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# Genetic diversity among the extant reference varieties of tetraploid cotton (*Gossypium hirsutum* L.)

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**ABSTRACT :** An experiment conducted for maintenance of tetraploid extant reference cotton varieties has explicated the genetic variability, association and diversity among them for yield and fiber improvement during 2017-2018 at CICR, Regional station, Coimbatore. The highest variation was observed for seed cotton yield /plant and bolls /plant. The traits such as seed cotton yield/plant, bolls /plant, seed index, boll weight and plant height recorded high heritability along with high genetic advance as per cent of mean. Studies on correlation of traits have shown, highly significant positive association of boll/plant, boll weight and seed index with seed cotton yield /plant. The path analysis has shown, highly significant and positive direct effect for bolls/plant and boll weight. Therefore, these traits can directly be used for selection of progenies for improvement. The Principal Component Analysis of data extracted with four significant components (PCs) that had Eigen value >1 and these values accounted for a cumulative variation of 73.744%. In PC I, the traits like seed index, fiber strength, plant height, sympodia, bolls, boll weight, fiber length and seed cotton yield /plant showed considerable positive factor loadings. The cluster analysis grouped the genotypes into three clusters. Among them, cluster III accompanied the maximum genotypes and have contributed much towards yield and yield attributing traits. These highly divergent genotypes have ample scope for utilization in cotton crop improvement.

**Key words :** Correlation, diversity, extant variability, path analysis, varieties

Cotton is the most important fiber and cash crop of India which play a key role in the industrial and agricultural economy. The upland cotton (*Gossypium hirsutum* L.) is the world's leading fiber producing crop and is grown in more than 80 countries of the world (Dutt *et al.*, 2004). This has attained main focus of research because its cultivars meet 90 per cent of the bulk demand of world's cotton (Wendel *et al.*, 1992). Cotton in India provides direct livelihood to nearly 6 million farmers and about 40 -50 million people are employed in cotton trade and its processing.

Estimation of genetic relationships among crop species will provide the nature of genetic diversity. The studies on genetics of germplasm will helps in the estimation of variability, correlations, path coefficient analysis and quantification of degree of divergence which is of immense value in identifying diverse genotypes for recommendations of breeding programmes to improve quality as well as quantity. Seed cotton yield is a polygenically inherited trait resulting from multiplicative interaction of its contributing traits which are highly influenced by the environment. Correlation and path coefficient analysis form a basis for selection and helps in understanding those components affecting yield improvement through their direct and indirect effects.

Studies on genetic divergence are of considerable practical interest, since crop improvement involves utilization of trait variability for economic end uses. The wide range of genetic diversity observed in Indian cotton has been exploited to improve seed cotton yield and more importantly, the fiber quality. In this line, the present investigation was carried out for further utilization of the variability, interrelationship and diversity exists among the extant reference varieties of tetraploid cotton.

## MATERIALS AND METHODS

The material for the present investigation consisted of 86 tetraploid (*G.hirsutum* L.) cotton genotypes planted during winter season of 2017-2018 at Central Institute for Cotton Research, Regional station, Coimbatore (Table 5). The plantings were done in randomized block design with two replications. Each variety was sown in 10 rows adopting, 90 cm space between rows and 60 cm between plants. Recommended agronomic, cultural and plant protection practices for upland cotton was adopted till the harvest of the crop. Observations on plant height (cm), sympodia /plant, bolls / plant were recorded on five randomly selected plants in each replication. In each plot 10 randomly selected bolls were collected weighed and the average was expressed as boll weight-1 (g), The seed index (g) was computed by taking the average weight of 100 seeds in eight replications. Ginning (%) was arrived adopting the formula lint weight/kapas weight x100. The fiber traits such as fiber length (2.5% span length mm), fiber strength (g/tex), fiber fineness (Mic.), fiber uniformity (%) were estimated through High Volume Instrument (Premier) under ICC mode. The seed cotton was harvested individually in five randomly selected plants in each plot and expressed as SCY /plant (g). The data thus generated were subjected for computation of Mean, Range, Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), Heritability, Genetic Advance, Correlation Coefficients as per the statistical procedure of Johnson *et al.,* (1955). The path analysis was done as per the method suggested by Deway and Lu (1959). Principal component analyses was executed based on 11quantitative traits as to find out the relative importance of different traits in capturing the genetic variation. Scatter plot was drawn for visual assessment of components or factors which can explain the variability at most that exists in the generated data using software PAST 3 (Hammer *et al.,* 2001). The factors subjected for cluster analysis was based on Euclidean distances and wards minimum variance of Agglomerative hierarchical clustering arrived with the help of XLSTAT software. For arriving hierarchical cluster, analysis of pooled data was performed using scores of dissimilarity matrix (Ward, 1963).

