RESEARCH PAPER

Analysis of Fibre Quality in a *Gossypium Hirsutum* × *G. Barbadense* Backcross Introgression Population

S. M. PALVE[1*], P. K. MANDHYAN[2], V. N. WAGHMARE[3] and N. KATE[4]

[1]*Principal Scientist*, [3]*Head & Director*, [4]*Assistant Chief Technical Officer*,
Division of Crop Improvement, ICAR - Central Institute for Cotton Research (CICR), Nagpur-440 010. INDIA
[2]*Principal Scientist, ICAR - Central Institute for Research on Cotton Technology (CIRCOT),*
Adenwala Road, Matunga, Mumbai - 400019, INDIA

Abstract

Attempts to introgress genes from *G. barbadense* into upland cotton have resulted in achieving stable introgression of fibre quality traits and disease resistance in the background of upland cotton. For the present study, F_1 generated crossing Suraj (*G. hirsutum*) as the recipient parent and Suvin (*G. barbadense*) as the donor parent in 2013. The F1 (Suraj × Suvin) was backcrossed to Suraj to produce BC_1F_1 population during 2014. In 2018 data was collected on 19 BC_1F_4 progenies for fibre quality traits i. e. Nep (count/g), SCn(count/g), L (w) mm, L (n) mm and SFC (n) using Advanced Fibre Information Sysem (AFIS) with the objective of selecting lines with least negatively related traits values for further use in cotton breeding. Five BC_1F_4 progenies namely, SPS36-94, SPS37-94, SPS41-94, SPS46-31 and SPS 49-31 were identified as promising for all the fibre quality traits combining lower mean values of nep (cnt/g), seed coat nep (cnt/g) short fibre content by number (%<12.7mm) and higher values of length by weight (mm), length by number (mm) and upper quartile length by weight (mm). The results of present study indicate that release of abundant genetic variation in fibre quality traits in the BC_1F_4 progenies produced by backcrossing and continuous self-pollination.

Keywords : Advance fibre Information System, back crosses, cotton, correlations, fibre quality traits, *G. barbadense,* introgression progenies, yield components, upland cotton,

*For Correspondence : E-mail : smpalve@gmail.com

Introduction

Cotton (*Gossypium* spp.) is one of the most important cash crops and resource for the textile industry world wide. In India, upland cotton (*G. hirsutum* L.) occupies majority of areas over 95 % under cultivation. *G. barbadense* L. (Sea island, Egyptian or Pima cotton) possesses excellent fibre quality traits and used as the donor for fire quality improvement of upland cotton (*G. hirsutum* L.). However, this cotton has relatively limited adaptability and low yield thus occupies insignificant area (< 1%) particularly in Southern States of India.

Attempts to incorporate genes from *G. barbadense* into upland cotton have resulted in achieving stable introgression fibre properties and disease resistance. Species Polycross (SP) and John Cotton (JC) were initiated by U. S. Cotton breeders during 1960s and 1970s by attempting crosses between wild tetraploid species and cultivars of *G. hirsutum*. SP germplasm population was derived from multiple crosses among twelve cotton cultivars and strains of four tetraploid species, i. e. *G. barbadense L., G. Tomentosum Nutt., G. Mustelinum* Watt., and *G. Darwinii* Watt. JC germplasm population was resulted from multiple crosses between Acala 1517 type cultivars and *G. barbadense*. Both these germplasms underwent multiple generations of random mating and selfing. The uniqueness of the Acala cotton has been attributed to its unique breeding history in which germplasm from *G. barbadense* and a three species hybrid (ATH, *G. arboreum* × *G. Thurberi* × *G. hirsutum*) had been introgressed (Smith and Cothren, 1999). Interspecific introgression has also contributed significantly to the development of high quality of Pee Dee germplasm lines (May, 2001). The Pee Dee germplasms involved multiple introgressions from the Triple Hybrid, *G. barbadense* and Acalas using multiple breeding methods involving random mating, backcrossing and composite crossing in addition to pedigree selection. The sealand 542 and 883 cultivars developed from a interspecific cross between the *G. barbadense* cultivar "Bleak Hall" and the upland cotton cultivar "Coker Wilds" (Culp and Harrell 1974; Bowman *et al.,* 2006) at the USDA-ARS Pee Dee Experiment station in the 1930s.

