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Genetic variability Correlation and path analysis for seed cotton yield and fiber quality traits in BT cotton (*Gossypium hirsutum* L.)

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ABSTRACT

A field experiment was conducted during *kharif* 2025-26 at Regional Agricultural Research Station (RARS), Lam, Guntur using randomized block design used to estimate genetic variability, correlation and path analysis for seed cotton yield and fiber quality traits in Bt cotton (*Gossypium hirsutum* L.). The experimental material comprised of 4 lines, 4 testers, 16 hybrids and two standard BG-II checks (Rasi Swift and RCH 659). Analysis of variance revealed significant differences among the genotypes, suggesting substantial variability in experimental material. High GCV and PCV was observed for plant height, number of monopodia , number of sympodia, number of bolls per plant, seed index and seed cotton yield. High heritability along with high genetic advance as per cent of mean observed for plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, lint index, seed index, ginning out turn, seed cotton yield per plant, upper half mean length and micronaire, indicating that direct phenotypic selection may be effective. Correlation analysis revealed that plant height, number of sympodia, number of bolls per plant, lint index and ginning out turn showed positive and significant association with seed cotton yield. Path analysis revealed that plant height, number of sympodia per plant and number of bolls per plant showed positive direct effects with significant association, indicating that improvement in these traits may improve the seed cotton yield.

Key Words: *Correlation, Genetic variability, Heritability and Path coefficient analysis*

Cotton (*Gossypium* spp.) is a crop of prosperity having influence on man and matter and is called as 'King of fiber' and 'White Gold'. Cotton is one of the most important commercial crops and forms the backbone of Indian textile industry. No other fiber has the desirable characteristics that are found in cotton. It belongs to the Malvaceae family. Out of 50 species available, 45 are diploid (2n=26) with only two cultivated species *i.e., Gossypium herbaceum* L. and *Gossypium arboreum* L. (Old world cotton), while 5 species are naturally tetraploid (2n=52) with only two cultivated species *i.e.*, *Gossypium hirsutum* L. (Upland cotton) and *Gossypium barbadense* L. (Egyptian cotton, New world cotton). Cotton is an allotetraploid species, *Gossypium hirsutum* L. that contributes to more than 90% of the world's cotton production (Farooq *et al.,* 2024). A field experiment was conducted during *kharif* 2025-26 at Regional Agricultural Research Station (RARS), Lam, Guntur using randomized block design used to estimate genetic variability, correlation and path analysis for seed cotton yield and fiber quality traits in Bt cotton (*Gossypium hirsutum* L.). The experimental material comprised of 4 lines, 4 testers, 16 hybrids and two standard BG-II checks (Rasi Swift and RCH 659). Andhra Pradesh produced 4.47 lakh ha, the production was 9.39 lakh bales of 170 kg/bale and the productivity was 357 kg/ha (All India Coordinated Research Project on Cotton – Annual Report 2025-26).

Effective utilization of genetic variability enables plant breeders to develop superior genotypes with improved yield and desirable traits. Correlation analysis method is used for the study of association between the different characters in plants and for selection of significant characters that can contribute to improve seed cotton yield. The degree and strength of these associations provide information for selecting superior genotypes and developing effective breeding strategies for crop improvement (Chaudhry *et al.* (2022). Path analysis splits the correlation into direct and indirect effects, which provide information about the traits

Table 1. Analysis of variance for seed cotton yield, its attributing traits and fiber quality traits

Source	Mean Sum of Squares (MSS)														
	d.f	DFF	PH (cm)	NMP	NSP	NB	BW (g)	LI (g)	SI (g)	GOT (%)	SCY (g)	UHML (mm)	UI (%)	MIC (µg/inch)	TEN (g/tex)
Replication	1	0.01	550.6	0.001	3	45.6	0.44	0.5	4.3	6.58	1381	2.36	0.07	0.02	0.96
Treatment	25	38.19 **	8972.3 **	0.93 **	43.58 **	291.89 **	2.49 **	2.45 **	9.58 **	55.25 **	3405.2 **	64.42 **	35.55 **	0.88 **	21.33 **
Error	26	3.77	158.1	0.008	1.7	1.24	0.21	0.2	0.7	7.42	362.3	2.25	5.35	0.07	2.88

that directly or indirectly affect the seed cotton yield. Considering the significance of genetic variability and character association in crop improvement, the present study was conducted to estimate genetic variability, heritability, correlation and path coefficient analysis for seed cotton yield, its attributing traits and fiber quality traits.

