Received: 21 Mar 2024 | Revised: 15 Dec 2024 | Accepted: 19 Dec 2024

Electronic Journal of Plant Breeding

Research Note

Analysis of variability, heritability and trait association in four F_2 populations of *Gossypium hirsutum* L.

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Abstract
Cotton is a prime crop of industrial importance. The assessment of variability provides scope for planning the breeding programmes. This study was conducted at Tamil Nadu Agricultural University, Coimbatore in F_2 generation for the crosses *viz.*, CO 17 x KC 2, TVH 002 x KC 3, TVH002 x RAHC 1039 and TCH 1894 x NDLH 32 to estimate the variability, trait heritability and correlation among traits. In this experiment, high PCV paired with high GCV was noted for number of monopodia per plant as well as boll weight in all the four crosses. High heritability along with high genetic advance as per cent of mean were noted among all the crosses for seed index, boll weight, plant height and lint index. The plant yield of a single plant in all the crosses was noted to be significant and positively correlated with lint index, number of bolls per plant, internode length, boll weight and plant height.

Keywords: Correlation, F_2 population, Heritability, Variance

Cotton is a major commercial crop in India and plays a crucial role in the global textile industry. Six countries India, China, Pakistan, Australia, the United States, and Brazil are recognized as the top cotton producers worldwide (Shuli *et al.*, 2018). As the primary natural fiber used in textiles, cotton holds immense economic value (Kumar *et al.*, 2019). The genetic variation observed in key crop traits is largely attributed to its pollination type, which is predominantly cross-pollinated.

This variation in the gene pool is vital for an effective breeding program. Creating genetic variability is a prerequisite for selection (Ranganatha *et al.*, 2013). A broad genetic variability allows for more efficient selection within breeding populations (Ahsan *et al.*, 2015). Understanding the extent of variability present in a population is crucial to designing effective breeding strategies for improving various traits (Dhivya *et al.*, 2014). By assessing heritable traits through broad-sense heritability values, plant breeders can predict the likelihood of traits being passed from parents to offspring (Nandini *et al.*, 2018).

To further explore the genetic variability and heritability of yield attributes in cotton, this study was conducted using four F_2 populations.

This study was carried out in the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore, to determine the variability, trait heritability and correlation among various quantitative traits in the F_2 generation of the crosses *viz.*, CO 17 x KC 2, TVH 002 x KC 3, TVH002 x RAHC 1039 and TCH 1894 x NDLH 32. The experimental crop was raised during summer 2022. In each population, individual F_2 progenies *i.e.*, 200 progenies in CO 17 x KC 2, 146 progenies in TVH 002 x KC 3, 241 progenies in TVH 002 x RAHC 1039 and 157 progenies in TCH 1894 x NDLH 32 along with their respective parents were sown with a spacing of 90 cm between rows and 30 cm between the plants in a row and standard agronomic practices were followed. Data were noted for the quantitative characters *i.e.*, days to first flowering, plant height, internode length, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, single plant yield, ginning outturn, seed index, lint index, upper half mean length, uniformity ratio, bundle strength, elongation percentage and fiber fineness, in all the four crosses.

Variability studies: Phenotypic and genotypic variances, phenotypic and genotypic co-efficients of variability were calculated based on the method suggested by Singh and Chaudhary (1985) and they were classified as low (<10%), moderate (10-20%) and high (>20%). Broad sense heritability was calculated using the formula proposed by Lush (1940).

According to Johnson *et al*. (1955), broad sense heritability was classified as low (less than 30%), moderate (30-60%) and high (more than 60%). Genetic advance as percent of mean was worked out as per the method proposed by Johnson *et al.* (1955) and designated as low (less than 10%), moderate (10-20%) and high (greater than 20%).

Correlation analysis: The degree or the direction of association between two or more variables is known as correlation. The simple correlation coefficients were worked out as per the formula given by Falconer (1996). Testing the significance of the correlation coefficients was done by comparing correlation coefficients with Fisher and Yates (1953) table values at n-2 degrees of freedom, where the 'n' represents number of paired observations utilized for analysis.

