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**Research Article**

# Assessment of genetic variability and correlation analysis of seed and seed cotton yield attributing traits of tetraploid cotton genotypes (*G. hirsutum* L.)

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## Abstract

The nature and magnitude of genetic divergence, variability and correlation were estimated in 110 extant varieties of cotton using Mahalanobis $D^2$ statistics by considering 20 quantitative characters to reveal a considerable amount of diversity in the material. The genotypes were grouped into ten clusters. Cluster I constituted a maximum number of accessions (80). The genotypes falling in cluster VIII (32.329) had the maximum divergence, which was closely followed by cluster IX (28.032), cluster X (23.674) and cluster I (15.717). The inter cluster distance was maximum between cluster VIII and IX (45.242) suggesting that the genotypes representing these clusters may be used as parents for future crop improvement programme. Traits like yield per plant, number of bolls per plant, sympodial length, number of sympodia per plant, dry matter of seedlings and plant height were the major contributors for genetic divergence. ANOVA revealed the presence of considerable amount of variability among the genotypes. High estimates of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for yield per plant, number of bolls per plant, sympodial length, number of sympodia per plant, dry matter of seedlings and plant height. High heritability coupled with high genetic advance as per cent of mean was recorded for yield per plant, number of bolls per plant, dry matter of seedlings, sympodial length, number of sympodia per plant, plant height, speed of germination, shoot length, boll weight per plant, vigour index and fibre fineness. In correlation analysis, seed cotton yield was significant and positively correlated with number of bolls per plant followed by boll weight, plant height, seed index and fibre length. Hence, selections based on the above characters will result in genotypes with high seed cotton yield.

**Key words**
Cotton, , Genetic diversity, Correlation analysis, clustering

## Introduction

Cotton is an important commercial crop providing raw material to the textile industry. It is an important natural fibre crop of global importance and widely referred as 'King of fibre crops' (Thiyagu *et al.* 2010). In crop improvement programme, knowledge on nature of gene action and inheritance of traits is essential as to choose a suitable breeding methodology. Study of genetic divergence is the basis for crop breeding. In order to assess the degree of diversity, a potential tool Multivariate analysis using $D^2$ statistics was used (Mahalanobis, 1936). Analysis of genetic diversity is important for the selection of parents to recover superior transgressive segregates (Patro and Ravisankar, 2004). Several workers have emphasized the importance of genetic divergence in the process of selection of desirable parents (Murthy and Arunachalam, (1996) and Rahman *et al.* (1997)). Knowledge of the existence of diversity among the germplasm lines and genetic relationships among breeding stocks could be an invaluable aid. Success of crop improvement programme largely depends on nature and magnitude of genetic variability, genetic advancement and character association of attributes on yield. Correlation studies among the economic traits are also important to estimate the inter relationship among the yield attributing traits.

This article is aimed at the estimation of genetic diversity and variability among cotton varieties, to determine the grouping pattern of genotypes in a different cluster, to identify yield and fibre quality attributing traits and to identify genetically diverse genotypes for further exploitation. This study is based on the evaluation of 110 extant cotton varieties.

## Material and methods

he field trial comprised of 110 extant varieties of cotton was conducted at Central Institute for Cotton Research, Regional Station, Coimbatore during winter 2011-2014.The study was conducted in a randomized block design with three replications maintaining a distance of 90 cm between rows and 60 cm between plants. Standard agronomic practices and plant protection measures were taken. The biometric observations were recorded on five randomly selected plants per replication for plant height (cm), sympodial length (cm), number of sympodia plant$^{-1}$, number of bolls plant$^{-1}$, boll weight$^{-1}$ (g), seed index, ginning (%), fibre length (mm), uniformity ratio, elongation, strength (g/tex), fineness (micronaire), maturity (%), seed cotton yield plant$^{-1}$ (g), germination (%), speed of germination, root length (cm), shoot length (cm), vigour index and dry matter of seedlings (mg 10 seedling$^{-1}$) . Mahalanobis (1936) $D^2$ statistic was computed to estimate the intra and inter cluster distances due to the grouping of genotypes into clusters. The mean, range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), correlation coefficient and genetic advance were calculated as per the standard statistical procedure of Johnson *et al*. (1955).