## RESULTS AND DISCUSSION

The results of the present investigation showed that the values of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the traits (Table 1). The phenotypic coefficient of variation ranged from 3.55 to 33.64 per cent. The highest PCV was observed for seed cotton yield /plant

**Table 1.** Variability traits for fiber, yield and yield attributing traits in extant tetraploid cotton genotypes

| Characters | **Mean** | PCV | GCV | Heritability (%) | Genetic advance as (%) of mean |
|---|---|---|---|---|---|
| Plant height (cm) | **124.62** | 12.46 | 11.56 | 86.09 | 22.09 |
| Sympodia/plant | **21.49** | 14.77 | 11.89 | 64.81 | 19.72 |
| Bolls/plant | **35.44** | 30.16 | 29.10 | 93.15 | 57.86 |
| Boll weight (g) | **3.86** | 13.50 | 12.14 | 80.79 | 22.47 |
| Seed index (g) | **9.65** | 12.18 | 12.00 | 97.03 | 24.34 |
| Ginning (%) | **34.24** | 8.71 | 8.53 | 95.98 | 17.21 |
| Fiber length (cm) | **27.36** | 6.64 | 6.08 | 83.89 | 11.48 |
| Fiber strength (g/tex) | **21.97** | 6.81 | 5.74 | 71.18 | 9.98 |
| Fiber fineness (Mic.) | **3.77** | 17.00 | 15.82 | 86.50 | 30.30 |
| Fiber uniformity (%) | **49.04** | 3.55 | 3.01 | 71.74 | 5.25 |
| SCY/plant (g) | **137.99** | 33.67 | 33.29 | 97.73 | 67.72 |

(33.64%) and bolls /plant (30.16). The genotypic coefficient of variation obtained for various yield and yield attributing characters ranged from 3.01 to 33.25 per cent. The highest GCV were observed for seed cotton yield /plant (33.25%) followed by bolls /plant (29.01%). A close and parallel relationship between phenotypic and genotypic variance for all the characters was diserved. The highest PCV and GCV were recorded for seed cotton yield /plant and bolls / plant. Similar observations were established by Dheva and Potdukhe, (2002); Preetha and Raveendran (2007) and Dhivya *et al.* (2014). Moderate PCV and GCV were observed for sympodia/plant, plant height, seed index, boll weight and fiber fineness.

High estimates of heritability (above 60%) in broad sense were recorded for all the characters from sympodia /plant (64.81) to seed cotton yield plant -1 (97.73). Nevertheless, the

**Table 2.** Genotypic correlation coefficients between fiber and yield component traits with seed cotton yield of extant tetraploid cotton genotypes

| Characters | PH | SYM | Bolls | BW | SI | GI | FL | FS | FF | FU | SCYP |
|---|---|---|---|---|---|---|---|---|---|---|---|
| PH | 1.000 | 0.582$^{**}$ | 0.262$^{*}$ | 0.043 | 0.155 | 0.011 | -0.021 | 0.154 | -0.170 | -0.011 | 0.241$^{*}$ |
| SYM | | 1.000 | 0.316$^{**}$ | -0.075 | 0.136 | -0.087 | -0.007 | 0.401$^{**}$ | -0.245 | 0.089 | 0.253$^{*}$ |
| Bolls | | | 1.000 | 0.070 | 0.073 | -0.039 | -0.229$^{*}$ | 0.239 | -0.020 | 0.344$^{**}$ | 0.896$^{**}$ |
| BW | | | | 1.000 | 0.644$^{**}$ | -0.042 | 0.176 | 0.007 | -0.062 | -0.197 | 0.488$^{**}$ |
| SI | | | | | 1.000 | -0.276$^{*}$ | 0.364$^{**}$ | 0.276$^{*}$ | -0.354$^{**}$ | -0.409$^{**}$ | 0.308$^{**}$ |
| GI | | | | | | 1.000 | -0.115 | -0.319$^{**}$ | 0.418$^{**}$ | 0.133 | -0.038 |
| FL | | | | | | | 1.000 | 0.333$^{**}$ | -0.135 | -0.844$^{**}$ | -0.127 |
| FS | | | | | | | | 1.000 | -0.514$^{**}$ | -0.227 | 0.225 |
| FF | | | | | | | | | 1.000 | 0.399$^{**}$ | -0.045 |
| FU | | | | | | | | | | 1.000 | 0.203 |

