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Research Article

Genetic analysis of fibre quality and yield related traits in desi cotton (*Gossypium arboreum* L.)

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Abstract

The present investigation was undertaken in 48 desi cotton genotypes to study the genetic divergence and character association for fibre quality and yield related traits. The results of Mahalanobis D² analysis indicated the presence of considerable genetic divergence among the genotypes. They were grouped into nine clusters. The crosses made between the genotypes of cluster V (NDLA-3066) with cluster VII (NDLA 3105-5) followed by cluster IX (NDLA 3147-2) with cluster VII (NDLA 3105-5) and cluster VI (NDLA-2974) with cluster VII (NDLA 3105-5) are expected to give desirable segregants. Of the 15 characters studied, elongation percentage, seed cotton yield, UHML, bundle strength and lint yield contributed maximum towards divergence. The correlation study showed significant positive association of boll weight and lint yield with seed cotton yield per plant at both phenotypic and genotypic levels. So, increase in seed cotton yield per plant can be attained by the improvement of boll weight and lint yield in breeding programme.

Keywords: Desi cotton, genetic divergence, correlation, clusters, fibre quality, yield.

INTRODUCTION

Cotton (*Gossypium spp.*), known as the “King of fiber crops,” is one of the most important natural fibre and cash crops of India. It provides the basic raw material (cotton fibre) to the cotton textile industry. Cotton also referred to as “White Gold,” plays a dominant role in the industrial and agricultural economy of the country. It sustains millions of people in sectors such as agriculture, textile mills, ginning factories, and business (Imran *et al.*, 2011). Around 60 million people rely on its cultivation, commerce, and processing for living. Globally, cotton is cultivated over an area of 33.18 m ha with a production of 25.73 m tonnes and a productivity of 775 kg ha⁻¹. In India, it is grown in an area of 12.65 m ha with a production of 5.9 m tonnes and a productivity of 466 kg ha⁻¹ [International Cotton Advisory Committee (ICAC) data portal, 2021-22].

Domestication of *Gossypium arboreum* initiated at Indus valley (Hutchinson, 1954) and from there, it spread to various parts of the world. During this expansion, it became adapted to a large range of climatic and soil conditions and adopted distinct genetic and morphological features. *G. arboreum* fibres display various colours (e.g., white, off-white and tan) and some of the accessions produce fibres with very high strength (Ashraf *et al.*, 2018). Desi cotton produces two types of fibres. One is short and coarse fibre and the other type is good quality spinnable fibre (Kranthi, 2015). In addition, desi cotton has absorbent property because of which it is used more efficiently in surgical and first aid treatment (Meena *et al.*, 2022). There is a significant demand for short-staple cotton for denims and mattresses. *G.*

arboresum is well known for possessing many favourable attributes than upland cotton, mainly well adapted to dry land conditions as well as amenable to low input cultivation practices (Iqbal *et al.*, 2019).

Genetic diversity in the experimental material is generally considered as a vital criterion for choosing genetically diverse parents required for efficient and successful hybridization programme, which in turn results in the production of high yielding lines (Melchinger, 1999). Satish (2021) reported that seed cotton yield followed by lint index, boll weight, number of bolls per plant, ginning out-turn, plant height, seed index, days to 50 % flowering contributed maximum towards genetic divergence. Meena *et al.* (2022) reported that inter-cluster distances were greater than intra-cluster distances, indicating that the crosses between genotypes of the diverse clusters can be made to create suitable transgressive segregants. Correlation coefficient analysis measures the magnitude of the relationship between various plant characters and determines the component characters on which selection can be based for improvement in seed cotton yield and fibre quality. Jangid *et al.* (2022) reported that seed cotton yield exhibited a highly significant and positive correlation with lint yield, number of bolls per plant and boll weight.

Keeping in view the importance of genetic analysis of desi cotton genotypes for fibre quality and yield related traits, the present investigation was carried out with the objectives of the assessment of genetic diversity among the diverse desi cotton genotypes for yield and fibre related traits and also to study the character association among the different yield and fibre related traits.

