J. Farm Sci., 34(2): (126-133) 2021

RESEARCH PAPER

Diverse genetic resource from inter-specific hybridization in cotton *Gossypium* spp.

S. ANJAN GOWDA[1] AND I. S. KATAGERI[2]

[1&2]Department of Genetics and Plant Breeding, College of Agriculture, Dharwad
University of Agricultural Sciences, Dharwad - 580 008, Karnataka, India
[2]E-mail: katageriis@uasd.in

(Received: January, 2021 ; Accepted: June, 2021)

Abstract: The inter specific cotton mapping population (*Gossypium hirsutum* cv DS-28 x *Gossypium barbadense* cv SBYF-425) was evaluated during 2017-18 and 2018-19 at the University of Agricultural Sciences Dharwad. As expected from the interspecific hybridization, higher variability was observed in the advanced generations of the lines. The presence of higher variability was represented by wide range of individuals identified. The range observed was from 7.61-64.84 g/plant of seed cotton yield, 2.04 to 5.89 g of boll weight, 27.83 to 43.61 % of lint percentage, 24.74 to 33.71 mm of upper half mean length, 23.83-33.48 g/tex of fiber strength and 2.92 to 4.63 of micronaire. As the evaluated lines are beyond F_{13} & F_{14} generations, they are genetically stable and uniform. Some of them were having high seed cotton yield with fiber quality (RIL-77, 88, 93 & 133), suitable for spinning yarn above 60's counts and can be released as varieties or they can also be used as parents in developing intra-hirsutum commercial hybrids. There are also lines which were not having combination of desirable traits, but are highly desirable for single traits, such lines could be utilized as donor parents in further breeding programme.

Key words: Cotton, Fiber quality, Genetic resource, Recombinant inbred lines

Introduction

Cotton is a natural gift of the nature to humanity. A part from secondary applications in household textiles, wipes, hygiene/health products, and the automotive industry, it nurtures one of the most essential human requirements, namely clothes. Cotton is grown in 105 countries, with a total export value of $15.62 billion US dollars. Cotton employs about 100 million people, with the cotton-related industry employing another 250 million. (Anon., 2015). Gossypium is a genus with 51 species and eight genomes (A, B, C, D, E, F, G, and K) (Katageri *et al*., 2020). Only four species are cultivated for natural textile fiber worldwide; of these, *Gossypium hirsutum* and *G. barbadense* are tetraploid (2n = 4x = 52) with an AD-genome and are referred to as new world cotton. Old world cotton species *G. arboreum* and *G. herbaceum* have a diploid (2n = 2x = 26) A-genome. Due to its higher yield potentiality with 30-50's counts spin capacity, *G. hirsutum* accounts for 95 percent of total cotton cultivation, while *G. barbadense*, *G. arboreum*, and *G. herbaceum* account for the remaining area of cultivation. *G. barbadense* is known for producing raw cotton with the highest fiber strength and length, as well as the finest fiber fineness; it can be spun up to 60-120's counts yarn, which *G. hirsutum* cannot. *G. barbadense* has only been cultivated in a few parts of Egypt and India due to its low yielding capacity, vulnerability to sucking pests, and sensitivity to moisture stress, but it is the best genetic resource for improving the fiber quality of *G. hirsutum* (Wu *et al*., 2019).

Advances in spinning technology necessitate raw cotton fiber that is longer and stronger. One mm increase in raw cotton fiber length increases yarn strength by 0.816 g/tex, and one g/tex increase in raw cotton boosts yarn strength by 0.51 g/tex (Jackowski and Frydrych, 1999). Many attempts have been made to transfer *G. barbadense*'s superior fiber quality traits to the high-yielding *G. hirsutum* (Lacape *et al*., 2003). *G. hirsutum*, on the other hand, has not completely realized the fiber characteristics of *G. barbadense*. Therefore, in the present study lines developed from interspecific cross following single seed descent method to constitute a mapping population (Choudki *et al*., 2012a: Choudki *et al*., 2012b) were evaluated.

