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# Genetic Variability and Correlation Analysis for Fibre Quality Traits in Diploid Cotton (*Gossypium* spp)

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**Abstract:** The present investigation was carried out to study genetic parameters of fibre quality traits in diploid cotton comprising of *Gossypium herbacium* var Jayadhar and *G arboreum* var DLSa17 along with their recombinant inbred lines (RILs). Results revealed highest variance for uniformity ratio (3.30) and the lowest for micronaire (0.20). All the traits exhibited low estimates of phenotypic and genotypic coefficients of variation. Among the traits lowest GCV and PCV were observed for uniformity ratio whereas highest GCV was recorded for fibre elongation and highest PCV for micronaire. 2.5 per cent span length and fibre elongation exhibited high heritability coupled with moderate genetic advance as per cent mean whereas fibre strength recorded moderate heritability with low genetic advance as per cent mean. Low heritability coupled with low genetic advance was observed for micronaire indicating that this trait is controlled by non-additive genes and simple selection would not be effective.

**Key words:** Correlation · Diploid cotton · Fibre quality · Genetic variability

## INTRODUCTION

Cotton is one of the most important commercial crops grown in India. It is the world's leading natural fibre crop and it is the cornerstone of textile industries worldwide. Cotton known as the king of fibres and in recent times called as white gold is the most vital crop of commerce to many countries including India. Cotton is primarily grown for its fibre which is the most important raw material for textile industry. Both yield and quality of fibre are equally important in cotton. Inspite of several competitions from synthetic fibres cotton continues to enjoy a place of prime importance in textile industry. In India, cotton provides means of livelihood to millions of farmers and workers and sustains cotton textile industry which annually produces cloth of the value exceeding a thousand crore rupees. In total, cotton has become a highly agro-industrial crop. Fibre quality can be attributed by a set of the measurable properties that affect the spinning performance of the fibre. Among them, fibre strength, fibre length and fibre fineness are the primary quality properties that influence textile processing. Genetic improvement continues to be key in meeting this agricultural challenge. Cotton fibre quality properties, as measured by fibre bundles, display additive quantitative inheritance, which has facilitated a steady genetic advance in cotton improvement [1]. Enhanced fibre quality properties may be due to either introgression of new genes or new combinations of existing genes [2].

India has a pride place in the global cotton scenario, it has the distinction of having the largest cotton area of 117.73 lakh hectares, production of 330.0 lakh bales (1 bale = 170 kg lint) and productivity of 496.39 kg per ha [3]. Perhaps India is the only country in the world where in all the four cultivated species, viz. *G. herbaceum, G. arboreum, G. hirsutum* and *G. barbadense* are grown on commercial scale. In India, diploid cotton (*G. herbaceum* and *G. arboreum*) is grown from time immemorial. Conversion of poor fibre quality diploids into superior quality cottons makes cultivation of such cottons as

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remunerative [4]. At this juncture, a rethinking is required on how far *desi* cotton can be introduced in intensive management situation for sustainable cotton production. Even though genetic variability in *desi* cotton so far is exploited only in rainfed situations, initial studies on *desi* cotton have indicated that *desi* cotton also respond to protective irrigation and intensification. The success of any breeding programme depends on the spectrum of genetic variability present in the population. A wider spectrum of variability will enhance the chances of selecting a desired genotype. Heritability is a good index of the transmission of characters from parents to their off spring. Heritability along with genetic advance is useful in estimating the influence of environment. Therefore, an attempt has been made in the present investigation to estimate the magnitude genetic variability, heritability and genetic advance for fibre quality traits in diploid cotton.

## MATERIALS AND METHODS

**Genetic Material:** The experimental material for the present investigation consisted of 154 recombinant inbred lines developed from cross between *G herbacium* var Jayadhar and *G arboreum* var DLSa17. The salient features of the parents are given in Table 1. The population was evaluated at ARS, Hanumanamatti in augmented design during kharif 2012. The crop was sown with the spacing of 90 cm between rows and 20 cm between plants. All the recommended package of practices for diploid cotton was followed to raise the crop. The fibre quality analysis was carried out at CIRCOT, Mumbai. The analysis of variance (ANOVA) for all characters was carried out separately. Phenotypic and genotypic components of variances were estimated following Burton and Devane method [5]. Heritability in broad sense was estimated as per Hanson method [6] and genetic advance as per cent of mean was estimated following Johnson method [7].

