

Research Article

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Insights into the genetic divergence in Asiatic cotton (*Gossypium arboreum* L.) germplasm for fibre-quality traits

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Abstract

Asiatic cotton (*Gossypium arboreum* L.) has evolved in the Indian subcontinent and is known for its adaptability to low-input management conditions. In the present study, 300 diverse *G. arboreum* lines, including 100 Nandyal arboreum breeding lines (NAB), 132 Arboreum germplasm collections (AGC) and 68 long-linted arboreum genotypes (LLA), were evaluated for fibre quality to assess the diversity among them and to identify promising genotypes with desirable fibre traits. Significant variations were observed among the genotypes for the studied fibre-quality traits. Principal component analysis showed that the traits micronaire (Mic) and elongation percentage ($E\%$) followed by upper half mean length (UHML) and bundle tenacity (tenacity) were the most significant contributors to variation. Cluster analysis based on the Euclidian distance method showed 16 clusters among 300 *G. arboreum* genotypes. The genotypes in cluster 4 have desirable UHML, tenacity and UI (uniformity index) traits, and cluster 12 has Mic and $E\%$ traits. Furthermore, the number of genotypes with desirable fibre-quality traits was found to be higher in the AGC group than in the LLA and NAB groups. The trait tenacity followed by the UHML showed relatively higher Shannon–Weiner diversity index values across different genotypic groups. Based on the superior performance, the genotypes PA 847, PA 809, PA 837, PA 863, NDLA 3147-2, NDLA 2974 and NDLA 3081 were found to be having desirable fibre traits. The identified promising genotypes are valuable genetic resources for improving fibre quality in *G. arboreum* cotton.

Introduction

Cotton is a cash crop grown to provide natural fibre to the textile industry. The genus *Gossypium* consists of 45 diploid and seven tetraploid species, including four cultivated species, namely, *G. hirsutum*, *G. barbadense*, *G. arboreum* and *G. herbaceum*. Among them, *G. hirsutum* is known as upland cotton, which occupies 95% of cotton production globally (Iqbal *et al.*, 2022). However, *G. arboreum* is Asiatic cotton originating in the Indian subcontinent, accounting for 2% of world cotton production (Ksenia *et al.*, 2020). From 2021 to 2022, cotton was cultivated in an area of 33.18 m ha worldwide with production and productivity of 25.73 m tonnes and 775 kg/ha, respectively (International Cotton Advisory Committee data portal, 2021–22) (ICAC; <https://icac.org/>). The area under Asiatic diploid cotton declined gradually after the introduction of Bt cotton (Narayanan *et al.*, 2014; Kranti, 2015). However, *G. arboreum* mainly exhibits some adaptive traits, such as the ability to grow under low-input management conditions and tolerance to drought, pests and diseases (Mehetre *et al.*, 2003). Despite desirable traits, its fibre is coarse, short, weak in strength and not suitable for spinning in the modern textile industry when compared with upland cotton (Romeu-Dalmau *et al.*, 2015). Even though the quality of the fibre is poor, it is mainly used for the preparation of denim, upholstery fabric and for surgical purposes due to its absorbent properties (Meena *et al.*, 2016).

The fibre quality in cotton is based on fibre length, bundle strength, micronaire, uniformity index and elongation percentage (Ibrahim *et al.*, 2019). The spinning efficiency of the fibre mainly depends on the length of the fibre. Longer fibres are stronger and finer and produce lengthy yarns (Naoumkina *et al.*, 2019). The bundle strength of fibre mainly affects the equal stretchability of individual fibres and the natural quality of fabric after processing (Mathangadeera *et al.*, 2020). The micronaire value is used as an indication of fibre maturity and fineness. The low micronaire of fibre results in the formation of neps or knots during spinning, thereby breaking the yarn (Hussain *et al.*, 2002). However, high micronaire results in mature and coarse fibres (Han *et al.*, 1998). The uniformity index refers to the ratio of the mean length and upper half mean length of fibres (Azzouz *et al.*, 2008). The fibre with



a low uniformity index causes difficulty in spinning, which results in poor yarn quality (Hequet *et al.*, 2006). The elongation of fibres is a measure of toughness and ductility. The high degree of elongation enhances the weaving capability of fibre and results in high-end product quality (Delhom *et al.*, 2022). These fibre traits are greatly affected by fluctuations in growth conditions as well as the environment (Darawsheh *et al.*, 2022). The fibre quality of *G. hirsutum* is moderate with long staple cotton (Ijaz *et al.*, 2019). However, *G. barbadense* is known for extra-long staple cotton with strong and fine fibres (Hu *et al.*, 2019). The fibres of *G. arboreum* and *G. herbaceum* are coarse and short-staple fibres (Axmedov *et al.*, 2022). The fibre quality of *G. arboreum* exhibits more vulnerability and poor quality as it grows mainly in marginal environmental conditions (Wang *et al.*, 2012). However, *G. arboreum* is more resilient to climate change, and the improvement of fibre quality gives a competitive advantage compared to upland cotton.