Material and methods

Our mapping population consisted of 220 recombinant inbred lines generated from a cross between Ds-28 (*G. hirsutum*) and SBYF-425 (*G. barbadense*). The female parent DS-28 is an agronomically superior parent with higher boll weight (4.21g), lint percentage (40.06%), and seed cotton yield (33.69g), whereas the SBYF-425 is superior in fiber quality traits such as fiber length (33.13), fiber strength (33.49), optimum fiber finess (3.64), higher uniformity index (89.94), and elongation percentage (6.33%) but has a low seed cotton yield (21.51g). The 220 RILs and checks (DS-28, SBYF-425, MCU-5, Sahana, CNH120MB, and Suraj) were sown in an Augmented design with ten blocks, each block containing twenty-two RILs with no replication and six checks replicated. Evaluations were conducted during Kharif 2018 (F_{13} generation) at the University of Agricultural Sciences, Dharwad's Main Agricultural Research Station, and during Kharif 2019 (F_{14} generation) at the Agricultural Research Station, Dharwad. The length of the bed was 6.1 meters, with a spacing of 0.20 meters between plants and 0.90 meters between rows. The plant height in centimeters (PH), the number of monopodial branches (MON), the number of sympodial branches (SYM), the number of bolls per plant (BN), and the weight of the bolls in grams (BWT) were recorded. To calculate boll weight, twenty fully opened bolls per line were picked and weighed to determine the average boll weight. The 20 bolls and total harvest from each RIL were combined, cleaned to eliminate trash, weighed, and converted to per plant seed cotton yield in gram (SCY) and were subjected to ginning. Lint percentage (LP) was calculated using the formula LP = [(seed cotton weight- seed weight)/ seed cotton weight]*100, seed index in grams (SI) was calculated by weighing 100 seeds and lint index (LI) was calculated using the formula LI= (SI-LP)/(100-LP). For fiber quality data, cleaned 150-200g lint was analyzed in a compact (Statex) high-volume instrument (HVI mode). Fiber length was measured in millimeters (UHML), fiber strength was measured in grammes per tex (FS), fiber fineness was measured in micronaire values (MIC), uniformity ratio (FU), maturity ratio (FM), and elongation percentage (FEL) were recorded.

The DAU test function of the agricolae package in R Studio was used to conduct the statistical analysis of the augmented design. The adjusted mean values were used in downstream analyses such as variability statistics, principal component analysis and correlation analysis. The genotypic variance (GV) was estimated using the formula GV = (RILs

Table 1. Augmented anova for yield, its attributing and fiber quality traits in the *G. hirsutum*cv DS-28 x *G. barbadense* cv SBYF-425 RIL mapping population during 2017-18

	DF	PH	MON	SYM	BN	BWT	SI	LP
Block (Eliminating Treatment effect)	9	142.59*	0.04	15.53***	13.59**	0.44*	0.32	6.65
Treatment (Eliminating Block effect)	225	121.06**	0.36***	7.28**	17.87***	0.36**	0.97***	9.46**
Checks	5	405.95***	0.94***	7.37	45.46***	1.87***	4.87***	56.44***
RILs	219	111.54**	0.37***	8.88***	18.02***	0.33*	0.92***	9.98**
Checks vs RILs	1	780.80***	0.72***	16.12*	5.29	0.04	14.80***	2.2
Error	45	62.44	0.06	3.86	3.55	0.19	0.35	4.64
CV (%)	-	7.9	18.9	17.6	15.7	11.8	6.7	5.6
C.D. @ 5%	-	24.31	0.73	6.04	5.8	1.34	1.82	6.62

	DF	LI	SCY	UHML	FS	MIC	FU	FEL	FM
Block (Eliminating Treatment effect)	9	0.63	163.85**	1.19	5.67**	0.08	23.07	0.04**	0.005
Treatment (Eliminating Block effect)	225	0.83**	199.44***	7.24***	7.64***	0.16***	22.27*	0.07***	0.004**
Checks	5	5.46***	1627.97***	86.19***	118.60***	1.27***	40.33*	0.72***	0.03***
RILs	219	0.81**	171.15***	4.10**	3.75**	0.14***	21.43*	0.05***	0.004**
Checks vs RILs	1	4.34**	324.48*	347.85***	342.98***	0.36*	265.89***	3.4735***	0.001
Error	45	0.38	57.75	2.23	1.7	0.06	12.76	0.02	0
CV (%)	-	11.2	18	5.3	4.9	6.7	4.1	2.2	8
C.D. @ 5%	-	1.9	23.36	4.59	4.02	0.77	10.99	0.39	0.15

