J. Cotton Res. Dev. **35**(2), 173-180 (July, 2021) **ISSN No. 0972-8619**

Genetic variability for seed cotton yield components and fibre quality traits in introgressed populations of interspecific crosses between *Gossypium hirsutum* L. × *G. barbadense* L.

S. M. PALVE*, V. N. WAGHMARE, P. K. MANDHYAN AND N. KATE
Division of Crop Improvement, ICAR-Central Institute for Cotton Research, Nagpur 440010
**Email: smpalve@gmail.com*

ABSTRACT: A backcross inbred populations was developed between cultivated species of *Gossypium hirsutum* and *G. barbadense*. Data on yield components and fibre quality traits was collected on 201 BC_1F_4 individual single plant selections (SPS) of 19 progenies. The results indicated that the average values of introgression lines for all the yield components except boll had higher values than parental genotypes Suraj and Suvin. Thus positive transgression was found in majority of BC_1F_4 families. For ginning percentage, progeny 40-94 had maximum value of 47.2 per cent followed by SPS 47-31 (45.7%). Wide variation was observed for boll weight (2.5 to 8.4g) while SPS 40-94 had maximum variation for seed index ranging from 9.2 to 3.3. The results clearly showed that introgressed lines CNH 20378, CNH 20387, CNH 204710 and CNH 204910 had higher ginning outurn percent compared to the recipient parent Suraj and donor parent Suvin. CNH 204710 demonstrated highest ginning per cent of 43.9, boll weight of 4.8 g, upper half mean length (UHML) of 29.0 mm and fibre strength of 26.4 g/tex. CNH 20378 had ginning percent of 43.4, boll weight of 4.5 g, staple length of 29.4 mm and fibre strength of 28.7 g/tex. Introgressed line CNH 20387 showed ginning percent of 43.4, boll weight of 4.3g, UHML of 28.8 mm and fibre strength of 28.0 g/tex. Introgressed line CNH 204910 had ginning per cent of 43.3, boll weight of 4.6g, UHML of 28.3 mm and fibre strength of 25.8 g/tex. Amongst the introgressed lines, CNH 203111 had highest elongation with value of 6.3 per cent followed by CNH 20338 (6.2%) and CNH 20475 (6.0 %). The identified introgressed lines showed transgression for improved ginning percentage, boll weight and elongation percent. These lines could be used for further improving ginning outturn and lint yield in upland cotton.

Key words: Cotton, ginning outturn, *Gossypium barbadense*, *G. hirsutum*, interspecific crosses, introgression, quality traits

Cotton (*Gossypium* spp.) is an important economic crop worldwide which provides renewable fibres for the textile industry. *G. hirsutum* referred as upland cotton, contributes more than 90 per cent of the global cotton acreage and production. *G. barbadense* L., referred as Pima or Egyptian cotton, accounts for 8 per cent of the cotton production in the world (Shim *et al.*, 2018). *G. barbadense* has superior extra-long, strong and fine fibre properties which make it an ideal choice for providing new genetic variation useful for improving fibre quality in upland cotton.

G. hirsutum and *G. barbadense* are largely inter-fertile and each displays a series of distinctive characteristics in their agronomic performance, adaptability and fibre quality. The transgressive segregants derived from interspecific segregating populations of *G. hirsutum* and *G. barbadense* have different sets of dominant and recessive alleles for the same traits *i.e.*, extremely short to tall plant height, short/cluster to long fruiting branch, bolls to prolific bearer, very early to late maturity, very coarse to fine and shorter and weaker fibres than upland cotton. Application of approaches such as conventional breeding, cytological applications and molecular approaches to incorporate genes form *G. barbadense* into upland cotton has resulted into valuable genetic resources such as chromosome segment substitution lines (Stelly *et al.*, 2005; Peng *et al.*, 2008, Shi *et al.*, 2020), backcross inbred lines (Lacape *et al.*, 2005; Chee *et al.*, 2005a, b; Zhang

