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CHARACTERIZATION OF INDIGENOUS *GOSSYPIUM ARBOREUM* L. GENOTYPES FOR VARIOUS FIBER QUALITY TRAITS

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Abstract

Diploid cotton (*Gossypium arboreum* L.) being an “Old World” cultivated cotton species, evolved in Indo-Pak subcontinent, has been known for conferring resistance to biotic and abiotic stresses. To the extent of our knowledge, there is no comprehensive report available on the characterization of *G. arboreum* germplasm. Hence, the present study was conducted to characterize 26 *G. arboreum* genotypes by deploying univariate and multivariate analysis in 2010 at NIBGE, Faisalabad. All these genotypes were characterized for boll weight, GOT percentage, micronaire value, staple length, fiber bundle strength and uniformity index. Genotypic variation was significant ($p<0.01$) for all the analyzed traits except boll weight. Maximum boll weight (2.47g) was observed for genotype 23718. GOT ranged from 18.75% (Haroonabad) to 36.94% (DC-116).The finest fiber was obtained from synthetic (4.37 µg/inch) and this genotype also exhibited the higher values for staple length (23.81 mm) and fiber bundle strength (27.37 g/tex). Range for uniformity index was observed from 76.19% (Garohill) to 77.98% (212). Principal component analysis (PCA) exhibited that first five components accounted for >63% of the total variability. Cluster analysis identified four groups based on their agronomic properties. Significant relationships among different traits can be useful to select best genotypes having good fiber quality traits. These genotypes may prove a valuable resource to fuel the breeding efforts for not only broadening the genetic base of the newly developed material but can also add synergy to various cotton genomic projects.

Key words: Diploid cotton, *Gossypium arobreum* L., Characterization, GOT percentage, Fiber quality.

Introduction

Cotton is the most important natural fiber crop. Cotton seeds are the major source of edible oil as well as cotton meal throughout the world (Pillay & Myers, 1999; Rahman *et al*., 2005; Sunilkumar *et al*., 2006). The genus *Gossypium* contains 45 diploid and 6 allotetraploid species which spread across temperate and tropical regions of Africa, Australia Central and South America, Arabia, Indian subcontinent, the Galapagos and Huawei (Fryxell, 1992). On the basis of chromosomal affinity studies, species of the genus *Gossypium* are grouped into eight (A-G & K) diploid genomes (Beasley, 1940; Endrizzi *et al*., 1985; Stewart, 1994). Members of each genome group have morphological resemblance but they rarely form hybrids with species of other genome groups. Both diploid cotton species, *G. arboreum* L. and *G. herbaceum* L., (n=x=13) are the cultivated “Old World” cotton species of genus *Gossypium*. The *G. arboreum* might be evolved from *G. herbaceum* because *G. arboreum* differs from *G. herbaceum* only at single reciprocal chromosomal translocation (Gerstel, 1953; Hutchinson, 1954). In Pakistan, Asiatic cotton also called desi cotton is still successfully grown in some regions with mediocre soil environments and rough management practices.

A better understanding of genotypic and phenotypic correlation among various traits in plants provide invaluable information to initiate the successful breeding programs (Li *et al*., 2008). The knowledge of existing association between various traits of interest may significantly improve the interpretation of findings, thus providing sound basis for planning more resourceful crop improvement programs. Estimating the magnitude of genotypic diversity in various traits of agronomic interest among various genotypes/cultivars of *G. arboreum* may lead to open up new opportunities for initiating the breeding programs for the improvement of the corresponding trait. Assessment of the genetic variability can be achieved by using morphological measurements and phenotypic characterization (Tahir, 2010).