## Results and Discussion

An efficient crop breeding programme requires genetic diversity in the genotypes involved, to produce high yielding varieties (Murthy and Arunachalam, 1996). Genetic diversity analysis through the cluster analysis using D2 statistics is in accordance to Mahalanobis (1936), was carried out with seed cotton yield attributing traits, seed and fibre quality traits that were recorded in 110 extant varieties. The analysis brought out 10 clusters of genotypes as presented in Table 1. Among the clusters, cluster I was the largest having 80 genotypes followed by cluster X (9), cluster IX (5), cluster VIII (4) and the rest contains two genotypes each. The pattern of group constellation proved the existence of the significant amount of variability. The clustering pattern of the genotypes revealed that the clustering did not follow any particular pattern of clustering with respect to the origin (Ushakumari and Rangaswamy, 1997).The distance among intra and inter clusters, revealed that inter cluster distances was greater than intra cluster distances which suggest considerable amount of genetic diversity among genotypes (Table 2). The maximum intra-cluster distance was observed for cluster VIII (32.329) followed by the cluster IX (28.032), cluster X (23.674), cluster I (15.717) and so on. The high intra cluster distance in cluster VIII indicated the presence of wide genetic diversity among the genotypes in this cluster *viz.,* GSB 39, L 389, BC 68 2WW and L 604.

The widest inter cluster distance was found between cluster VIII and IX (45.242) followed by cluster IX and X (34.675), cluster VII and VIII (32.903) and so on. The nearest inter cluster distance was found between cluster II and III (7.824) followed by cluster III and V (8.643), cluster IV and VII (8.898) and so on. The maximum genetic divergence between the cluster points to the fact that hybridization among the genotypes included with them would produce potential and meaningful hybrids and desirable segregants. Use of genetically distant genotypes as parents to get the most promising breeding material had also been suggested by Jain and Yadav (2001), Gururajan and Manickam (2002), Sakhti *et al.* (2009) and Kulkarni *et al.* (2011). However, Altaher and Singh (2003) proved that more number of heterotic combinations with high heterosis was from parents grouped into divergent groups like clusters VIII and IX.

The contribution of individual characters to the divergence has been worked out in terms of number of times it appeared first (Table 3). This study helps to identify diversity in the different proportion which ultimately helps to decide utilization of genetic material for the improvement of specific characters. Among the twenty characters studied, the highest contribution to the divergence was seed index followed by fibre fineness, germination per cent and dry matter of seedlings.

The means of quantitative traits of various clusters (Table 4) have shown considerable differences between the cluster means for different characters. Cluster I had maximum mean values for yield per plant, germination per cent and shoot length; cluster VI recorded the highest mean values for number of sympodia per plant, boll weight per plant, dry matter of seedlings and fibre quality traits like fibre strength, fibre fineness and maturity; cluster V recorded high mean values for sympodial length, fibre elongation and vigour index. A similar result was reported by Ranjan *et al.,* (2014). Thus, it was observed that genotype or genotypes grouped under cluster VI ranked first by having 11 characters (1-2 scores) at desirable direction followed by genotypes under cluster V with eight characters (1-3 scores), cluster I with seven characters (1-3 scores) and cluster IV with five characters (1-3 scores). Genotypes grouped under cluster II (last rank) recorded nine characters in the negative direction (4-8 scores). Therefore use of genotypes in clusters VI, V, I and IV would be desirable to generate the variability in the desired direction. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Based on the *per se* performance of the best genotypes within the clusters, may be directly selected and used as a potential parent for the development of hybrid.

Mostly, crop improvement depends on the amount of genetic variability present among the characters under consideration. Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated in field crops. In the present investigation, it was observed in all the traits that phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) (Table 5). This implied that apparent variation was not only due to genotype but also due to the influence of environment.

The range of phenotypic coefficient of variation was from 3.32 to 41.41 per cent. The highest PCV was observed for yield per plant (41.41%), the number of bolls per plant (37.16%), sympodial length (32.04%), number of sympodia per plant (26.19%), plant height (24.43%) and dry matter of seedlings (23.79%).

The values for the genotypic coefficient of variation obtained for various yield and yield attributing characters ranged from 2.97 to 37.01 per cent. The highest GCV were observed for yield per plant (37.01%), number of bolls per plant (32.48%), sympodial length (25.61%), number of sympodia per plant (22.95%), plant height (22.04%) and dry matter of seedlings (22.11%). Moderate PCV and GCV were observed for shoot length, speed of germination, vigour index, root length, boll weight per plant and fibre fineness.