MATERIALS AND METHODS

The present investigation was carried out using 48 diverse desi cotton genotypes developed at Regional Agricultural Research Station, Nandyal (**Table 1**). The experiment was carried in a Randomized Block Design (RBD) with three replications during *kharif*, 2021-22. Each genotype was grown in two rows with a row length of 5 m and spacing of 60 cm between the rows and 30 cm between the plants. All recommended crop management practices were followed for good crop growth and establishment.

Observations were recorded on five randomly selected plants per accession for six morphological traits *viz.*, plant height, bolls per plant, boll weight, ginning percentage, lint index and seed index were recorded in each replication. In addition, four morphological characters, days to 50 % flowering, days to maturity, seed cotton yield and lint

Table 1. Details of germplasm accessions utilized for study

S. No	Genotype	Parentage	S. No	Genotype	Parentage
1	Aravinda	Desi A-2462 x A 5262	25	NDLA-3115-2	Srinandi x NACH-18
2	Srinandi	Racherla x Local Desi type	26	NDLA-3091	Aravinda x 2954
3	Yaganti	Aravinda x H-507	27	NDLA-3116-3	Yaganti x ARBA-79-08
4	NDLA-2985	2708 x DSAV-2	28	NDLA-3109-4	Aravinda x NACH-18
5	NDLA-3116-4	Yaganti x ARBA-7908	29	NDLA- 3111-5	Srinandi x MRDC-235
6	NDLA-2953	NDLA-2913 x AC-40	30	NDLA-3109	Aravinda x NACH-18
7	NDLA-3005	2463 x HD 444	31	NDLA-3139-3	Yaganti x DAS 1041
8	NDLA-3066	2933 x 2937	32	NDLA-3128-2	MRDC-235 x Yaganti
9	NDLA-2974	Aravinda x 401	33	NDLA-3105-5	Aravinda x ARBA-79-08
10	NDLA-3014	2463 x NANDI 405	34	NDLA-3129-1	NACH-6 x Srinandi
11	NDLA-3038	2463 x 2941	35	NDLA-3140	Srinandi x Swadeshi-651
12	NDLA-3043	Aravinda x 610	36	NDLA-3143-1	Yaganti x Swadeshi-651
13	NDLA-3037	2463 x 2938	37	NDLA-3147-1	3068 x Yaganti
14	NDLA-2946	NDLA-2708 x AC-349513	38	NDLA-3151-1	NDLA-3070 x MRDC-235
15	NDLA-2930	NDLA-2708 x B-5	39	NDLA-3152-1	NDLA-3091 x NACH-18
16	NDLA-2963	NDLA-2913 x NDLA-30811	40	NDLA-3154-3	CCA-3 x Yaganti
17	NDLA-2965	NDLA-2708 x RC-1	41	NDLA-3148-2	3068 x RG-690
18	NDLA-3028	NDLA-2463 x NDLA-2949	42	NDLA-3122-2	Srinandi x FDK-178
19	NDLA-2958	NDLA-2462 x Kalugotla	43	NDLA-3155-3	SV-385 x RG-690
20	NDLA-2976	Aravinda x AKH 4	44	NDLA-3147-2	CCA-3 x RG-690
21	NDLA-3020	GB 30 x 2463	45	NDLA-3149-2	PA-740 x RG-690
22	NDLA-3094	Aravinda x 2977	46	NDLA-3142-1	Srinandi x CNA-1007
23	NDLA-3104-4	Aravinda x CIBA-357	47	NDLA-3146-2	Yaganti x CNA-1007
24	NDLA-3113	Srinandi x MRDC-233	48	NDLA-3146-1	Yaganti x CNA-1007

yield were recorded on plot basis. Fibre quality traits viz., Upper half mean length (UHML), micronaire, bundle strength, uniformity index and elongation percentage were measured using High Volume Instrumentation (HVI-900-SA; Uster) operated in the HVI mode at ICAR-Central Institute for Research on Cotton Technology, Regional Unit, Coimbatore, India. The statistical analysis including descriptive statistics, analysis of variance, Mahalanobis D^2 analysis and Pearson's correlation coefficient analysis were performed using INDOSTAT statistical software.