PH: Plant height (cm)
MON: Number of monopodial branches
SYM: Number of sympodial branches
BN: Number of bolls per plant
BWT: Boll weight (g)
SCY: Seed cotton yield per plant (g)
LP: Lint percentage:
SI: Seed index (g)
LI: Lint index
FS: Fiber strength (g/tex)
MIC: Micronaire value
FU: Fiber uniformity ratio
FM: Fiber maturity ratio
FEL: Fiber elongation (%)

Table 2. Augmented anova for yield, its attributing and fiber quality traits in the *G. hirsutum*cv DS-28 x *G. barbadense* cv SBYF-425 RIL mapping population during 2018-19

	DF	PH	MON	SYM	BN	BW	SI	LI
Block (Eliminating Treatment effect)	9	376.53**	0.196	4.82	17.89	0.498	0.319	0.256
Treatment (Eliminating Block effect)	225	241.74**	0.515**	4.19**	22.32	0.880**	1.87**	0.698**
Checks	5	169.76	2.74**	9.55**	68.62**	1.65**	3.65**	3.107**
RILs	219	242.13**	0.44**	3.97*	20.10*	0.833**	1.77**	0.635**
Checks vs RILs	1	589.22*	2.61**	19.37**	230.95**	6.44**	12.79**	0.011
Error	45	126.28	0.209	2.35	16.81	0.445	0.39	0.179
CV (%)	-	10.67	19.54	12.26	17.63	17.28	13.96	15
C.D. @ 5%	-	25.26	1.029	3.44	9.21	1.5	1.4	0.952

	DF	LP	SCY	UHML	FS	MIC	UI	FM	FEL
Block (Eliminating Treatment effect)	9	1.76	53601.8	0.00024**	0.00011**	-0.0001**	0.0013**	0.00**	0.00002**
Treatment (Eliminating Block effect)	225	8.22**	52278.1**	5.36**	7.34**	0.142**	8.78**	0.0037**	0.032**
Checks	5	57.26**	2086966.0**	56.92**	92.39**	0.595**	55.23**	0.0279**	0.247**
RILs	219	6.63**	449309.9**	3.60**	4.844**	0.131**	7.10**	0.0030**	0.023**
Checks vs RILs	1	64.19**	7792200.1**	81.91**	45.029**	0.00026**	99.07**	0.0122**	0.688**
Error	45	1.82	232495.5	-0.00008	0.00001	0	-0.00004	0	0
CV (%)	-	7.19	19.93	6.77	7.83	9.95	3.13	9.6	2.81
C.D. @ 5%	-	3.03	1083.89	0.0196	0.0077	0.0023	0.0135	0.0005	0.0027

PH: Plant height (cm)
MON: Number of monopodial branches
SYM: Number of sympodial branches
BN: Number of bolls per plant
BWT: Boll weight (g)
SCY: Seed cotton yield per plant (g)
LP: Lint percentage:
SI: Seed index (g)
LI: Lint index
FS: Fiber strength (g/tex)
MIC: Micronaire value
FU: Fiber uniformity ratio
FM: Fiber maturity ratio
FEL: Fiber elongation (%)

Table 3. Variability and heritability for yield, its component and fiber quality traits, in the *G. hirsutum*cv DS-28 x *G. barbadense* cv SBYF-425 RIL mapping population