Comprehensive knowledge about the nature and potential of the existing genotypes and the degree of association among different agronomic and yield related traits is a prerequisite to initiate any breeding project (Badr, 2003; Soomro *et al*., 2005 & 2008; Batool *et al*., 2010; Khan *et al*., 2010). Major agronomic traits like boll weight, ginning out turn, micronaire value, staple length, fiber bundle strength and uniformity index have a gigantic impact in varietal development. In multiple cotton studies, correlations among different agronomic traits, especially fiber related traits have been documented. Seed cotton yield (SCY) was positively correlated with ginning out turn (GOT) and boll weight (Muthuswamy & Vivekanandan, 2004), number of bolls/plant, number of sympodia and GOT (Verma *et al*., 2006), monopodial branches, node of first fruiting branch, boll weight and boll number (Iqbal *et al*., 2006). Correlation study for phenotypic and fiber related traits was also reported by Sun-Junling *et al*. (2006), suggesting heritability of genetic variation in irradiated progenies of cotton. Fiber strength was negatively correlated with GOT (Miller & Rawlings, 1967; Meredith & Bridge, 1971; Smith & Coyle, 1997; Zeng *et al*., 2007). Malik *et al*. (2013) reported a positive significant association among fibre strength, fibre length, fibre uniformity, GOT and lint per seed, in a set of 20 colored and white genotypes of cotton. Alkuddsi *et al*. (2013) reported a significant positive association of seed cotton yield with average boll weight, lint index and GOT.

The detailed information regarding the nature and degree of genetic variability depends upon the type of estimation technique (Ndour, 1998; Bajracharya *et al*., 2006). The multivariate analysis techniques like principal component analysis (PCA), principal coordinate analysis (PCoA) and Mahalonbi's D^2 statistics as well as cluster analysis (Lin & Thompson, 1975) have been used widely for measuring the magnitude of genetic variability in diverse germplasm collections (Thompson & Nelson, 1998; Brown-Guedira *et al*., 2000). The key advantage of PCA analysis over the other technique is that each genotype is assigned to only single distinct group and it also demonstrates the significance of largest contributor towards the total variation on each axis of differentiation (Sharma, 2006). On the other hand, correlation co-efficient defines simple relations among traits, however, it does not always determine influential results about the determination of selection criteria of plants (Cakmakci *et al*., 1998).

The demand of improved cotton varieties is increasing but response to prevailing demand is not accelerated accordingly due to lack of significant genetic diversity in available germplasm stock (Van Esbroeck & Bowman, 1998; Paterson *et al*., 2004). A thorough understanding of genetic diversity and breeding potential of *G.arboreum*, accessions are vital for the genetic improvement of cotton fiber quality and productivity. Therefore, for the development of novel genotypes of cotton with superior fibre and high yield potential, genetically diverse parents should be used in breeding program (Bhatt, 1970; Punitha & Raveendran, 2004)

In the light of the above, this study was planned to investigate the correlation pattern among different agronomic traits in *G. arboreum* genotypes and the degree of similarity/dissimilarity among these cotton accessions using a multivariate statistical approach.

Material and Methods

The experiment was carried out during the year 2010 cropping season at National Institute for Biotechnology and Genetic Engineering (NIBGE), Faisalabad (73^o 74 E and 30^o 31.5 N, 605 feet above sea level), Pakistan. Climatic conditions at the experimental sites are given in Fig. 1.

A total of 26 diploid cotton genotypes were used for this study (Table 1). The experiment was laid out in randomized complete block design (RCBD) with two replications. The plot size was $5m^2$ and the all the genotypes were sown on May 23, 2010. Standard agronomic practices were applied. Forty bolls were hand-picked from each genotype. Bolls were weighed on electrical balance and average boll weight was calculated, then the samples were ginned on saw-gin machine and lint weight was calculated to determine GOT. Fiber traits were measured by using High Volume Instrument (HVI).

Table 1. *Gossypium arboreum* genotypes used in this study.

Sr.No.	Names	Genome	Parentage
1.	Rohi	A_2	Haroonabad local x D9
2.	LDL-113	A_2	Farmer field selection
3.	No.18	A_2	Farmer field selection
4.	FDH-113	A_2	Farmer field selection
5.	No-36	A_2	Farmer field selection
6.	No-29	A_2	Farmer field selection
7.	212	A_2	Farmer field selection
8.	Barnecum	A_2	Farmer field selection
9.	FDH-786	A_2	Farmer field selection
10.	451-R	A_2	Farmer field selection
11.	23718	A_2	Farmer field selection
12.	M-11	A_2	Farmer field selection
13.	Garohill	A_2	Farmer field selection
14.	D-9	A_2	Farmer field selection
15.	HK-244	A_2	Farmer field selection
16.	M-17	A_2	Farmer field selection
17.	Synthetic	A_2	Farmer field selection
18.	FDH-228	A_2	TD-1 x (Comilla x FDH-170): 2002
19.	No-17	A_2	Farmer field selection
20.	Haroonabad	A_2	Farmer field selection
21.	27518	A_2	Farmer field selection
22.	FH-786	A_2	Farmer field selection
23.	231-R	A_2	Farmer field selection
24.	450-R	A_2	Farmer field selection
25.	DC-116	A_2	Farmer field selection
26.	No-35	A_2	Farmer field selection