RESULTS AND DISCUSSION

The data collected from the experimental material was subjected to the analysis of variance and is presented in the **Table 2**. It is perceptible from the analysis of variance that the treatment differences for all the characters were significant for all the genotypes indicating the presence of sufficient variability among the genotypes. Similar results were reported by Keerio *et al.* (2022) and Meena *et al.* (2022). The descriptive statistics including mean, range, coefficient of variation, broad sense heritability and genetic advance of evaluated traits are presented in **Table 3**. The seed cotton yield ranged from 281 kg/ha to 1008.40 kg/ha with a mean value of 624.01 kg/ha. The elongation percentage ranged from 5.63% to 8.66% among the evaluated genotypes. The phenotypic and genotypic coefficient of variations ranged from 3.05% to 30.01% and 1.91% to 28.12% for days to maturity and lint yield, respectively. The highest broad sense heritability was observed for ginning percentage

(98.90) followed by bundle strength (98.80) and UHML (98.40), whereas, the lowest broad sense heritability was observed for elongation percentage (24.20). The highest genetic advance was observed for lint yield (54.29) followed by seed cotton yield (51.39) and seed index (34.00). The lowest genetic advance was observed for days to maturity (2.46).

From the study, it was observed that the traits lint index, seed index, seed cotton yield and lint yield showed high heritability and high genetic advance indicating the presence of additive gene action. High heritability and high genetic advance for seed cotton yield, lint yield and boll weight were reported by Gnanasekaran *et al.* (2018) and Parre and Patil (2021). The traits ginning percentage, UHML, micronaire and bundle strength showed high heritability and medium genetic advance. The traits plant height and uniformity index showed high heritability and low genetic advance. The trait boll weight showed medium heritability with medium genetic advance. The traits days to 50% flowering, days to maturity and bolls per plant showed medium heritability with low genetic advance. The trait elongation percentage showed low heritability coupled with low genetic advance. The traits showing high or medium or low heritability coupled with either medium or low genetic advance indicate the predominance of non-additive gene action in their expression. High heritability coupled with low genetic advance for ginning percentage and bundle strength were reported by Jarwar *et al.* (2018) and Komala *et al.* (2018).

Table 2. Analysis of variance for fibre and yield components in desi cotton

S. No.	Character	Mean sum of squares		
		Replications	Treatments	Error
	Degrees of freedom	2	47	94
1.	Plant height (cm)	4.4236	155.4502**	11.3597
2.	Days to 50% flowering	0.1875	15.3178**	2.9109
3.	Days to maturity	0.3402	22.1554**	7.5672
4.	Number of bolls per plant	1.0989	13.0676**	4.9591
5.	Boll weight (g)	0.0538	0.2592**	0.0914
6.	Ginning percentage (%)	0.2986	29.0272**	0.1054
7.	Lint index (g)	0.0525	0.6191**	0.0893
8.	Seed index (g)	0.1727	2.0599**	0.0563
9.	Seed cotton yield (Kg ha ⁻¹)	1252.7970	88003.2967**	4242.7066
10.	Lint yield (Kg ha ⁻¹)	195.1371	12905.9824**	569.6156
11.	UHML (mm)	0.0875	10.0772**	0.0554
12.	Micronaire ($\mu\text{g inch}^{-1}$)	0.0146	0.9445**	0.0267
13.	Bundle strength (g tex ⁻¹)	0.0136	6.8164**	0.0265
14.	Uniformity index (%)	0.1875	16.0128**	2.6697
15.	Elongation percentage (%)	0.0896	0.8069**	0.4121

** - Significantly different at 1 % probability level

Table 3. Estimates of mean, variability, heritability (broad sense) and genetic advance as per cent of mean for fibre and yield components in desi cotton