	PH	MON	SYM	BN	BWT	SI	LP	LI	SCY	UHML	FS	MIC	FU	FEL	FM
Mean	100.14	0.88	13.95	11.40	3.68	8.68	38.10	5.36	34.81	27.85	27.27	3.89	85.57	5.79	0.65
Minimum	62.16	0.01	7.30	2.90	2.04	5.87	27.83	3.18	7.61	24.74	23.83	2.92	74.29	5.17	0.51
Maximum	137.34	2.60	32.15	30.74	5.89	11.46	43.61	7.60	64.84	33.71	33.48	4.63	95.61	6.47	0.84
h^2	0.49	0.89	0.48	0.67	0.56	0.69	0.52	0.50	0.65	0.59	0.62	0.59	0.38	0.73	0.53
GV	104.53	0.24	4.14	8.47	0.18	0.57	4.07	0.31	79.92	1.46	1.58	0.06	6.08	0.03	0.00
PV	201.49	0.28	8.53	11.34	0.32	0.83	7.78	0.60	121.51	2.77	2.68	0.11	15.66	0.04	0.00
GCV (%)	9.03	51.98	9.62	11.52	8.99	7.58	4.81	8.27	19.82	3.80	3.97	5.63	2.63	2.60	5.04
PCV (%)	12.62	54.42	14.17	14.73	11.77	9.13	6.67	11.65	24.55	5.07	5.09	7.36	4.25	3.04	6.96
ECV (%)	3.58	2.44	4.54	3.21	2.78	1.55	1.86	3.38	4.72	1.26	1.13	1.73	1.62	0.44	1.93
DS-28	89.98	1.21	12.46	9.93	4.21	8.79	40.06	5.90	33.69	29.32	27.86	3.94	85.29	5.83	0.58
SBYF-425	107.03	0.40	12.49	10.50	2.84	8.65	35.97	4.88	21.51	33.13	33.49	3.64	89.84	6.33	0.57
MCU-5	96.15	0.86	13.25	11.07	3.81	9.93	35.78	5.55	30.73	32.10	31.00	3.53	88.99	6.09	0.54
Sahana	100.90	1.13	14.07	11.04	3.94	9.08	40.05	6.08	39.04	27.93	27.51	4.05	86.55	5.86	0.59
CNH120MB	101.55	0.96	14.53	13.62	3.79	9.34	34.89	5.01	47.55	26.79	26.32	4.32	86.90	5.80	0.60
Suraj	97.75	0.88	14.08	10.98	4.15	9.61	38.41	6.01	38.12	30.30	30.15	4.00	87.93	6.05	0.55

PH: Plant height (cm)
BN: Number of bolls per plant
LP: Lint percentage:
FS: Fiber strength (g/tex)
FM: Fiber maturity ratio
MON: Number of monopodial branches
BWT: Boll weight (g)
SI: Seed index (g)
MIC: Micronaire value
FEL: Fiber elongation (%)
SYM: Number of sympodial branches
SCY: Seed cotton yield per plant (g)
LI: Lint index
FU: Fiber uniformity ratio

Table 4. Principal component analysis summary and Eigenvectors for various traits in the mapping population