* Significant at 5%; ** Significant at 1%

PH - Plant Height (cm), SYM - Sympodia/plant, Bolls - Bolls/plant, BW - Boll weight (g), SI - Seed Index (g), GI - Ginning (%) , FL - Fiber length (cm), FS - Fiber strength (g/tex), FF - Fiber fineness (Mic.), FU - Fiber uniformity (%), SCYP - Seed cotton yield/plant (g)

**Table 3.** Direct and indirect effects of yield and fiber quality traits of extant tetraploid cotton genotypes

| | PH | SYM | Bolls | BW | SI | GI | FL | FS | FF | FU | SCYP |
|---|---|---|---|---|---|---|---|---|---|---|---|
| PH | -**0.022** | 0.023 | 0.228 | 0.020 | -0.012 | 0.001 | 0.002 | 0.008 | -0.008 | 0.002 | $0.241^{*}$ |
| SYM | -0.013 | **0.039** | 0.275 | -0.036 | -0.011 | 0.001 | 0.001 | 0.020 | -0.011 | -0.012 | $0.253^{*}$ |
| Bolls | -0.006 | 0.012 | **0.873** | 0.033 | -0.006 | 0.000 | 0.025 | 0.012 | -0.001 | -0.047 | $0.896^{**}$ |
| BW | -0.001 | -0.003 | 0.061 | **0.475** | -0.050 | 0.001 | -0.019 | 0.000 | -0.003 | 0.027 | $0.488^{**}$ |
| SI | -0.003 | 0.005 | 0.063 | 0.306 | -**0.078** | 0.000 | -0.039 | 0.014 | -0.016 | 0.056 | $0.308^{**}$ |
| GI | 0.002 | -0.003 | -0.034 | -0.020 | 0.022 | **0.001** | 0.012 | -0.016 | 0.019 | -0.018 | -0.038 |
| FL | 0.001 | 0.000 | -0.200 | 0.083 | -0.028 | 0.000 | -**0.108** | 0.017 | -0.006 | 0.116 | -0.127 |
| FS | -0.003 | 0.016 | 0.208 | 0.003 | -0.022 | 0.000 | -0.036 | **0.051** | -0.023 | 0.031 | 0.225 |
| FF | 0.004 | -0.010 | -0.018 | -0.029 | 0.028 | 0.001 | 0.015 | -0.026 | **0.046** | -0.055 | -0.045 |
| FU | 0.0003 | 0.003 | 0.300 | -0.094 | 0.032 | 0.000 | 0.091 | -0.012 | 0.018 | **-0.137** | 0.203 |

Residual effect: 0.102

PH - Plant Height (cm), SYM - Sympodia/plant, Bolls - Bolls/plant, BW - Boll weight (g), SI - Seed Index (g), GI - Ginning (%) , FL - Fiber length (cm), FS - Fiber strength (g/tex), FF - Fiber fineness (Mic.), FU - Fiber uniformity (%), SCYP - Seed cotton yield/plant (g)

heritability estimates in conjunction with predicted genetic advance will be more reliable. Johnson *et al.,* (1955) reported that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. The genetic advance for all the quantitative characters ranged from 5.25 (Fiber uniformity %) to 67.72 (seed cotton yield /plant). High heritability coupled with high genetic advance were registered for seed cotton yield plant -1, bolls plant -1, fiber fineness, seed index, boll weight and plant height suggesting