Genetic Variability (PCV and GCV): The study observed high phenotypic coefficient of variation (PCV) coupled with high genotypic coefficient of variation (GCV) for traits such as the number of monopodia per plant and boll weight across all crosses (**Table 1**). Similar findings were reported by Monisha (2018). These traits with substantial variability present a considerable scope for selection. Conversely, low PCV and low GCV were recorded for ginning outturn, aligning with the observations of Amanu *et al*. (2022). Additionally, low PCV and GCV were detected for uniformity ratio, upper half mean length, elongation percentage, and days to first flowering across all crosses. Moderate levels of PCV and GCV were observed for the seed index, consistent with the findings of Dhivya *et al*. (2014).

For plant height, high PCV and high GCV were observed in the crosses CO 17 × KC 2 and TVH 002 × RAHC 1039. Similarly, the number of sympodia per plant exhibited high PCV and high GCV across all crosses, except for TCH 1894 × NDLH 32, which demonstrated high PCV but moderate GCV. The number of bolls per plant displayed high PCV and high GCV in all crosses, except for TVH 002 × KC 3, which showed high PCV but moderate GCV. These findings align with the results of Hampannavar *et al*. (2020) and Soomro (2020). However, the significant disparity between PCV and GCV for the number of bolls per plant indicates a substantial environmental influence on this trait.

Single plant yield exhibited high PCV and high GCV in the crosses CO 17 × KC 2 and TCH 1894 × NDLH 32. Notably, no significant differences were observed between PCV and GCV values for fiber quality parameters across all crosses, consistent with the findings of Salem *et al.* (2021).

Transgressive Segregants: The evaluation of transgressive segregants in four cotton crosses CO 17 × KC 2, TVH 002 × KC 3, TVH 002 × RAHC 1039, and TCH 1894 × NDLH 32 revealed diverse genetic mechanisms and trait distributions. Each cross exhibited distinct patterns of skewness and kurtosis, indicating different underlying genetic actions. In the CO 17 × KC 2 cross, additive gene action was identified for the number of bolls per plant, boll weight, and bundle strength. Positive skewness in traits such as the number of bolls per plant, boll weight, and single plant yield suggested complementary gene action. Meanwhile, traits like days to first flowering and ginning outturn exhibited platykurtic distributions, consistent with the findings of Nandini *et al.* (2018), indicating broad variability that is advantageous for selection. For the TVH 002 × KC 3 cross, positive skewness was observed for days to first flowering. Platykurtic curves were noted for internode length, days to first flowering, number of monopodia, and ginning outturn. Fiber fineness and upper half mean length demonstrated negative skewness, as reported by Smith *et al.* (2010), indicating duplicate gene action. This cross exhibited both broad variability and additive gene action for multiple traits. In the TVH 002 × RAHC 1039 cross, positive skewness was recorded for plant height and internode length, while platykurtic distributions were observed for days to first flowering and the number of monopodia, suggesting traits with wide variability. The TCH 1894 × NDLH 32 cross displayed positive skewness for the number of bolls per plant and boll weight, accompanied by leptokurtic distributions, indicative of narrow variability. These observations align with the findings of Orabi *et al.* (2017).

Heritability and Genetic Advance: All the crosses demonstrated high heritability coupled with high genetic advance as a percentage of the mean for traits such as boll weight, plant height, lint index, and seed index (**Table 1**). These findings are consistent with previous studies conducted by Khan *et al*. (2009), Reddy and Sarma (2014), and Ahsan *et al.* (2015). High heritability along with moderate genetic advance as a percentage of the mean was observed for the upper half mean length in all crosses. In contrast, high heritability combined with low genetic advance as a percentage of the mean was recorded for the uniformity ratio, corroborating the findings of Gopikrishnan *et al.* (2013), who also reported

Table 1. Genetic variability and heritability in F_2 populations of the crosses CO17 x KC2, TVH002 x KC3, TVH002 x RAHC 1039 and TCH1894 x NDLH32

