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# Unveiling Genetic Variation in Egyptian cotton (*Gossypium barbadense* L.) germplasm: A Combined Approach of Morphological Characterization and Multivariate Analysis

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## Research Article

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## ABSTRACT

Cotton (*Gossypium* sp) is a commercial crop that is predominantly grown in tropical and subtropical regions, with India emerging as the largest producer globally. This study focused on the genetic diversity and morphological characterization of *Gossypium barbadense* L., the second most cultivated cotton species. Comprehensive data encompassing qualitative and quantitative traits, spanning morphological attributes to yield-contributing parameters, were documented and analyzed using appropriate statistical analysis. The findings indicate the significance of specific attributes *viz.*, the number of monopodia and sympodia per plant, boll weight, and fiber fineness, which emerged as highly reliable markers for selection. These traits exhibit elevated genotypic and phenotypic coefficients of variation, along with substantial heritability ($h^2$) and genetic advance as percent of mean. Multivariate analysis, Principal component analysis divided the total variance into 14 components, and cluster analysis segregated the germplasm into five distinct clusters, highlighting the substantial genetic variation.

**Keywords:** *G. barbadense*; Variability; DUS characterization; Multivariate analysis

## INTRODUCTION

Cotton (*Gossypium* sp) in a commercial crop that is grown predominantly in the tropical and subtropics. India is the major producer of cotton, producing 5.31 million metric tons, or 21% of the world's total cotton production. India is the primary habitat of all four major cotton species: *G. hirsutum, G. arboreum, G. herbaceum*, and *G. barbadense. G. hirsutum* is the source of 94% of hybrid cotton produced in India. Egyptian cotton (*G. barbadense* L.) is grown for its extra-long, sturdy, and finest fibre [1], which is the second most cultivated species, growing less than 2% in the world. The southern regions of India are the primary producers of long and Extra-Long Staple (ELS) cotton, and demand for this product continues to expand annually. India currently produces 2 lakh hectares of ELS cotton, however only approximately 4 lakh bales are available to meet the country's requirements, and the demand is approximately 9 lakh bales.

Because germplasm has a higher level of genetic variation than other material, it is composed of gene and allele diversity lines that give varying ranges of yields and fiber quality attributes. The value of germplasm can be determined only when it is properly characterized. Characterization and evaluation of germplasm and quantification of genetically diverse genotypes are indispensable for the pragmatic use of plant genetic resources and for determining evolutionary relationships [2]. To identify the desired genotypes, leaf, stem, and floral morphological traits are being used in cotton [3]. Successful breeding program depends on the complete knowledge and understanding of the genetic diversity within and among genetic resources of the available germplasm, enabling plant breeders to choose parental sources that will generate diverse populations for selection.

In addition to deciphering the genetic diversity of crop germplasm utilizing quantitative traits, variations in the germplasm collections could be investigated by employing qualitative traits. Genetic variability between genotypes and both direct and indirect consequences have been extensively explored through Principal Component Analysis (PCA), correlation analysis, and clustering approaches [4]. Hence, the present investigation was conducted with the objectives of acknowledging the traits suitable for DUS testing and analyzing the genetic diversity existing in the *G. barbadense* accessions through morphological characterization using qualitative descriptors, variability, correlation, and multivariate analysis among the genotypes (Table 1).

**Table 1.** Morphological description of *Gossypium barbadense* accessions.

| S. no. | Descriptor traits | Categories | Scores | Type of assessment | Number of genotypes | Frequency % |
|---|---|---|---|---|---|---|
| 1 | Leaf colour | Green | 1 | VS | 74 | 74 |
| | | Light green | 2 | | 26 | 26 |
| 2 | Leaf hairiness | Sparse | 1 | VS | 93 | 93 |
| | | Medium | 5 | | 2 | 2 |
| | | Dense | 9 | | 5 | 5 |
| 3 | Leaf appearance | Cup | 1 | VS | 3 | 3 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | flat | 2 | | 97 | 97 |
| 4 | Leaf shape | Palmate | 1 | VS | 40 | 40 |
| | | Semi-digitate | 2 | | 60 | 60 |
| 5 | Petiole pigmentation | Absent | 1 | VS | 5 | 5 |
| | | Present | 2 | | 95 | 95 |
| 6 | Stem pigmentation | Absent | 1 | VS | 15 | 15 |
| | | Present | 9 | | 85 | 85 |
| 7 | Petal colour | Cream | 1 | VS | 75 | 75 |
| | | Yellow | 2 | | 25 | 25 |
| 8 | Petal spot | Absent | 1 | VS | 6 | 6 |
| | | Present | 2 | | 94 | 94 |
| 9 | Boll shape | Round | 3 | VG | 6 | 6 |
| | | Ovate | 5 | | 37 | 37 |
| | | Elliptical | 7 | | 57 | 57 |
| 10 | Boll size | Medium | 1 | VG | 43 | 43 |
| | | Large | 2 | | 42 | 42 |
| | | Small | 3 | | 15 | 15 |