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14	PC15
PH	-0.02	0.23	-0.35	0.39	-0.29	-0.18	0.17	0.22	0.38	-0.51	0.09	0.25	-0.04	0.01	0.02
MON	0.12	-0.10	-0.27	-0.37	0.09	-0.22	0.78	0.10	0.06	0.27	0.01	0.10	0.08	0.01	0.00
SYM	-0.12	0.15	-0.43	0.24	-0.26	-0.23	-0.23	0.29	-0.41	0.53	0.10	-0.01	0.03	0.03	0.00
BN	-0.02	0.03	-0.42	-0.53	-0.28	0.18	-0.20	-0.34	0.02	-0.09	0.34	0.03	-0.39	0.05	0.01
BWT	0.16	0.28	-0.10	0.30	0.32	0.23	0.30	-0.27	-0.61	-0.22	0.18	0.08	-0.15	0.04	0.00
SI	-0.21	0.42	0.11	0.03	0.00	-0.40	0.02	-0.53	0.14	0.15	-0.04	0.04	0.08	0.01	-0.53
LP	0.35	0.26	0.03	-0.22	0.31	0.10	-0.22	0.50	0.07	0.01	0.11	0.22	-0.14	0.04	-0.52
LI	0.11	0.52	0.11	-0.15	0.27	-0.23	-0.15	-0.03	0.16	0.14	0.04	0.18	-0.05	-0.04	0.67
SCY	0.23	0.27	-0.40	-0.21	0.00	0.15	-0.12	-0.06	-0.06	-0.21	-0.43	-0.30	0.55	-0.04	-0.01
UHML	-0.47	0.13	0.10	-0.23	-0.02	0.02	0.05	0.18	-0.19	-0.17	-0.26	0.16	0.00	0.71	0.04
FS	-0.47	0.15	-0.03	-0.16	0.05	0.07	0.08	0.18	-0.15	-0.09	-0.37	0.07	-0.30	-0.65	-0.04
MIC	0.20	0.36	0.26	0.01	-0.35	0.04	0.23	0.16	0.03	0.05	-0.06	-0.63	-0.37	0.11	0.00
FU	-0.21	0.18	-0.16	0.24	0.10	0.68	0.11	-0.06	0.41	0.41	-0.06	0.06	0.01	0.10	0.00
FEL	-0.41	0.17	0.10	-0.13	0.10	0.08	0.07	0.20	0.00	-0.13	0.65	-0.31	0.41	-0.14	0.00
FM	0.16	0.18	0.37	-0.12	-0.58	0.26	0.11	-0.01	-0.19	0.07	0.04	0.46	0.30	-0.16	0.01
Standard deviation	1.79	1.63	1.30	1.14	1.03	0.96	0.92	0.84	0.81	0.76	0.68	0.64	0.61	0.33	0.06
Proportion of Variance	0.21	0.18	0.11	0.09	0.07	0.06	0.06	0.05	0.04	0.04	0.03	0.03	0.02	0.01	0.00
Cumulative Proportion	0.21	0.39	0.50	0.59	0.66	0.72	0.78	0.83	0.87	0.91	0.94	0.97	0.99	1.00	1.00

PH: Plant height (cm)
BN: Number of bolls per plant
LP: Lint percentage:
FS: Fiber strength (g/tex)
FM: Fiber maturity ratio
MON: Number of monopodial branches
BWT: Boll weight (g)
SI: Seed index (g)
MIC: Micronaire value
FEL: Fiber elongation (%)
SYM: Number of sympodial branches
SCY: Seed cotton yield per plant (g)
LI: Lint index
FU: Fiber uniformity ratio

Mean sum of squares – Error Mean sum of squares). Then, using the formula PV=(GV + Error Mean Sum of Squares), the phenotypic variance (PV) is estimated. The ratio of GV and PV is used to calculate broad sense heritability. The coefficient of variability is computed using formula, CV = (standard deviation / mean) *100. The prcomp function was used to perform principal component analysis (PCA), and the biplot function was used to plot PC1 *vs* PC2, ward's D^2 analysis was performed using the dist and hclust functions, and the biplot of PC1 *vs* PC2 was merged with clustering using the ggplot2 package. The corrplot package in RStudio was used to conduct correlation analysis, and all non-significant correlations at the 0.05 level of significance were cross-marked in the correlation plot.

Results and discussion

Cotton breeders in India and around the world have been attempting to convert medium-staple *G. hirsutum* into extra-long-staple cotton for at least 40 years, but with only partial success with inter-specific hybrid cultivars like Varalaxmi (Katarki 1972) and many hybrids flooding the market now. MCU 5, a long-staple cotton variety developed from an interspecific cross involving *G. barbadense*, is still being cultivated in India. However, due to preferential elimination of *barbadense* alleles and reversion to *hirsutum* alleles at the end of F_6 and subsequent generations, the maximum potential of *G. barbadense* has yet to be realized in *G. hirsutum* (Gore*, et al.* 2014; Reinisch *et al.,* 1994; Zhang and Percy 2007). So the, targeted/precise introgression of *barbadense* chromosomal segments into *hirsutum* is needed and marker-assisted selection is being considered as a potential technique for precise introgression. However, to map the responsible genomic targets/quantitative trait loci, there is a need for good quality mapping population with high variability of target trait. Cotton fiber quality traits are mapped using both interspecific (*G. hirsutum* x *G. barbadense*) and intraspecific (*G. hirsutum* x *G. hirsutum* and/or *G. barbadense* x *G. barbadense*) populations. The goal of creating an interspecific mapping population between *G. hirsutum* and *G. barbadense* species is for realizing a greater number of polymorphic markers to get a saturated linkage map and to realize high phenotypic variability in the population (Katageri *et al.,* 1989, Soregoan *et al.,* 2006 and 2007, Choukadi *et al.*, 2012a, Choukadi *et al.,* 2012b). Therefore, the RIL mapping population developed from interspecific hybridization was evaluated.