MATERIAL AND METHODS

The experiment was carried out during *kharif*, 2025-26 at Regional Agricultural Research Station (RARS), Lam Farm, Guntur. Experiment with 4 lines (LHBT 10, LHBT 24, LHBT 17 and LHBT 9), 4 testers (LHBT 16, LHBT 2385, LHBT 2388 and LHBT 2389), 16 hybrids and two standard BG-II checks (Rasi Swift and RCH 659). They are in sown in two replications using Randomized Block Design with spacing of 105 × 60 cm.

Data recorded for traits namely, days to 50% flowering (recorded on plot basis), plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), lint index (g), seed index (g), ginning out turn (%), seed cotton yield per plant (g) and fiber quality traits such as, upper half mean length (UHML) (mm), uniformity index (%), micronaire (µg/inch), tenacity (g/tex) were recorded on plot basis.

RESULTS AND DISCUSSION

The analysis of variance revealed substantial variances among 26 genotypes for all the traits studied, representing the existence of substantial genetic variability among the parental lines as well as in hybrids (Table 1). Mean performance revealed that LHBT 10 and LHBT 9 among the lines and LHBT 16 and LHBT 2385 from testers were found to be superior for seed cotton yield and its attributing traits. Among the hybrids, LHBT 24 × LHBT 2389, LHBT 24 × LHBT 2388, LHBT 10 × LHBT 2389 and LHBT 24 × LHBT 2385 were found to be superior for seed cotton yield, whereas LHBT 17 was found to be superior for fiber quality traits, suggesting its potential for evaluation in future cotton breeding programmes.

Plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, seed index and seed cotton yield per plant exhibited high PCV and GCV (Table 2). Sahar *et al.*

Table 2. Estimates of genetic parameters for seed cotton yield, its attributing traits and fiber quality traits

Traits	GCV (%)	PCV (%)	h^2_{bs} (%)	GA	GAM (%)
Days to 50% flowering	6.60	7.29	82.0	7.73	12.31
Plant height (cm)	29.13	29.65	96.5	134.36	58.97
Number of monopodia per plant	72.23	72.89	98.2	1.39	147.56
Number of sympodia per plant	26.27	27.33	92.5	9.06	52.05
Number of bolls per plant	32.85	32.99	99.2	24.72	67.39
Boll weight (g)	19.40	21.19	83.8	2.01	36.58
Lint index (g)	19.20	20.66	86.4	2.04	36.78
Seed index (g)	20.01	21.35	87.3	4.06	38.39
Ginning out turn (%)	14.91	17.07	76.3	8.80	26.83
Seed cotton yield/ Plant (g)	20.26	22.81	78.9	70.91	37.09
Upper half mean length (mm)	19.45	20.14	93.2	11.08	38.68
Uniformity Index (%)	4.71	5.48	73.8	6.87	8.34
Micronaire (µg/inch)	13.33	14.45	85.1	1.21	25.33
Tenacity (g/tex)	9.91	11.35	76.1	5.45	17.81

Table 3. Genotypic (below diagonal) and phenotypic (above diagonal) correlation matrix for seed cotton yield, its attributing traits and fiber quality traits in cotton (*Gossypium hirsutum* L.)