**Note:** VG: Visual assessment by a single observation of a group of plants or parts of plants; VS: Visual assessment by a single observation of individual plants or parts of plants

## MATERIALS AND METHODS

### Plant material

A total of 100 accessions of *Gossypium barbadense* L. germplasm along with 4 standard check varieties namely suvin, CO 18, CCB-51 and CCB–143B were raised in Augmented block design I in uniform environmental conditions at the Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, India during the winter of 2023 and the recommended sequence of procedures was followed to enhance crop growth throughout the cropping season.

### Data observation

Five plants per accession were selected at random to document observations. Data concerning eighteen qualitative attributes at the appropriate development phase, namely leaf colour, leaf hairiness, leaf shape, leaf appearance, petiole pigmentation, flower petal colour, petal spot, anther colour, filament colour, position of stigma, stem pigmentation, bearing habit, boll shape, boll pitting, boll size, boll colour, boll tip and bract type, were documented employing the DUS criteria suggested by PPV and FRA, 2001. Characteristics such as leaf colour, leaf hairiness, leaf petiole pigmentation, leaf shape and leaf appearance were recorded based on a visual inspection of the plant's fourth leaf from the top. The presence or absence of pigmentation on the stem, flower characteristics such as petal colour, petal spot, the position of stigma and at the peak of flowering, the coloration of the anther and filaments was noted. During boll maturity stage, boll colour, boll shape, prominence of boll tip and boll pitting were documented. Data on various seed cotton yield contributing traits (Quantitative traits) like days to 50% flowering, plant height (cm), number of monopodia/plants, number of sympodia, boll weight (g), lint index (g), seed index (g), ginning out turn (%), and fibre quality parameters like Upper Half Mean Length (UHML) (mm), uniformity index (%), micronaire (µg/inch), fibre strength (g/ tex) and elongation (%) were measured using High Volume Instrumentation.

### Statistical analysis

The data collected is analysed using an analysis of variance approach as suggested by Federer and Raghavarao. In this investigation, utilizing methodologies established by Burton and DeVane, the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were computed. Concurrently, heritability in broad sense ($h^2$) and Genetic Advance as a percentage of the Mean (GAM) were determined, following the formulations delineated by Johnson et al. Correlation studies were performed using R studio. Additionally, multivariate analyses such as Principal Component Analysis (PCA) and cluster analysis were performed utilizing the statistical package Minitab version 17.

## RESULTS

Qualitative traits are less affected by the environment than quantitative characteristics, they are significantly more useful in characterizing germplasm. Observation on 18 qualitative traits were recorded for 100 genotypes and the scores were analyzed. Variation was absent for the characters *viz.*, anther colour, filament colour, position of stigma, bearing habit, boll colour, boll tip, boll pitting and bract types, meanwhile the remaining ten attributes have been identified to show variation under study.

The majority of genotypes contained green leaves (74%) and the remaining 26 genotypes were found to have light green leaves. Three categories of leaf hairiness were observed namely, sparse hairs (93%), medium hairs (2%) and dense hairs in the 5 genotypes. In leaf appearance, majority of leaves were observed to have flat appearance (97%) and remaining 3 genotypes were observed to have a cup appearance. The genotypes were categorised as two distinct classes based on their leaf shape: 60 genotypes showed semi-digitate leaves, whereas 40 genotypes were identified as having palmate leaves. The trait of petiole pigmentation was documented in 95 genotypes (95%) and absent in five genotypes *viz.*, RRB 224, SBS (YF), SBS 49, 3530, 5391–T.

In 85 genotypes (85%), the trait stem pigmentation was present, and in 15 genotypes (15%), it was not present. Regarding flower petal colour, yellow flowers were documented in 75 genotypes (75%) and cream-coloured flowers were found in 25 genotypes. The trait petal spot was found in 94 genotypes (94%) and absent in six genotypes: EC 136452/B, ERB 4488, GIZA, EC 101783, GIZA 14647, and Marred. A higher frequency of elliptical bolls (57%) was observed in 57 genotypes, whereas ovate-shaped bolls were observed in 37 genotypes (37%) and round-shaped bolls were observed in 6 genotypes. Regarding boll size, three categories of boll size were observed, among which 42 genotypes were observed with medium-sized bolls (42%), 15 genotypes with large-sized bolls, and 43 genotypes with small-sized bolls. All the genotypes in *G. barbadense* were observed with exerted stigma, yellow anther, cream filament, green bolls, pitted bolls with pointed boll tip, normal bract, and solitary bearing habit.