The demand for high-yielding good fibre quality *G. arboreum* varieties is increasing, but the return to such demand is lagging due to the lack of significant diversity among the available germplasms (Razzaq *et al.*, 2021). In addition, breeding for both high-yielding and desirable fibre-quality traits is a difficult task due to the negative correlation between the traits (Yu *et al.*, 2013). In addition, the magnitude and diversity among the genotypes depend on estimation methods (Bajracharya *et al.*, 2006). Multivariate statistical methods such as principal component analysis (PCA) and cluster analysis are used to study multiple traits at a time and make comparisons of a large number of genotypes (Jarwar *et al.*, 2019). Furthermore, correlation studies reveal the nature and magnitude of relationships among the studied traits. The grouping of genotypes into different categories enables a better understanding of the presence of variability among the genotypes (Bhatti *et al.*, 2020). Additionally, the estimation of diversity indexes provides the quantitative measurement of biological variability in a group of genotypes (Mayank and Singh, 2013). The absolute knowledge of the presence of genetic diversity and the potentiality of existing genotypes among the available *G. arboreum* germplasm is needed to initiate the breeding programme.

Given the importance of the *G. arboreum* germplasm in the development of varieties with desirable fibre quality, the study was designed with the objectives of (i) phenotypic characterization of *G. arboreum* germplasm lines for different fibre-quality traits, (ii) identification of the most contributing traits of variation among the *G. arboreum* genotypes, (iii) quantitative estimation of diversity among the *G. arboreum* germplasm lines of different genotypic groups and (iv) identification of promising *G. arboreum* genotypes for different fibre-quality traits.

Materials and methods

Plant material and field experiment

Three hundred diverse *G. arboreum* genotypes, including 100 Nandyal arboreum breeding lines (NAB), 132 Arboreum germplasm collections (AGC) and 68 long-linted arboreum genotypes (LLA), were studied for fibre-quality traits. The details of genotypes along with their source of origin are mentioned in Table S1. The selected genotypes for the study represent the *G. arboreum* breeding lines developed at Acharya N G Ranga Agricultural University, Regional Agricultural Research Station (RARS), Nandyal, India, as well as the diverse germplasm accessions of India. The study was conducted at the Regional

Agricultural Research Station, Nandyal, India for two years (2021/2022 and 2022/2023) under rainfed conditions. Nandyal is located at 15°28'N latitude and 78°28'E longitude at an altitude of 211.76 m above mean sea level and has a tropical climate with distinct seasons. The soil type in this location is black soil (*vertisols*) with a deep and cracking clay texture. The seasonal average maximum and minimum temperatures, relative humidity, total precipitation and maximum bright sunshine hours per day in both years are presented in Table S2. The seeds were sown in late-June each year. All genotypes were evaluated in a 15 × 20 alpha lattice design with three replications per genotype. All agronomic management practices were the same in both experimental years and followed as per the All India Coordinated Research Project on Cotton recommendations.

Trait measurement

The seed cotton was picked from 10 individual plants per genotype from each replication and ginned using cloy gin available at RARS, Nandyal. The lint samples of all 300 genotypes were sent to the ICAR-Central Institute for Research on Cotton Technology, Regional Unit, Coimbatore, India for measurement of fibre traits using High Volume Instrumentation (HVI-900-SA; Uster) operated in the HVI mode. The fibre traits measured included upper half mean length (UHML) (mm), bundle tenacity (tenacity) (g/tex), micronaire (Mic) (µg/inch), uniformity index (UI) (%) and bundle elongation in percentage (E%). The UHML measured under HVI mode is the average length by the number of fibres in the largest half distributed by weight (Sahar *et al.*, 2021).

Statistical analysis

The pooled data generated on fibre-quality traits over 2 years were subjected to descriptive statistics, analysis of variance, Pearson's correlation, PCA and cluster analysis using STAR (Statistical Tool for Agricultural Research) 2.1.0 software according to Reddy *et al.* (2020a). In PCA, according to Gatten's lower bound principle, the principal components having more than one eigenvalue are only considered for explaining the percentage contribution of variation (Reddy *et al.*, 2021). The cluster analysis was carried out as per the Ward's minimum variance method based on Euclidian distances.

The diverse Asiatic cotton genotypes were categorized into high, medium and low groups as per the distinctness, uniformity and stability (DUS) guidelines (<https://plantauthority.gov.in/crop-dus-guidelines>) under each category of all genotypes, NAB, AGC and LLA for each fibre trait (Table S3).

The polymorphic diversity index, Shannon–Weiner diversity index (*H*), was estimated by using the following formula (Reddy *et al.*, 2020b):

$$H = - \sum_{i=1}^s n_i (\ln n_i)$$

where n_i is the number of genotypes belonging to the i th class and s is the total number of classes.