Table 1: Salient features of the parents used in the present investigation

| Traits | Jayadhar | DLSa17 |
|---|---|---|
| Seed cotton Yield (kg/ha) | 600-800 | 1000-1200 |
| 2.5% Span Length (mm) | 20-22 | 25-27 |
| Fibre strength (g/tex) | 15-17 | 20-22 |
| Elongation (%) | 4-5 | 5-6 |
| Micronaire (ìg/inch) | 4.9-5 | 4-4.4 |
| Duration (days) | 190-200 | 150-165 |

## RESULTS AND DISCUSSION

**Genetic Variability:** Analysis of variance indicated significant variability for important fiber quality traits *viz.* 2.5 per cent span length (mm) and fibre elongation (%) (Table 2). This indicated that the RIL population developed using diverse parents belonging to *G. herbaceum* and *G. arboreum* species could be effectively utilized in improvement of fibre quality traits in diploid cotton. Significant differences were found among the recombinant inbred lines for 2.5% span length which corresponds to findings of Ahmed *et al.* [8] and Hussain *et al.* [9]. Observations on 2.5 per cent span length indicated the presence of wide variation (22.84 to 30.00 mm) (Table 3). The variation for fibre strength varied from 16.42 to 23.7 g/tex. Micronaire (fibre fineness) ranged from 3.20 to 5.60 ìg/inch with the mean value of 4.42 ìg/inch. Such type of variation was also observed by Kohel *et al*. [2] and Lazo *et al*. [10] and Paterson *et al*. [11] in $F_2$ population of cross between *hirsutum* and *barbadense*, Ulloa and Meredith [12] in $F_2$ populations derived from intraspecific crosses involving hirsutums. However recent trend of identification of major QTLs for this trait is useful to identify linkage between molecular marker and major QTLs. The phenotypic coefficient of variation (PCV) was found to be greater than genotypic coefficient of variation (GCV) for all the characters, indicating environmental influence on these traits. Similar results were also reported by Tomar and Singh [13 & 14], Krishnadoss and Kadambavanasundaram [15] and Sakthi *et al*. [16]. 2.5 per cent span length, fibre strength, micronaire, uniformity ratio and fibre elongation showed low PCV and GCV estimates which indicated that one has to either create or locate source of high variability of wider spectrum for effective selection and improvement in these characters. Saeed Ahmad *et al*. [17], Preetha and Raveendran [18] and Venkatesan [19] in their studies found similar trends.

High heritability values were observed for 2.5 per cent span length and fibre elongation indicated that the additive gene effects are more important as reported by Tomar and Singh [13, 14]. Similar results were reported by Dheva and Potdukhe [20], Preetha and Raveendran [18] and Ganesan and Raveendran [21]. Therefore, simple selection method will be effective for the improvement of these traits. However, Falconer and Mackey [22] suggested that estimates of heritability are subject to environmental conditions and therefore may be used with great care and caution in plant improvement programme. High level of heritability for fibre quality traits also revealed that these traits are amenable for QTL analysis,

Table 2: ANOVA for the fibre quality traits

| | DF | 2.5 % SL | Fibre Strength (g/tex) | Micronaire (g/inch) | Uniformity Ratio (%) | Elongation (%) |
|---|---|---|---|---|---|---|
| Block(ignoring treatments) | 6 | 10.27** | 16.09** | 0.47* | 11.19** | 1.92** |
| Treatment (eliminating Blocks) | 156 | 2.30** | 1.91 | 0.19 | 3.01 | 0.17** |
| Checks | 2 | 7.14** | 12.04** | 0.72* | 8.19** | 0.45** |
| Checks + Var vs. Var. | 154 | 2.23* | 1.78 | 0.18 | 2.95 | 0.16** |
| Block (Eliminating check+Var.) | 6 | 1.00 | 0.39 | 0.07 | 1.52 | 0.06 |
| Entries(Ignoring Blocks) | 156 | 2.65** | 2.56* | 0.20 | 3.34* | 0.24** |
| Varieties | 153 | 2.59** | 2.38 | 0.19 | 3.32* | 0.22** |
| Checks vs. Varieties | 1 | 2.55 | 3.43 | 0.01 | 3.89 | 3.17** |
| ERROR | 12 | 0.66 | 1.07 | 0.15 | 3.36 | 0.04 |