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Plant height (cm)	113.40	98	134.33	6.79	6.11	80.90	11.32
2	Days to 50% flowering	62.47	56.66	67.00	4.24	3.25	58.70	5.13
3	Days to maturity	115.31	110.00	120.00	3.05	1.91	39.10	2.46
4	Number of bolls per plant	21.98	17.40	27.10	12.58	7.47	35.30	9.14
5	Boll weight (g)	1.98	1.33	2.53	19.30	11.89	37.90	15.08
6	Ginning percentage (%)	36.59	31.13	43.06	8.53	8.48	98.90	17.38
7	Lint index (g)	2.91	2.26	4.26	17.66	14.39	66.40	24.17
8	Seed index (g)	4.75	3.20	6.26	17.90	17.18	92.20	34.00
9	Seed cotton yield (Kg ha ⁻¹)	624.01	281.10	1008.40	28.73	26.77	86.80	51.39
10	Lint yield (Kg ha ⁻¹)	227.99	104.13	377.73	30.01	28.12	87.80	54.29
11	UHML (mm)	23.74	19.63	26.66	7.76	7.69	98.40	15.72
12	Micronaire (µg inch ⁻¹)	5.82	4.96	7.00	9.89	9.48	92.00	18.74
13	Bundle strength (g tex ⁻¹)	22.64	19.56	26.63	6.68	6.64	98.80	13.60
14	Uniformity index (%)	80.18	75.66	84.33	3.32	2.63	62.50	4.28
15	Elongation percentage (%)	6.32	5.63	8.66	11.65	5.73	24.20	5.81

PCV-Phenotypic coefficient of variation, GCV-Genotypic coefficient of variation

The relative contributions of the characters studied towards the divergence of genotypes are presented in **Table 4**. Among the characters, elongation percentage (21.37 %) contributed maximum to the total variation followed by seed cotton yield (19.77 %), UHML (14.72 %), bundle strength (12.68%), lint yield (12.68 %), ginning percentage (10.82 %), lint index (6.74 %), plant height (0.62 %), micronaire (0.53 %) and uniformity index (0.09 %). The genotypes namely, NDLA 3147-2 (8.66%) and NDLA-2974 (7.56%) recorded very high elongation percentage. The maximum diversity of elongation percentage may be due to the wide range of elongation percentage among all genotypes. The characters that contributed least to the genetic diversity were micronaire (0.53%) and uniformity index (0.09%). The characters that showed no contribution towards genetic divergence were days to 50% flowering, days to maturity, number of bolls per plant, boll weight and seed index. Reddy *et al.* (2015) and Mangi *et al.* (2021) also reported that elongation percentage contributed maximum towards diversity in their study. Bhimate *et al.* (2019) and Satish (2021) reported that seed cotton yield contributed maximum towards diversity in their study.

The 48 genotypes were grouped into nine clusters using Tocher's method based on D^2 values in which the genotypes belonging to the same cluster had an average minimum D^2 value, than that of genotypes present in different clusters. Out of nine clusters formed, cluster I was the largest comprising of maximum number of

26 genotypes (**Table 5**). The mono-genotypic clusters formed in the present study represented existence of wide diversity among the germplasm under study. Cluster means for 15 traits for all the nine clusters are presented in the **Table 6**. The average intra and inter-cluster distances D^2 values were estimated and are presented in **Table 7**. The inter cluster distance ranged from 276.90 (between cluster VI and IX) to 2344.34 (between cluster V and VII). Comparison between inter and intra cluster D^2 values revealed that inter cluster D^2 values were greater than intra cluster D^2 values. The inter cluster distances were greater than intra cluster except in some clusters as reported by Satish *et al.* (2009), Sakthi *et al.* (2009) and Kulkarni *et al.* (2011). The maximum inter cluster D^2 value was observed between cluster V and cluster VII (2344.34) followed by cluster VII and cluster IX (2253.23) and cluster VI and cluster VII (1927.78). Based on these studies, crosses made between the genotypes of cluster V (NDLA-3066) with cluster VII (NDLA 3105-5) followed by cluster IX (NDLA 3147-2) with cluster VII (NDLA 3105-5) and cluster VI (NDLA-2974) with cluster VII (NDLA 3105-5) are expected to give desirable segregants. Inter-crossing between the genotypes which are divergent in nature lead to wide genetic base in the source population and greater opportunity for crossing over to occur, which releases the hidden variability by breaking undesirable linkages.