Results

Genetic variability for fibre-quality traits

The data generated on fibre traits of 300 genotypes over 2 years are presented in Table S4. The analysis of variance for fibre traits

showed the presence of significant differences among the studied genotypes (Table S5). However, the years mean squares were significant for all the traits except for UI. The highly significant interaction effects between genotype \times year were observed for all the studied fibre traits. The total sum of squares of treatments accounts for the total variation partitioning for genotype, year and genotype \times year interaction. The percentage contribution to the total variability ranges from 41.29% (UI) to 80.83% (UHML) for genotypes, 0.01% (Mic) to 0.97% (*E*%) for the year and 17.94% (UHML) to 58.61% (UI) for genotype \times year interaction. Thus, the highest contribution of genotypic variability of the total variability resulted in high broad sense heritability (>50) for all the traits except for UI. The genotype \times year interaction showed a higher contribution for the trait UI. The extent of variation among the studied fibre traits is presented in Fig. 1. The frequency distribution of fibre traits showed a near-normal distribution among all genotypes, NAB, AGC and LLA groups. Among all 300 Asiatic cotton genotypes, the UHML ranged from 15.8 to 31 mm, with a mean value of 24.9 mm (Table S6). The highest mean value of UHML (27.51 mm) was observed in the LLA group, ranging from 24 to 31 mm. The mean value of tenacity was 24.86 g/tex, ranging from 15.6 to 32.2 g/tex in all genotypic groups. Furthermore, the highest mean value of tenacity (27.79 g/tex) was observed in the LLA group, ranging from 23.1 to 32.2 g/tex. Mic ranged from 3.5 to 7.1 $\mu\text{g}/\text{inch}$, with a mean value of 5.37 $\mu\text{g}/\text{inch}$ among all the studied genotypes. However, the highest mean value of Mic (5.6 $\mu\text{g}/\text{inch}$) was observed in the AGC group, ranging from 3.5 to 7.1 $\mu\text{g}/\text{inch}$. The UI ranged from 75 to 86%, with a mean value of 81.23% in all genotypic groups of 300 Asiatic cotton genotypes. In addition, the highest mean value of UI (82.31%) was observed in the LLA group, ranging from 79 to 86%. The mean value of *E*% was 6.09%, ranging from 4.3 to 8.9% among all genotypes. The highest mean value of *E*% (6.24%) was observed in the NAB group, ranging from 5.5 to 8.9% among 100 genotypes.

Pearson correlations among fibre traits

Pearson correlation coefficients among fibre traits in all four categories of genotypes were analysed and are presented in Table 1. Highly significant and positive correlations were observed between UHML and tenacity in the AGC ($r^2 = 0.91$), followed by the A ($r^2 = 0.90$), NAB ($r^2 = 0.86$) and LLA ($r^2 = 0.70$) groups. However, highly significant and negative correlations were observed between UHML and Mic ($r^2 = -0.76$), followed by tenacity and Mic ($r^2 = -0.72$), in the AGC group. In all four categories of genotypes, significant and positive correlations were observed between the fibre traits UHML, tenacity and UI only. In addition, significant and negative correlations were observed between UHML and *E*% and between tenacity and *E*% in all genotypic groups. The fibre trait Mic showed significant and negative correlations with UHML, tenacity and UI and a positive correlation with *E*% in all categories of genotypic groups except for LLA. Further, among the 300 genotypes, one genotype had a Mic value of <3.5 , 75 had 3.5–5.0 and 224 had >5.0 . The correlation of genotypes with Mic values 3.5–5 showed negative correlations with UHML, tenacity and *E*% and a significant positive correlation with UI (Table S7). However, the genotypes with Mic value >5.0 showed a significant negative correlation with UHML, tenacity and UI and a significant positive correlation with *E*%. The traits UI and *E*% showed significant and negative correlations in the A ($r^2 = -0.21$) and AGC ($r^2 = -0.25$) groups.

The results showed that the relationship between UHML and tenacity followed by tenacity and UI was stronger in all cotton genotypic groups.

Principal component analysis

PCA was performed to identify the most contributing variation of traits in the four cotton genotypic groups. The scree plots of genotypes depicted that one principal component (PC1) in the A and AGC groups and two principal components (PC1 and PC2) in the NAB and LLA groups showed eigenvalues of more than one (Fig. 2). The eigenvalues of PC2 in A and AGC groups are found to be 0.82 and 0.9, respectively (Table 2). These principal components explained 61, 75, 64 and 67% of the variation in the A, NAB, AGC and LLA groups, respectively. The fibre traits Mic and *E*% were the most contributing traits of variation in the A and AGC groups. In the NAB group, the most contributing traits of variation were Mic and *E*% in PC1 and Mic and UHML in PC2. However, the traits tenacity and UHML in PC1 and Mic and UI in PC2 were the most contributing traits of variation in the LLA group. The biplots generated through PCA revealed that the genotypes NDLA 3147-2, NDLA 3081, RG 856, RG 846 and PBD 17 in the A group; NDLA 3042, NDLA 3081, NDLA 3147-2, NDLA 2996 and NDLA 2978 in the NAB group; RG 856, RG 846, PBD 17 and FDK 260 in the AGC group; and PA 847, PA 807, PAIG 380, PA 837 and PA 864 in the LLA group were different from other genotypes with placement on positive side and showed higher estimates based on the combination of desirable traits. Overall, Mic and *E*%, followed by UHML and tenacity, were the most contributing variations of traits in all Asiatic cotton genotypic groups.