S. No.	TRAIT	CROSS	VP	VG	VE	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)
1	Days to first flowering	CO17 x KC2	5.95	5.23	0.72	4.36	4.09	87.91	4.42	7.89
		TVH002 x KC3	5.45	2.13	3.32	4.17	2.61	39.03	1.88	3.36
		TVH002 x RAHC 1039	6.24	2.76	3.48	4.42	2.94	44.24	2.28	4.03
		TCH1894 x NDLH32	5.97	0.57	5.40	4.35	1.35	9.58	0.48	0.86
2	Plant height	CO17 x KC2	268.21	254.58	13.62	21.56	21.00	94.92	32.02	42.15
		TVH002 x KC3	147.38	110.49	36.90	18.85	16.32	74.97	18.75	29.12
		TVH002 x RAHC 1039	235.09	210.45	24.65	21.88	20.70	89.52	28.27	40.34
		TCH1894 x NDLH32	192.08	156.65	35.44	19.46	17.58	81.55	23.28	32.70
3	Internode length	CO17 x KC2	0.55	0.48	0.08	15.55	14.46	86.46	1.33	27.70
		TVH002 x KC3	0.64	0.35	0.29	16.60	12.31	54.99	0.90	18.81
		TVH002 x RAHC 1039	0.46	0.17	0.30	16.18	9.69	35.86	0.50	11.95
		TCH1894 x NDLH32	0.53	0.28	0.26	15.64	11.26	51.84	0.78	16.70
4	Number of monopodia per plant	CO17 x KC2	0.71	0.51	0.20	111.06	94.19	71.93	1.25	164.55
		TVH002 x KC3	0.64	0.24	0.40	82.45	50.69	37.80	0.62	64.20
		TVH002 x RAHC 1039	0.61	0.37	0.24	130.14	101.52	60.86	0.98	163.15
		TCH1894 x NDLH32	0.80	0.40	0.40	68.65	48.41	49.73	0.91	70.33
5	Number of sympodia per plant	CO17 x KC2	10.98	5.06	5.92	26.09	17.71	46.08	3.15	24.77
		TVH002 x KC3	8.90	2.66	6.24	26.74	14.62	29.89	1.84	16.46
		TVH002 x RAHC 1039	11.72	5.60	6.12	31.96	22.09	47.77	3.37	31.45
		TCH1894 x NDLH32	9.22	1.78	7.44	26.41	11.60	19.29	1.21	10.49
6	Number of bolls per plant	CO17 x KC2	21.76	16.76	5.00	50.87	44.65	77.02	7.40	80.72
		TVH002 x KC3	27.56	1.60	25.96	49.04	11.83	5.82	0.63	5.88
		TVH002 x RAHC 1039	32.76	15.00	17.76	54.11	36.62	45.79	5.40	51.04
		TCH1894 x NDLH32	29.42	16.66	12.76	44.93	33.81	56.62	6.33	52.41
7	Boll weight	CO17 x KC2	0.68	0.46	0.23	29.99	24.50	66.71	1.14	41.21
		TVH002 x KC3	0.46	0.42	0.04	25.71	24.52	90.97	1.27	48.17
		TVH002 x RAHC 1039	0.68	0.58	0.10	33.16	30.62	85.24	1.45	58.23
		TCH1894 x NDLH32	0.62	0.48	0.14	28.64	25.19	77.31	1.26	45.62
8	Single plant yield	CO17 x KC2	195.58	41.95	153.63	55.64	25.77	21.45	6.18	24.58
		TVH002 x KC3	242.61	0.83	241.78	55.53	3.25	0.34	0.11	0.39
		TVH002 x RAHC 1039	192.19	2.76	189.43	54.26	6.51	1.44	0.41	1.61
		TCH1894 x NDLH32	334.39	142.69	191.70	54.13	35.36	42.67	16.07	47.58
9	Ginning outturn	CO17 x KC2	3.67	2.61	1.06	6.37	5.37	71.09	2.80	9.32
		TVH002 x KC3	4.30	3.12	1.17	6.89	5.88	72.75	3.11	10.32
		TVH002 x RAHC 1039	3.29	2.07	1.23	6.35	5.03	62.77	2.35	8.21
		TCH1894 x NDLH32	3.60	2.81	0.79	6.18	5.45	77.97	3.05	9.92
10	Seed index	CO17 x KC2	1.57	1.06	0.51	15.43	12.70	67.71	1.75	21.52
		TVH002 x KC3	1.97	1.78	0.18	16.87	16.06	90.63	2.62	31.49
		TVH002 x RAHC 1039	2.76	2.58	0.18	19.76	19.09	93.38	3.20	38.00
		TCH1894 x NDLH32	2.12	1.96	0.16	17.82	17.11	92.24	2.77	33.85
11	Lint index	CO17 x KC2	0.36	0.28	0.09	17.19	15.04	76.48	0.95	27.09
		TVH002 x KC3	0.40	0.35	0.04	17.60	16.60	88.98	1.15	32.26
		TVH002 x RAHC 1039	0.48	0.44	0.05	20.62	19.60	90.40	1.29	38.39
		TCH1894 x NDLH32	0.48	0.46	0.03	19.13	18.59	94.38	1.35	37.19

Table 1. Continued..