### Analysis of variance

The outcomes of the analysis of variance implied significant differences among the 100 germplasm accessions for the characters evaluated. These findings, elucidated in Table 2, highlights significant variability existing among the accessions.

Variability studies.

**Table 2.** Analysis of variance (ANOVA) for 14 quantitative traits.

| **Source of variation** | **df** | **D5F** | **PH** | **NMP** | **NSP** | **BW** | **GOT** | **LI** | **SI** | **SPY** | **UHML** | **Mic** | **FS** | **UI** | **EL** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Treatments | 103 | 42.97 | 300.79 | 0.493 | 30.97 | 0.5269 | 14.693 | 0.7018 | 2.1826 | 415.26 | 5.5705 | 0.628 | 19.21 | 2.49 | 0.06 |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Checks | 3 | 7.5 | 243.24 | 0.1946 | 45.14 | 0.0112 | 26.91 | 0.1501 | 0.1883 | 1007.63 | 2.9 | 0.022 | 35.49 | 1.34 | 0.09 |
| Test entries | 99 | 43.64$^{**}$ | 225.01$^{**}$ | 0.507$^{**}$ | 29.69$^{**}$ | 0.544$^{**}$ | 14.12$^{**}$ | 0.329$^{**}$ | 1.36$^{**}$ | 354.79 | 3.95$^{**}$ | 0.652$^{**}$ | 17.71 | 2.41 | 0.06$^{**}$ |
| Check *vs.* test | 1 | 83.12 | 7975.74 | 0.0036 | 114.96 | 0.3807 | 34.33 | 39.25 | 89.28 | 4625.44 | 173.03 | 0.031 | 118.8 | 13.89 | 0.02 |
| Error | 4 | 0.75 | 9.68 | 0.0247 | 1.285 | 0.0288 | 1.4375 | 0.0198 | 0.0075 | 196.47 | 1.28 | 0.026 | 7.556 | 1.646 | 0.008 |

**Note:** $^{*}$Indicates significance at 5% level; $^{**}$Indicates significance at 1% level; Df: Degrees of freedom; PH: Plant Height; NMP: Number of Monopodia per Plant; NSP: Number of Sympodia per Plant; BW: Boll Weight; GOT: Ginning Outturn; LI: Lint Index; SI: Seed Index; SPY: Single Plant Yield; UHML: Upper Half Mean Length; Mic: Fibre fineness, UI: Uniformity ratio; EL: Elongation percentage

The data on genetic parameters, including Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), broad sense heritability ($h^2$), and Genetic Advance as a percentage of the Mean (GAM), for fourteen studied traits are furnished in Table 3. The differences between GCV and PCV for traits observed *in G. barbadense* accessions were minimal with respect to each trait. For the following traits, high GCV as well as high PCV were noted: Number of monopodia per plant (37.72%, 36.5%), number of sympodia per plant (34.19%, 33.19%), boll weight (21.66%, 20.96%), and fibre fineness (21.3%, 20.83%). Moderate PCV in addition to moderate GCV was documented for traits such as plant height (19.89%, 19.45%), seed index (12.94%, 12.89%), lint index (11.54%, 11.08%), and fibre strength (12.92%, 10.21%). Low PCV coupled with Low GCV was recorded for attributes such as days to 50% flowering (9.31%, 9.22%), Upper half mean length (6.52%, 6.1%), Elongation percentage (4.37%, 3.95%), and uniformity ratio (1.94%, 1.52%). Moderate PCV coupled with low GCV was observed for ginning outturn (11.58%, 5.81%). High PCV with Moderate GCV was noted for single plant yield (56.41%, 10.91%).

