Genetic Variability Analysis for Fibre Quality Traits in Tetraploid Cotton (*Gossypium* spp.)

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ABSTRACT: *The present study was undertaken for the estimation of genetic variability, heritability and genetic advance of fibre quality traits in tetraploid cotton comprising of Gossypium hirsutum var. KC2 and G. barbadense var. Suvin along with their recombinant inbred lines (RILs). A wide range of variation was found for almost all the traits. All the characters showed very small difference between genotypic coefficient of variation (GCV) and respective phenotypic coefficient of variation (PCV), indicated that all the characters were least affected by environment. Moderate PCV and GCV estimates were obtained for micronaire value, 2.5% span length and elongation per cent and hence the best possibilities of improvements are through selection. High heritability with low genetic advance as per cent mean was observed for 2.5% span length and uniformity ratio, indicating non-additive gene effects and heterosis breeding can be resorted for improving these traits.*

Keywords: Genetic variability, Heritability, Genetic advance, Fibre quality, Tetraploid cotton.

INTRODUCTION

The Fabric of Our Lives, cotton (*Gossypium* spp.), is the most used textile fibre in the world and it has great impact in the global economy and hence it is also popularly known as white gold. In 2013-2014, the world's cotton production is estimated at 116.67 million bales of 480 lakh bales, which is 6.402 million bales lesser than the previous year 2012-2013. This is due to reduction in the area of cultivation in many countries (Anonymous, 2014a). India continued to maintain the largest area under cotton and second largest producer of cotton next to China with 35.29 per cent and 24 per cent of world cotton area and production, respectively. India also sustained the position of being the second largest consumer and exporter of cotton and it is expected to export 7.5 million bales and expected to also consume 23 million bales in 2013-2014 (Anonymous, 2014b). India has the distinction of growing all the four cotton cultivable species *viz., Gossypium arboreum, G. herbaceum, G. barbadense* and *G. hirsutum*. Among the four species, the tetraploid (or allopolyploid) species *G. hirsutum* L. and *G. barbadense* L. accounted

for 90 and 8 per cent of the world cotton production, respectively (Zhang *et al.*, 2008). Usually *G. hirsutum* accessions possess high yield but poor fibre qualities and *G. barbadense* lines have good fibre quality traits but with low yield.

Cotton produces unicellular seed trichomes commonly called as "fibres". Demands for enhancement of fibre quality traits such as fibre length and fibre strength have been increasing because of changes in spinning technology in the textile industry. Cotton fibre properties are essential predictors of yarn performance. The suites of fibre quality traits that collectively affect the utility of the fibre for the textile industry include the length, the strength, the fineness and the colour. These properties have been shown to be moderately to highly heritable (Lacape *et al.*, 2003). 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 (Meredith and Bridge, 1971). Enhanced fibre quality properties may be due to either

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Table 1
Mean performance of parents and mean and range of F$_3$'s for fibre quality traits

S. No.	Characters	Mean KC2 (P$_1$)	SUVIN (P$_2$)	F$_3$	Minimum	Maximum
1.	2.5% span length (mm)	24.70	30.10	28.50	22.60	34.00
2.	Bundle strength (g/tex)	19.08	29.50	23.50	14.90	31.60
3.	Micronaire value (mg/inch)	4.42	3.70	3.20	2.20	4.70
4.	Uniformity ratio (%)	49.40	50.00	46.90	43.80	54.80
5.	Elongation per cent (%)	5.00	6.56	5.40	4.10	7.00

introgression of new genes or new combinations of existing genes (Kohel *et al.*, 2001).

Knowledge of the nature and magnitude of genotypic and phenotypic variability present in any crop species plays a vital role in formulating successful breeding programme for evolving superior cultivars. Effectiveness of selection directly depends upon the amount of heritability and expected genetic advance as per cent of mean for that character. The present investigation was carried out to estimate the magnitude of genetic variability, heritability and genetic advance for fibre quality traits in tetraploid cotton.