S. No.	TRAIT	CROSS	VP	VG	VE	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)
12	Upper half mean length	CO17 x KC2	4.08	3.94	0.14	8.69	8.54	96.57	4.02	17.28
		TVH002 x KC3	2.55	2.24	0.31	6.82	6.39	87.96	2.89	12.35
		TVH002 x RAHC 1039	2.27	1.95	0.32	6.35	5.89	86.02	2.67	11.25
		TCH1894 x NDLH32	3.47	3.23	0.23	7.91	7.64	93.23	3.58	15.19
13	Uniformity ratio	CO17 x KC2	1.09	0.88	0.21	2.20	1.98	80.61	1.73	3.66
		TVH002 x KC3	0.61	0.46	0.15	1.66	1.44	75.54	1.22	2.58
		TVH002 x RAHC 1039	0.65	0.52	0.13	1.71	1.53	80.72	1.34	2.84
		TCH1894 x NDLH32	0.58	0.40	0.17	1.61	1.34	70.10	1.10	2.32
14	Bundle strength	CO17 x KC2	5.06	4.93	0.14	10.21	10.06	97.25	4.51	20.45
		TVH002 x KC3	2.64	2.47	0.16	7.22	6.99	93.77	3.14	13.94
		TVH002 x RAHC 1039	3.09	2.85	0.25	7.75	7.44	92.07	3.33	14.71
		TCH1894 x NDLH32	3.40	3.23	0.17	8.13	7.92	95.01	3.61	15.90
15	Elongation percentage	CO17 x KC2	0.14	0.07	0.07	6.85	4.96	52.43	0.41	7.40
		TVH002 x KC3	0.28	0.25	0.03	9.94	9.31	87.64	0.96	17.95
		TVH002 x RAHC 1039	0.13	0.11	0.03	6.58	5.90	80.50	0.60	10.91
		TCH1894 x NDLH32	0.10	0.08	0.02	5.60	5.11	83.11	0.53	9.59
16	Fiber fineness	CO17 x KC2	0.19	0.16	0.03	9.52	8.79	85.21	0.76	16.71
		TVH002 x KC3	0.26	0.23	0.03	11.06	10.39	88.28	0.93	20.10
		TVH002 x RAHC 1039	0.28	0.24	0.04	10.97	10.22	86.78	0.94	19.61
		TCH1894 x NDLH32	0.32	0.29	0.04	11.75	11.09	89.04	1.04	21.55

VP- Phenotypic variance
VG- Genotypic variance
VE- Environmental variance
PCV- Phenotypic Coefficient of Variance
GCV- Genotypic Coefficient of Variance
h^2- Heritability
GA- Genetic Advance
GAM- Genetic Advance as per cent of mean

low genetic advance for this trait. Plant height exhibited additive gene action across all crosses. Similarly, additive gene action was observed for the number of bolls per plant and internode length in the CO 17 × KC 2 cross, aligning with the results of Sajjad *et al.* (2015). Sympodia per plant, however, showed significant environmental influence in the crosses TVH 002 × RAHC 1039 and CO 17 × KC 2. Boll weight displayed additive gene action across all crosses, while single plant yield was heavily influenced by environmental factors. Additive gene action was also evident for lint index and seed index in all crosses. Additionally, the CO 17 × KC 2 cross exhibited additive gene action for bundle strength, consistent with findings reported by Gnanasekaran *et al.* (2020). Additive gene action was further observed for fiber fineness in the TCH 1894 × NDLH 32 and TVH 002 × KC 3 crosses.

Correlation Analysis: The correlation analysis of quantitative traits across the four cotton crosses TVH 002 × KC 3, CO 17 × KC 2, TCH 1894 × NDLH 32, and TVH 002 × RAHC 1039 is presented in **Tables 2**, **3, 4, and 5**.

Direct Phenotypic Association of Component Traits with Seed Cotton Yield: Single plant yield in all the crosses exhibited a significant and positive correlation with traits such as internode length, plant height, number of bolls per plant, lint index, and boll weight. These findings are in alignment with those reported by Dedaniya and Pethani (1994), Gite *et al.* (2006), and Ekinci *et al.* (2010). Additionally, single plant yield was significantly and positively correlated with the seed index and the number of sympodia in all crosses except CO 17 × KC 2. In the cross TVH 002 × RAHC 1039, a significant positive correlation was observed between single plant yield and the number of monopodia per plant, consistent with the findings of Iqbal *et al.* (2006). However, negative associations were identified between yield and fiber quality parameters, as previously reported by Scholl and Miller (1976).