*@ 5%, **@ 1%

Table 3: Mean, Range, variance, GCV, PCV, $h^2$ and GAM for fibre quality traits

| Traits | Mean±SE | Minimum | Maximum | Variance | GCV (%) | PCV (%) | $h^2$ (%) | GAM |
|---|---|---|---|---|---|---|---|---|
| 2.5 % SL (mm) | 26.27±0.13 | 22.84 | 30.00 | 2.60 | 5.05 | 5.92 | 72.75 | 11.38 |
| Fibre strength (g/tex) | 19.40±0.12 | 16.42 | 23.70 | 2.38 | 5.64 | 7.76 | 52.73 | 10.81 |
| Micronaire (ig /inch) | 4.42±0.04 | 3.20 | 5.60 | 0.20 | 4.86 | 9.91 | 24.00 | 6.28 |
| Uniformity Ratio (%) | 49.37±0.15 | 45.00 | 53.00 | 3.30 | 2.71 | 3.59 | 56.83 | 5.39 |
| Elongation (%) | 5.45±0.04 | 4.60 | 6.50 | 0.22 | 7.35 | 8.23 | 79.78 | 17.33 |

SE- Standard Error

Table 4: Association among productivity and fibre quality traits in Jayadhar X DLSa17 RILs

| | X1 | X2 | X3 | X4 | X5 |
|---|---|---|---|---|---|
| X1 | 1.00 | | | | |
| X2 | 0.41** | 1.00 | | | |
| X3 | -0.28** | -0.17* | 1.00 | | |
| X4 | -0.17* | 0.27** | 0.28** | 1.00 | |
| X5 | 0.48** | 0.11 | -0.09 | -0.01 | 1.00 |

Significance: ** @ 1%, * @ 5%

X1: 2.5% span length (mm) X2: Fibre strength (g/tex)

X3: Micronaire (µg/inch) X4: Uniformity ratio (%)

X5: Elongation (%)

since they are not much affected by environment [11]. Taking into consideration the amount of variability, heritability and genetic advance as percent of mean in the present study, it may be concluded that selection would be effective in cotton for 2.5 per cent span length and fibre elongation.

**Correlation Analysis:** Fibre length was significantly and positively associated with fibre strength and fibre elongation (Table 4). Significant negative correlation was observed between fibre strength and micronaire. A similar positive correlation between fibre strength and fibre length was also observed by earlier investigators using an exotic upland AM panel [23]. Some of the earlier studies also indicated negative correlations between micronaire and fibre length, micronaire and fibre strength, fibre strength and elongation in an upland and diploid association mapping panel [24, 25]. Thus, for undertaking selection programme for fibre quality traits in interspecific cross combinations, selection based on 2.5 per cent span length, fibre strength and micronaire can be considered for improvement of fibre quality.

## REFERENCES


1. Meredith, W.R. and R.R. Bridge, 1971. Breakup of linkage blocks in *Gossypium hirsutum* L. Crop Sci., 11 : 659-668.
2. Kohel, R.J., J. Yu, Y.H. Park and G.R. Lazo, 2001. Molecular mapping and characterization of traits controlling fiber quality in cotton. Euphytica, 121(2): 163-172.
3. Anonymous, 2012. All India Coordinated Cotton Improvement Project Report.
4. Katageri, I.S., S. Chandrakant, B.M. Khadi, H.M. Vamadevaih and K. Narayan, 2004. Transfer of fibre length, strength and fineness from Tetraploid to Diploids in *Gossypium spp*. International Cotton Genome Initiative ICGI–2004 Workshop, October 10-13, 2004, held at Hyderabad, India.
5. Burton, G.W. and E.M. Devane, 1953. Estimating heritability in fall fescue (Festecd cirunclindcede) from replicated clonal material. Agron. J., 45: 478-481.
6. Hanson, C.H., H.G. Robinson and R.E. Comstock, 1956. Biometrical studies of yield in segregating populations of Korean Lespediza. Agron. J., 48 : 268-272.