2011; Yu *et al.*, 2013), recombinant inbred lines (RILs) and random mating populations derived introgressed lines (Ma and Liu 1982; Cantrell and Davis 2000; Liu *et al.*, 2005; Jenkins *et al.*, 2008, Waghmare *et al.*, 2016). Yu *et al.*, 2013 developed backcross inbred lines (BIL) population through two generation of backcrossing followed by several generations of self-pollination. Zeng *et al.*, 2016 reported that repeated self-pollination minimized hybrid breakdown and stabilized the chromosome segments from G. *barbadense* in Upland cotton. Martinez *et al.*, 2018 reported that New Mexico Introgrssion lines 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) provided an improved source of Upper Half Mean Length (Brown *et al.*, 2019).

In the present investigation, introgressed populations derived from crosses between *G. hirsutum* and *G. barbadense* and backcrosses were evaluated for seed cotton yield components and fibre quality traits. The extent of genetic variability generated and successful identification of promising superior progenies has been discussed.

MATERIALS AND METHODS

A widely adapted *G. hirsutum* var. Suraj and G. *barbadense* var. Suvin were selected for the study. The crosses were made between Suraj as female parent and Suvin as the male parent during 2013-2014 at ICAR-Central Institute for Cotton Research, Nagpur. The F_1 (Suraj × Suvin) was then backcrossed to Suraj to produce BC_1 F_1 population during 2014. In 2015, BC_1 F_1 population was grown and extensively self-pollinated. In the subsequent generations upto BC_1 F_6, continued self-pollination of selected single plant progenies. The field experiment was conducted during 2018-2019 (BC_1 F_4), 2019-2020 (BC_1F_5), and 2020-2021 (BC_1 F_6) at ICAR-CICR, Nagpur wherein 19 BC_1 families of 4-14 plants per family (totalling 201 plants) were tested for yield components and fibre properties. The observations were recorded for plant height (PH), monopodia (MO), sympodial branches (SY), bolls/plant (BN), boll weight (BW), ginning percentage (GOT %) and seed index (SI). At maturity, seed cotton harvested from each line was used for calculating ginning outturn percentage. The lint of individual single plants during 2018-2019 and bulk of progeny rows in 2019-2020 and 2020-2021 was tested for fibre quality traits using High volume instrument (HVI) at ICAR-Central Institute for Research on Cotton Technology, Mumbai. Results of the best performing twenty lines were presented (Table 2). Fibre quality traits included upper half mean length (UHML), uniformity ratio (UR), micronaire value (MV), fibre strength (FS) and elongation percentage (E%). Descriptive statistical parameters, such as mean values, standard deviation and range were computed for each trait. WASP 2.0 (Web Based Agricultural Statistics Software Package) was used for descriptive statistical analysis.

RESULTS AND DISCUSSION

The mean values of seed cotton yield components are presented in Table 1. The results of the descriptive statistical analysis of yield components indicated that the average values of BC_1 F_4 progenies for plant height, monopodia, sympodia, ginning percentage, boll weight and seed index were higher than both the parental varieties Suraj and Suvin. The variation in plant height was highest followed by boll number, ginning percentage, boll weight and seed index. Progeny SPS40-94 had highest range of ginning percent with minimum value of 40.8 per cent and maximum of 47.2 per cent followed by SPS47-31 (39.3-45.7%) as compared to parents Suraj and Suvin with mean values of 35.6 and 31.6 per cent, respectively. For seed index, progeny SPS 41-94 had highest variation for seed index (9.2–13.3). For boll number, SPS 48-31 had wide variation which varied from 13.0 – 32.0. For plant height, it was observed that all the progenies had higher mean plant height than that of parents

Table1. Descriptive statistical analysis of yield components in introgressed progenies