Inter-Correlation Among Yield Components: Plant height was significantly and positively correlated with internode length, the number of bolls per plant, and the number of sympodia per plant in all crosses, consistent with Kumar *et al.* (2019). A significant positive correlation between plant height and the number of monopodia per plant was also observed in all crosses, as reported by Arunkumar and Murthy (2020), except for the cross TVH 002 × RAHC 1039. Plant height showed a negative correlation with

Table 2. Correlation co-efficient analysis in the cross CO 17 x KC 2

	DFF	PH	IL	NM	NS	NBP	BW	GOT	SI	LI	UHML	UR	BS	EL	FF	SPY
DFF	1.000															
PH	-0.035	1.000														
IL	0.132	0.417**	1.000													
NM	0.053	0.214**	0.038	1.000												
NS	-0.128	0.775**	0.199**	0.162*	1.000											
NBP	-0.062	0.328**	0.133	0.084	0.243**	1.000										
BW	0.019	-0.029	0.103	-0.049	-0.200**	-0.088	1.000									
GOT	-0.007	0.055	-0.095	-0.010	0.058	0.056	0.122	1.000								
SI	-0.081	0.014	-0.028	-0.094	0.036	0.075	0.102	-0.066	1.000							
LI	-0.078	0.035	-0.070	-0.099	0.062	0.091	0.148*	0.465**	0.850**	1.000						
UHML	-0.069	-0.006	-0.090	0.085	-0.002	0.157*	-0.026	0.109	0.007	0.064	1.000					
UR	0.099	0.045	0.048	0.010	0.072	-0.019	0.130	0.080	0.060	0.096	-0.266**	1.000				
BS	0.066	-0.008	-0.007	-0.133	0.027	0.072	-0.040	0.158*	-0.007	0.085	0.264**	-0.204**	1.000			
EL	-0.144*	-0.043	-0.039	0.026	0.032	0.007	-0.108	-0.039	-0.049	-0.051	0.074	-0.180*	0.119	1.000		
FF	-0.085	0.000	-0.056	0.065	-0.037	0.006	0.037	-0.066	0.118	0.068	0.002	0.000	-0.106	-0.027	1.000	
SPY	-0.036	0.266**	0.162*	0.053	0.113	0.841**	0.407**	0.080	0.131	0.152*	0.138	0.054	0.012	-0.023	0.027	1.000

*significant at 5%, **significant at 1%

DFF- Days to first flowering
PH- Plant height
IL- Internode length
NM- Number of monopodia per plant
NS- Number of sympodia per plant
NBP- Number of bolls per plant
BW- Boll weight
GOT- Ginning outturn
SI- Seed index
LI- Lint index
UHML- Upper half mean length
UR- Uniformity ratio
BS- Bundle strength
EL- Elongation percentage
FF- Fiber fineness
SPY- Single plant yield