In the present study, it was observed that a close correspondence between phenotypic and genotypic variance for plant height, boll weight per plant, seed index, ginning (%), fibre length, fibre uniformity ratio, fibre elongation, fibre strength, fibre fineness, fibre maturity, germination per cent, speed of germination, vigour index and dry matter of seedlings indicating less environmental influence. However, traits like sympodial length, number of sympodia per plant, number of bolls per plant and yield per plant showed higher variation indicating the influence of environment on these characters. The highest PCV and GCV were recorded for yield per plant, number of bolls per plant, sympodial length, number of sympodia per plant, dry matter of seedlings and plant height. In earlier studies by Dheva and Potdukhe (2002), Preetha and Raveendran (2007) and Dhivya *et al.* (2014) also showed the highest PCV and GCV estimates for single plant yield.

In a broader sense high estimate of heritability (above 60%) was recorded for all the characters under study, however, for root length it was 58.08 per cent. It was reported that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion (Johnson, 1955). A perusal of genetic advance for all the quantitative characters ranged from 5.48 % (fibre uniformity ratio) to 68.14% (yield/plant (g)). High heritability coupled with high genetic advance was registered for yield per plant, number of bolls per plant, dry matter of seedlings, sympodial length, number of sympodia per plant, plant height, speed of germination, shoot length, boll weight per plant, vigour index and fibre fineness suggesting predominance of additive gene action in the expression of these traits.

The correlation coefficients provide a reliable measure of association among the characters and help to differentiate very important associates useful in breeding from those of the non-vital ones (Falconer, 1981). The genotypic correlation coefficient between seed cotton yield with nineteen biometric characters such as yield components and fibre quality traits were worked out and presented in Table 6.

In the present study, seed cotton yield has a significant and positive correlation with five traits namely number of bolls per plant (0.947) followed by boll weight (0.533), plant height (0.315), seed index (0.207) and fibre length (0.196). Hence, selections based on the above characters will aid in selecting genotypes with high per plant seed cotton yield. Similar results for positive correlation between yield and number of boll per plant, boll weight and fibre length were reported by Kalpande *et al.* (2008), Reddy and Reddy (2008) and Thiyagu *et al.* (2010).

Regarding inter correlation, plant height had significant positive inter correlation with sympodial length, number of sympodia per plant and boll number per plant. Sympodial length had significant correlation with number of sympodia Boll number exhibited significant positive inter correlation with boll weight; boll weight had positive inter correlation with seed index and fibre length; Seed index with fibre length; fibre uniformity with fibre strength; fibre fineness with fibre maturity; germination percentage with speed of germination; fibre length negatively inter correlated with fibre elongation; ginning per cent with germination percentage.

The present study showed ten clusters when cluster analysis was done with 110 genotypes. Cluster I constituted maximum number of genotypes (80). The genotypes falling in cluster VIII (32.329) had the maximum divergence. The inter cluster distance was maximum between cluster VIII and IX (45.242) followed by IX and X (34.675). Hence, the genotypes in these clusters may be used as parents for generation of new cultivars. In the variability studies, the traits like per plant yield, boll number, sympodial length, number of sympodia per plant, dry matter of seedlings and plant height recorded high variability, heritability and genetic advance as per cent of mean. Seed cotton yield was significantly and positively correlated with five traits namely number of bolls per plant, boll weight, plant height, seed index and fibre length. Therefore, selections based on these traits would be useful for further crop improvement.

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**Table 1. Cluster composition of 110 cotton germplasm**