Cluster analysis

The cluster analysis using Ward's method resulted in the grouping of genotypes into 16, 9, 8 and 7 clusters based on five fibre traits in the A, NAB, AGC and LLA genotypic groups, respectively (Table 3 and Table S8). The constellation plot of different genotypic groups is presented in Fig. S1. Among the 16 clusters formed from the A genotypic group, the maximum and minimum numbers of genotypes were observed in cluster 1 (55) and cluster 15 (2), respectively. The maximum and minimum mean values for UHML and tenacity were found in clusters 5 and 16, respectively. The mean value of the fibre trait Mic was highest in cluster 12 and lowest in cluster 3. The highest and lowest mean values for UI were observed in clusters 4 and 12, respectively. However, the maximum and minimum mean values were found in clusters 15 and 5, respectively, for trait *E*%. Overall, the UHML, tenacity and UI traits were in the desirable direction in cluster 4, followed by cluster 5. The traits Mic and *E*% were in the desirable direction in clusters 12 and 15.

Diversity patterns in different genotypic groups

A clear variation in fibre-quality traits was observed between different genotypic groups by comparing the studied traits. The number of Asiatic cotton genotypes in the A, NAB, AGC and LLA groups was categorized into low, medium and high classes (Table 4) as per the DUS guidelines (<https://plantaauthority.gov.in/crop-dus-guidelines>). The classification mainly showed the distribution of genotypes into all performance classes for the studied fibre traits in each category of genotypic groups. Interestingly, none of the

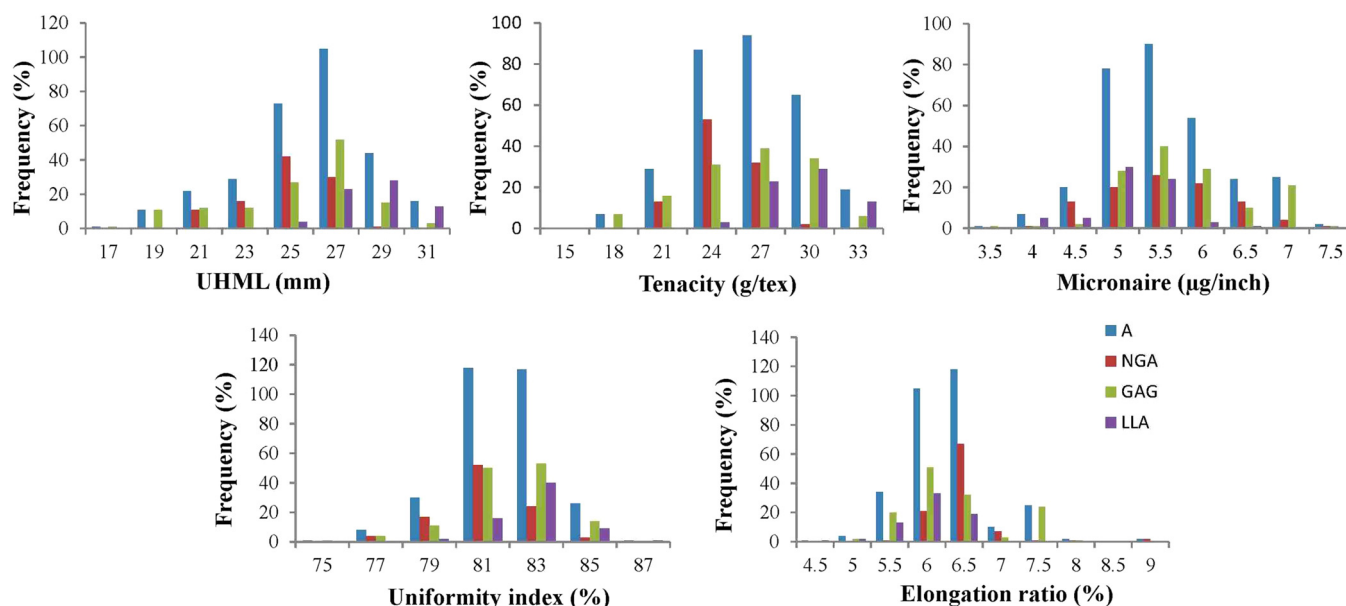


Figure 1. Frequency distribution of fibre traits in Asiatic cotton genotypes. UHML, upper half mean length; Tenacity, bundle tenacity; Mic, micronaire; UI, uniformity index; E%, bundle elongation in %; A, all genotypes; NAB, Nandyal arboreum breeding lines; AGC, arboreum germplasm collections; LLA, long-limbed arboreum.

genotypes were observed for the Mic and E% traits under the low-performance class or for UI under the high-performance class in the NAB group. No genotype was grouped for the E% trait under the high-performance class in the AGC and LLA groups. Furthermore, no genotype was found for the UHML, tenacity and Mic traits under the low class in the LLA genotypic group. Among all the studied traits, a higher proportion of genotypes were observed under the high class for the traits UHML, tenacity

and Mic in all four genotypic groups except for tenacity in the NAB group. In addition, a greater number of genotypes for UI and E% was observed under the medium class in all four genotypic groups. A lower proportion of genotypes for the UHML, tenacity and Mic traits was observed under the low-performance class in all four genotypic groups. Furthermore, a lower proportion of genotypes for UI was observed under the high-performance class in all four genotypic groups. However, for trait E%, a lower proportion of