Traits	DFF	PH (cm)	NMP	NSP	NBP	BW (g)	LI (g)	SI (g)	GOT (%)	UHML (mm)	UI (%)	MIC (µg/inch)	TEN (g/tex)	SCY (g)
DFF	**1**	0.361**	0.469**	-0.037	0.282*	-0.327*	-0.203	-0.049	-0.151	-0.172	-0.079	-0.044	0.124	-0.085
PH (cm)	0.372**	**1**	0.027	0.438**	0.304*	-0.161	0.161	-0.328*	0.468**	0.429**	0.223	-0.410*	0.196	0.350*
NMP	0.540**	0.028	**1**	-0.181	-0.205	0.16	-0.446**	-0.02	-0.123	-0.203	0.008	0.212	0.173	-0.063
NSP	-0.111	0.448**	-0.179	**1**	0.368**	-0.294*	0.065	-0.065	0.214	0.026	-0.16	0.048	-0.17	0.418**
NBP	0.297*	0.308*	-0.2	0.397**	**1**	-0.784**	0.242	-0.013	0.05	-0.355**	-0.277*	0.163	-0.223	0.417**
BW (g)	-0.40**	-0.167	0.173	-0.370**	-0.838**	**1**	0.009	-0.003	0.236	0.347*	0.495**	-0.129	0.358**	0.145
LI (g)	-0.232	0.208	-0.492**	0.067	0.271	0.008	**1**	-0.323*	0.535*	0.262	0.201	-0.139	0.176	0.319*
SI (g)	-0.045	-0.347*	-0.018	-0.087	-0.015	0.003	-0.401**	**1**	-0.409**	-0.399**	-0.095	0.054	-0.03	-0.011
GOT (%)	-0.226	0.533**	-0.131	0.237	0.04	0.361**	0.578**	-0.372**	**1**	0.502**	0.478**	-0.209	0.330*	0.428**
UHML (mm)	-0.207	0.466**	-0.206	0.001	-0.381**	0.411**	0.306*	-0.443**	0.582**	**1**	0.477**	-0.668**	0.455**	0.048
UI (%)	-0.083	0.254	-0.005	-0.22	-0.330*	0.696**	0.344*	-0.169	0.679**	0.528**	**1**	-0.385**	0.711**	0.221
MIC (µg/inch)	0.016	-0.454**	0.215	0.081	0.177	-0.162	-0.161	0.055	-0.242	-0.739**	-0.448**	**1**	-0.473**	0.02
TEN (g/tex)	0.117	0.296*	0.21	-0.219	-0.251	0.495**	0.226	-0.166	0.483**	0.513**	0.881**	-0.595**	**1**	0.194
SCY (g)	-0.114	0.457**	-0.06	0.538**	0.463**	0.05	0.431**	-0.041	0.655**	0.099	0.359**	-0.013	0.291*	**1**

DFF= Days to 50% 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 (%); **UHML**= Upper Half Mean Length (mm); **UI**= Uniformity index (%); **MIC**= Micronaire (µg/inch) and **TEN**=Tenacity (g/tex); SCY (g) = Seed Cotton Yield

Table 4. Phenotypic and genotypic direct and indirect effects of seed cotton yield and its component traits on seed cotton yield