| Clusters | No. of genotypes | Name of genotypes |
|---|---|---|
| I | 80 | 70 E, AB 6, AC738, ACP 71, AH 107, AK 23 B, American nectariless, Bikaneri Nerma, B N ,B N 1, NC71, NC99, Ca/H- 128, Ca/ H- 129, Ca/ MH -133, MDH 89, CPD 420, CPD 423, CPD 428, CSH -8, CSH -19, DHY 286 – 1, DHY 286 1R, DS 28 F, G COT 18, Gujarat 67, H 1098, H 1117, H 1157, HLS 329, K 34007, Kanchana, BN RED, LRA 5166, M 12, M 2, NC108, NC102, MCU 13, MCU 3, MCU 4, MCU 7, MCU 8, NCH 11, NH 452, PH 325, PH 93, PRS 74, PUSA 8-6, REBA B50, RHC 003, RS -2013, RS- 810, RS-875, RST -9, SH – 2379, Suman, T 7, TCH 1218, H 1220, VC 21, VC 22, VC 31, VC 32, Vikas, Vikaram, H 974, HGMS -1, HHM -1, F 286, J 34, LH 1134, F 320, LH 372, J 205, LSS, LH 886, Badnawar 1, Khandwa 3, GSHV 112 |
| II | 2 | JK 35, Khandwa2MB |
| III | 2 | PG 5, PG 6 |
| IV | 2 | AKH 081, F 505 |
| V | 2 | G.COT. 10, LH 1556 |
| VI | 2 | F 1378, PIL 8 |
| VII | 2 | F 1861, LH 900 |
| VIII | 4 | GSB 39, L 389, BC 68 2WW, L 604 |
| IX | 5 | SRT-GMS 1, GSAV 1056, HS 6, RHC 006, LRA 5166SB |
| X | 9 | Deviraj, F 1054, F 846, G.COT. 100, G.COT.16, PIL 43, Surat Dwarf, EC 344034, KH 11 |

**Table 2. Average intra (diagonal) and inter cluster distances in cotton**

| Clusters | I | II | III | IV | V | VI | VII | VIII | IX | X |
|---|---|---|---|---|---|---|---|---|---|---|
| I | 15.717 | 13.209 | 14.215 | 13.683 | 14.654 | 14.098 | 14.722 | 30.166 | 27.747 | 21.552 |
| II | | 5.233 | 7.824 | 10.072 | 11.560 | 12.391 | 12.493 | 28.993 | 26.238 | 19.252 |
| III | | | 5.704 | 12.796 | 8.643 | 13.151 | 14.609 | 27.466 | 28.683 | 18.172 |
| IV | | | | 6.897 | 14.857 | 11.277 | 8.898 | 32.836 | 22.155 | 21.737 |
| V | | | | | 7.233 | 11.366 | 14.989 | 24.979 | 30.73 | 17.058 |
| VI | | | | | | 7.466 | 9.790 | 28.499 | 26.154 | 19.771 |
| VII | | | | | | | 7.694 | 32.903 | 22.275 | 21.981 |
| VIII | | | | | | | | 32.329 | 45.242 | 28.929 |
| IX | | | | | | | | | 28.032 | 34.675 |
| X | | | | | | | | | | 23.674 |

**Table 3. Relative contribution of different traits towards divergence**

| SL.No. | Characters | No. of first rank | Contribution (%) |
|---|---|---|---|
| 1 | Plant height (cm) | 8 | 0.13 |
| 2 | Sympodial length (cm) | 5 | 0.08 |
| 3 | No. of sympodia/ plant | 1 | 0.02 |
| 4 | No. of bolls/plant | 19 | 0.32 |
| 5 | Boll weight/plant (g) | 29 | 0.48 |
| 6 | Seed Index | 1302 | 21.72 |
| 7 | Ginning (%) | 65 | 1.08 |
| 8 | Fibre length (mm) | 279 | 4.65 |
| 9 | Fibre Uniformity ratio | 9 | 0.15 |
| 10 | Fibre elongation | 20 | 0.33 |
| 11 | Fibre strength (g/tex) | 22 | 0.37 |
| 12 | Fibre fineness (micronaire value) | 1184 | 19.75 |
| 13 | Fibre maturity (%) | 429 | 7.16 |
| 14 | Germination percent | 1055 | 17.60 |
| 15 | Speed of germination | 138 | 2.30 |
| 16 | Root length (cm) | 147 | 2.45 |
| 17 | Shoot length (cm) | 17 | 0.28 |
| 18 | Vigour Index | 462 | 7.71 |
| 19 | Dry matter of seedlings | 705 | 11.76 |
| 20 | Yield/plant (g) | 99 | 1.65 |