**Table 3.** Variability components of the characters studied.

| Traits | PV | GV | GCV (%) | PCV (%) | $h^2$ | GA | GA as % of mean |
|---|---|---|---|---|---|---|---|
| Days to 50% flowering | 43.65 | 42.81 | 9.22 | 9.31 | 98.09 | 13.37 | 18.84 |
| Plant height (cm) | 218.44 | 208.83 | 19.45 | 19.89 | 95.6 | 29.15 | 39.23 |
| Number of monopodia/plants | 0.51 | 0.47 | 36.5 | 37.72 | 93.61 | 1.38 | 72.85 |
| Number of sympodia/plant | 29.7 | 27.99 | 33.19 | 34.19 | 94.24 | 10.59 | 66.48 |
| Boll weight (g) | 0.54 | 0.51 | 20.96 | 21.66 | 93.64 | 1.42 | 41.84 |
| Ginning outturn (%) | 5.67 | 4.24 | 5.81 | 11.58 | 58.71 | 4.62 | 14.03 |
| Lint index | 0.33 | 0.3 | 11.08 | 11.54 | 92.16 | 1.09 | 21.95 |
| Seed index | 1.36 | 1.35 | 12.89 | 12.94 | 99.27 | 2.39 | 26.5 |
| Single plant yield (g) | 190.6 | 36.05 | 10.91 | 56.41 | 18.97 | 5.39 | 9.8 |
| Upper half mean length (mm) | 3.96 | 3.46 | 6.1 | 6.52 | 87.42 | 3.59 | 11.76 |
| Fibre fineness (µg/inch) | 0.52 | 0.49 | 20.83 | 21.3 | 95.69 | 1.42 | 42.04 |
| Fibre strength (g/tex) | 15.94 | 9.95 | 10.21 | 12.92 | 62.41 | 5.14 | 16.64 |
| Uniformity ratio (%) | 2.41 | 1.48 | 1.52 | 1.94 | 61.23 | 1.96 | 2.45 |
| Elongation (%) | 0.06 | 0.05 | 3.95 | 4.37 | 81.91 | 0.42 | 7.38 |

In *G. barbadense* accessions, substantially high heritability was recorded for seed index (99.27%) followed by days to 50% flowering (98.09%), fibre fineness (95.69%), plant height (95.6%), number of sympodia per plant (94.24%), boll weight (93.64%), number of monopodia per plant (93.61%), lint index (92.16%), upper half mean length (87.42%), elongation percentage (81.91%), fibre strength (62.41%) and uniformity ratio (61.23%). Moderate heritability was observed for the ginning outturn (58.71%) and low heritability was documented for single plant yield (18.97%).

For a selection programme to be more effective, it is crucial to consider both heritability estimates and predicted genetic advance. Elevated heritability along with genetic advance as percent of mean was recorded in number of monopodia per plant (93.61%, 72.85%), number of sympodia per plant (94.24%, 66.48%), fibre fineness (95.69%, 42.04%), boll weight (93.64%, 41.84%), plant height (95.6%, 39.23%), seed index (99.27%, 26.5%) and lint index (92.16%, 21.95%). High heritability with moderate genetic advance as percent of mean was documented in days to 50% flowering (98.09%, 18.84%), fibre strength (62.41%, 16.64%), upper half mean length (87.42%, 11.76%). High heritability combined with low genetic advance as per cent of mean was observed in the elongation percentage (81.91%, 7.38%) and uniformity ratio (61.23%, 2.45%). Medium heritability in addition to medium genetic advance as percent of mean was noted in the ginning outturn (58.71%, 14.03%). Low heritability and low genetic advance as percent of mean was recorded in single plant yield (18.97%, 9.8%).

## Correlation studies

Correlation coefficient is a tool used in plant breeding to ascertain the extent of relationship between two or more variables. Days to 50% flowering exhibited a significant negative correlation with single plant yield, while a substantial inverse relationship was observed between the lint index and seed index. Moreover, a significant negative correlation was noted between the number of monopodia per plant and the number of sympodia per plant. The uniformity ratio and seed index displayed significant negative correlations with the ginning outturn. Additionally, the lint index exhibited a significant positive correlation with both seed index and fiber fineness. Fibre quality traits like upper half mean length displayed positive significant correlations with fiber strength, elongation percentage, and uniformity ratio. Conversely, fiber fineness showed a significant negative correlation with fiber strength, upper half mean length, and elongation ratio, while demonstrating a significant positive association with the lint index. Moreover, the uniformity ratio exhibited a significant positive correlation with both fiber strength and upper half mean length. Notably, for fiber strength, elongation percentage displayed a positive significant correlation with both fiber strength and upper half mean length (Table 4).