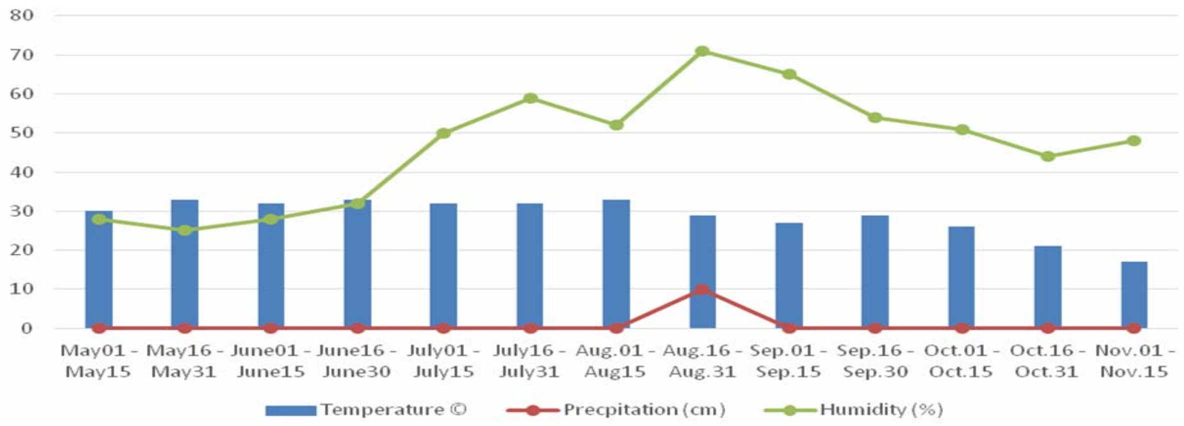

Fig. 1. Climatic conditions over the period of trial, 2010.

Statistical analysis: The means, standard error (S.E), coefficient of variation (C.V) and range for all the six traits were calculated. Analysis of variance was carried out using Statistix 8.1 to see the genotypic variation. In order to see the association among all the traits under study, all the possible correlation coefficients were recorded by using SPSS16. To investigate the importance of different traits in the explanation of multivariate polymorphism among cotton genotypes, principal component analysis (PCA) was deployed with the aid of STATISTICA software (statsoft version 12 statsoft, Inc., Tulsa, Okla, USA). Six principal component were deduced on the basis of relative scores. In order to evident the groups among genotypes, cluster analysis was performed to determine the hierarchical similarity among cotton genotypes. From the PCA values, a Euclidean distance matrix was laid down (Flores *et al*., 1997) to construct a relative dendrogram. The genotypes were grouped by deploying Ward's minimum variance method. The reference line on the dendrogram was drawn where the number of clusters was equal to more or less 20% of the total distance. 1st and 2nd principal component axes scores were plotted to enhance the visualization of genotype differences.

Results

The descriptive statistic (i.e. mean, S.E, C.V and range) for the six phenotypic traits are given in Table 2. A high range of variation was found among all the traits under study. A wide range (1.00-2.27 g) of genetic variation was calculated for boll weight, having mean value of 1.86 g. GOT being an important agronomic trait ranged from 18.75% (Haroonabad) to 36.94% (DC-116). Micronaire value ranged from 4.37µg/inch for Synthetic to 6.79µg/inch for FH-786. Staple length ranged from 12.91 mm for DC-116 versus 23.81 mm for Synthetic. Fiber strength showed a high level of divergence from 25.06 (DC-116) to 27.37 (Synthetic) g/tex. A genotype 212 showed the maximum uniformity (77.98%) while a genotype (Garohill) showed less uniformity (76.19%).

Analysis of variance (ANOVA) using RCBD showed statistically significant differences among all the genotypes for GOT, micronaire value, staple length, fiber bundle strength and uniformity index and non-significant for boll weight (Table 3).