MATERIALS AND METHODS

The experimental material for the present investigation consisted of 142 F$_3$ progenies derived from an inter-specific cross between *G. hirsutum* var. KC2 and *G. barbadense* var. Suvin. KC 2 is a medium duration variety with medium staple length and suitable for cultivating under rainfed black soil tract of Tuticorin, Tirunelveli and Virudhunagar districts of Tamil Nadu. It is highly resistant to jassids (*Amarasca sp.*) and exhibited medium yield and also shows relatively better drought tolerance. On the other hand, Suvin is known for its exceptionally extra-long and strong fibre quality characters but with relatively poor yield, under both irrigated and water stress conditions besides susceptible to several pest and diseases. These two lines have also shown significant dissimilarity at molecular level and hence they were selected for mapping population development. Along with F$_3$ plants, five rows of each parent were grown in the field at Department of Cotton, Tamil Nadu Agricultural University, Coimbatore during 2012-2013. The crop was sown with the spacing of 90 cm between rows and 45 cm between plants. All the recommended package of practices for tetraploid cotton was followed to raise the crop. Each and every selected individual plant was again selfed by adopting clay smear method

described by Ramanatha Iyer (1936) for advancing them to F$_4$ and F$_5$ generations for future genetic analysis.

The fibre quality characters *viz.*, 2.5 per cent span length (mm), bundle strength (g tex^{-1}), micronaire value (μg/inch), uniformity ratio (%) and elongation per cent (%) were estimated by High Volume Instrument installed at Cotton Breeding Station, Tamil Nadu Agricultural University, Coimbatore. Phenotypic and genotypic coefficient of variation (PCV and GCV) was computed using the formula adopted by Burton (1952) and categorized of the range of variation was done as proposed by Sivasubramaniam and Menon (1973). Heritability (h^2) in broad sense was computed using the formula according to Lush (1940) and it was classified according to Robinson *et al.* (1949). Genetic advance (GA) as per cent of mean was estimated, adopted the method suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Variation is very important for the plant breeders and selection is effective when magnitude of variability in the breeding population is too enough. Observations on 2.5 per cent span length indicated the presence of wide variation (22.60 to 34.00 mm) (Table 1). The variation for bundle strength varied from 14.90 to 31.60 g/tex. The F$_3$ recorded a lower mean value of 3.20 μg/inch for micronaire when compared to parents (4.42 μg/inch and 3.70 μg/inch), with a range of 2.20 to 4.70 μg/inch in F$_3$. The mean uniformity ratio (46.90%) of F$_3$ was intermediate between the two parents (49.40% for P$_1$ and 50% for P$_2$), with the maximum of 54.80% and the minimum of 43.80%. Elongation per cent ranged between 4.10% and 7.00% in F$_3$ and the mean values recorded in P$_1$, P$_2$ and F$_3$ were 5.00%, 6.56% and 5.40% respectively. Such type of variation was also observed by Kohel *et al.* (2001); Prasad *et al.* (2005); Santoshkumar *et al.* (2012); Dhivya *et al.* (2014); Ahsan

Table 2
Components of variance for fibre quality traits

S.No	Characters	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (%)	Genetic advance as percentage of mean
1.	2.5% span length (mm)	9.98	9.42	11.09	10.77	94.38	5.91
2.	Bundle strength (g/tex)	4.97	3.17	9.49	7.58	63.78	11.83
3.	Micronaire value (mg/inch)	0.32	0.14	17.68	11.69	43.75	18.56
4.	Uniformity ratio (%)	7.98	6.51	6.02	5.44	81.58	3.99
5.	Elongation per cent (%)	0.70	0.50	15.49	13.09	71.43	16.48

et al. (2015) and Lazo *et al.* (1994) and Paterson *et al.* (2003) in F$_2$ population of cross between *G. hirsutum* and *G. barbadense*, Ulloa and Meredith (2000) and Ranganatha *et al.* (2013) in F$_2$ populations derived from intraspecific crosses involving *hirsutums*, Malagouda *et al.* (2014) in RIL populations derived from inter-specific cross involving *G. herbacium* and *G. arboreum*. However recent trend of identification of major QTLs for this trait is useful to identify linkage between molecular marker and major QTLs.

The estimates of phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation, heritability in broad sense and genetic advance as per cent of mean for 5 fibre traits are presented in Table 2. The knowledge of nature and magnitude of variability available in the genotypes for different characters is an important prerequisite for making simultaneous selection over more number of characters to bring remarkable improvement in

cotton. The values of phenotypic variance were more than the genotypic variance for all the characters. High phenotypic and genotypic variance were observed for 2.5% span length (9.98; 9.42) and uniformity ratio (7.98; 6.51). Micronaire value (0.32; 0.14) and elongation per cent (0.70; 0.50) were showed the lowest genotypic and phenotypic variance.