Phylogenetic analyses of both nuclear and cytoplasmic DNA sequences indicate that *G. hirsutum* and *G. barbadense*

are closely related (Small and Wendel, 1999) and these species cross easily to yield hybrids that show normal meiosis and produce fertile progeny. Inspite of difficulties like hybrid breakdown (Stephens, 1949; Dai *et al.*, 2016), distorted genetic segregation in early (Reinisch *et al.,* 1994) and advanced generations (Jiang *et al.,* 2000), linkage drag, a high level of epistasis between fibre quality quantitative trait loci (QTLs) and genetic backgrounds harbouring different unlinked introgressed alleles (Chee *et al.* 2005a, 2005b) in interspecific gene transfer between *G. hirustum* and *G. barbadense,* significant achievements have been achieved. Introgression is widely acknowledged as a potential source of valuable genetic variation, and growing efforts were invested in analysis of interspecific crosses conferring transgressive variation (Lacape *et al.,* 2005). Recent example of success in introgression breeding is release of RMBUP - 4, a random mated barbadense Upland population. RMBUP - 4 derived from crosses between 18 Upland chromosome segment introgression lines (CSL) each containing a Pima chromosome or an arm and three Upland cotton cultivars, followed by random mating for five cycles (Jenkins *et al.,* 2013). Yu *et al.* (2013) reported the development of backcross inbred lines (BIL) population through two generation of backcrossing followed by several generations of self-pollination. Repeated self-pollination minimized hybrid breakdown and stabilized the chromosome segments transferred from *G. barbadense* to Upland cotton. MD 10-5 is a multi-parent advanced generation inter-cross population, derived from a random mated Barbadense Upland population (Zeng *et al.,* 2016). MBI 19915 chromo some segment introgressed line with excellent fibre quality selected from the $BC_5 F_{3:5}$ of an interspecific cross between *Gossypium hirsutum* and *G. barbadense* (Song *et al.,* 2017). New Mexico introgrssion lines (Multi-parent advanced generation intercross designated as New Mexico Introgrssion lines) (Martinez et al., 2018) were released for resistance to Verticillium wilt. GA R01-40-08, a germplasm line derived from the cross of 'Tamcot 2111' (*G. hirsutum*) with 'Pima S-6' (*G. barbadense* L) provides an improved source of fibre length (Brown *et al.,* 2019).

In India, a remarkable success has been achieved in improvement of fibre quality, particularly fibre length and strength of upland cotton. MCU 5 is the first extra-long stable variety of *G. hirsutum* derived from multiple crosses involving *G. barbadense* (Sea Island) as one of the parents. The objective of the present study was to minimize effects of hybrid breakdown and segregation distortions in later generations by using conventional backcross breeding, three-way and multiple crosses with subsequent self-pollination for the development of desirable introgression lines of *G. hirsutum.* With the modernization of Indian textile industry, higher quality cotton specially high fibre strength is desired. Therefore, efforts were made to select interspecific introgressed lines in the background of upland cotton having better fibre properties suiting

to industries requirements and also as source material for future breeding programme. BC_1F_4 introgrssion progenies were evaluated for fibre properties using Advanced Fibre Information System (AFIS) with the objective of selecting materials for further cotton genetics and breeding.

Materials and methods

The F_1 was made using Suraj as the recipient parent and Suvin as the donor parent in 2013-14. The F_1 (Suraj × Suvin) was then backcrossed to Suraj to produce BC1F1 population during 2014. In 2015, BC_1F_1 population was grown and self-pollinated. In subsequent years, selected single plant selection progenies were continuous self-pollinated. In 2018 data was collected on 201 BC_1F_4 individual single plant selections from 19 progenies. The field experiment was conducted with 19 BC_1F_4 families of 4-14 plants per family and tested for yield components and fibre properties. Non-replicated 19 BC_1F_4 progenies were planted with two checks Suraj and Suvin in each block. The length of each plot was 4.5 m with two rows spaced 0.6 m apart. Recommended package of practices were followed for raising a crop under irrigation at ICAR-Central Institute for Cotton Research, Nagpur.