Correlation matrices showed a significant associations between the phenotypic traits (Table 4). Micronaire value showed a significant negative correlation with the staple length and fiber bundle strength but it was positively correlated with GOT. The staple length was positively correlated with fiber bundle strength while it was negatively correlated with GOT. Negative correlation was also observed between the fiber bundle strength and GOT percentage. Average boll weight was positively correlated with uniformity index.

Table 2. Descriptive statistics of six phenotypic traits.

Sr. No.	Traits	Mean ± S.E	Range	CV (%)
1.	Average boll weight (g)	1.86 ± 0.08	1.00-2.47	23.14 %
2.	Ginning out turn (%)	28.95 ± 1.04	18.75-36.94	18.31 %
3.	Micronair value (µg/inch)	5.47 ± 0.12	4.37-6.79	11.41 %
4.	Staple length (upper-half mean length (mm)	16.29 ± 0.50	12.91-23.81	15.67 %
5.	Fiber strength (g/tex)	26.33 ± 0.13	25.06-27.37	2.53 %
6.	Uniformity index (%)	77.09 ± 0.10	76.19-77.98	0.69 %

Table 3. Analysis of variance (ANOVA).

Sr.#	Traits	Mean squares		
		R df=1	G df=25	Error df=25
1.	Average boll weight (g)	2.36	$0.40^{N.S}$	0.30
2.	Ginning out turn (%)	0.88	56.27**	0.55
3.	Micronaire value (µg/inch)	0.01	0.78**	0.04
4.	Staple length (upper-half mean length (mm)	0.43	13.04**	0.19
5.	Fiber strength (g/tex)	0.77	0.89**	0.07
6.	Uniformity index (%)	2.23	0.58*	0.29

R= Replication, G = Genotype
**= Significant at 1% probability level
*= Significant at 1% probability level
N.S.= Non-significant

Table 4. Correlation coefficients among six agronomic traits of 26 cotton genotypes.

	Average boll weight (g)	Ginning out turn (%)	Micronair value (µg/inch)	Staple length (mm)	Fiber strength (g/tex)	Uniformity index (%)
Average boll weight (g)	1					
Ginning out turn (%)	.149	1				
Micronair value (µg/inch)	0.219	0.868**	1			
Staple length (mm)	-.034	-.948**	-0.829**	1		
Fiber strength (g/tex)	-.153	-.948**	-0.884**	.897**	1	
Uniformity index (%)	.486*	.170	0.295	-.145	-.200	1

**= Correlation is significant at the 0.01 level
*= Correlation is significant at the 0.05 level

In order to find the variation pattern, and also to detect the relationships among the phenotypic traits, PCA was carried out. Eigenvalues, cumulative percentage of the eigenvalues and the eigenvectors showing the association between original data and each principal component are given in Table 5. Out of the six principal components, first five components (PC1 to PC5) accounted for >63% of the total variation. PC1 showed the 63.18% of the total variation, PC2 explained 23.49% of the total variation, PC3 and PC4 explained 8.61% and 2.75% of the total variation respectively, 1.44% and 0.53% of the total variation was explained by PC5 and PC6, respectively. The characteristics of each principal component were calculated on the basis of estimated factor loadings. PC1 was colligated with boll weight, micronaire value, staple length, fiber bundle strength and uniformity index. PC2 and PC3 were related with GOT and uniformity index. PC4 was related with the micronaire value. Scatter diagram of the first two principal components distributed these 26 cotton genotypes into four groups (Fig. 2).

Due to pronounced difficulty in grouping of genotypes with PCA analysis, cluster analysis was performed to group these genotypes. The genotypes studied were grouped into four clusters by deploying Ward’s minimal distance method. The clusters contained three to nine genotypes, depending upon the similarity of specific traits. Both the clusters I and IV comprised of nine genotypes each, while cluster II contained five genotypes. Cluster III was consisted of three genotypes. The relative correlation among different genotypes is shown in Fig. 3. In the present study, the mean performance of six phenotypic traits for each cluster showed a wide range of variation. Cluster wise mean and general mean for each phenotypic trait is reported in Table 6.

Table 5. PCA of the six characters associated with 26 cotton genotypes, showing eigen-values and the proportions of the variation associated with first six axes and eigenvectors of characters.