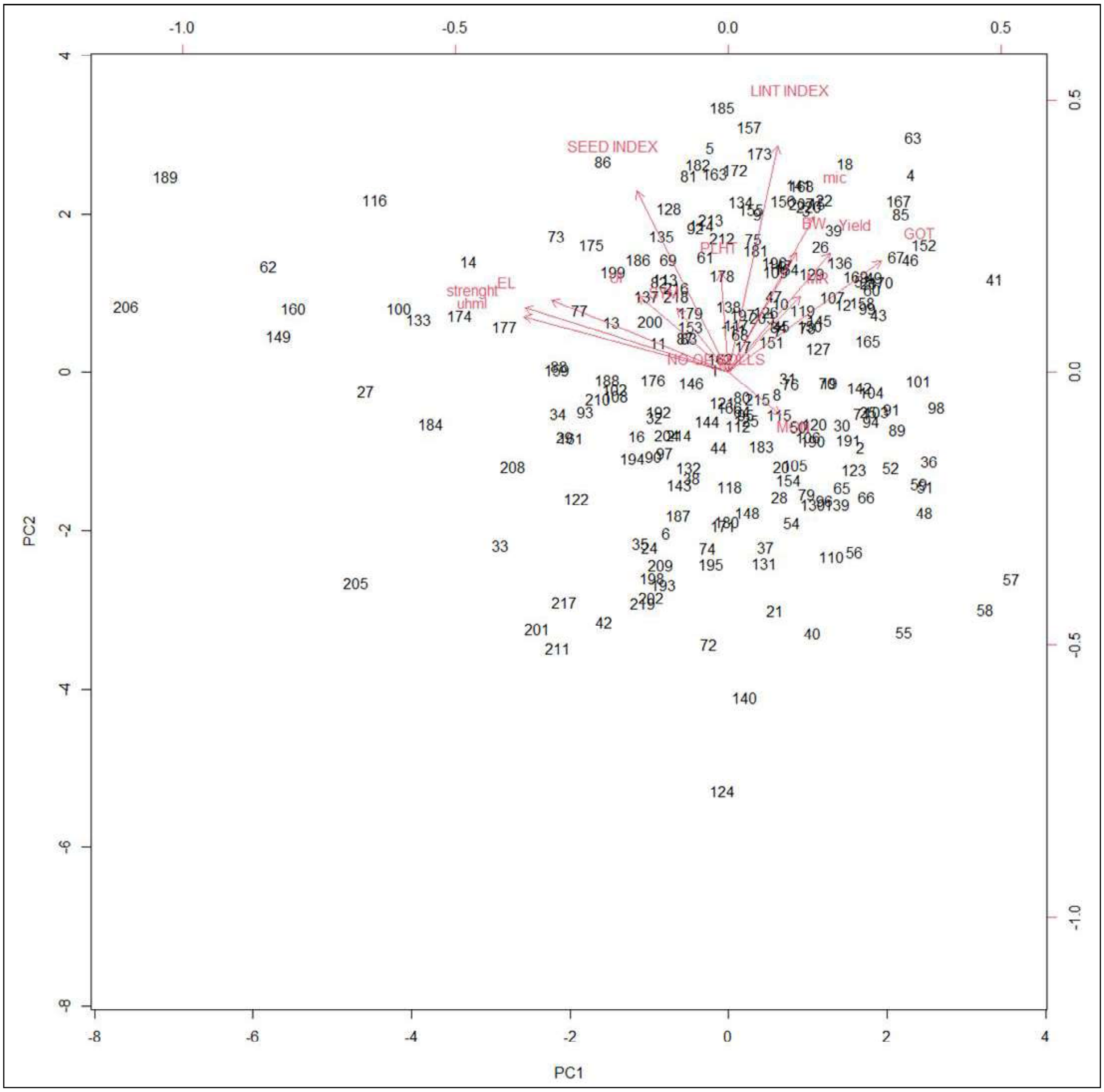

Fig. 1. Scatter plot of PC1 Vs PC2 for various traits under study in the *G. hirsutum* cv DS-28 x *G. barbadense* cv SBYF 425 RIL mapping population

