015</b>	0.007	0.000	-0.001	-0.004	-0.010	<b>0.251</b>
<b>NOM</b>	0.000	0.000	-0.027	-0.008	0.408	0.010	<b>0.010</b>	0.002	-0.004	0.000	-0.005	<b>0.386</b>
<b>NOS</b>	-0.004	0.007	-0.028	-0.001	0.619	0.000	0.001	<b>0.017</b>	-0.005	-0.003	-0.013	<b>0.589</b>
<b>SL</b>	0.001	-0.004	0.042	0.000	-0.158	-0.001	-0.002	-0.004	<b>0.024</b>	-0.007	0.000	<b>-0.107</b>
<b>BS</b>	0.000	0.000	-0.012	-0.002	-0.006	0.004	0.000	0.004	0.014	<b>-0.012</b>	-0.009	<b>-0.020</b>
<b>FF</b>	-0.002	0.007	-0.041	-0.002	0.558	0.007	0.002	0.009	-0.001	-0.005	<b>-0.022</b>	<b>0.510</b>

Residuals are **0.00176**, \*GC- Genotypic correlation coefficient

The remaining characteristics, which are fibre length (0.024), boll number (0.023), number of sympod (0.017), plant height (0.015) and number of monopod (0.024), all had a significant impact on seed cotton yield. The number of monopods, sympods, boll weight, ginning out turn, plant height, fibre fineness and number of monopods all had a significant indirect effect on the seed cotton yield through lint yield. Thus, choosing these traits will simultaneously increase seed cotton yield.

## CONCLUSIONS

Research into correlation and path coefficients assists in trait selection, determining the direction of selection, and expediting the breeding process by offering breeders a deeper comprehension of trait relationships. Studies focus on correlation and path coefficients assists in trait selection, determining the direction of selection and expediting the breeding process by offering breeders a deeper comprehension of trait relationships.

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**Conflict of Interest.** None.

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