Table 1. Pearson correlations among fibre traits of *G. arboreum* genotypes in different genotypic groups

Group	Fibre trait	UHML (mm)	Tenacity (g/tex)	Mic (µg/inch)	UI (%)
A (N = 300)	Tenacity (g/tex)	0.90***			
	Mic (µg/inch)	-0.63***	-0.59***		
	UI (%)	0.56***	0.58***	-0.34***	
	E%	-0.38***	-0.37***	0.27***	-0.21***
NAB (N = 100)	Tenacity (g/tex)	0.86***			
	Mic (µg/inch)	-0.43***	-0.57***		
	UI (%)	0.26**	0.31**	-0.21*	
	E%	-0.47***	-0.36***	0.25**	0.16
AGC (N = 132)	Tenacity (g/tex)	0.91***			
	Mic (µg/inch)	-0.76***	-0.72***		
	UI (%)	0.61***	0.60***	-0.52***	
	E%	-0.22*	-0.24**	0.26**	-0.25**
LLA (N = 68)	Tenacity (g/tex)	0.70***			
	Mic (µg/inch)	-0.15	-0.13		
	UI (%)	0.34**	0.40***	0.21	
	E%	-0.31**	-0.32**	-0.03	-0.16

UHML, upper half mean length; Tenacity, bundle tenacity; Mic, micronaire; UI, uniformity index; E%, bundle elongation in %; A, all genotypes; NAB, Nandyal arboreum breeding lines; AGC, arboreum germplasm collections; LLA, long-limbed arboreum.
** and *** significant at $P < 0.01$ and $P < 0.001$, respectively.

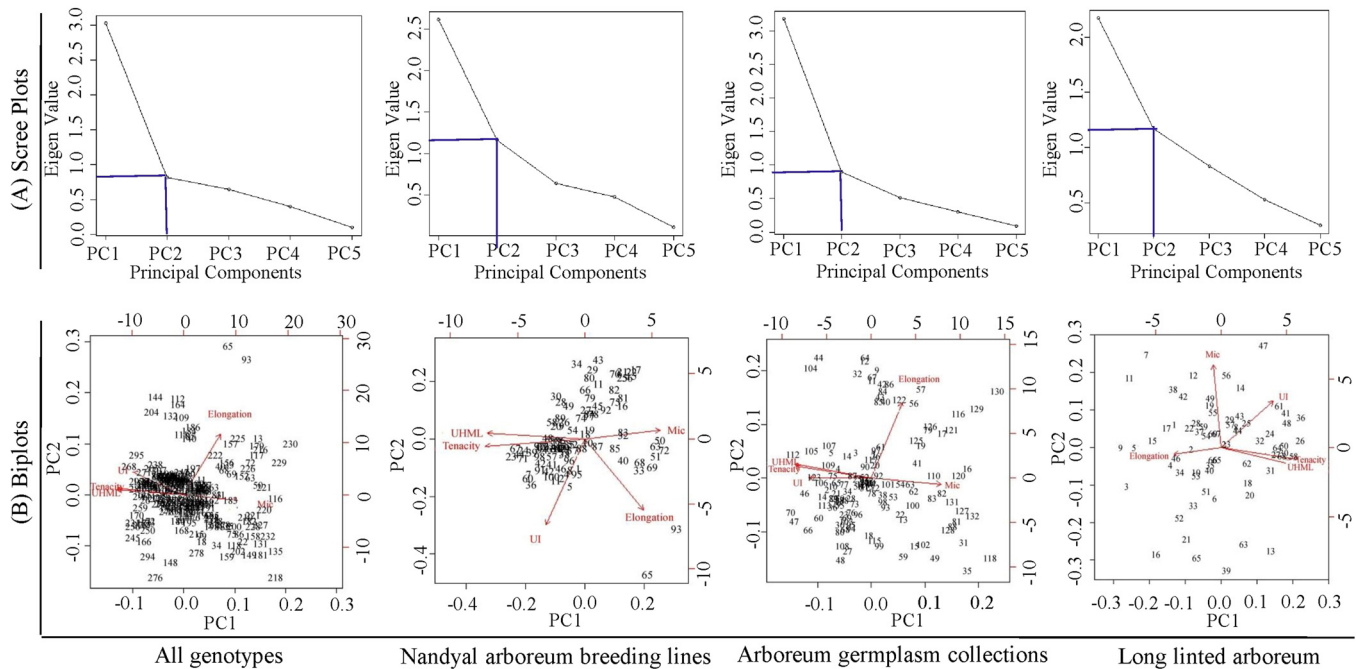


Figure 2. PCA of fibre traits in Asiatic cotton genotypic groups: (A) scree plots and (B) biplots of the first two principal components show the variation among the fibre-quality traits.

genotypes was found in the low-performance class in the A and NAB groups and in the high-performance class in the AGC and LLA groups. This indicates that among the NAB, AGC and LLA groups, a greater number of genotypes with desirable fibre-quality traits are present in the order AGC > LLA > NAB.