	P/ G	DFF	PH	NMP	NSP	NBP	BW	LI	SI	GOT	UHML	UI (%)	MIC	TEN	SCY (g)
DFF	**P**	**-0.153**	0.016	0.641	-0.01	0.389	-0.394	0.002	-0.003	0.007	-0.027	0.008	-0.001	0.018	-0.085
	G	**-0.698**	0.125	0.568	-0.057	0.495	-0.222	-0.129	-0.024	0.314	-0.265	-0.137	0.01	-0.095	-0.114
PH	**P**	-0.055	**0.044**	0.003	0.123	0.419	-0.194	-0.002	-0.023	-0.022	0.069	-0.023	-0.016	0.028	0.350*
	G	-0.26	**0.335**	0.03	0.229	0.513	-0.091	0.115	-0.179	-0.738	0.595	0.42	-0.273	-0.239	0.457**
NMP	**P**	-0.071	0.001	**0.136**	-0.051	-0.282	0.193	0.006	-0.001	0.005	-0.032	-0.008	0.008	0.025	-0.063
	G	-0.377	0.009	**1.051**	-0.092	-0.334	0.094	-0.272	-0.01	0.183	-0.263	-0.01	0.13	-0.17	-0.06
NSP	**P**	0.005	0.019	-0.024	**0.028**	0.508	-0.354	-0.009	-0.004	-0.01	0.004	0.016	0.001	-0.024	0.418**
	G	0.077	0.15	-0.189	**0.511**	0.662	-0.201	0.037	-0.045	-0.33	0.002	-0.363	0.049	0.177	0.538**
NBP	**P**	-0.043	0.013	-0.028	0.103	**1.379**	-0.946	-0.003	-0.009	-0.002	-0.057	0.028	0.006	-0.032	0.417**
	G	-0.207	0.103	-0.211	0.203	**1.666**	-0.455	0.15	-0.008	-0.057	-0.486	-0.544	0.107	0.203	0.463**
BW	**P**	0.05	-0.007	0.021	-0.082	-1.082	**1.206**	-0.001	-0.002	-0.011	0.056	-0.051	-0.005	0.051	0.145
	G	0.286	-0.056	0.183	-0.189	-1.397	**0.543**	0.005	0.002	-0.501	0.525	1.148	-0.098	-0.4	0.05
LI	**P**	0.031	0.007	-0.061	0.018	0.334	0.011	**-0.014**	-0.023	-0.025	0.042	-0.02	-0.005	0.025	0.319*
	G	0.163	0.07	-0.517	0.035	0.452	0.004	**0.553**	-0.207	-0.801	0.391	0.568	-0.097	-0.183	0.431**
SI	**P**	0.007	-0.014	-0.002	-0.018	-0.018	-0.004	0.004	**0.071**	0.019	-0.064	0.009	0.002	-0.004	-0.011
	G	0.032	-0.116	-0.02	-0.045	-0.026	0.002	-0.222	**0.515**	0.515	-0.565	-0.279	0.033	0.134	-0.041
GOT	**P**	0.023	0.02	-0.016	0.06	0.07	0.285	-0.007	-0.029	**-0.048**	0.081	-0.049	-0.008	0.048	0.428**
	G	0.158	0.179	-0.139	0.122	0.068	0.196	0.32	-0.192	**-0.385**	0.743	1.121	-0.146	-0.39	0.655**
UHML	**P**	0.026	0.019	-0.027	0.007	-0.49	0.419	-0.003	-0.028	-0.024	**0.161**	-0.049	-0.027	0.065	0.048
	G	0.145	0.156	-0.217	0.001	-0.634	0.223	0.17	-0.228	-0.806	**1.276**	0.872	-0.444	-0.415	0.099
UI	**P**	0.012	0.009	0.001	-0.045	-0.382	0.598	-0.002	-0.006	-0.023	0.076	**-0.103**	-0.015	0.103	0.221
	G	0.058	0.085	-0.006	-0.112	-0.55	0.378	0.191	-0.087	-0.941	0.675	**1.65**	-0.269	-0.711	0.359**
MIC	**P**	0.006	-0.018	0.029	0.01	0.225	-0.156	0.002	0.003	0.01	-0.107	0.039	**0.04**	-0.068	0.02
	G	-0.012	-0.152	0.227	0.041	0.296	-0.088	-0.09	0.029	0.336	-0.943	-0.74	**0.601**	0.481	-0.013
TEN	**P**	-0.019	0.008	0.023	-0.047	-0.307	0.432	-0.002	-0.002	-0.015	0.073	-0.073	-0.019	**0.144**	0.194
	G	-0.082	0.099	0.221	-0.112	-0.419	0.269	0.125	-0.086	-0.67	0.655	1.454	-0.358	**-0.807**	0.291*
Phenotypic residual effect = 0.122; Genotypic residual effect = 0.030															