boll weight in TVH 002 × RAHC 1039 but was positively correlated with boll weight in TVH 002 × KC 3. Days to first flowering exhibited significant negative correlations with elongation percentage in CO 17 × KC 2, seed index in TVH 002 × KC 3, and uniformity ratio and fiber fineness in TVH 002 × RAHC 1039. Internode length demonstrated a significant positive correlation with the number of sympodia per plant in all crosses and with the number of bolls per plant in all crosses except CO 17 × KC 2. Seed index exhibited a positive correlation with lint index across all crosses, consistent with the observations of Wadeyar and Kajjidoni (2014). similar observations were reported by Waldia and Jatasra (1980), in desi cotton. The number of monopodia per plant was significantly and positively correlated with the number of sympodia per plant in CO 17 × KC 2 and TVH 002 × KC 3. Additionally, it was positively correlated with the number of bolls per plant in TVH 002 × KC 3 and TCH 1894 × NDLH 32, as reported by Sahar *et al.* (2021). In TVH 002 × RAHC 1039, monopodia per plant were significantly correlated with the seed index. The number of sympodia per plant showed a significant positive correlation with the number of bolls per plant in all crosses but a significant negative correlation with boll weight in CO 17 × KC 2 and TVH 002 × RAHC 1039. The number of bolls per plant was significantly and positively correlated with seed index and lint index in all crosses except CO 17 × KC 2. Positive associations between the number of bolls per plant and seed index were previously reported by Channa *et al.* (2016). In the CO 17 × KC 2 cross, the number of bolls per plant exhibited a positive correlation with the upper half mean length but a negative correlation with boll weight and uniformity ratio in TVH 002 × RAHC 1039. Boll weight showed significant positive correlations with lint index and seed index in all crosses, except for the CO 17 × KC 2 cross. Negative correlations between boll weight and ginning outturn in TVH 002 × KC 3 were consistent with the findings of Kaushik *et al*. (2005). Ginning outturn was positively correlated with lint index across all crosses and with bundle strength in CO 17 × KC 2, as suggested by Dedaniya *et al*. (2020). Conversely, ginning outturn was negatively correlated with seed index in TVH 002 × KC 3. Lint index exhibited a positive correlation with bundle strength in TCH 1894 × NDLH 32 but showed a significant negative correlation with fiber fineness in TVH 002 × KC 3. Upper half mean length was positively correlated with bundle strength in all crosses except TVH 002 × KC 3, as reported by Thiyagu *et al.* (2010), but was negatively correlated with uniformity ratio in CO 17 × KC 2 and TCH 1894 × NDLH 32. Uniformity ratio displayed significant

Table 3. Correlation co-efficient analysis in the cross TVH 002 x KC 3

	DFF	PH	IL	NM	NS	NBP	BW	GOT	SI	LI	UHML	UR	BS	EL	FF	SPY
DFF	1.000															
PH	-0.008	1.000														
IL	0.046	0.343**	1.000													
NM	0.127	0.237**	0.006	1.000												
NS	-0.021	0.711**	0.198*	0.208*	1.000											
NBP	-0.006	0.352**	0.209*	0.177*	0.307**	1.000										
BW	-0.098	0.204*	0.068	-0.049	0.052	0.038	1.000									
GOT	0.107	-0.115	0.018	0.024	0.010	-0.021	-0.206*	1.000								
SI	-0.191*	0.149	0.016	-0.008	0.111	0.268**	0.374**	-0.248**	1.000							
LI	-0.125	0.079	0.026	0.006	0.105	0.260**	0.238**	0.333**	0.827**	1.000						
UHML	0.026	0.008	0.102	0.006	0.032	-0.097	-0.005	0.036	-0.127	-0.093	1.000					
UR	-0.163	-0.001	-0.099	0.073	0.087	0.015	-0.046	-0.068	0.152	0.108	-0.106	1.000				
BS	0.021	0.020	-0.005	0.060	0.039	0.069	-0.018	-0.071	0.080	0.041	-0.004	0.012	1.000			
EL	-0.155	0.055	-0.100	0.012	0.107	0.098	-0.026	-0.135	0.016	-0.067	-0.107	0.058	-0.126	1.000		
FF	-0.038	0.046	-0.002	0.076	0.131	-0.066	0.064	-0.167*	-0.134	-0.231**	0.001	-0.069	0.058	0.117	1.000	
SPY	-0.062	0.399**	0.208*	0.159	0.282**	0.868**	0.480**	-0.117	0.382**	0.313**	-0.067	-0.010	0.055	0.068	-0.033	1.000