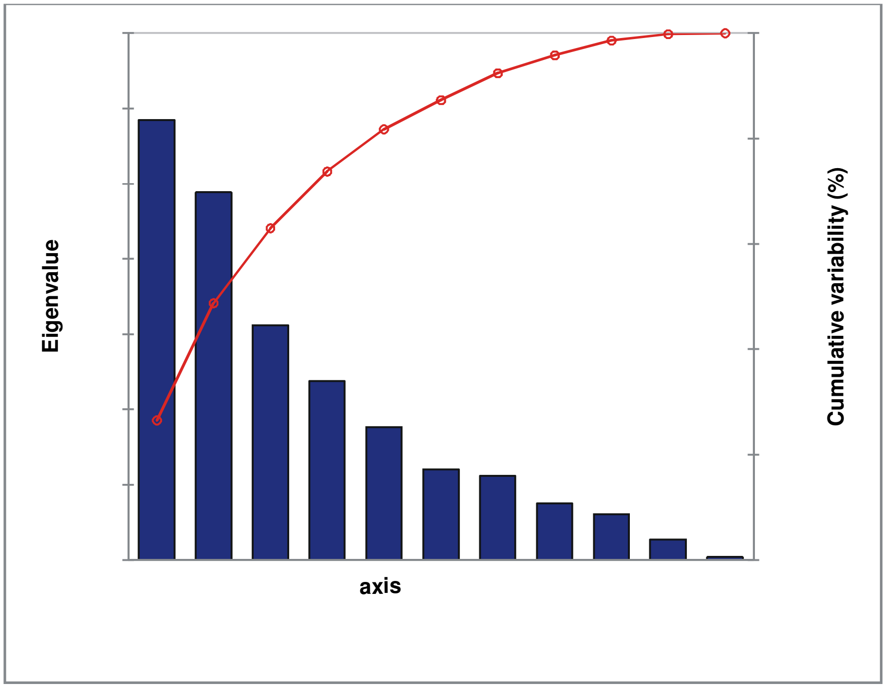

**Fig 1.** Screen plot of tetraploid cotton genotypes

**Table 4.** Principal component analysis for yield and yield contributing traits in extant tetraploid cotton genotypes

| Characters | Principal components | | | |
|---|---|---|---|---|
| | PCA 1 | PCA 2 | PCA 3 | PCA 4 |
| Plant height (cm) | 0.401 | 0.337 | -0.304 | 0.566 |
| No. of sympodia | 0.451 | 0.356 | -0.505 | 0.394 |
| Bolls/plant | 0.397 | 0.788 | 0.071 | -0.093 |
| Boll weight (g) | 0.486 | 0.000 | 0.742 | 0.015 |
| Seed Index (g) | 0.726 | -0.199 | 0.389 | 0.013 |
| Ginning (%) | -0.428 | 0.173 | 0.243 | 0.617 |
| Fiber length (mm) | 0.426 | -0.664 | 0.058 | 0.320 |
| Fiber strength (g/tex) | 0.646 | -0.048 | -0.406 | -0.186 |
| Fiber fineness (Mic.) | -0.603 | 0.219 | 0.363 | 0.344 |
| Fiber uniformity % | -0.433 | 0.742 | -0.075 | -0.250 |
| Seed cotton yield (g) | 0.551 | 0.686 | 0.375 | -0.069 |
| **Eigen values** | **2.922** | **2.442** | **1.560** | **1.188** |
| **Variability (%)** | **26.563** | **22.200** | **14.185** | **10.796** |
| **Cumulative variability (%)** | **26.563** | **48.763** | **62.948** | **73.744** |

the predominance of additive gene action.

The correlation co efficient provides a dependable measure of association among the characters and helps to distinguish essential associates (Falconer, 1981). The correlation coefficients of characters attributed to seed cotton yield /plant were estimated and the results are presented in Table 2. Highly significant and positive correlation of seed cotton yield /plant with boll number/plant (0.896), boll weight (0.488), seed index (0.308) was observed. Followed to this, sympodia/plant (0.253) and plant height (0.241) recorded positive significant correlation with yield. This indicated that increase in seed cotton yield/plant might be due to corresponding increase of the above traits. Association of seed cotton yield with boll weight was reported in earlier studies (Alkuddsi *et al.,* 2013); bolls and boll weight (Farooq *et al.,* 2014) and bolls (Ekinci *et al.*, 2010).