The Shannon–Weiner diversity index (H) values were estimated to study the diversity among Asiatic cotton genotypes in all four genotypic groups. The H diversity index values varied with an average of 0.63 for the studied fibre traits in the A group of all 300 genotypes. Furthermore, the H diversity index values were high in the A group only. The average value of the H diversity index was observed to be high in the AGC group among the NAB, AGC and LLA groups. The fibre trait tenacity followed by UHML showed high values of the H diversity index in the A and AGC groups. The traits UHML followed by tenacity and UI followed by Mic showed higher H diversity index values in the NAB and LLA groups, respectively. Overall, the traits tenacity and UHML showed a relatively higher level of variation, while $E\%$ was less variable across the different Asiatic cotton genotypic groups except for the LLA group.

Grouping of genotypes for fibre-quality traits

According to the mean values for each trait, the five contrasting genotypes are presented in Table S9. The best five genotypes showed trait values of more than 30 mm, 31 g/tex, 6.9 $\mu\text{g}/\text{inch}$, 85% and 7.5% for UHML, tenacity, Mic, UI and $E\%$, respectively. The lowermost genotypes showed trait values of less than 19.9 mm, 24.4 g/tex, 4.6 $\mu\text{g}/\text{inch}$, 80% and 5.8% for UHML, tenacity, Mic, UI and $E\%$, respectively. Among the studied genotypes, CNA 1039 (31 mm) followed by GAM 255 (30.3 mm) and PA 837 (30.3 mm) were found to be superior for the UHML trait. For tenacity, the genotypes PA 793 (32 g/tex) and PA 741 (32 g/tex) were superior among the studied genotypes. Furthermore, RG 801 (7.1 $\mu\text{g}/\text{inch}$) followed by NDLA 3147-2 (7 $\mu\text{g}/\text{inch}$), NDLA 3091 (7 $\mu\text{g}/\text{inch}$) and RG 784 (7 $\mu\text{g}/\text{inch}$) had high Mic

values. The genotypes PA 809 (86%), followed by PA 863 (85%), CNA 1038 (85%), CNA 1058 (85%), CNA 1075 (85%) and PA 837 (85%), were superior for the UI trait among the studied genotypes. For the trait $E\%$, the genotypes NDLA 3081 (8.9%) followed by NDLA 3147-2 (8.8%) were superior across the studied genotypes. Interestingly, the genotype PA 847 was found to have superiority for UHML (30 mm), Mic (6 $\mu\text{g}/\text{inch}$) and UI (85%) among the studied genotypes across the different genotypic groups. Furthermore, the genotype PA 809 was superior for UHML (30.2 mm), tenacity (31 g/tex) and UI (86%). The genotypes PA 837 and PA 863 were found to be superior for UHML and UI. However, for the traits Mic and $E\%$, the genotypes NDLA 3147-2, NDLA 3091 and NDLA 2974 are desirable among the studied genotypes. Furthermore, the genotype NDLA 3081 was found to be superior with desirable traits for UI and $E\%$.

Discussion

The results of the study demonstrated a clear understanding of the presence of variability among the studied genotypes for fibre quality. The LLA lines evaluated in the study are comparable to other *G. arboreum* lines in the NAB and AGC groups in terms of higher values for the traits UHML (>24 mm), tenacity (>25 g/tex) and UI (>85%). These LLA lines can be utilized in *G. arboreum* fibre quality improvement programme to meet the demands of the textile industry (Chinchane and Baig, 2018). Further, the improved long-linted *G. arboreum* varieties possess high toughness and rigidity and are suitable alternatives to the medium-long staple *G. hirsutum* varieties (Chandra and Sreenivasan, 2011). The significant difference among the genotypes with a wide range of mean values enables the improvement of fibre quality in *G. arboreum* genotypes. The significant genotype \times year effect suggests that the genotypes fluctuated considerably for stability for respective traits. This indicates that testing years were different due to

Table 2. PCA of five fibre traits of *G. arboreum* genotypes in different genotypic groups

Fibre trait	A		NAB		AGC		LLA	
	PC1	PC2	PC1	PC2	PC1	PC2	PC1	PC2
UHML (mm)	-0.53	0.08	-0.56	0.05	-0.52	0.18	0.58	-0.18
Tenacity (g/tex)	-0.53	0.10	-0.57	-0.07	-0.52	0.15	0.60	-0.12
Mic ($\mu\text{g}/\text{inch}$)	0.43	-0.08	0.44	0.08	0.48	-0.08	-0.06	0.85
UI (%)	-0.40	0.34	-0.22	-0.77	-0.43	-0.01	0.41	0.48
E %	0.30	0.93	0.34	-0.63	0.21	0.97	-0.37	-0.07
Eigenvalue	3.03	0.82	2.61	1.16	3.18	0.90	2.17	1.17
Variance (%)	0.61	0.16	0.52	0.23	0.64	0.18	0.43	0.23
Cumulative variance (%)	0.61	0.77	0.52	0.75	0.64	0.82	0.43	0.67
Most contributing traits	Mic, E%	Mic, UI	Mic, E%	Mic, UHML	Mic, E%	E% UHML	Tenacity, UHML	Mic, UI