In present investigation the phenotypic coefficient of variations were greater than genotypic coefficient of variations (Fig. 1). The differences between them were of lower magnitude, that is, they were more or less close to each other. This indicates that there is small effect of environment on characters and selection may be effective. Abbas *et al.* (2013) and Erande *et al.* (2014) also reported greater PCV values than GCV values for all the traits. Micronaire value (17.68; 11.69), 2.5% span length (11.09; 10.77) and elongation per cent (15.49; 13.09)
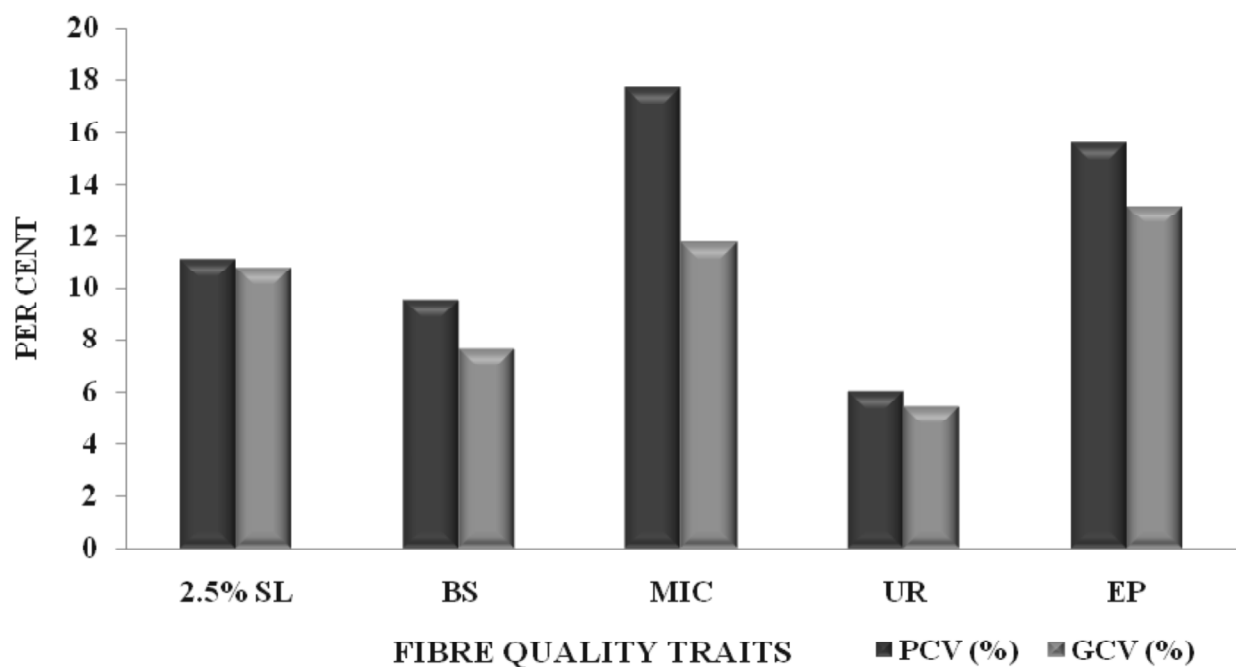