Seed cotton yield is a polygenically controlled complex character resulting from multiplicative interaction of yield

Table 4. Contribution of different characters towards divergence in 48 desi cotton genotypes

S. No.	Character	Contribution (%)	Times ranked 1 st
1.	Plant height (cm)	0.62	7
2.	Days to 50% flowering	0.00	0
3.	Days to maturity	0.00	0
4.	Number of bolls per plant	0.00	0
5.	Boll weight (g)	0.00	0
6.	Ginning percentage (%)	10.82	122
7.	Lint index (g)	6.74	76
8.	Seed index (g)	0.00	0
9.	Seed cotton yield (kg ha ⁻¹)	19.77	223
10.	Lint yield (Kg ha ⁻¹)	12.68	143
11.	UHML (mm)	14.72	166
12.	Micronaire ($\mu\text{g inch}^{-1}$)	0.53	6
13.	Bundle strength (g tex ⁻¹)	12.68	143
14.	Uniformity index (%)	0.09	1
15.	Elongation percentage (%)	21.37	241

Table 5. Grouping of genotypes into nine clusters using Tocher's method

Cluster	Total number of genotypes	Cluster members
I	26	Aravinda, NDLA-2965, NDLA-2963, NDLA-3037, NDLA-3115-2, NDLA-3094, NDLA-3028, NDLA-3038, NDLA-2985, NDLA-3111-5, NDLA-2958, NDLA-2976, NDLA-3005, NDLA-3043, NDLA-3091, NDLA-2946, NDLA-3116-4, NDLA-3142-1, NDLA-3147-1, NDLA-3109, NDLA-3014, NDLA-3149-2, NDLA-3151-1, NDLA-3020, NDLA-3155-2 and Srinandi.
II	8	NDLA-3143-1, NDLA-3155-3, Yaganti, NDLA-3152-1, NDLA-3139-3, NDLA-3146-1, NDLA-3146-2 and NDLA-3129-1
III	4	NDLA-3154-3, NDLA-3148-2, NDLA-3140 and NDLA-2953
IV	5	NDLA-3113, NDLA-3109-4, NDLA-2930, NDLA-3116-3 and NDLA-3104-4
V	1	NDLA-3066
VI	1	NDLA-2974
VII	1	NDLA 3128-2
VIII	1	NDLA 3105-5
IX	1	NDLA 3147-2

components. The cumulative effects of such characters determine the dependent variable, yield. The study of correlation between yield and its component traits are of considerable importance in selection programmes. The genotypic and phenotypic correlation coefficients between seed cotton yield and other component characters and among themselves were estimated and presented in the **Table 8**. Seed cotton yield showed significant and positive correlation with boll weight (0.297 and 0.231) and lint yield (0.937 and 0.944) at genotypic and phenotypic levels, respectively. But is showed significant negative correlation with lint index (-0.227), uniformity index (-0.175) and elongation percentage (-0.604) at genotypic levels. Boll weight showed significant and positive correlation with ginning percentage (0.557 and 0.343), lint

yield (0.457 and 0.315) and uniformity index (0.308 and 0.220) at genotypic and phenotypic levels, respectively. Bolls per plant showed significant and positive correlation with micronaire (0.439 and 0.240) at both genotypic and phenotypic levels, respectively and with only elongation percentage (0.589) at phenotypic level.