**Fig.2.** PCA factor loadings of component 1

The close relationship between yield and yield attributing traits will be exploited in selection programme which might be helpful in developing high yielding genotypes. As regard to inter correlation, plant height has positive significant inter correlation with sympodia / plant and boll numbers /plant. Number of sympodia has positive significant inter correlation with boll numbers /plant and fiber strength. Number of bolls /plant has positive significant inter correlation with fiber uniformity. Boll weight has positive inter correlation with seed index. Seed index has positive association with fiber length and fiber strength, Ginning per cent with fiber fineness; fiber length with fiber strength; fiber fineness with fiber uniformity. These results clearly indicated that selection for any one of these traits leads to concurrent improvement of other traits as well as seed cotton yield. It was found that linkage was the primary cause for negative correlation between yield and fiber quality traits. To break this association Meredith and Bridge, 1971 has recommended inter mating. The fiber quality traits exhibited positive inter correlation among themselves with significance as conformed with the findings of Dutt *et al.,* (2004), Basbag and Gencer (2007) and Thiyagu *et al.,* (2010). Fiber quality traits like fiber length, fiber strength, fiber fineness and fiber uniformity had positively significant inter correlation with seed index, sympodia and bolls (Altaher and Singh, 2003; Sakthi *et al.,* 2007 and Thiyagu *et al.,* 2010).

Path co-efficient analysis was done in order to study the direct and indirect effects of individual component characters on the dependent variable, seed cotton yield /plant. Study on path coefficient enables to concentrate on the variable which shows high direct effect on seed cotton yield. This ultimately results in selection with one or few important traits (Dewey and Lu, 1959). The genotypic correlation

**Table 5.** Clustering of extant tetraploid cotton genotypes

| Clusters | Sub groups | Genotypes | Name of genotypes |
|---|---|---|---|
| I | 1 | 2 | CSH 19, JLH 168 |
| | 2 | 7 | Gujarat67, SH 2379, RS 2013, F 1378, GSHV 112, MCU 10, Sumangala |
| | 3 | 15 | Khandwa 3, HS 6, H1220, Sahana, VC 21, PRS 74, TCH 1716, DHY286-1, HC-122-66, F 505, Laxmi, EC 344034, P-15-1, Khandwa 2, Supriya |
| II | 1 | 6 | G Cot. 12, NH 452, G. Cot 18, L 604, G.Cot.10, Abadhita |
| | 2 | 1 | American Nectariless |
| | 3 | 18 | G COT 16, ACP71, Bikaneri Nerma, Narasimha, Suman, MCU 8, RMPBS 155, PKV Rajat, Pratima, MCU 12, NH 545, BN Red, F1054, Extream Okra, MCU 11, REBA B 50, J 34, MCU 9 |
| III | 1 | 16 | KC 3, P-15 DP, G.Cot. 100, H1098, JCC-1, JK 4, LH 900, Sivanandhi, MCU 13, P-15, Deviraj, MCU 5, H 974, Surabhi, H1117, Pusa 8-6 |
| | 2 | 20 | Badnawar, HLS 329, LH113, MCU 3, LRA 5166, PG 6, T7, JK 35, RHC 003, Anjali, RS 875, F 320, F 846, NCH 11, GLM-5, CPD 423, F1861, MCU 5 VT, H 1157, H1236, Kanchana |