**Table 4.** Correlation matrix among the 14 characters studied.

| Traits | D5F | PH | NMP | NSP | BW | GOT | LI | SI | SPY | UHML | MIC | FS | UI | EL |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| D5F | 1 | | | | | | | | | | | | | |
| PH | 0.1 | 1 | | | | | | | | | | | | |
| NMP | -0.04 | 0.17 | 1 | | | | | | | | | | | |
| NSP | 0.05 | -0.18 | -0.23$^{*}$ | 1 | | | | | | | | | | |
| BW | 0.06 | -0.09 | 0.02 | 0.1 | 1 | | | | | | | | | |
| GOT | 0.06 | 0.04 | -0.08 | 0.001 | -0.11 | 1 | | | | | | | | |
| LI | -0.28$^{**}$ | -0.04 | 0.13 | -0.001 | 0.04 | 0.12 | 1 | | | | | | | |
| SI | -0.24$^{*}$ | -0.01 | 0.1 | -0.12 | 0.052 | -0.23$^{*}$ | 0.66$^{**}$ | 1 | | | | | | |
| SPY | -0.30$^{**}$ | -0.15 | -0.008 | 0.05 | 0.08 | -0.04 | 0.11 | -0.03 | 1 | | | | | |
| UHML | -0.03 | -0.12 | 0.05 | -0.1 | -0.08 | 0.04 | -0.1 | 0.06 | -0.1 | 1 | | | | |
| MIC | -0.16 | -0.03 | -0.15 | -0.04 | -0.03 | 0.16 | 0.23$^{*}$ | 0.07 | 0.02 | -0.43$^{**}$ | 1 | | | |
| FS | 0.002 | -0.06 | 0.11 | -0.11 | 0.02 | -0.14 | -0.02 | 0.14 | -0.04 | 0.7$^{**}$ | -0.65$^{**}$ | 1 | | |
| UI | 0.01 | 0.09 | 0.11 | -0.1 | 0.002 | -0.22$^{*}$ | -0.01 | 0.09 | 0.05 | 0.20$^{*}$ | -0.17 | 0.33$^{**}$ | 1 | |
| EL | -0.01 | -0.12 | 0.03 | -0.12 | -0.02 | -0.009 | 0.05 | 0.08 | 0.01 | 0.65$^{**}$ | -0.39$^{**}$ | 0.78$^{**}$ | 0.17 | 1 |

**Note:** [*]Indicates significance at 5% level; [**]Indicates significance at 1% level; PH: Plant Height; NMP: Number of Monopodia per Plant; NSP: Number of Sympodia per Plant; BW: Boll Weight, GOT: Ginning Outturn; LI: Lint Index; SI: Seed Index; SPY: Single Plant Yield; UHML: Upper Half Mean Length, Mic: Fibre fineness; UI: Uniformity ratio; EL: Elongation percentage

## Multivariate analysis

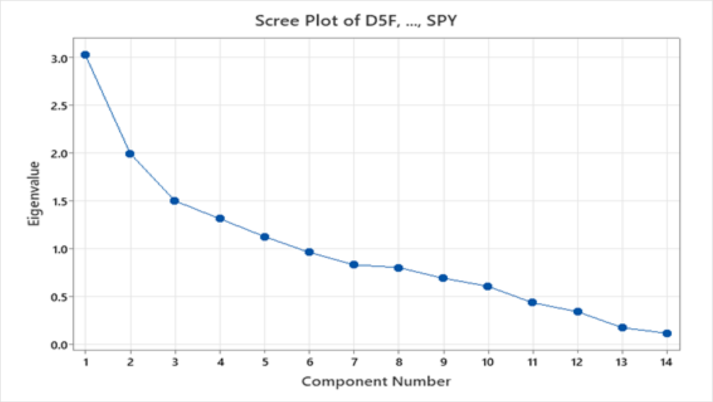
Multivariate analysis has been demonstrated to be a useful method for handling germplasm collection.

## Principal component analysis

To examine the genetic divergence among the 100 germplasm accessions, Principal Component Analysis (PCA) was employed to examine the mean values of all fourteen traits under investigation. Out of the fourteen PCs, the first five had eigen values greater than one (>1) and had maximum contribution to total variability. The corresponding eigen values of PC 1, 2, 3, 4, 5 were 3.02, 1.99, 1.50, 1.31 and 1.13 respectively which had contributed 21.6%, 14.3%, 10.8%, 9.4% and 8.1% variance to the total variation of 64.2%.

The germplasm with high PC 1 value were characterized by Fibre fineness, ginning outturn and number of sympodia per plant significantly contributed to the variation observed among the genotypes under investigation. PC 2 revealed higher and positive values for days to 50% flowering, plant height, number of sympodia per plant and ginning outturn. PC 3 has high and positive value for traits: Days to 50% flowering, plant height, number of monopodia per plant, seed index, fibre fineness and uniformity ratio. PC 4 showed high and positive values for traits including ginning outturn, lint index, upper half mean length, fiber strength, fiber fineness, and elongation percentage. PC 5 displayed high and positive values for plant height, number of monopodia per plant, ginning outturn, single plant yield, upper half mean length, fibre fineness and uniformity ratio. The association between eigen values and principal components is shown by a scree plot, and PC 1 indicated the highest variability of 21.6% with an eigen value of 3.02. PC 13 and PC 14 showed the least variability, with eigen values of 0.18 and 0.122, respectively (Figure 1).