*significant at 5%, **significant at 1%

Table 4. Correlation co-efficient analysis in the cross TVH 002 x RAHC 1039

	DFF	PH	IL	NM	NS	NBP	BW	GOT	SI	LI	UHML	UR	BS	EL	FF	SPY
DFF	1.000															
PH	0.051	1.000														
IL	0.032	0.387**	1.000													
NM	-0.092	0.056	0.085	1.000												
NS	0.018	0.835**	0.271**	-0.014	1.000											
NBP	-0.043	0.380**	0.187**	0.114	0.472**	1.000										
BW	0.042	-0.158*	0.025	0.096	-0.279**	-0.182**	1.000									
GOT	0.068	-0.018	0.050	-0.091	-0.092	-0.013	0.052	1.000								
SI	-0.022	0.108	0.031	0.141*	0.149*	0.212**	0.164*	-0.129	1.000							
LI	0.004	0.090	0.054	0.095	0.098	0.193**	0.179**	0.315**	0.896**	1.000						
UHML	0.021	0.055	0.027	-0.051	0.068	0.016	-0.026	-0.014	0.017	0.007	1.000					
UR	0.087	-0.069	-0.002	0.090	-0.143*	-0.200**	0.094	0.004	0.064	0.061	-0.064	1.000				
BS	0.109	0.042	-0.034	-0.026	0.002	-0.075	-0.047	0.040	-0.069	-0.050	0.376**	-0.025	1.000			
EL	-0.034	0.025	0.066	0.016	0.015	0.042	0.060	-0.007	-0.018	-0.011	0.058	-0.047	0.052	1.000		
FF	0.055	-0.060	-0.057	-0.024	-0.055	-0.096	-0.048	0.032	-0.004	0.014	0.037	-0.019	0.115	0.123	1.000	
SPY	-0.035	0.276**	0.212**	0.180**	0.305**	0.855**	0.285**	0.010	0.262**	0.254**	0.003	-0.132*	-0.091	0.073	-0.100	1.000

*significant at 5%, **significant at 1%

DFF- Days to first flowering
PH- Plant height
IL- Internode length
NM- Number of monopodia per plant
NS- Number of sympodia per plant
NBP- Number of bolls per plant
BW- Boll weight
GOT- Ginning outturn
SI- Seed index
LI- Lint index
UHML- Upper half mean length
UR- Uniformity ratio
BS- Bundle strength
EL- Elongation percentage
FF- Fiber fineness
SPY- Single plant yield

Table 5. Correlation co-efficient analysis in the cross TCH 1894 x NDLH 32

	DFF	PH	IL	NM	NS	NBP	BW	GOT	SI	LI	UHML	UR	BS	EL	FF	SPY
DFF	1.000															
PH	-0.045	1.000														
IL	0.079	0.358**	1.000													
NM	-0.022	0.181*	0.030	1.000												
NS	-0.073	0.728**	0.236**	0.129	1.000											
NBP	0.037	0.320**	0.351**	0.168*	0.234**	1.000										
BW	0.110	-0.020	0.041	-0.006	-0.050	0.127	1.000									
GOT	-0.056	-0.015	0.098	-0.048	-0.066	0.006	-0.043	1.000								
SI	0.093	0.038	0.063	0.211**	0.142	0.316**	0.246**	-0.107	1.000							
LI	0.055	0.034	0.110	0.181*	0.112	0.297**	0.208**	0.368**	0.882**	1.000						
UHML	0.096	-0.064	0.069	-0.081	-0.107	0.048	0.155	-0.007	0.138	0.118	1.000					
UR	-0.245**	0.108	0.049	0.081	0.124	0.015	0.064	0.056	-0.035	-0.005	-0.252**	1.000				
BS	0.066	-0.002	0.051	0.062	-0.060	0.028	-0.020	0.068	0.139	0.161*	0.367**	-0.136	1.000			
EL	0.094	-0.020	0.061	0.070	-0.034	0.103	0.079	0.074	0.033	0.063	0.154	-0.033	0.213**	1.000		
FF	-0.230**	-0.038	-0.085	0.029	-0.089	-0.013	-0.132	0.006	-0.062	-0.059	0.053	0.039	-0.016	-0.025	1.000	
SPY	0.065	0.237**	0.287**	0.132	0.161*	0.834**	0.598**	0.023	0.424**	0.410**	0.101	0.047	0.007	0.094	-0.067	1.000

*significant at 5%, **significant at 1%

DFF- Days to first flowering
PH- Plant height
IL- Internode length
NM- Number of monopodia per plant
NS- Number of sympodia per plant
NBP- Number of bolls per plant
BW- Boll weight
GOT- Ginning outturn
SI- Seed index
LI- Lint index
UHML- Upper half mean length
UR- Uniformity ratio
BS- Bundle strength
EL- Elongation percentage
FF- Fiber fineness
SPY- Single plant yield

negative correlations with bundle strength and elongation percentage in CO 17 × KC 2.

These correlations underscore the importance of careful monitoring and selection of heritable traits contributing to economically important characteristics. Selecting traits with additive gene action can facilitate the development of stable, fixed genotypes. However, caution must be exercised to avoid fixing undesirable traits linked to economically significant ones, as this could hinder genetic improvement during generation advancement. Successive careful monitoring of the traits and their genetic mechanisms, improved cotton genotypes with enhanced yield and quality attributes can be attained while minimizing undesirable associations.

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