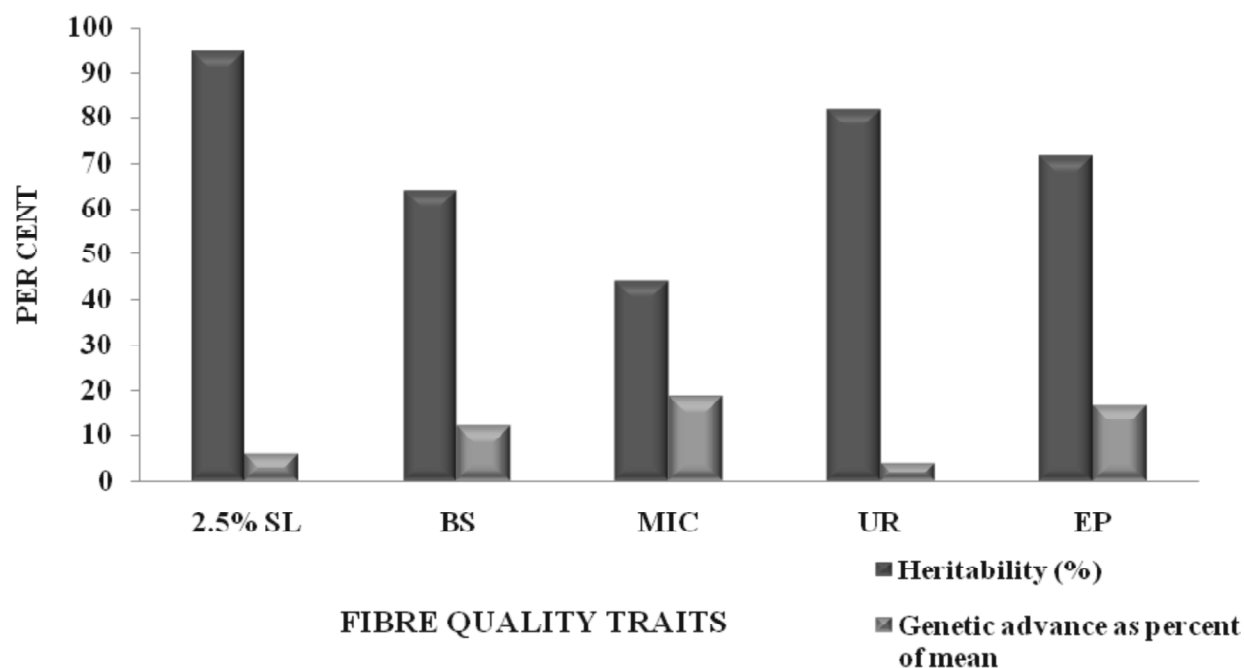**Figure 1: PCV and GCV estimates for fibre quality traits**

Figure 2: Heritability and genetic advance as percentage of mean for fibre quality traits

showed moderate estimates of phenotypic and genotypic coefficients of variation indicating diversity among the material studied depicting the possibility of improvement in the quality by further selection in segregating generations. Similar results were also reported by Dheva and Potdukhe (2002) for micronaire value, Kumari and Subbaramamma (2006) for 2.5% span length, and Santoshkumar *et al.* (2012) for elongation per cent. Low values of genotypic and phenotypic coefficients of variation were observed for bundle strength (9.49; 7.58) and uniformity ratio (6.02; 5.44) indicating narrow range of variability for these traits thereby restricting the scope for selection. These results are in agreement with the findings of Vinodhana *et al.* (2013) and Dhivya *et al.* (2014).

The heritability estimates were high for 2.5% span length (94.38), bundle strength (63.78), uniformity ratio (81.58) and elongation per cent (71.43). These results are in agreement with the results reported by Preetha and Raveendran (2007), Venkatesan (2008), Santoshkumar *et al.* (2012), Dinakaran *et al.* (2012) and Erande *et al.* (2014). High level of heritability for fibre quality traits revealed that these traits are amenable for QTL analysis, since they are not much affected by environment (Paterson *et al.*, 2003). Moderate heritability value was observed for micronaire value (43.75). Neelam and Potdukhe (2002) and Prasad *et al.* (2005) have also reported

similar results in their studies. High heritability denotes the amenability of the traits in selection process. Johnson *et al.* (1955) indicated that high values of heritability is not always an indication of high genetic gain. If heritability is mainly due to non-additive gene effect, the expected genetic advance would be low, and if there is additive gene effect, a high genetic advance may be expected (Panse, 1957).

Moderate heritability coupled with moderate genetic advance was observed for micronaire value (43.75; 18.56) indicating the operation of both additive and non-additive gene action in the inheritance of this trait (Table 2 and Fig. 2). The present findings are in agreement with the results reported by Rao and Reddy (2001) and Prasad *et al.* (2005). Estimates of high heritability and moderate genetic advance were observed for bundle strength (63.78; 11.83) and elongation per cent (71.43; 16.48). Similar results were reported by Dinakaran *et al.* (2012) and Santoshkumar *et al.* (2012) for elongation per cent. High heritability coupled with low genetic advance was observed for 2.5% span length (94.38; 5.91) and uniformity ratio (81.58; 3.99). This suggests that these characters were under the control of non-additive gene action and heterosis breeding can be resorted for improving these characters. The reports of Santoshkumar *et al.* (2012) for 2.5% span length and Preetha and Raveendran (2007) and Venkatesan

(2008) for uniformity ratio were also in accordance with the results obtained in the present study. Taking into consideration the amount of variability, heritability and genetic advance as per cent of mean in the present study, it may be concluded that selection would be effective in cotton for 2.5% span length, uniformity ratio and elongation per cent for developing superior fibre quality cotton varieties.

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