There is little information available on Advanced Fiber Information System (AFIS) data and the benefits of using it in breeding programmes. The AFIS test provides several length parameters deduced from individual fibre measurements. The length is measured based on single fibres in order to get a true fibre length distribution within a cotton sample. The "by number" distribution shows the true fibre length distribution in the sample. The "by weight" distribution is based on the weight of the fibres and is always biased towards the longer fibres since the longer fibres weigh more than the short fibres. Upper quartile length is equivalent to the classer's staple. AFIS neps count (cnt/g) is the total sum of fibre neps and seed coat neps per gram of fibres. Neps are small entanglements of cotton fibre and can be classified as either biological or mechanical neps. Bulk lint obtained from hand-harvested open bolls from the 19 BC_1F_4 families used to analyse data by the AFIS, Zellweger Uster, instrument in the fiber testing laboratory at the ICAR-Central Institute for Research on Cotton Technology, Mumbai, India. Six fibre quality traits were measured including mean length by weight (Lw), length by number (Ln), upper quartile length by weight (UQLw), short fiber content by number SFC(n), nep count per gram Nep (Cnt/g) and seed coat nep count per gram SCN (Cnt/g). SFC is the percentage by number or weight of fibres less than 0.5 inches (12.7mm). SFC is an important quality parameter that negatively impacts yarn quality and finished products. WASP 2.0 (Web Based Agricultural Statistics Software Package) was used for the descriptive statistical analysis and correlation analysis of among fibre quality traits for the BC_1F_4 lines.

Results and Discussion

The results of the descriptive statistical analysis of fibre quality traits, Nep (cnt/g), SCn (cnt/g), L(w) mm, UQL (w) mm, L (n) mm and SFC (n) are shown in **Table 1**. The average value 55.79 nep (cnt/g) of BC_1F_4 progenies was lower than those of the recipient parent Suraj (130 cnt/g) and donor parent Suvin (63 cnt/g). Eleven BC_1F_4 progenies had lower mean values of nep (cnt/g) than the both the parents. Among 19 progenies, SPS41-94 had lowest value of 27 nep (cnt/g) followed by SPS36-94 and SPS 37-94 (35 nep cnt/g) and SPS50-31(37 nep cnt/g). Neps are small fiber entanglements

that are formed during cultivation, harvesting, and ginning. It causes imperfection of yarn and fabric. For SCN (cnt/g), contrasting phenotypic differences were observed between parents Suraj and Suvin. Suvin had lowest value of 1 SCN (cnt/g) while Suraj had value of 17 SCN (cnt/g).

Average value of the BC_1F_4 progeny was 7.53 Scn (cnt/g). Among progenies, SPS41-94 had lowest value of zero (cnt/g) followed by SPS44-31 (1 SCN cnt/g) and SPS36-94, SPS37-94, SPS40-94 with 2 SCn (cnt/g). It is interesting to note that all the 19 BC_1F_4 progenies had lower mean values of SCN (cnt/g) than the recipient parent,

Table 1: Mean data 32-50 single plant selection progenies bulk (2018-19)