	Principal component axis					
	1	**2**	**3**	**4**	**5**	**6**
Eigenvalues	3.791	1.410	0.516	0.165	0.087	0.032
Cumulative variation (%)	63.18	86.67	95.28	98.03	99.47	100
Character	**Eigenvectors**					
Average boll weight (g)	**-0.970**	0.144	-0.059	0.118	-0.019	-0.142
Ginning out turn (%)	-0.245	**-0.832**	**-0.499**	0.035	0.020	0.012
Micronaire value (µg/inch)	**-0.938**	-0.006	0.011	**-0.334**	0.088	-0.004
Staple length (mm)	**0.937**	-0.225	-0.039	-0.191	-0.163	-0.080
Fiber strength (g/tex)	**0.964**	-0.115	0.033	0.001	0.227	-0.069
Uniformity index (%)	**-0.318**	**-0.795**	**0.514**	0.041	-0.012	-0.006

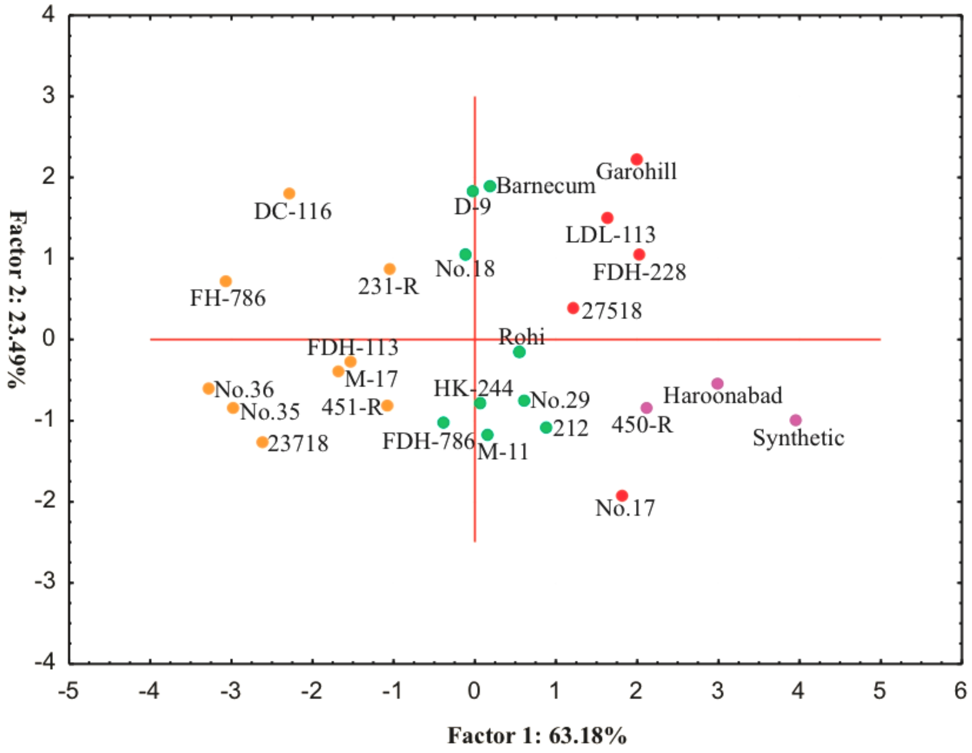

Fig. 2. Distribution of cotton genotypes based on first two principal components.

Table 6. Cluster means and general mean for the studied traits in *G. arboretum*.

Character	I	II	III	IV	Over all mean
Average boll weight (g)	1.79	1.50	2.07	1.98	1.86
Ginning out turn (%)	28.63	24.69	19.56	33.99	28.95
Micronair value (µg/inch)	5.35	4.86	4.83	6.05	5.47
Staple length (mm)	16.20	17.81	21.31	14.19	16.29
Fiber strength (g/tex)	26.48	26.84	27.26	25.65	26.33
Uniformity index (%)	77.18	76.81	76.87	77.32	77.09

Discussion

Fiber quality and lint traits are very complex because they are associated with many morphysiological mechanisms. Past breeding efforts for improving fiber quality traits in *G. hirsutum* have been successful, however improving *G. arboreum* germplasm received very little attention in cotton breeding programs, although highly significant genotypic effects for six phenotypic traits examined in these 26 cotton genotypes reflected pronounced genetic variation in *G. arboreum* germplasm. Crop phenology, well fitted to the available resources of the production environment has a gigantic role to maximize crop yields by agronomy or plant breeding (Richards, 1989; Shorter *et al*., 1991).The main objective to use these diverse genotypes was to remove the hurdles that have limited the success of improving the yield and fiber quality in *G. arboreum*.