**Table 4. Cluster mean values for different quantitative traits in cotton**

| Characters/ Cluster | I | II | III | IV | V | VI | VII | VIII | IX | X |
|---|---|---|---|---|---|---|---|---|---|---|
| Plant height (cm) | 93.89 (4) | 76.75 (10) | 109.25 (3) | 111.75 (2) | 93.50 (5) | 85.75 (8) | 85.75 (8) | 90.38 (6) | 120.10 (1) | 87.44 (7) |
| Sympodial length (cm) | 26.79 (8) | 19.75 (10) | 32.25 (2) | 31.75 (4) | 33.75 (1) | 32.25 (2) | 29.75 (7) | 23.50 (9) | 30.70 (5) | 30.61 (6) |
| No. of sympodia/plant | 18.09 (9) | 16.50 (10) | 21.50 (5) | 21.00 (6) | 22.00 (4) | 26.75 (1) | 26.75 (1) | 18.38 (8) | 25.60 (3) | 20.00 (7) |
| No. of bolls/plant | 24.11 (3) | 14.75 (10) | 21.00 (6) | 29.00 (1) | 23.50 (4) | 27.00 (2) | 22.50 (5) | 20.25 (8) | 15.60 (9) | 20.72 (7) |
| Boll weight/plant (g) | 4.41 (7) | 4.59 (3) | 4.59 (3) | 4.52 (5) | 4.60 (2) | 4.77 (1) | 4.36 (8) | 4.35 (9) | 3.38 (10) | 4.43 (6) |
| Seed Index | 9.72 (5) | 9.69 (6) | 10.07 (4) | 9.19 (9) | 10.35 (3) | 9.63 (6) | 9.29 (8) | 11.38 (1) | 8.33 (10) | 10.47 (2) |
| Ginning (%) | 36.50 (3) | 35.75 (5) | 33.39 (10) | 37.05 (1) | 36.96 (2) | 35.03 (7) | 36.44 (4) | 33.93 (8) | 35.68 (6) | 33.75 (9) |
| Fibre length (mm) | 27.32 (4) | 27.33 (3) | 26.25 (8) | 26.68 (7) | 26.78 (6) | 27.75 (2) | 25.58 (9) | 30.36 (1) | 25.11 (10) | 26.79 (5) |
| Fibre Uniformity ratio | 50.60 (5) | 50.63 (4) | 52.20 (1) | 49.48 (9) | 50.28 (8) | 50.30 (7) | 50.80 (3) | 48.61 (10) | 51.60 (2) | 50.58 (6) |
| Fibre elongation | 6.56 (7) | 6.38 (9) | 6.53 (8) | 6.78 (2) | 6.80 (1) | 6.73 (4) | 6.58 (6) | 6.29 (10) | 6.75 (3) | 6.59 (5) |
| Fibre strength (g/tex) | 21.37 (6) | 22.26 (5) | 22.23 (4) | 20.93 (8) | 22.85 (3) | 23.95 (1) | 19.77 (10) | 23.90 (2) | 20.83 (9) | 21.23 (7) |
| Fibre fineness (micronaire ) | 4.42 (7) | 4.13 (10) | 4.17 (9) | 4.28 (8) | 4.65 (4) | 5.07 (1) | 4.90 (2) | 4.90 (2) | 4.65 (4) | 4.55 (6) |
| Fibre maturity (%) | 76.04 (7) | 72.50 (9) | 68.75 (10) | 76.50 (6) | 73.50 (8) | 83.00 (1) | 81.25 (3) | 81.75 (2) | 80.70 (4) | 76.94 (5) |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Germination percent | 19.42 (1) | 15.40 (9) | 15.70 (7) | 16.63 (5) | 16.73 (4) | 18.15 (2) | 17.28 (3) | 15.58 (8) | 15.83 (6) | 14.17 (10) |
| Speed of germination | 9.89 (4) | 10.93 (1) | 9.43 (6) | 9.38 (7) | 8.85 (10) | 9.30 (8) | 10.20 (3) | 10.29 (2) | 9.50 (5) | 9.22 (9) |
| Root length (cm) | 9.24 (1) | 6.58 (10) | 6.83 (9) | 8.98 (3) | 7.70 (5) | 7.93 (4) | 7.50 (8) | 9.15 (2) | 7.65 (7) | 7.68 (6) |
| Shoot length (cm) | 1799.90 (1) | 1616.50 (6) | 1518.63 (8) | 1689.35 (3) | 1490.78 (9) | 1625.33 (5) | 1642.13 (4) | 1734.65 (2) | 1542.37 (7) | 1425.78 (10) |
| Vigour Index | 0.46 (3) | 0.35 (9) | 0.32 (10) | 0.46 (3) | 0.51 (1) | 0.40 (7) | 0.44 (5) | 0.47 (2) | 0.36 (8) | 0.42 (6) |
| Dry matter of seedlings | 107.24 (4) | 68.25 (9) | 96.04 (6) | 128.30 (2) | 107.89 (3) | 128.99 (1) | 96.33 (5) | 90.70 (8) | 52.42 (10) | 91.35 (7) |
| Yield/plant (g) | 94.11 (1) | 92.50 (5) | 93.50 (3) | 92.00 (6) | 90.00 (7) | 94.00 (2) | 93.00 (4) | 88.75 (9) | 89.60 (8) | 82.89 (10) |
| Total | 90 | 143 | 122 | 98 | 90 | 72 | 106 | 108 | 127 | 136 |
| Rank | II | X | VII | IV | II | I | V | VI | VIII | IX |