SPS	Ne Cnt/ g	SCN Cnt/g	Lw mm	Ln mm	UQLw mm	SFC (n) % <12.7mm
32-94	79	6	23.1	18.8	28.2	25.6
33-94	78	15	24.9	20.9	29.8	20.5
34-94	56	8	24.4	20.8	29.0	18.6
35-94	68	9	24.2	20.3	29.0	21.7
36-94	35	2	24.8	20.9	29.3	19.0
37-94	35	2	26.3	22.4	31.1	17.7
38-94	45	7	24.7	20.1	30.4	24.3
39-94	86	10	23.3	18.5	29.0	29.2
40-94	43	2	25.9	21.5	31.0	19.2
41-94	27	0	24.3	20.6	28.7	19.0
42-94	38	9	25.0	20.8	30.2	21.3
43-94	55	14	25.3	21.1	30.4	20.1
44-31	47	1	21.2	17.5	25.8	27.0
45-31	43	6	23.6	19.5	28.4	23.5
46-31	70	8	25.1	20.7	35.2	22.2
47-31	65	12	25.0	21.0	30.0	19.7
48-31	77	14	24.4	20.5	28.8	20.3
49-31	76	15	26.6	22.3	31.8	19.1
50-31	37	3	23.5	20.2	27.7	18.0
SPS M±SD	55.79±18.44	7.53±4.96	24.51±1.24	20.44±1.20	29.67±1.92	21.37±3.20
Min.-Max.	27.0-86.0	0.0-15.0	21.2-26.6.0	17.5-22.4	25.8-35.2	17.7-29.2
Suraj	130	17	26.0	21.1	31.9	23.6
Suvin	63	1	33.3	26.7	41.5	19.1

Suraj. Seed coat fragment is a portion of a cotton seed, usually black or dark brown in color, broken from a mature or immature seed to which fibers and linters may or may not be attached (American Society for Testing and Materials).

The mean values of the BC_1F_4 progenies was close to recurrent parent Suraj for length by weight (Lw), length by number (Ln) and upper quartile length by weight (UQLw). The recipient parent Suraj and BC_1F_4 progenies had value of 26.0, 21.1, 31.9 and 24.51, 20.44, 29.67 for length by weight (Lw), length by number (Ln) and upper quartile length by weight (UQLw), respectively. However, a donor parent Suvin had higher values of 33.3, 26.7, 41.5 for length by weight (Lw), length by number (Ln) and upper quartile length by weight (UQLw), respectively than the recipient parent Suraj and 19 BC_1F_4 progenies. There was a difference of 9.4 (25.8mm-35.2mm) for upper quartile length by weight (UQLw) in introgrssion progenies compared to the recipient parent Suraj indicating generation of variability and positive transgression. SPS46-31 had upper quartile length by weight of 35.2 mm higher than the recipient parent Suraj. SPS37-94 and SPS49-31 had higher values of length by number (mm) and length by weight than the parent Suraj. Chee *et al.* (2005b) observed transgressive segregation in fibre length traits (Lw, Ln, UQLw, SFCn, SFCw) for all the phenotypes in the BC_3F_2 progenies. Kelly *et al.* (2012) used lines with the longest fiber length combined with the lowest short fiber content for further assessment and eventual selection if fiber had a desirable length distribution in F_2 and F_3 generations.

For quality trait short fibre content by number (%, <12.7), BC_1F_4 families had lower average value of 21.37% than the recipient parent Suraj (23.6%), close to the mid-parent value of recipient and donor parent Suvin (19.1%) indicated that introgressed progenies produced cotton with lower quantities of short fibre (less than 12.7 mm). SPS34-94 and SPS50-31 had lowest values of 18.6 and 18.0 short fibre content by number (%12.7), respectively than both the parents. Majority of the progenies i. e. 15 BC_1F_4 progenies had lower values [SFC(n)] than the recipient parent Suraj. Kelly *et al.* (2012) found that improvement in fibre length could effectively be done using either HVI or AFIS data, and that differences in fibre quality improvement were minimal between the two fibre testing methods.