SPS	Parameters	N	PH	MO	SY	BN	GOT	BW	SI
32-94	Mean± SD	10	125.2±6.5	1.8±0.8	19.8±3.4	15.4±4.0	43.9±0.7	5.1±0.5	11.39±0.79
	Min. –Max.		116.0-134.0	1.0-3.0	14.0-22.0	11.0-22.0	29.0-44.8	4.0-8.4	10.1-12.8
33-94	Mean± SD	11	126.4±19.6	1.6±0.6	18.0±2.9	16.4±3.4	43.4±1.4	5.3±0.5	10.83±1.01
	Min. –Max.		104.0-136.0	1.0-2.0	14.0-21.0	13.0-22.0	41.2-45.9	2.5-6.3	8.4-12.3
34-94	Mean± SD	10	136.2±14.6	1.6±1.1	19.2±1.3	16.6±3.9	42.1±0.4	5.2±0.8	11.6±0.53
	Min. –Max.		124.0-160.0	1.0-3.0	18.0-21.0	12.0-21.0	40.4-43.3	4.3-6.4	9.8-12.8
35-94	Mean± SD	13	136.2±14.6	1.6±1.1	19.2±1.3	16.6±3.9	42.4±3.0	4.9±0.8	11.1±1.38
	Min. –Max.		124.0-160.0	1.0-3.0	18.0-21.0	13.0-21.0	37.8-45.2	3.7-6.3	7.1-12.7
36-94	Mean± SD	4	119.0±7.8	2.0±1.2	19.4±1.7	17.0±4.4	42.5±1.6	5.2±0.9	11.6±0.98
	Min. –Max.		111.0-130.0	1.0-4.0	18.0-22.0	12.0-22.0	40.5-44.4	3.8-5.9	10.3-12.4
37-94	Mean± SD	9	119.6±7.9	1.9±1.6	15.7±0.8	15.3±4.9	42.6±1.6	5.1±0.5	11.6±0.94
	Min. –Max.		108.0-127.0	1.0-4.0	15.0-17.0	11.0-25.0	40.2-44.8	4.8-5.9	9.5-12.6
38-94	Mean± SD	10	104.0±10.7	2.0±0.9	14.7±1.2	13.7±4.6	42.8±1.3	5.1±0.3	11.5±0.82
	Min. –Max.		94.0-118.0	1.0-3.0	13.0-16.0	8.0-21.0	40.8-45.4	4.0-5.5	10.0-12.6
39-94	Mean± SD	12	104.6±9.6	1.8±0.5	15.4±3.3	12.0±3.4	41.7±0.8	4.7±0.5	11.36±0.93
	Min. –Max.		91.0-118.0	1.0-2.0	12.0-19.0	8.0-16.0	40.4-43.3	4.0-5.9	9.2-12.4
40-94	Mean± SD	12	109.2±7.7	1.2±1.1	18.4±2.8	14.8±2.2	43.8±2.3	4.8±0.3	10.88±1.17
	Min. –Max.		104.0-121.0	1.0-3.0	15.0-22.0	12.0-17.0	40.8-47.2	4.4-5.9	9.2-13.3
41-94	Mean± SD	12	104.2±10.1	1.8±0.8	15.2±1.6	13.4±2.9	41.9±0.9	5.6±0.2	11.2±0.86
	Min. –Max.		102.0-119.0	1.0-3.0	14.0-18.0	11.0-18.0	40.3-43.9	4.1-5.8	10.0-12.4
42-94	Mean± SD	8	100.8±5.0	2.2±0.8	14.8±1.1	12.6±1.9	43.3±0.9	4.5±0.3	11.13±0.61
	Min. –Max.		96.0-108.0	1.0-3.0	14.0-16.0	11.0-16.0	41.9-44.2	3.9-5.0	10.2-11.8