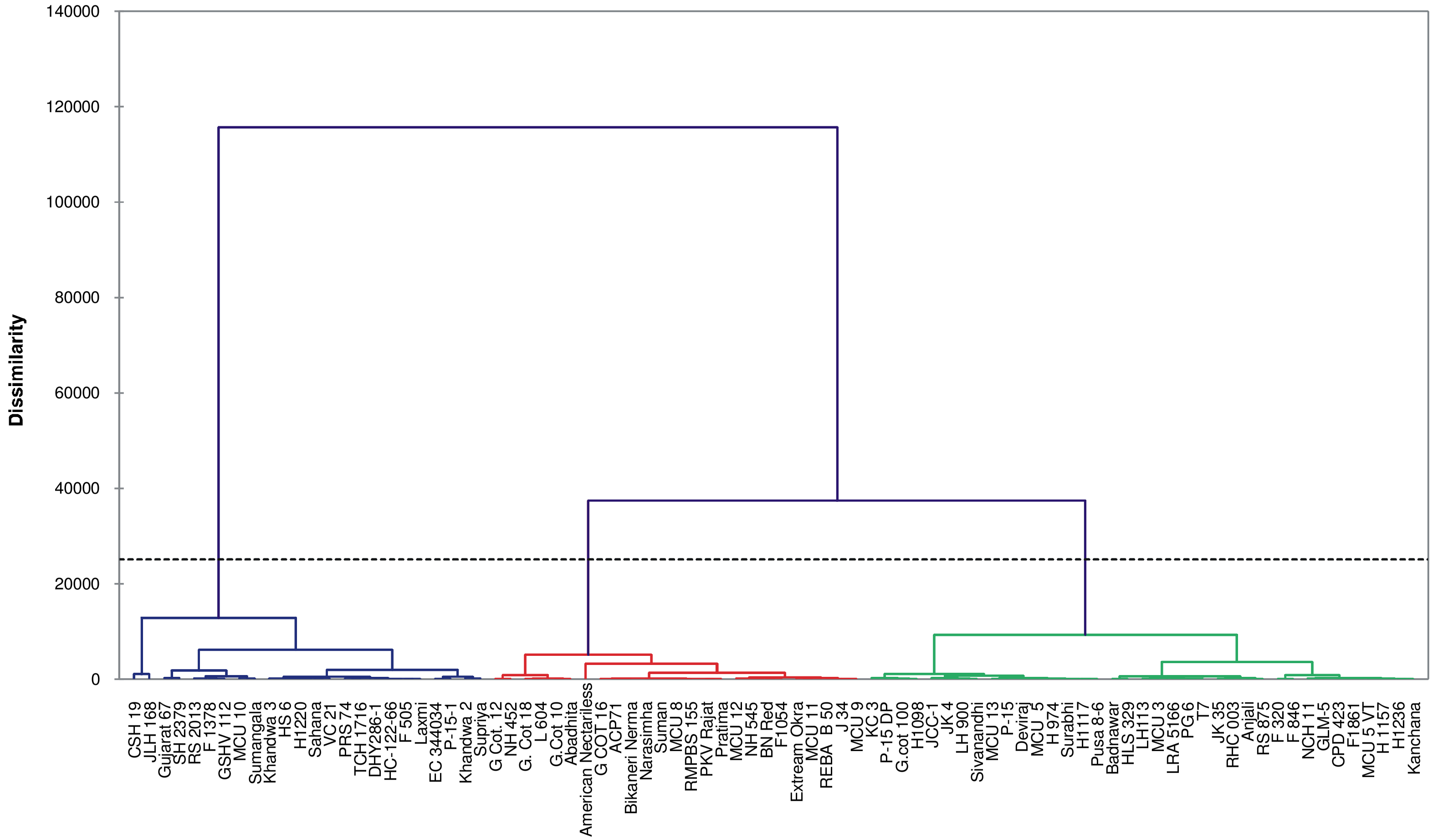

**Fig.3.** Clustering of 86 extant cotton genotypes based on 11 morphological traits

coefficients of seed cotton yield with other yield and fiber quality traits were further partitioned into direct and indirect effects (Table 3).

The component of residual effect of path analysis in yield and fiber quality traits was 0.102. The lower residual effect indicated that the characters chosen for path analysis were adequate and appropriate. Very high positive direct effect was observed for bolls/plant (0.873) and boll weight (0.475). Thiyagu *et al.,* (2010) also observed similar results for direct effects. Altaher and Singh (2003) also reported that the trait like lint index, bolls/plant and boll weight has positive direct effect on yield. The remaining characters namely fiber strength (0.051), fiber fineness (0.046), sympodia per plant (0.039) recorded positive effect on seed cotton yield /plant. The traits like fiber uniformity, plant height, sympodia /plant, and fiber strength recorded positive indirect effect on seed cotton yield / plant through bolls /plant. The positive indirect effect of seed index on seed cotton yield /plant through boll weight was observed. So selection of these traits will lead to concurrent improvement of yield in cotton.