Results of the Pearson's correlation coefficient among different quality traits is presented in **Table 2.** Significant and positive correlations (0.727) were noted between Nep (cnt/g) with SCN (cnt/g). Length by weight (Lw) had significant positive correlation with upper quartile length by weight (UQLw) (0.927) and length by number (Ln) (0.973) while significant negative correlation with short fiber content by number (-0.457). However, Length by number (Ln) also showed significant negative correlation with short fiber content by number (SFCn) (-0.646). Similarly, Ulloa (2006) found number of neps was positively correlated to seed coats neps, and short and immature fibre content, and negatively correlated to mean fibre fineness and maturity ratio in comparison between $F_{2:3}$ and $F_{2:6}$ generations. Cultivars possessing a genetic capacity for

higher fibre quality can build and sustain greater marketability and price. Consequently, the development of cotton cultivars possessing enhanced cotton fibre quality is essential for sustaining long-term cotton production in any region (Bourland, 2015).

BC_1F_4 progenies SPS36-94, SPS37-94, SPS41-94, SPS46-31and SPS49-31 are promising for all the fibre quality traits combining lower mean values of nep (cnt/g), seed coat nep (cnt/g) short fibre content by number (%<12.7mm) and higher values of length by weight (mm), length by number (mm) and upper quartile length by weight (mm). Thus, these results indicate release of abundant genetic variation for fibre quality traits in the BC1F4 progenies produced by backcrossing and continuous self-pollination.

Table 2: Correlations between fibre quality traits

Nep (Cnt/g)	SCN (Cnt/g)	Lw (mm)	UQLw (mm)	Ln (mm)	SFC (n) %<12.7mm
Nep (Cnt/g)	0.727**	0.108	0.199	-0.003	0.386
SCN (Cnt/g)		-0.041	-0.024	-0.059	0.117
Lw (mm)			0.927*	0.973*	-0.457*
UQ Lw (mm)				0.861*	-0.269
Ln (mm)					-0.646**

*, ** = Significant at 0.05% and 0.01% probability levels, respectively.

References

Bourland, F.M. (2015) - Breeding for Improved Cotton Fibre Quality - *Cotton Statistics and News.* No. 52, pp 1-4.

Bowman, D. T., Gutierrez, O. A., Percy, R. G., Calhoun, D. S., May, O. L. (2006) - Pedigrees of upland and pima cotton cultivars released between 1970 and 2005 - *Miss. Agric. Exp. Stn. Bull.,* 1155.

Brown, N., Shen X., Lubbers, E. L., Kumar, P., McBlanchett, J., Smith, C. W., Jones, D., Paterson, A. H. and Chee, P. W. (2019) - Registration of GAR 01-40-08, a *Gossypium hirsutum* Upland Cotton germplasm Line with qFLChr.1 introgressed from *Gossypium barbadense* conferring improved fibre length - *J. Plant Reg.,* **13**:406-410.

Chee, P., Draye, X., Jiang, C. X., Decanini, L., Delmonte, T. A., Bredhauer, R., Smith, C. W. and Paterson, A. H. (2005a) - Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: I. Fiber elongation - *Theor. Appl. Genet.,* **111**:757-763.

Chee, P., Draye, X., Jiang, C. X., Decanini, L., Delmonte, T. A., Bredhauer, R., Smith, C. W. and Paterson, A. H. (2005b) - Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: III. Fiber length -*Theor. Appl. Genet.,* **111**:772-781.

Culp, T. W. and Harrell, D. C. (1974) - Breeding quality cotton at the Pee Dee Experiment Station Florence, SC, USDA-ARS Publ. 30. U. S. Gov. Print Office, Washington, DC.

Dai, B., Guo, H., Huang, C., Zhang, X. and Lin, Z. (2016) - Genomic heterozygosity and hybrid breakdown in cotton (Gossypium): different traits, different effects. *BMC Genetics,* **17**:58 (https://doi10.1186/s12863-016-0366-5).

Jenkins, J. N., McCarty, J. C., Hayes, R., Jones, D. C. (2013) - Registration of RMBUP-C4, a random mated population with *Gossypium hirsutum* L. alleles, introgressed into Upland cotton germplasm - *J. Plant Reg.,* 7:224-228.

Jiang, C. X., Chee, P. W., Draye, X., Morrell, P.L., Smith, C.W. and Paterson, A. H. (2000) - Multilocus interactions restrict gene introgression in interspecific populations of polyploidy *Gossypium* (cotton) - *Evolution,* **54**:798-814.