UHML, upper half mean length; Tenacity, bundle tenacity; Mic, micronaire; UI, uniformity index; E %, bundle elongation in %; A, all genotypes; NAB, Nandyal arboreum breeding lines; AGC, arboreum germplasm collections; LLA, long-linted arboretum; PC, principal component.

varying temperatures, relative humidity and precipitation during the crop growth period. However, the genotypic variability contributed the greatest proportion for all the traits except for UI. Snider *et al.* (2013) found that 69.8% of the variability is affected by the interaction effect for uniformity (in our study it is 58.6%). Baxevanos *et al.* (2013) reported that the contribution of genotypic variability is strong for lint % and elongation %, moderate for length, strength and uniformity and least for micronaire, short fibre index and fibre colour traits. Further, a consensus exists that the uniformity index (Campbell and Jones, 2005; Campbell *et al.*, 2012) and micronaire (Bradow and Davidonis, 2000; Meredith *et al.*, 2012) are primarily affected by environment, whereas contrasting results were reported for length and

strength (Bradow and Davidonis, 2000; Aguado *et al.*, 2010). The correlation estimates for the traits across the years showed values higher than 0.7 in A, NAB, AGC and LLA genotypic groups indicating the positive linear association between trait values in both experimental years. This shows that interaction is simple and not able to affect the ranking of genotypes across the years (Carvalho *et al.*, 2022). The obtained results were in agreement with previous findings in cotton (Singh *et al.*, 2014; Lingaiah *et al.*, 2020). Therefore, the best genotypes can be recommended based on the predicted genotypic values for each trait.

The highly significant and positive correlations were observed between UHML, bundle tenacity and UI traits in the study. The trait Mic showed a negative correlation with UHML, tenacity

Table 3. Cluster-wise mean values of 300 *G. arboreum* genotypes for fibre-quality traits

Cluster	Number of genotypes	UHML (mm)	Tenacity (g/tex)	Mic ($\mu\text{g}/\text{inch}$)	UI (%)	E%
1	55	26.21	26.01	5.14	82.85	5.91
2	29	26.20	26.97	5.07	81.31	5.51
3	19	27.10	27.69	4.26	81.48	6.19
4	12	28.59	29.70	5.44	84.50	5.91
5	18	29.06	30.07	4.92	82.67	5.32
6	14	22.44	21.75	5.94	77.46	5.92
7	24	24.53	23.38	5.76	81.61	6.15
8	9	25.97	26.98	5.86	80.47	5.95
9	25	23.02	22.26	5.87	80.16	5.93
10	43	24.60	24.04	4.84	80.45	6.20
11	13	26.08	27.36	5.22	81.92	7.27
12	4	19.89	19.06	6.78	76.44	7.54
13	18	20.02	19.75	6.72	79.28	6.74
14	7	21.84	21.23	5.47	79.57	7.06
15	2	19.23	19.30	6.21	83.20	8.83
16	8	18.41	18.63	6.48	81.63	5.91

UHML, upper half mean length; Tenacity, bundle tenacity; Mic, micronaire; UI, uniformity index; E%, bundle elongation in %.

Table 4. Performance categories and diversity index values of *G. arboreum* genotypes in different genotypic groups for fibre traits

Fibre traits	Low	Medium	High	H
All genotypes				
UHML (mm)	24	71	205	0.80
Tenacity (g/tex)	25	132	143	0.92
Mic ($\mu\text{g}/\text{inch}$)	1	75	224	0.58
UI (%)	93	199	8	0.73
E%	5	293	2	0.12
Nandyal arboreum breeding lines				
UHML (mm)	5	47	48	0.86
Tenacity (g/tex)	8	77	15	0.69
Mic ($\mu\text{g}/\text{inch}$)	0	30	70	0.61
UI (%)	43	57	0	0.68
E%	0	98	02	0.10
Arboreum germplasm collections				
UHML (mm)	19	23	90	0.84
Tenacity (g/tex)	17	46	69	0.97
Mic ($\mu\text{g}/\text{inch}$)	1	22	109	0.49
UI (%)	41	90	1	0.66
E%	2	130	0	0.08
Long-linted arboreum				
UHML (mm)	0	1	67	0.08
Tenacity (g/tex)	0	9	59	0.39
Mic ($\mu\text{g}/\text{inch}$)	0	23	45	0.64
UI (%)	9	52	7	0.71
E%	3	65	0	0.18

UHML, upper half mean length; Tenacity, bundle tenacity; Mic, micronaire; UI, uniformity index, E%, bundle elongation in %, H, Shannon-Weiner diversity index.