* () Parenthesis indicates rank of clusters

**Table 5. Estimation of genetic parameters for 20 quantitative traits in cotton**

| SI. No. | Parameters | Mean | Minimum | Maximum | GCV (%) | PCV (%) | Heritability | Genetic advance as % of mean |
|---|---|---|---|---|---|---|---|---|
| 1 | Plant height (cm) | 94.42 | 51.00 | 170.00 | 22.04 | 24.43 | 81.38 | 40.95 |
| 2 | Sympodial length (cm) | 27.50 | 11.00 | 52.50 | 25.61 | 32.04 | 63.92 | 42.19 |
| 3 | No. of sympodia/plant | 19.07 | 11.00 | 37.50 | 22.95 | 26.19 | 76.77 | 41.42 |
| 4 | No. of bolls/plant | 23.19 | 10.00 | 55.00 | 32.48 | 37.16 | 76.40 | 58.48 |
| 5 | Boll weight/plant (g) | 4.38 | 2.44 | 5.61 | 13.12 | 13.88 | 89.25 | 25.53 |
| 6 | Seed Index | 9.78 | 6.35 | 12.68 | 9.07 | 9.10 | 99.32 | 18.62 |
| 7 | Ginning (%) | 35.68 | 22.64 | 40.38 | 6.70 | 6.71 | 99.71 | 13.78 |
| 8 | Fibre length (mm) | 27.22 | 21.60 | 37.75 | 6.80 | 6.99 | 94.63 | 13.62 |
| 9 | Fibre Uniformity ratio | 50.58 | 46.50 | 54.15 | 2.97 | 3.32 | 80.16 | 5.48 |
| 10 | Fibre elongation | 6.57 | 5.00 | 7.20 | 4.55 | 5.22 | 76.22 | 8.19 |
| 11 | Fibre strength (g/tex) | 21.50 | 16.84 | 31.85 | 9.05 | 10.22 | 78.38 | 16.51 |
| 12 | Fibre fineness (micronaire value) | 4.47 | 3.48 | 6.91 | 11.03 | 11.18 | 97.25 | 22.41 |
| 13 | Fibre maturity (%) | 76.52 | 66.00 | 104.00 | 6.88 | 7.06 | 95.11 | 13.83 |
| 14 | Germination percent | 92.62 | 48.00 | 100.00 | 37.01 | 41.41 | 79.89 | 68.14 |
| 15 | Speed of germination | 18.38 | 5.93 | 24.95 | 7.13 | 8.05 | 78.38 | 13.00 |
| 16 | Root length (cm) | 9.81 | 7.60 | 15.89 | 17.74 | 18.46 | 92.27 | 35.10 |
| 17 | Shoot length (cm) | 8.86 | 5.20 | 12.43 | 10.87 | 14.27 | 58.08 | 17.07 |
| 18 | Vigour Index | 1733.09 | 636.36 | 2285.00 | 16.96 | 18.63 | 82.82 | 31.79 |
| 19 | Dry matter of seedlings | 0.45 | 0.26 | 0.66 | 13.38 | 15.42 | 75.25 | 23.91 |
| 20 | Yield/plant (g) | 102.52 | 24.19 | 240.56 | 22.11 | 23.79 | 86.40 | 42.34 |