Kelly, C. M., Hequet E. F. and Dever J. K. (2012) - Interpretation of AFIS and HVI fiber property measurements in breeding for cotton fiber quality improvement - *J. Cotton Science,* **16**:1-16 (http://journal.cotton.org).

Lacape, J. M., Nguyen T. B., Courtois B., Belot, J. L., Giband, M., Gourlot, J. P., Gawryziak, G, Roques, S. and Hau, B. (2005) - QTL analysis of cotton fiber quality using multiple *Gossypium hirsutum × Gossypium barbadense* backcross generations - *Crop Sci.,* **45**:123-140.

Martinez, G., Abdelraheem, A., Darapuneni, M., Jenkins, J. N., McCarty, J. C. and Zhang, J. (2018) - Evaluation of a multi-parent advanced generation intercross (MAGIC) introgressed line population for Verticillium wilt resistance in upland cotton -*Euphytica,* **214**:197 (https://doi.org/10.1007/s10681-018-2278-0).

May, O. L. (2001) - Registration of PD 94045 germplasm line of Upland cotton - *Crop Sci.,* **41**:279-280.

Reinisch, A. J., Dong, J. M., Brubaker, C. L., Stelly, D. M., Wendel, J. F. and Paterson, A. H. (1994) - A detailed RFLP map of cotton, *Gossypium hirsutum × Gossypium barbadense :* Chromosome organization and evolution in a disomic polyploid genome - *Genetics.,* **138**:829-847.

Small, R.L. and Wendel, J. F. (1999) - The mitochondrial genome of allotetraploid cotton (*Gossypium* L.) - J. Heredity, **90**: 251-253.

Smith, C.W. and Cothren, J.T. (1999) - Cotton : Origin, History, Technology and Production. John Wiley & Sons, Inc., New York, NY.

Song W., Wang M., Su W., Lu Q., Xiao X., Cai J., Zhang Z., Li S., Li P., Gong J., Gong W., Shang H., Liu A., Li. J., Chen T., Ge Q., Shi Y., Yuan Y. (2017) - Genetic and phenotypic effects of chromosome segments introgressed from *Gossypium barbadense* into *Gossypium hirsutum. PLoSONE* -**12**: e0184882 *(https://doi.org/ 10.1371/journal.pone.0184882)*

Stephens, S. G. (1949) - The cytogenetics of speciation in *Gossypium* 1. Selective elimination of the donor parent genotype in interspecific backcrosses - *Genetics,* **34**:627-637.

Ulloa, M. (2006) - Heritability and Correlations of Agronomic and Fiber Traits in an Okra-Leaf Upland Cotton Population - *Crop Sci.,* **46**:1508-1514.

WASP 2.0 Web Based Agricultural Statistics Software Package (2018) - ICAR-Research Complex for Goa, Ela, Old Goa, 403402, India.

Yu J., Zhang K., Li S., Yu S., Zhai H., Wu M., Li X., Fan S., Song M., Yang D., Li Y. and Zhang J. (2013) - Mapping quantitative trait loci or lint yield and fibre quality across environments in a *Gossypium hirsutum × Gossypium barbadense* backcross inbred lione population. *Theor. Appl. Genet. -* **126***:275-287 (https://doi:10.1007/s00122-012-1980-x PMID: 23064252)*

Zeng, L., Rex, O. M. and Meredith W. R. (2016) - Registration of cotton germplasm line

---

Cotton Facts: Spinning and Weaving (ICAC, 2003)

- Spinning is the process of making yarn from loose fibers. The most crucial part of spinning is the insertion of twist into a continuous strand of overlap- ping fibers to form a yarn. Twisting is preceded by many operations, such   as carding, drawing, etc., which also form part of the spinning process.

- Cotton was first spun by use of machinery in England in 1730. Developments in spinning machinery in 1730 and saw gins in 1793 paved the way to make cotton the most important natural fiber in the world.