**Table 6.** Cluster wise average values of 11 morpho agronomic traits of 86 extant cotton genotypes

| Characters | Cluster 1 | Cluster 2 | Cluster 3 |
|---|---|---|---|
| Plant height (cm) | 120.55 | 121.44 | 133.73 |
| No. of sympodia | 20.09 | 21.61 | 22.77 |
| Bolls/plant | 23.56 | 36.10 | 46.79 |
| Boll weight (g) | 3.71 | 3.76 | 4.15 |
| Seed Index (g) | 9.60 | 9.33 | 10.21 |
| Ginning (%) | 34.14 | 34.52 | 33.92 |
| Fiber length (mm) | 27.62 | 27.46 | 26.91 |
| Fiber strength (g/tex) | 21.59 | 21.97 | 22.34 |
| Fiber fineness (Mic.) | 3.75 | 3.83 | 3.68 |
| Fiber uniformity (%) | 48.33 | 49.35 | 49.32 |
| Seed cotton yield (g) | 86.99 | 135.41 | 195.07 |

**Table 7.** Distance between clusters of 86 extant cotton genotypes

| Clusters | 1 | 2 | 3 |
|---|---|---|---|
| 1 | - | 50.057 | 111.376 |
| 2 | | - | 61.876 |
| 3 | - | - | - |

Cluster and principal component analyses can be jointly used to explain the variations in plant materials with high genetic diversity. Sunseri *et al.,* (2010) proposed that the genetic variability assessment between populations is not only for their protection and registration but also for conservation of germplasm and breeding purposes. In the present study, four significant principal components (PCs) extracted had Eigen value >1 and this values accounted for a cumulative variation of 73.74 per cent indicating the great influence of identified traits on the phenotype of population panel. Screen plot exhibited variance percentage associated with each principal component attained by drawing a graph between Eigen value and PC numbers (Fig. 1). However, the remaining components contributed only 26.256 per cent towards the total diversity for this set of cotton genotypes. The first principal component (PC I) explained the most variability accounted for 26.563 per cent followed by second component 22.200 per cent, third for 14.185 per cent and fourth for 10.796 per cent of total variation (Table 4).

The different morphological traits that contribute for total variation were considered for each component. The traits like seed index, fiber strength, plant height, sympodia, bolls, boll weight, fiber length and seed cotton yield /plant showed considerable positive factor loadings on PC I while ginning (%), fiber uniformity and fiber fineness showed negative loadings (Fig. 2). Similarly Abasianyanga Isong *et al.,* (2017) reported that principal component in cotton with the highest variability contributed by seed cotton yield, uniformity ratio, boll weight, sympodia, bolls/plant and plant height. The second PC was related to diversity among cotton genotypes due to seed cotton yield /plant, fiber uniformity, bolls, sympodia and plant height with their positive loadings. The PC III due to boll weight, seed cotton yield /plant, seed index, fiber fineness and PC IV elucidated by diversity among the genotypes for ginning per cent, plant height and sympodia with positive loadings.

Cluster analysis using agglomerative hierarchial clustering exhibited a distinct pattern of group formation (Fig. 3). The dendrogram depicted three distinct clusters. Among the clusters, cluster 3 comprised of 36 genotypes grouped into two classes each consisting of 16 and 20 genotypes. Cluster 2 consists of 25 genotypes and cluster 1 with 24 genotypes, respectively (Table 5).

Cluster analysis using unweighted paired group method using arithmetic average showed distinct pattern of group formation (Table 6). The genotypes in cluster 3 showed higher values for yield and yield attributing traits like plant height, sympodia, bolls/plant, boll weight, seed index and seed cotton yield/plant. The genotypes in cluster 2 mainly contributing fiber quality traits like ginning (%), fiber strength, fiber fineness and fiber uniformity. So selection of the genotypes in cluster 3 will be very much useful for improving yield. The inter cluster distance (Table 7) was maximum in between cluster 1 and 3 indicates wide range of diversity. Choosing of genotypes in distant clusters was very much useful for breeding programme for obtaining a wide spectrum of variation among the segregants.

## CONCLUSION

From this study, it may be concluded that high variability expressed in seed cotton yield and bolls may reward for yield improvement in the event of selection based on these traits. Seed cotton yield had significant association with boll/ plant, boll weight, seed index, sympodia/plant and plant height was observed. Principal component analysis has identified characters like seed index, fiber strength, plant height, sympodia, bolls, boll weight, fiber length and seed cotton yield /plant that plays prominent role in classifying the variation existing among the cotton genotypes. Thus the results of principal component analysis revealed the existing level of genetic variation and explain the traits contributing for this diversity; this will provide an opportunity to identify parents for improving various morphological traits which have greater impact, not only on seed cotton yield but also on the establishment on distinctiveness.

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