**Table 6. Genotypic correlation coefficients between yield components and fibre quality traits with seed cotton yield**

| | **P.ht.** | **SYL** | **N SY** | **BN** | **BW** | **SI** | **G%** | **FL** | **FU** | **FE** |
|---|---|---|---|---|---|---|---|---|---|---|
| P.ht | 1 | 0.617** | 0.585** | 0.308** | 0.087 | -0.104 | 0.155 | 0.02 | -0.122 | 0.046 |
| SYL | | 1 | 0.585** | 0.143 | 0.111 | 0.047 | -0.067 | 0.087 | -0.074 | 0.061 |
| NSY | | | 1 | 0.113 | -0.047 | -0.12 | -0.066 | -0.017 | -0.149 | 0.112 |
| BN | | | | 1 | 0.254** | 0.034 | 0.083 | 0.100 | -0.132 | -0.017 |
| BW | | | | | 1 | 0.572** | 0.166 | 0.279** | -0.219 | 0.069 |
| SI | | | | | | 1 | -0.122 | 0.459** | -0.251 | -0.213 |
| G% | | | | | | | 1 | 0.115 | -0.063 | 0.022 |
| FL | | | | | | | | 1 | -0.732 | -0.331** |
| FU | | | | | | | | | 1 | -0.113 |
| FE | | | | | | | | | | 1 |

*Significant at P=0.05, **Significant at P=0.01

P.hgt- plant height (cm) FU –Fibre uniformity SL – Shoot length (cm)
SYL – Sympodial length (cm) FE – Fibre elongation VI – Vigour index
NSY- Number of sympodia FS – Fibre strength (g/tex) DMS- Dry matter of seedlings
BN – Boll number FF – Fibre fineness YP –Yield per plant (g)
BW – Boll weight (g) FM – Fibre maturity
SI – Seed index Gm% -Germination per cent
G% - Ginning per cent SG – Speed of germination
FL – Fibre length (2.5mm) RL – Root length (cm)

**Contd.., Table 6. Genotypic correlation coefficients between yield components and fibre quality traits with seed cotton yield**

| | FS | FF | FM | Gm% | SG | RL | SL | VI | DMS | YP |
|---|---|---|---|---|---|---|---|---|---|---|
| P.ht | -0.102 | -0.14 | -0.023 | 0.117 | -0.038 | -0.022 | 0.108 | 0.103 | -0.034 | 0.315** |
| SYL | -0.031 | -0.189 | -0.207 | 0.018 | -0.130 | -0.014 | -0.008 | -0.011 | 0.018 | 0.186 |
| NSY | -0.067 | -0.082 | 0.052 | 0.003 | -0.155 | -0.077 | -0.111 | -0.100 | -0.083 | 0.093 |
| BN | -0.119 | -0.09 | 0.026 | 0.044 | 0.072 | -0.142 | 0.089 | 0.012 | 0.030 | 0.947** |
| BW | -0.126 | 0.039 | -0.008 | 0.190 | 0.109 | -0.072 | 0.113 | 0.122 | 0.158 | 0.533** |
| SI | 0.200 | -0.009 | -0.106 | 0.031 | -0.027 | -0.072 | 0.090 | 0.036 | 0.256** | 0.207* |
| G% | -0.240 | -0.104 | -0.019 | 0.335** | 0.293 | 0.033 | 0.155 | 0.255** | 0.177 | 0.129 |
| FL | 0.069 | -0.181 | -0.174 | 0.210 | 0.178 | 0.021 | 0.240* | 0.240 | 0.283** | 0.196* |
| FU | 0.293** | 0.100 | 0.033 | -0.079 | -0.076 | 0.013 | -0.201 | -0.142 | -0.213 | -0.188 |
| FE | -0.599 | 0.118 | 0.146 | -0.091 | -0.049 | -0.103 | -0.129 | -0.156 | -0.147 | 0.011 |
| FS | 1 | -0.084 | -0.138 | 0.115 | 0.038 | 0.098 | 0.088 | 0.145 | 0.149 | -0.149 |
| FF | | 1 | 0.853** | -0.269 | -0.131 | 0.037 | -0.058 | -0.117 | -0.126 | -0.052 |
| FM | | | 1 | -0.275 | -0.109 | 0.030 | -0.055 | -0.124 | -0.110 | 0.035 |
| Gm% | | | | 1 | 0.671** | 0.084 | 0.354** | 0.683** | 0.256** | 0.100 |
| SG | | | | | 1 | -0.105 | 0.687** | 0.667** | 0.639** | 0.094 |
| RL | | | | | | 1 | 0.124 | 0.522** | -0.121 | -0.13 |
| SL | | | | | | | 1 | 0.806** | 0.778** | 0.105 |
| VI | | | | | | | | 1 | 0.527** | 0.052 |
| DMS | | | | | | | | | 1 | 0.067 |
| YP | | | | | | | | | | 1 |

*Significant at P=0.05, **Significant at P=0.01