A wide range of mean values was found for the analyzed traits. Average boll weight ranged from 1.00 to 2.47g. Significant difference for GOT among the studied genotypes was found and ranged 18.75 to 36.94%., indicating that these genotypes were bred for high GOT. Fiber fineness is measured in terms of micronair value, affects the staple length and fiber bundle strength. The studied genotypes showed a range of 4.37–6.79 ug/inch but the micronair value for most of the genotypes was comparable with cultivated tetraploid cotton. The high micronair value (>5.0 ug/inch) and very low micronair value referred to coarse and immature fiber, respectively (Chandra & Sreenivasan, 2011). The efficient use of *G. arboreum* genotypes on modern high speed machines in textile industry has always been handicapped due to its short staple length but the genotypes used for this study ranged from 12.91 to 23.81 mm, indicating the high potential for the improvement of staple length among these genotypes. The fiber bundle strength of the analyzed genotypes showed a range of 25.06 to 27.37 g/tex. These values show that fiber bundle strength is found to be at par with those of the modern *G. hirsutum* cultivars, suggesting the need of *G. arboreum* to be manipulated to cater to the requirements of modern textile industry. Uniformity index was in the range of 76.19 to 77.98 %, which reveals that yarn spun from such fibers will be uniform in size and fiber wastage will be minimum. Low uniformity index will lead to more short fiber contents and such genotypes are difficult to spun and ultimately deteriorate the fiber quality.

In ANOVA, genotypic differences were highly significant for all the traits examined except boll weight, indicating the presence of genetic variability among these genotypes for phenotypic traits. These results suggest that these genotypes are useful germplasm resource for lint yield and fiber quality improvement in *G. arboreum*.

Genotypic correlations were highly significant as compared to phenotypic and also low for environmental correlations. These results are in accordance with Desalegn *et al*., (2009) who reported that in most cases, the phenotypic correlation was lower than genotypic correlation, clearly indicating that traits were mainly directed by genetic effects. Boll weight, GOT, micronaire value, staple length, fiber bundle strength and uniformity index are the major goals in cotton breeding. Boll weight was found to be positively correlated with uniformity index. The highest contribution of boll weight has been discussed by Krishnarao & Mary (1990). Micronaire value is an important criterion for selection. The micronaire value was negatively correlated with staple length and fiber bundle strength but positively correlated with GOT. Staple length and fiber bundle strength were found to be positively correlated. Both of these characters have high impact in varietal development. Association between fiber bundle strength and GOT was found to be negative, these results were in accordance with previous findings (Miller & Rawlings, 1967; Meredith & Bridge, 1971; Smith & Coyle, 1997; Zeng *et al*., 2007).

Correlation analysis assumes the association between single traits while multivariate analysis provides accurate measurements of similarities and dissimilarities and also measures the relative shares of various traits to the total variation in the germplasm (Rezai & Frey, 1990; Pezzotti *et al*., 1994; Flores *et al*., 1997; Panthee *et al*., 2006). Moreover grouping of the individuals by using multiple agronomic traits is very useful to identify the adaptation and improvement of the genotype (Souza & Sorrells, 1991). This study shows that each trait is a valuable source of variation in at least one principal component axis but there was not a single trait that could explain a sound degree of variation.

Firincioglu *et al*. (2009) stated that biplot diagrams are foremost in genotypes selection having the combination of desirable traits for use in breeding programs. Genotypes were present in the four quadrants of the graph indicating a high source of variation and desirable combination of traits. Cluster analysis calculated on the basis of principal components render significant inter and intra group variation. In the Fig. 3, dendrogram obtained consist of four major groups and subgroups, having similar agronomic traits among genotypes. All the analyzed genotypes were grouped into four clusters, which favor the results obtained through PCA.