and UI but was positively correlated with E%. Further, the correlation of genotypes with Mic values 3.5–5 with other fibre traits indicates that finer fibres contributed more to length, strength and thereby higher fibre UI (Hinchliffe *et al.*, 2023). Besides, the E% depends more on maturity rather than fineness (Manivannan, 2023). The obtained results are in agreement with previous findings of Mendez-Natera *et al.* (2012) and Khan *et al.* (2017). Furthermore, the correlation analysis provides the association between single traits. The multivariate analysis like PCA provides information on the most contributing variation of traits along with similarities and dissimilarities of various traits in the studied genotypes. The fibre traits Mic and E% in A, NAB and AGC groups and tenacity and UHML in the LLA group represent the major amount of variability. Thus, there is a similarity in PC1 for the distribution of traits in A, NAB and AGC groups. Furthermore, the Mic and UI in the A and LLA groups, Mic and UHML in NAB and E% and UHML in the AGC group represent the higher amount of variability in PC2. Thus, the range of variability among the genotypes for the studied traits caused the differences in data expression patterns in A, NAB, AGC and LLA genotypic groups (Ullah *et al.*, 2022). Since the biological explanation of principal components is exquisite, the

best approach is to determine the influence of each variable on each component individually. Overall, the traits Mic and E%, followed by UHML and tenacity, were the most contributing traits of variation among the studied *G. arboreum* genotypes.

The biplot diagram shows that genotypes NDLA 3147-2, NDLA 3081, RG 856, RG 846 and PBD 17 are placed on the positive side with higher estimates based on the combination of desirable fibre-quality traits among the studied genotypes. The genotypes in cluster 4 have desirable UHML, tenacity and UI traits, and cluster 12 has Mic and E% traits. The intercrossing of genotypes in these clusters would result in a high likelihood of obtaining the desirable segregants for the respective traits. However, the negative associations between fibre traits UHML, tenacity and UI with Mic and E% emphasize the selection of lines with better fibre-quality traits and use them in recurrent selection programmes (Clement *et al.*, 2012). Further, maintenance of large population size with robust testing and intermating of selected lines in early segregating generations provides the possibility of getting rare combinations with all desirable fibre-quality traits (Sun *et al.*, 2019). Further, the fibre traits, tenacity and UHML showed higher values of the H index, which represents the balanced distribution of genotypes with higher diversity (Morris *et al.*, 2014; Yadav *et al.*, 2018). The obtained findings coincide with earlier studies in diploid cotton (Li and Erpelding, 2016; Krishnamoorthi *et al.*, 2020).

The genotypes CNA 1039, GAM 255, PA 837, PA 809 and PA 847 showed longer fibres in the study indicating their efficiency in improving fibre quality in diploid cotton. Furthermore, the genotypes PA 793, PA 741, PAIG 373, PAIG 394 and PA 809 showed higher strength (>30 g/tex). These high-strength genotypes crossed with longer fibre genotypes resulted in the development of good spinnable genotypes (Chandra and Sreenivasan, 2011). The genotypes with micronaire values of >5.0 $\mu\text{g}/\text{inch}$ (coarse fibre) or <3.5 $\mu\text{g}/\text{inch}$ (immature fibre) are not useful for spinning the yarn (Ghanmi *et al.*, 2017). Further, among the studied number of genotypes, 75 in the A group, 30 in NAB, 22 in AGC and 23 in LLA showed a Mic value of 3.5–5.0. However, the micronaire value is the product of linear density and fibre maturity which enables it as a not absolute estimate of fibre fineness (Clement *et al.*, 2012). The fibre uniformity and elongation directly affect the strength and twist of the yarn (Parsi *et al.*, 2016). The genotypes PA 809, PA 863, CNA 1038, CNA 1058 and PA 847 for uniformity and NDLA 3081, NDLA 3147-2, RG 856, NDLA 2974 and CCA 2003 for elongation were superior in the study. Overall, the genotypes PA 847, PA 809, PA 837, PA 863, NDLA 3147-2, NDLA 2974 and NDLA 3081 are ideal with most of the desirable fibre traits. The present investigation revealed moderate-to-high variability within genotypes of the same group, but also high genetic diversity between the studied genotypic groups of *G. arboreum* cotton. Thus, the available genetic variability could be used as a genetic resource for establishing a strong foundation for future genetic improvement in Asiatic cotton.

Conclusion

In the present study, we found the presence of significant phenotypic variations among the *G. arboreum* germplasm lines for fibre-quality traits. Multivariate statistical methods will have discriminatory ability in the large-scale characterization of germplasms using multiple traits. Furthermore, the diversity indexes are useful in the expression of the magnitude of variability in

different genotypic groups for fibre traits. The fibre traits, including micronaire, elongation %, fibre length and tenacity are ideal selection criteria for selecting genotypes for fibre quality improvement in *G. arboreum* cotton. The study identified the presence of desirable fibre traits in genotypes of different clusters. The intercrossing of genotypes in these clusters would result in desirable segregants for the traits of interest. The study identified genotypes CNA 1039, GAM 255, PA 837, PA 809 and PA 847 for fibre length, PA 793, PA 741, PAIG 373, PAIG 394 and PA 809 for fibre strength and PA 809, PA 863, CNA 1038, CNA 1058 and PA 847 for uniformity, indicating their greater responsiveness to spinning. These genotypes can be utilized in the improvement of fibre quality *G. arboreum* breeding programmes.

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