43-94	Mean± SD	13	106.4±13.4	2.2±0.8	14.4±2.3	13.8±3.3	41.5±0.9	5.3±0.5	11.38±0.67
	Min. –Max.		89.0-125.0	1.0-3.0	12.0-18.0	11.0-19.0	37.9-43.1	4.6-5.9	10.1-12.1
44-31	Mean± SD	10	118.0±16.3	1.2±0.6	18.8±3.5	19.8±5.3	38.3±2.4	3.9±0.5	9.57±0.58
	Min. –Max.		100.0-139.0	1.0-2.0	18.0-27.0	14.0-28.0	35.6-41.4	3.2-5.5	8.4-10.3
45-31	Mean± SD	12	117.8±14.6	1.6±0.9	18.6±3.6	14.2±3.1	42.0±0.8	5.5±0.7	11.7±1.08
	Min. –Max.		104.0-133.0	1.0-3.0	14.0-24.0	11.0-19.0	40.6-43.2	4.3-6.1	9.8-13.9
46-31	Mean± SD	13	112.8±8.1	1.6±1.5	17.4±1.8	16.2±3.3	41.1±0.9	5.6±0.9	11.5±0.62
	Min. –Max.		99.0-118.0	1.0-4.0	15.0-19.0	13.0-20.0	38.2-42.2	2.9-6.4	10.6-13.3
47-31	Mean± SD	13	111.8±8.6	2.0±0.8	16.8±1.6	12.6±2.3	42.4±2.2	5.8±1.3	11.5±0.60
	Min. –Max.		100.0-118.0	1.0-3.0	14.0-19.0	9.0-15.0	39.3-45.7	4.2-7.6	10.3-12.7
48-31	Mean± SD	5	97.0±9.0	2.4±1.1	16.0±1.58	20.0±7.8	39.4±2.8	4.4±0.4	10.08±0.98
	Min. –Max.		93.0-11.0	1.0-4.0	14.0-18.0	13.0-32.0	36.0-42.1	3.9-5.0	8.9-11.2
49-31	Mean± SD	11	119.8±6.8	1.6±0.9	20.8±4.0	16.4±5.1	42.5±1.1	6.7±0.3	11.1±0.88
	Min. –Max.		111.0-126.0	1.0-3.0	16.0-25.0	12.0-25.0	40.0-44.0	4.9-6.5	9.9-13.0
50-31	Mean± SD	13	117.2±11.2	1.8±1.5	17.4±1.3	13.4±3.1	41.9±1.2	5.4±0.6	11.6±0.53
	Min. –Max.		104.0-135.0	0.0-4.0	16.0-18.0	10.0-18.0	38.6-43.5	4.5-6.5	10.3-12.3
Suraj	Mean± SD		94.67±21.21	1.67±0.71	15.00±2.12	21.00±4.24	35.6±1.1	4.7±0.62	10.6±0.39
	Min. –Max.		90.0-100.0	1.0-2.0	14.0-16.0	17.0-27.0	34.0-36.4	3.84-5.27	10.2-11.1
Suvin	Mean± SD		79.00±14.77	1.50±0.55	14.50±2.59	25.00±3.39	31.6±0.4	3.4±0.4	11.19±1.13
	Min.– Max.		64.0-94.0	1.0-2.0	13.0-16.0	5.0-18.0	31.2-32.0	3.0-4.1	9.6-12.5
	Mean ± SDN=201		115.2±14.8	1.8±1.00	17.4±2.92	15.2±4.34	41.88±2.00	5.14±0.81	11.23±0.98
	Range		**72**	**4**	**15**	**24**	**18.2**	**5.9**	**6.8**
	Min-maxN = 201		88.0-160.0	0.0-4.0	12.0-27.0	8.0-32.0	29.0-47.2	2.5-8.4	7.1-13.9