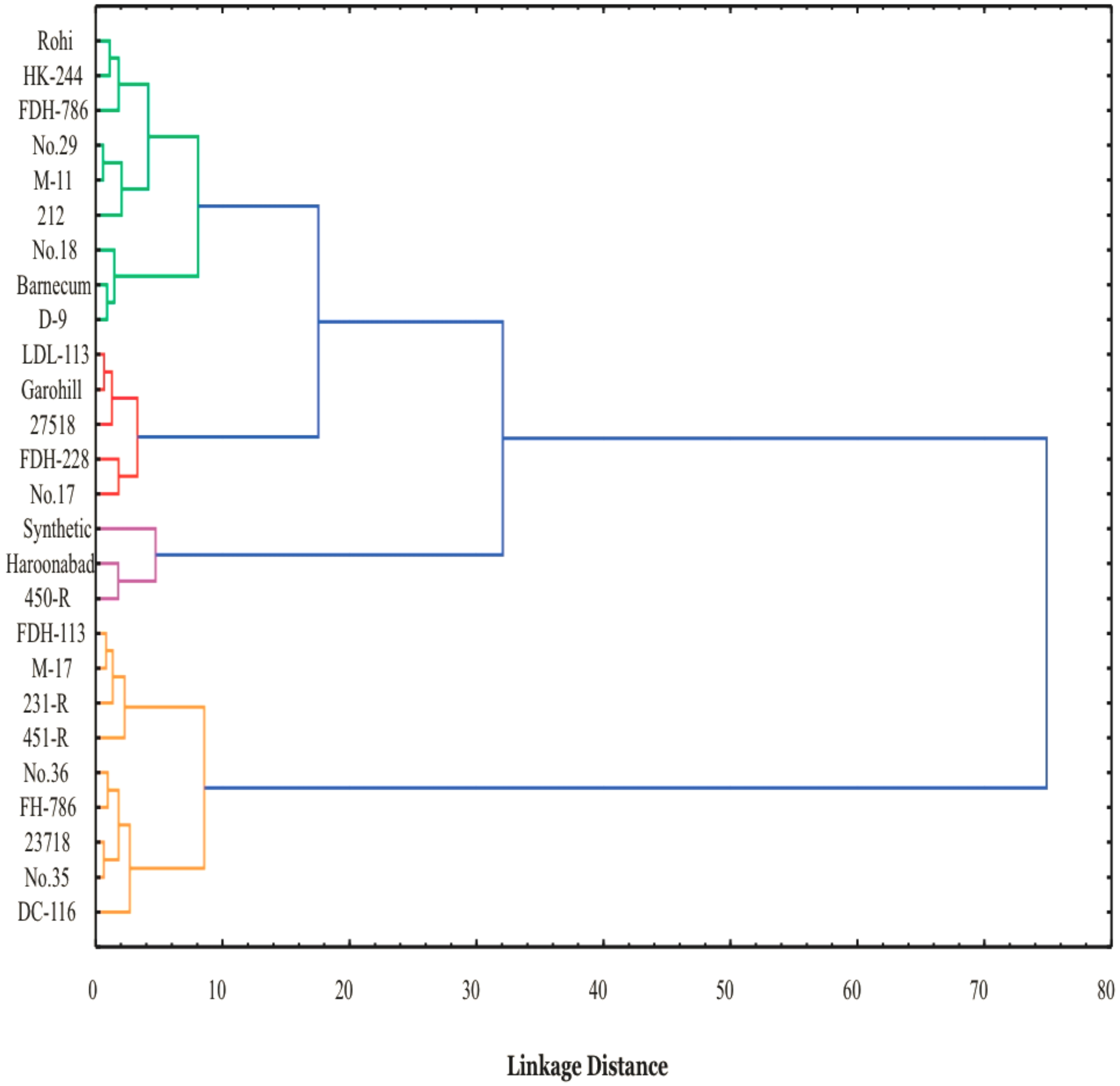

Fig. 3. Dendrogram generated by Ward's method of cluster analysis among the 26 cotton genotypes.

Conclusion

Large phenotypic variations for various yield related traits and fiber quality parameters exist among the indigenous *G. arboreum* genotypes. The analysis of variance in 26 cotton genotypes has laid down the foundation of information relating the association of traits which are useful for varietal selection in breeding projects. Moreover, absence of correlation among different traits permits useful recombinants to be used in breeding programs. Multivariate analysis is a valid system to evaluate germplasm in cotton, which has a key role to characterize the genotypes in terms of their adaptation and production, with high discriminatory capacity, in contrast to separate single trait analysis. Since this study is novel, and thus can also be used in various national and international genomic projects for cloning of the important genes.

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