Ginning percentage showed significant and positive correlation with lint yield (0.276 and 0.262), UHML (0.337 and 0.329), bundle strength (0.343 and 0.339) and uniformity index (0.387 and 0.306) at both genotypic and phenotypic levels, respectively. Lint index showed significant positive correlation with UHML (0.302 and 0.234) and bundle strength (0.290 and 0.242) at both genotypic and phenotypic levels, respectively. Seed

Table 6. Mean values of nine clusters for different fibre and yield traits estimated by Tocher's method among 48 desi cotton genotypes

S. No.	Character	Cluster number								
		I	II	III	IV	V	VI	VII	VIII	IX
1.	Plant height (cm)	114.85	114.04	114.00	110.20	102.33	109.00	107.33	107.33	112.33
2.	Days to 50% flowering	62.73	62.08	62.50	63.73	63.00	58.33	63.00	56.67	61.67
3.	Days to maturity	115.71	113.88	115.00	114.67	115.67	117.67	114.67	117.00	117.67
4.	Number of bolls per plant	21.97	20.73	25.08	21.67	24.20	20.73	17.40	22.90	24.33
5.	Boll weight (g)	1.86	2.17	2.04	2.19	2.07	1.57	2.20	2.47	2.40
6.	Ginning percentage (%)	35.56	40.70	37.88	32.76	32.50	34.43	42.10	43.07	38.87
7.	Lint index (g)	2.82	3.25	3.00	3.16	2.67	3.10	2.47	2.27	2.53
8.	Seed index (g)	5.07	4.14	4.09	4.84	5.23	5.97	3.57	4.07	3.77
9.	Seed cotton yield (Kg ha ⁻¹)	580.01	677.39	461.85	900.74	471.60	480.80	897.30	877.10	375.40
10.	Lint yield (Kg ha ⁻¹)	205.45	275.32	174.38	296.45	153.10	165.73	377.67	377.73	145.77
11.	UHML (mm)	23.42	25.45	24.65	23.42	20.67	21.43	26.40	23.37	19.63
12.	Micronaire ($\mu\text{g inch}^{-1}$)	5.96	5.40	5.51	5.57	6.80	6.90	4.97	6.30	6.97
13.	Bundle strength (g tex ⁻¹)	22.34	23.89	23.33	22.15	20.67	21.57	26.63	22.47	19.57
14.	Uniformity index (%)	80.00	82.00	81.25	79.07	77.67	76.67	79.33	77.00	82.00
15.	Elongation percentage (%)	6.29	6.22	6.03	6.16	7.30	7.57	6.00	5.90	8.67

Table 7. Average intra and inter D² values among nine clusters with 48 desi cotton genotypes

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
Cluster 1	198.91								
Cluster 2	475.15	169.55							
Cluster 3	408.86	523.65	298.22						
Cluster 4	452.69	789.84	925.78	253.57					
Cluster 5	343.69	1095.73	723.63	720.62	0.00				
Cluster 6	392.60	929.34	959.23	714.12	166.89	0.00			
Cluster 7	1330.21	492.48	1426.49	1475.68	2344.34	1927.78	0.00		
Cluster 8	809.33	404.73	660.99	1317.13	1438.24	1488.02	718.21	0.00	
Cluster 9	648.40	1126.18	1018.07	1340.87	311.81	276.90	2253.23	1368.78	0.00

index showed positive and significant correlation with micronaire at both genotypic (0.384) and phenotypic (0.353) levels. UHML showed significant and positive correlation with bundle strength (0.932 and 0.921), uniformity index (0.412 and 0.317) at genotypic and phenotypic levels, respectively. Micronaire showed significant and positive correlation with elongation percentage at genotypic (0.771) and phenotypic (0.352) levels. Bundle strength showed significant and positive correlation with uniformity index at genotypic (0.325) and phenotypic (0.256) levels. The character association analysis revealed that boll weight and lint yield were found to have significant positive association with seed cotton yield per plant at both genotypic and phenotypic levels, indicating close association of these characters with seed cotton yield and selection for high boll weight and lint yield could result in increased seed cotton yield. Similar findings were observed by Kakar *et al.* (2021) and Manan *et al.* (2022).

Genetic divergence analysis revealed that among all the quantitative and qualitative characters studied, elongation percentage contributed maximum to the total divergence followed by seed cotton yield, UHML, bundle strength, lint yield, ginning percentage, lint index, plant height, micronaire and uniformity index. The characters that contributed least to the genetic diversity were micronaire and uniformity index. The crosses made between the genotypes of cluster V (NDLA-3066) with cluster VII (NDLA 3105-5) having high inter cluster distance are expected to give desirable segregants. The characters *viz.*, boll weight and lint yield showed highly significant positive correlation with seed cotton yield per plant at both phenotypic and genotypic levels. The improvement of these characters simultaneously increases seed cotton yield per plant. So, while making simultaneous selections for improvement of seed cotton yield with these characters, a compromise has to be struck at the level of improvement with regard to the traits having negative association.