N = Number of individual plants sampled per family; SPS =Single plant selections; SD = Standard deviation; PH = Plant height (cm), MO = Monopodia; SY = Sympodia; BN = Boll Number; GOT = Ginning Outturn percentage; BW = Boll weight (g); SI = Seed index

Suraj and Suvin. Average plant height in progenies ranged from 88.0 to 160 cm. Progeny SPS 34-94 and SPS 35-94 had wide variation of 124.0 – 160.0 cm. Yu *et al.*, (2013) also reported transgressive segregation in backcross inbred lines (BIL) and observed normal distribution in yield and fibre quality traits. Nie *et al.*, (2015) showed that backcross inbred lines (BC_1F_8) had wide variations in plant architecture, seed size, and fuzz colour. Shi *et al.*, (2020) also reported abundant genetic variation in the introgression lines of *Gossypium hirsutum* × *G. barbadense* produced by advanced backcrossing and continuous self-crossing. Kumar *et al.*, (2019) observed continuous variation and transgressive segregation in $F_{2:3}$ and $F_{2:4}$ populations derived from crosses between Seal and population and upland cotton cultivars.

The mean values of twenty best performing introgression lines over three years for ginning outturn percentage, boll weight and two years data for fibre quality traits are given in Table 2. Amongst introgressed lines, CNH 204710 had highest value of 43.9 per cent followed by CNH 20378 and CNH 20387 (43.4%) and CNH 204910 (43.3 %). The donor parent Suvin had ginning outturn of 31.6 per cent. The results showed superiority of introgressed lines over the parents for GOT (%). Percy *et al.*, (2006) identified transgressive segregants in recombinant inbred population for both high and low lint per cent, with approximately 5 per cent of the lines exceeding the high lint pe rcent parent NM 24016. Shi *et al.*, (2008) found that lint percent is controlled by combined additive and dominance effects in hybrid combinations between *G. hirsutum* and *G. barbadense*.

CNH 203311, CNH 20494 and CNH 20495 had highest boll weight of 5.1, 5.0 and 4.8 g, respectively. For upper half mean length, introgrssion line CNH 20414 had highest fibre length of 29.9 mm followed by CNH 20507 (29.7 mm) and CNH 20453 (29.5 mm). Amongst introgressed lines, CNH 20378, CNH 20381 and

Table 2. Mean values of GOT (%), boll weight for 3 years (2018, 2019 and 2020) and fibre quality traits for 2 years (2018, 2019)

Sl. No.	Introgressed line	GOT	BW	UHML	UI (%)	MV	FS	FE
1	CNH 20338	43.0	4.6	29.2	84.5	3.8	27.9	6.2
2	CNH 203311	43.1	5.1	29.2	84.0	3.8	25.6	6.3
3	CNH 203511	42.6	4.0	29.1	84.0	4.0	26.9	6.1
4	CNH 20375	42.8	4.4	28.4	84.0	3.9	26.7	5.5
5	CNH 20378	43.4	4.5	29.5	83.5	4.1	28.6	5.8
6	CNH 20381	43.2	4.7	27.9	83.0	4.0	28.1	5.6
7	CNH 20384	42.7	4.7	29.3	85.0	4.3	28.8	5.6
8	CNH 20387	43.4	4.3	28.8	84.0	4.1	28.0	5.9
9	CNH 20397	43.2	4.3	29.5	85.0	4.4	28.5	5.9
10	CNH 20414	42.5	4.1	29.6	84.0	4.2	26.3	5.7
11	CNH 20421	43.4	4.1	28.9	83.5	4.1	25.6	5.6
12	CNH 20453	42.9	4.5	29.5	83.5	4.1	25.7	5.9
13	CNH 20475	42.4	4.6	29.4	83.5	3.9	27.5	6.0
14	CNH 204710	43.9	4.8	29.1	84.0	4.0	26.5	5.7
15	CNH 20494	42.8	5.0	29.0	84.0	4.2	26.5	5.7
16	CNH 20495	42.8	4.8	29.0	84.0	4.0	27.4	6.0
17	CNH 20498	43.1	4.8	28.8	83.5	4.1	26.9	5.8
18	CNH 204910	43.3	4.6	28.3	84.0	4.4	25.8	5.8
19	CNH 20502	43.0	4.4	29.5	84.5	4.5	26.6	5.6
20	CNH 20507	42.7	4.5	29.8	84.5	4.4	28.8	6.2
21	Suraj	35.9	4.5	31.2	85.5	3.7	27.2	5.5
22	NH 615	36.9	3.7	28.6	84.0	3.7	25.0	5.7
23	Suvin	31.6	2.5	38.4	86.5	3.3	31.4	5.8
	MAX	43.9	5.1	38.4	86.5	4.5	31.4	6.3
	MIN	31.6	2.5	27.9	83.0	3.3	25.0	5.5
	CV	2.3	12.6	2.5	1.2	10.2	6.9	6.0
	CD (p = 0.05)	1.6	0.9	1.5	NS	NS	NS	NS