**Figure 1.** Scree plot for fourteen principal components.



Scree plot demonstrates graph between eigen values and principal components where PC 1 displayed highest variability of 21.6% with eigen value of 3.02. Minimal variability was noted for PC 13 and PC 14 and displayed eigen values 0.18 and 0.122 respectively (Table 5).

Table 5. Principal component analysis of *G. barbadense* accessions for various yield contributing traits.

| Variables | PC1 | PC2 | PC3 | PC4 | PC5 |
|---|---|---|---|---|---|
| D5F | -0.016 | 0.425 | 0.183 | -0.059 | -0.446 |
| PH | 0.036 | 0.065 | 0.591 | -0.015 | 0.047 |
| NMP | -0.112 | -0.161 | 0.427 | -0.146 | 0.143 |
| NSP | 0.102 | 0.127 | -0.457 | -0.16 | -0.302 |
| BW | 0.006 | -0.049 | -0.18 | -0.45 | -0.33 |
| GOT | 0.107 | 0.104 | -0.043 | 0.651 | 0.018 |
| LI | 0.043 | -0.588 | -0.008 | 0.186 | -0.269 |
| SI | -0.08 | -0.572 | 0.101 | -0.023 | -0.363 |
| SPY | 0.035 | -0.202 | -0.343 | -0.209 | 0.587 |
| UHML | -0.465 | -0.037 | -0.099 | 0.245 | 0.007 |
| Mic | 0.406 | -0.196 | 0.002 | 0.183 | 0.034 |
| FS | -0.542 | -0.015 | -0.052 | 0.014 | -0.038 |
| UI | -0.238 | -0.073 | 0.174 | -0.325 | 0.164 |
| EL | -0.472 | -0.044 | -0.145 | 0.212 | -0.018 |
| Eigen value | 3.0259 | 1.9999 | 1.5053 | 1.3187 | 1.1323 |
| Proportion | 0.216 | 0.143 | 0.108 | 0.094 | 0.081 |
| Cumulative variance% | 0.216 | 0.359 | 0.467 | 0.561 | 0.642 |

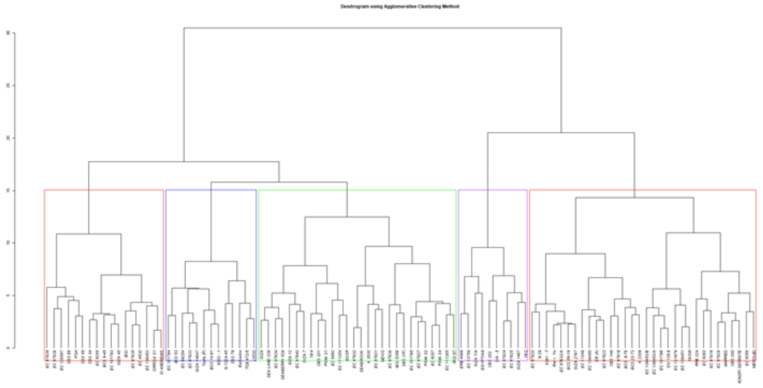
## Cluster analysis

Five major clusters *i.e.*, I, II, III, IV and V were formed by using the Wards linkage Table 6. According to May et al.,[5] more closely linked groups of cotton cultivars were found using cluster analysis. A dendrogram based on Euclidean distance was constructed to separate 100 germplasm into 5 main clusters (Figure 2). In current study, cluster I contains 13 genotypes and this cluster was subdivided into two sub-clusters I(a) and I(b). Cluster II consists of 32 genotypes and it also contains two sub-clusters II(a) and II (b) with 16 and 16 genotypes respectively. Cluster III consists of 17 genotypes which further divided into sub-clusters III(a) and III(b) with 6 and 11 genotypes respectively. Cluster IV consists of 28 genotypes which was subdivided into two subclasses IV(a) and IV(b) with 13 and 15 genotypes respectively. Cluster V consists of 10 genotypes which was subdivided into two subclasses V(a) and V(b) with 4 and 6 genotypes respectively.