Table 8. Correlation coefficients between seed cotton yield and yield component traits in desi cotton

	PH	DFF	DM	BPP	BW	GP	LI	SI	LY	HL	MIC	BS	UI	EP	SCY
PH	1.000	-0.121	0.176*	0.009	-0.162	-0.07	-0.016	0.077	-0.027	0.122	0.012	0.081	0.208*	-0.200*	-0.011
DFF	-0.071	1.000	0.158	0.000	-0.187*	-0.190*	0.191*	0.049	-0.138	0.134	-0.246**	0.127	-0.014	0.049	-0.049
DM	0.190*	0.052	1.000	0.303**	-0.125	-0.213*	0.044	0.257**	-0.152	-0.075	0.353**	-0.055	-0.462**	0.254**	-0.097
BPP	0.025	-0.013	0.157	1.000	-0.286**	-0.281**	-0.586**	0.145	-0.249**	-0.470**	0.439**	-0.504**	-0.156	-0.363**	-0.157
BW	-0.074	-0.163*	-0.161	0.019	1.000	0.557**	-0.134	-0.594**	0.457**	0.143	-0.218**	0.076	0.308**	-0.365**	0.297**
GP	-0.062	-0.144	-0.126	-0.156	0.343**	1.000	0.056	-0.623**	0.276**	0.337**	-0.247**	0.343**	0.387**	-0.144	-0.067
LI	-0.010	0.117	0.068	0.159	0.000	0.055	1.000	-0.144	-0.214**	0.302**	-0.336**	0.290**	0.051	-0.579**	-0.227**
SI	0.061	0.062	0.174*	0.098	-0.367**	-0.597**	-0.107	1.000	-0.229**	-0.364**	0.384**	-0.343**	-0.232**	-0.012	-0.035
LY	-0.017	-0.097	-0.067	0.129	0.315**	0.262**	0.021	-0.195*	1.000	0.1	-0.184*	0.112	-0.06	-0.631**	0.937**
HL	0.114	0.094	-0.046	-0.291**	0.090	0.329**	0.234**	-0.341**	0.086	1.000	-0.796**	0.932**	0.412**	-0.681**	-0.007
MIC	0.006	-0.167*	0.193*	0.240**	-0.109	-0.234**	-0.274**	0.353**	-0.161	-0.755**	1.000	-0.752**	-0.312**	0.771**	-0.125
BS	0.078	0.093	-0.041	-0.289**	0.035	0.339**	0.242**	-0.324**	0.107	0.921**	-0.718**	1.000	0.325**	-0.552**	-0.004
UI	0.130	-0.024	-0.272**	-0.096	0.220**	0.306**	0.005	-0.150	-0.058	0.317**	-0.216**	0.256**	1.000	-0.195*	-0.175*
EP	-0.069	-0.002	0.119	0.589**	0.020	-0.059	0.245**	0.010	-0.002	-0.347**	0.352**	-0.262**	-0.101	1.000	-0.604**
SCY	-0.003	-0.035	-0.040	0.193*	0.231**	-0.057	0.019	-0.020	0.944**	-0.014	-0.106	-0.002	-0.141	0.025	1.000

Above diagonal-genotypic and below diagonal-phenotypic correlation coefficients. PH-Plant height, DFF-Days to 50% flowering, DM-Days to maturity, BPP-Bolls per plant, BW-Boll weight, GP-Ginning percentage, LI-Lint index, SI-Seed index, LY-Lint yield, HL-UHML, MIC-Micronaire, BS-Bundle strength, UI-Uniformity index, EP-Elongation percentage, SCY-Seed cotton yield, *-Significantly different at 5% probability level, **-Significantly different at 1% probability level

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