GOT = Ginning Out Turn; BW = Boll Weight; UHML = Upper Half Mean Length (mm); UI = Uniformity index (%); MV = Micronaire Value (µg/inch); FS = Fiber Strength (g/tex); FE = Fiber Elongation (%)

CNH 20507 had highest fibre strength of 28.7 g/tex followed by CNH 20397 (28.5 g/tex) and CNH 20381 (28.1 g/tex). Introgression lines CNH 20378, CNH 20384, CNH 20397 and CNH 20507 for quality traits of fibre length, fibre strength, uniformity index, micronaire value and ginning outturn percentage were identified as promising lines. Lacape *et al.*, (2010) found that fibre length values in RILs were the most biased towards the G. *hirsutum* parent. Song *et al.*, (2017) reported the transgressive rate of $F_{2:3}$ generation was 53.60 per cent for boll weight, 46.97 per cent for lint percentage and 93.94 per cent for fibre length. Kannan *et al.*, (2011) also obtained high productive interspecific progenies (Gh × Gb) with high fibre strength that ranged from 30.0 to 35.7g/tex in BC_1 F_8 generation. Yu *et al.*, (2013) found improved fibre quality in length, strength, and micronaire than upland cotton. Lacape *et al.*, (2013) observed transgression for reproductive and quality traits among recombinant inbred line (RIL) population derived from an interspecific cross between G. *hirsutum* and G. *barbadense*. Chandnani *et al.* (2018) found transgressive segregation in BC_4 F_1 for all fiber quality traits *i.e.* upper half mean length, fibre strength, elongation, micronaire and uniformity index in both *G. hirsutum* and *G. barbadense* backgrounds.

Micronaire values varied from 3.8 (CNH 20338) to 4.5 (CNH20502) which is within acceptable micronaire range (3.5 to 4.9). Micronaire values less than 3.5 indicate immature fibres that are prone to break, dye poorly and create fibre entanglements (Han *et al.*, 1998). For elongation percentage, CNH 203311 had highest elongation percentage of 6.3 per cent followed by CNH20338 (6.2 %) and CNH 203511 (6.1 %) as compared to the parents Suraj (5.4%) and Suvin (5.7%). These results indicate positive transgression for elongation percent in backcross inbred lines. Fibre elongation which measures the degree of extensibility or elasticity of the fibres before a breaks occurs, are becoming increasingly important (May, 2000). Increase in elongation is associated with the improved yarn strength (Riley 1997). Chee *et al.*, (2005 a, b) reported that the BC_3 F_2 individuals showed a difference of 1.3 ranges between the lowest and highest fibre elongation values which carry only a small portion of the G. *barbadense* genome in an otherwise *G. hirsutum* background. Saha *et al.*, (2017) reported that a chromosome-specific recombinant inbred line (CS-B05shRIL) released on the basis of their improved elongation ranged from 7.37 to 7.84 per cent.

CONCLUSION

A backcross inbred lines developed from interspecific hybridization between *G. hirsutum* and *G. barbadense* were evaluated for yield components and fibre quality traits. The introgressed lines CNH 20378, CNH 20387, CNH 204710 and CNH 204910 were identified for higher ginning outturn per cent. Introgressed lines CNH 20378, CNH 20384, CNH 20397 and CNH 20507 were identified as promising lines for quality traits of fibre length, fibre strength, fibre uniformity, micronaire value and ginning outturn per cent. The identified introgressed lines showed transgression for yield components and quality traits. Thus, the present study demonstrated that these backcross inbred lines could be a resource for further cotton breeding.

REFERENCES

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 Regist.*, **13**: 406-10

.