7. Johnson, H.W., H.F. Robinson and R.E. Comstock, 1955. Genotypic and phenotypic correlation in soybean and their implications in selection. Agron. J. 47: 477-483.
8. Ahmed, Y.T., I.A. Khan and M. Zubair, 1997. Diallel analysis for seed cotton yield and its contributing traits in upland cotton (*G. hirsutum* L.). Indian J. Agric.. Sci., 67(12) : 583-585.
9. Hussain, B., A.A. Ghaffari, M.A. Amin and M.A. Khan, 1999. Genetic analysis of some agronomic traits in cotton. J. Agric. Res., 37: 1-8.
10. Lazo, G.R., Y.H. Park and R.J. Kohel, 1994. Identification of RAPD markers linked to fibre strength in *Gossypium hirsutum* and *G. barbadense* interspecific crosses. The biochemistry of cotton workshop, pp: 28-30.
11. Paterson, A.H., Y. Saranga, M. Menz, C.X. Jiang and R.J. Wright, 2003. QTL analysis of genotype x environment interactions affecting cotton fibre quality. Theoretical and Applied Genetics, 106: 384-396.
12. Ulloa, M. and W.R. Jr Meredith, 2000. Genetic linkage map and QTL analysis of agronomic and fibre quality traits in an intraspecific population. Journal of Cotton Science, 4: 161-170.
13. Tomar, S.K. and S.P. Singh, 1991. Genetic variability and association of characters in tree cotton (*Gossypium arboreum* L.). Indian J. Agric. Sci., 61(4): 255-258.
14. Tomar, S.K. and S.P. Singh, 1992. Correlation and path coefficient studies over environments in desi cotton (*Gossypium arboreum* L.). Indian J. Genet., 52(2): 187-191.
15. Krishnadoss, D. and Kadambavanasundaram, 1993. Indian J. Genet., 53: 55.
16. Sakthi, A.R., M. Kumar and R. Ravikesavan, 2007. J. Cotton Res. Dev., 21: 148.
17. Saeed Ahmad, K. Abdul, J. Abdul, H. Mohmood, M. Taj and I. Muhammad, 2003. J. Biolo. Sci., 3: 228.
18. Preetha, S. and T.S. Raveendran, 2007. Genetic variability and association in three different morphological groups of cotton. Asian J. Plant Sci., 6: 122.
19. Venkatesan, S., 2008. Genetic diversity analysis through morphological and molecular markers in cotton *(Gossypium spp.*), M.Sc.(Agric.). Thesis, T.N.A.U. Coimbatore. India.
20. Dheva, N.G. and N.R. Potdukhe, 2002. Study on variability and correlation in upland cotton for yield and its components. J. Indian Soc. Cotton Improv., 15: 148.
21. Ganesan, K.N. and T.S. Raveendran, 2007. Enhancing the breeding value of genotype through genetic selection in cotton (*Gossypium hirsutum* L.). Bull. Inst. Trop. Agri. Kyushu Univ., 30: 1-8.
22. Falconer, D.S. and T.F.C. Mackey, 1996. Introduction to Quantitative Genetics". Third Edition. Longman, London, pp: 65-92.
23. Abdurakhmonov, I.Y., R.J. Kohel,, J.Z. Yu, A.E. Pepper, A.A. Abdullaev, F.N. Kushanov, I.B. Salakhutdinov, Z.T. Buriev, S. Saha, B.E. Scheffler, H.N. Jenkins and A. Abdukarimov, 2008. Molecular diversity and association mapping of fiber quality traits in exotic *G. hirsutum* L. germplasm. Genomics, 92(6): 478-487.
24. Zeng, L., W.R. Jr Meredith, O.A. Gutierrez and D.L. Boykin, 2009. Identification of associations between SSR markers and fiber traits in an exotic germplasm derived from multiple crosses among *Gossypium* tetraploid species. Theoretical and Applied Genetics, 119(1): 93-103.
25. Kantartzi, S.K. and J.McD. Stewart, 2008. Association analysis of fiber traits in *Gossypium arboreum* accessions. Plant Breeding, 127: 173-179.