Table 6. Cluster membership for 100 *G. barbadense* L. genotypes.

| Clusters | Number of accessions | Germplasm |
|---|---|---|
| Cluster I | 13 | Barbados, BCS 10-91, EC 97633, EC 98254, EC 101784, G-122A-45, Giza 14647, IBSI 53, SBS 79, Tadla (P), TCB 472/5, 3530, 6002 - 1 |
| Cluster II | 32 | Bar x Xu, BCS 9-76, BCS 59-19, BCS 22-73, CBS 148, CBS 200, EB (A), EC 9256, EC 9260, EC 97618, EC 97619, EC 97620, EC 97623, EC 97628, EC 97632/A, EC 101786, EC 11248, EC 131979, EC 136450, EC 136451, EC 136452/A, EC 136452/B, Giza 2767, N 28, Menoubi, Monspi Serrate, Marred, K 2308, RRB 224, SIV 135-6, 16/2W, 5391 - T |
| Cluster III | 17 | BCS 9-45, CBS 34, EC 9255, EC 97626, EC 97635, EC 97639, EC 101783, EC 126597, EC 136453, Giza 45, EC 4530, PSH, Orrisa S1, IBSI, SBS 49, SBS 66, SI ANDREWS |
| Cluster IV | 28 | CBS 201, EC 9257, EC 97627, EC 97631, EC 97632, EC 97634, EC 97638, EC 97640, EC 111254, EC 111265, Giza 12, Giza 7, Giza, EC 4492, PIMA S4, PIMA S2, PIMA S1, NEVIS, K 3530, IBSI 57, IBSI 5356, EC 101785, SBS (YF), Seaberry 528, Seabrook, Sea land 339, 82/2R, 18\4 |
| Cluster V | 10 | CBS 202, EC 97624, EC 97625, ERB 4488, GIZA 7/A, EGYPTIAN, EC 13758, GIZA 1467, SIA – 5, 19\2 |

**Figure 2.** Clustering of 100 *G. barbadense* germplasm accessions based on Euclidean distance.



## DISCUSSION

Among the accessions, the majority of genotypes had green leaves and sparse pubescence followed by medium pubescence and glabrous leaves. In general, *G. barbadense* species are highly affected by sucking pests, especially jassids and whitefly [6]. Leaf hairiness plays a prominent role in pest resistance, where the glabrous trait is associated with reduced fibre yield [7] and dense pubescence is more susceptible to whitefly [8] and also increases gin trash. *G. barbadense* germplasm with medium pubescence can exhibit tolerance and potential genotypes can be selected for the improvement of whitefly-resistant cultivars. The majority of germplasm was identified to have a flat leaf appearance and the presence of stem and petiole pigmentation as well as petal spot indicated the usefulness of this character as a tool for the identification of specific genotypes. Among the genotypes, 60 genotypes showed semi–digitate leaf and 40 genotypes were recognized to have palmate leaf shape. Regarding boll traits, most of the germplasm accessions were observed to have elliptical and small sized bolls. Thus, DUS descriptor characterization of germplasm is advantageous for protecting and identifying varieties.

By studying genetic variability, breeders can identify individuals or lines with desirable traits that can be used as parents for crossbreeding programmes [9]. Genetic variability estimates pointed out that the differences between GCV and PCV are not very wide, primarily due to genetic factors and indicates the presence of considerable genetic variability. There is good potential for improvement through hybridization coupled with subsequent selection. High GCV and PCV for traits: Number of Monopodia per plant, number of sympodia per plant, boll weight, and fibre fineness showed an abundance of potential for genetic improvement of these traits by selection. Similar trend was observed by Chapara, et al. [10]. High heritability for traits like seed index, days to 50% flowering, fibre fineness, plant height, number of sympodia per plant, boll weight, number of monopodia per plant, lint index, upper half mean length, elongation percentage, fibre strength and uniformity ratio were documented. High heritability coupled with high GAM was noted in number of monopodia per plant, number of sympodia per plant, fibre fineness, boll weight, plant height, seed index and lint index. These findings implies that additive gene action is more prevalent in these traits' inheritance and that environmental influence has less of an effect on the expression of these traits. Therefore, these traits are highly reliable during selection. The results were in accordance with findings of Kumar, et al., [11] and Chapara, et al. [10].

In plant selection, computing the relationship between yield and its characteristics are crucial.

Seed cotton yield per plant showed a negative and significant association with days to 50% flowering, as indicated by previous studies [11]. The number of monopodia per plant has a significant negative correlation with number of sympodia per plant. A significant negative correlation exists between ginning outturn and both seed index and uniformity ratio. Similar findings are reported by Gnanasekaran et al., and Srinivas, et al. [12,13]. Lint index has a significant positive correlation with seed index and fiber fineness. Between seed index and lint index, a significant positive correlation was noticed. Similar findings were also reported by Amein, et al. [14]. The upper half mean length has a significantly correlates with fiber strength, elongation percentage, and uniformity ratio, as reported by Valu [15]. The correlation between fiber fineness with lint index was significant positive and with fiber strength, upper half mean length, and elongation ratio exhibited negative correlation. Positive significant correlation was observed between fiber strength and elongation percentage, upper half mean length, and uniformity ratio; which was in accordance with Reddy, et al. [16]. According to correlation studies, selection focused on favourable associations between these traits would be a very effective way to increase both yield and fibre quality. Selection should be performed cautiously for those traits that have negative correlation with seed cotton yield.