Cantrell, R. G. and Davis, D. D. 2000. Registration of NM24016, an interspecific-derived cotton genetic stock. *Crop Sci.*, **40**:1208.

Chandnani, R., Kim C., Guo, H., Shehzad, T., Wallace, J. G., He, D., Zhang, Z., Patel, J. D., Adhikari, J., Khanal, S. and Paterson, A. H. 2018. Genetic Analysis of Gossypium fiber quality traits in reciprocal advanced backcross populations. *Plant Genome*, **11**:170057 https://doi:10.3835/plantgenome2017.06.0057

Chee, P., Draye, X., Jiang, C. X., Decanini, L., Delmonte, T. A., Bredhauer, R., Smith, C. W. and Paterson, A. H. 2005(a). Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: I. *Fiber elongation. Theor. Appl. Genet.*, **111**:757-63.

Chee, P., Draye, X., Jiang, C. X., Decanini, L., Delmonte, T. A., Bredhauer, R., Smith, C. W., and Paterson, A. H., 2005(b). Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcross-self approach: III. Fiber length. *Theor. Appl. Genet.*, **111** : 772-81.

Han, Y. J., Lambert, W. E. and Bragg, C. K. 1998. White speck detection on dyed fabric using image analysis. *J. Cotton Sci.* **2**: 91-99.

Jenkins, J. N., McCarty, J. C., Gutierrez, O. A., Hayes, R. W., Bowman, D. T., Watson, C. E. and Jones, D. C. 2008. Registration of RMUP-C5, a random mated population of Upland Cotton germplasm. *J. Plant Regist.*, **2** : 239.

Kannan N., Selvakumar, P., Krishnamoorthy, R., Raja, D., Bhuvaneshwari, M., Subramanian, V. and Ramasami, M. 2011. Introgression of high fibre strength trait to upland cotton using marker assisted selection. In: *World Cotton Research Conference – 6*, Mumbai, pp 17-21.

Kumar, P., Singh, R., Lubbers, E. L., Shen, X., Paterson, A. H., Campbell, B. T., Jones, D. C. and Chee, P. W. 2019. Genetic evaluation of exotic chromatins from two obsolete interspecific introgression lines of upland cotton for fiber quality improvement. *Crop Sci.*, **59**:1-12.

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**:123-40.

Lacape J. M., Gawryziak, G., Cao, T. V., Viot, C., Liewellyn, D., Liu, S., Jacobs, J., Becker, D., Augusto, P., Barroso, V., Assuncao, J. H. D., Palai, O., Georges, S., Jean, J. and Giband, M. 2013. Mapping QTLs for traits related to phenology, morphology and yield components in an inter-specific *Gossypium hirsutum* × *G. barbadense* cotton RIL population. *Field Crops Res.*, **144** : 256-67.

Lacape, J. M., Liewellyn, D., Jacobs, J., Arioli, T., Becker, D., Calhoun, S., Al-Ghazi, Y., Liu, S., Palai, O., Georges, S., Giband, M., Assuncao, H. D., Augusto, P., Barroso, V., Claverie, M., Gawryziak, G., Jean, J., Vialle, M. and Viot, C. 2010. Meta-analysis of cotton fibre quality QTLs across diverse environments in a *Gossypium hirsutum* × G. *barbadense* RIL population. *BMC Plant Biol.*, **10**:132. http://www.biomedcentral.com/1471-2229/10/132.

Liu, J. S., Yang, B. X., Gao, Z. Y., Yang, S. J., Zheng, F., Yan, Y. and Ban, Z. J. 2005. High fiber strength medium and long staple cottons developed by hybridization between Upland and Sea-island cotton. *China Cottons*, **32**:12-14.

Ma, F. Z. and Liu, J. S. 1982. Genetic advances in economic traits of interspecific progenies between *Gossypium hirsutum* and *G. barbadense*. *J. China Agric Univ.*, **8**: 23-32.

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. 2000. Genetic variation or fibre quality. In: Basra A. S. (ed) *Cotton ibers-developmental biology, quality improvement and textile processing. Food products*, New York, pp183-229.