DFF= Days to 50% 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 (%); **UHML**= Upper Half Mean Length (mm); **UI**= Uniformity index (%); **MIC**= Micronaire (µg/inch) and **TEN**=Tenacity (g/tex).**G=Genotypic correlation; P= Phenotypic correlation**

(2021), Chapara *et al.* (2022) reported similar results for plant height, number of monopodia and number of sympodia per plant, for number of bolls per plant and for seed cotton yield per plant by Meena *et al.* (2022), Iqbal *et al.* (2023) and Kathiravan *et al.* (2025). Low GCV and PCV were observed for days to 50% flowering and uniformity index. These results are similar with Harini *et al.* (2025), Kanta *et al.* (2025) and Kathiravan *et al.* (2025) for days to 50% flowering and Vadodaria *et al.* (2025) for uniformity index.

The traits plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, lint index, seed index, ginning out turn, seed cotton yield per plant, upper half mean length and micronaire exhibited high heritability along with high genetic advance as percent of mean, suggesting the predominance of additive gene action and effective usefulness for direct phenotypic selection or simple selection. Whereas days to 50% flowering and tenacity recorded high heritability with moderate genetic advance as percent of mean, indicating that both additive gene action and non-additive gene action and efficiency of hybridization followed by selection (Table 2). Similar reports were reported by Harini *et al.* (2025) and Kanta *et al.* (2025) for days to 50% flowering, plant height, boll weight, lint index, seed index, uniformity index and tenacity, while Vadodaria *et al.* (2024) for number of sympodia per plant, ginning out turn, micronaire.

Correlation between seed cotton yield component traits and fiber quality traits with seed cotton yield, revealed that only five characters out of fourteen characters exhibited significant and positive association with seed cotton yield at both genotypic and phenotypic levels *viz.,* plant height (0.457** and 0.350*), number of sympodia per plant (0.538** and 0.418**), number of bolls per plant (0.463** and 0.417**), lint index (0.431** and 0.319*) and ginning out turn (0.655** and 0.428**), which representing their importance in selection criteria for yield improvement (Table 3). These results are in correspondence with Kadam *et al.* (2024) for plant height, Mawblei *et al.* (2022), Rani *et al.* (2024) and Kanta *et al.* (2025a) for number of sympodia per plant and number of bolls per plant, Hampannavar *et al.* (2020) for lint index and ginning out turn.

Path coefficient analysis which splits the correlation into direct and indirect effects, revealed that plant height (0.044 and 0.335), number of sympodia per plant (0.028 and 0.511) and number of bolls per plant (1.379 and 1.666) recorded positive direct effects along with positive significant association with seed cotton yield at both genotypic and phenotypic level, revealing their usefulness as reliable selection indices in cotton improvement programmes (Table 4). These results are in accordance with Kadam *et al.* (2024) for plant height, Arunkumar and Murthy (2020), Kanta *et al.* (2025a) and Kanta *et al.* (2025b) for number of sympodia per plant, Mawblei *et al.* (2022), Vadodaria *et al.* (2024) for number of bolls per plant.

CONCLUSION

Under the current study, analysis of variance revealed significant differences among 26 genotypes for 14 traits studied, indicating the existence of substantial variability among them. Mean performance revealed that the hybrid, LHBT 10 x LHBT 2389 exhibited highest seed cotton yield along with desirable fiber quality traits, indicating its potential for exploitation in future breeding programmes. Plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight lint index, seed index, ginning out turn, seed cotton yield per plant, upper half mean length and micronaire exhibited high heritability along with high genetic advance as percent of mean, indicating the predominance of additive gene action and direct phenotypic selection may be effective. Correlation studies confirmed that plant height, number of sympodia per plant, number of bolls per plant, lint index and ginning out turn showed positive association with seed cotton yield, these traits help in direct selection for improving seed cotton yield. Path analysis revealed that improvement in traits *viz.,* plant height, number of sympodia per plant and number of bolls per plant, directly helps in improving the seed cotton yield due to its positive direct effects and significant association with yield.

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