The total variance has been divided up into 14 components employing PCA. Out of the 14 PCs, the five PCs had the highest proportion of total variability and an eigenvalue greater than one. A scree plot shows the relationship between principal components and eigenvalues; PC 1 had the greatest variability, at 21.6%, with an eigenvalue of 3.02. PC 13 and PC 14 showed minimal variation, with eigenvalues of 0.18 and 0.122, respectively. Since PC 1 exhibited the highest variability, selection should be made using PC 1's genotypes.

## CONCLUSION

Cluster analysis showed that cluster II has the greater number of genotypes (32) while cluster V consists the least number of genotypes (10). The maximum inter-cluster distance was observed between cluster 1 and 5 (5.12) followed by 3 and 5 (5.07). The maximum inter-cluster distance indicates that genotypes were far more diverse than other clusters. Based on genetic diversity analysis, the genotypes from clusters I and V could be utilized as parents in hybridization programme. Maximum variation in the germplasm was found through analysis, which can be used in subsequent breeding programmes to obtain the desired genotypes.

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## AUTHOR CONTRIBUTIONS

HS collected and performed the analysis of the plant material, statistical analyses and wrote the manuscript. NP reviewed the manuscript and supervised all activities, participated in field research, data analysis and manuscript preparation. AS supervised all activities and participated in field research. NM and KG provided technical support for manuscript preparation. All authors have read and agreed to the publication of the final of the manuscript.

## CONFLICT OF INTEREST

The authors declare no conflict of interest regarding the publication of this manuscript.

## REFERENCES

1. Hussein EH, et al. Molecular characterization of cotton genotypes using PCR-based markers. J Appl Sci Res. 2007;3:1156–1169.
2. Zada M, et al. Assessment of genetic variation in Ethiopian mustard (*Brassica carinata* A. Braun) germplasm using multivariate techniques. Pak J Bot. 2013;45:583–593.
3. Iqbal MA, et al. Characterization of indigenous *Gossypium arboreum* L. Genotypes for various fiber quality traits. Pak J Bot. 2015;47:2347–2354.
4. Brown-Guedira G, et al. Evaluation of genetic diversity of soybean introductions and North American ancestors using RAPD and SSR markers. Crop Sci. 2000;40:815–823.
5. May OL, et al. Genetic diversity of US upland cotton cultivars released between 1980 and 1990. Crop Sci. 1995;35:1570–1574.
6. Dhamayanthi K, et al. Studies on leaf hairiness and sucking pest resistance in Egyptian cotton (*Gossypium barbadense* L.). 2020.
7. Bourland FM, et al. Relationships of plant trichomes to yield and fiber quality parameters in upland cotton. J Cotton Sci. 2017;21:296–305.
8. Miyazaki J, et al. Identification of host plant resistance to silverleaf whitefly in cotton: implications for breeding. Field Crops Res. 2013;154:145–152.
9. Subedi M. Developing *Chenopodium ficifolium* as a diploid model system relevant to genetic characterization and improvement of allotetraploid *C. quinoa*. 2020.
10. Chapara R, et al. Variability studies and genetic divergence in cotton (*Gossypium hirsutum* L.) germplasm using multivariate analysis. Electron J Plant Breed. 2022;13:1305–1311.
11. Kumar CPS, et al. Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). 2019:618-620.
12. Gnanasekaran M, et al. Studies on genetic variability correlation and path analysis in upland cotton. Electron J Plant Breed. 2020;11:981–986.
13. Srinivas B, et al. Genetic studies in yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). Agric Sci Dig Res J. 2014;34:285–288.
14. Amein M, et al. Correlation and path coefficient analysis for yield components traits in Egyptian cotton genotypes (*Gossypium barbadense* L.). Plant Arch. 2020;20:803–806.
15. Valu M, et al. Correlation, path coefficient and $D^2$ analysis study of seed cotton yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). J Pharmacogn Phytochem. 2021;10:222–230.
16. Reddy KB, et al. Correlation and path coefficient analysis in upland cotton (*Gossypium hirsutum* L.). J Res ANGRAU. 2015;43:25–35.