Nie, X., Tu, J., Wang, B., Zhou, X. and Lin, Z. 2015. A BIL population derived from *G. hirsutum* and *G. barbadense* provides a resource for cotton genetics and breeding. *PLoS ONE*, **10**: e0141064. doi:10.1371/journal.pone.0141064.

Percy, R. G., Cantrell, R. G. and Zhang, J. 2006. Genetic variation for agronomic and fiber properties in an introgressed recombinant inbred population of Cotton. *Crop Sci.*, **46**:1311–17.

Peng, W., Zhang, D. Y., Zian, L. U. Q., Zhen, G. W. and Zhen, Z. T. 2008. Development of *Gossypium barbadense* chromosome segment substitution lines in the genetic standard line TM -1 of *Gossypium hirsutum. Chinese Sci. Bull.*, **53**:1512-17.

Saha, S., Jenkins, J. N., McCarty, J. C., Hayes, R. W., Stelly, D. M. and Cambell, B. T. 2017. Four chromosome-specific (*Gossypium barbadense* Chromosome 5sh) Upland cotton RILs with improved elongation. *Jour. Pl. Regi.,* **11**:165-67.

Shi, Y. Z., Liu, A. Y., Li, J. W., Wang, S. F. and Yuan, Y. L. 2008. Heterosis and genetic analysis of boll weight and lint percentage of interspecific hybrid of G. *hirsutum* L. × G. *barbadense* L. *Chinese Agr. Sci. Bull.*, **24**: 139-43.

Shi, Y., Liu, A., Li, J., Zhang, J., Li, S., Zhang, J., Ma, L., He, R., Song, W., Guo, L., Lu, Q., Xiang, X., Gong, W., Gong, J., Ge, Q., Shang, H., Deng, X., Pa, J. and Yuan, Y. 2020. Examining two sets of introgression lines across multiple environments reveals background-independent and stably expressed quantitative trait loci of fiber quality in cotton. *Theor. Appl. Genet.*, 133: 2075-93.

Shim, J, Mangat, P. K. and Angeles-Shim, R. B. 2018. Natural variation in wild *Gossypium* species as a tool to broaden the genetic base of cultivated cotton. *J. Plant Sci. Curr. Res.*, **2**: 005.

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. and Yuan, Y. 2017. Genetic and phenotypic effects of chromosome segments introgressed from *Gossypium barbadense* into *Gossypium hirsutum. PLOS ONE*, **12**: https://doi.org/10.1371/journal.pone.0184882.

Stelly, D. M., Saha, S., Raska, D. A., Jenkins, J. N., McCarty, J. C. and Gutierrez, A. O. 2005. Registration of 14 Upland (*Gossypium hirsutum*) germplasm lines disomic for different *G. barbadense* chromosome or arm substitutions. *Crop Sci.*, **45**: 2663-65.

Waghmare, V. N., Rong, J., Rogers, C.J., Bowers, J. E., Chee, P. W., Gannaway, J. R., Katageri, I. and Paterson, A. H. 2016. Comparative transmission genetics of introgressed chromatin in *Gossypium* (cotton) polyploids. *Ameri. J. Bot.* **103**: 719-29.

WASP 2.0 Web Based Agricultural Statistics Software Package. 2018. *ICAR - Research Complex for Goa*, Ela Old Goa, 403-02, 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 for lint yield and fibre quality across environments in a *Gossypium hirsutum* × *Gossypium barbadense* backcross inbred line population. *Theor. Appl. Genet.*, **126**: 275-87.

Zhang, J. 2011. Twenty-five years of introgression breeding through interspecific hybridization between *Gossypium hirsutum* and *Gossypium barbadense*. *Proc. Beltwide Cotton Conference*, 711-16.

Zeng, L., Rex, O. M. and Meredith W. R. , Jr. 2016. Registration of cotton germplasm line, MD 10-5. J *Plant Regist.*, **10**: 47–50.

Received for publication : February 15, 2021
Accepted for publication : May 19, 2021