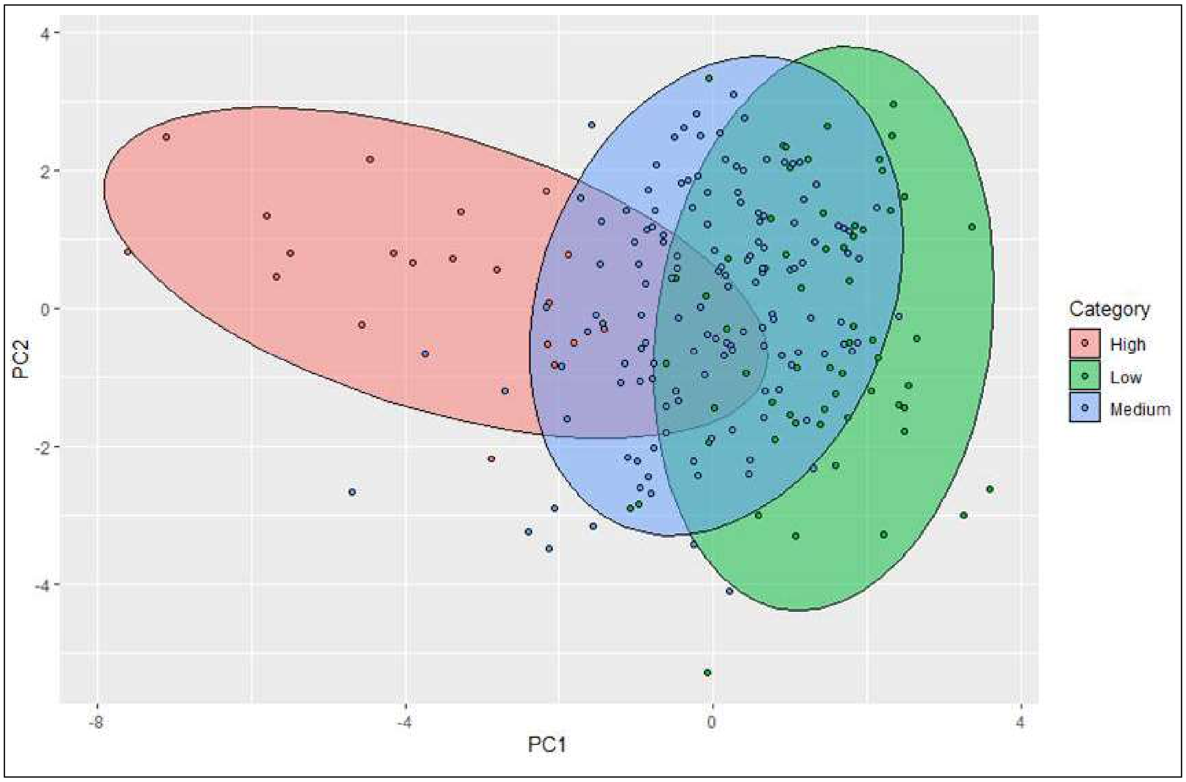

Fig. 2. Biplot of PC1 Vs PC2 with super imposed clusters for various traits under study in the *G. hirsutum* cv DS-28 x *G. barbadense* cv SBYF-425 RIL mapping population

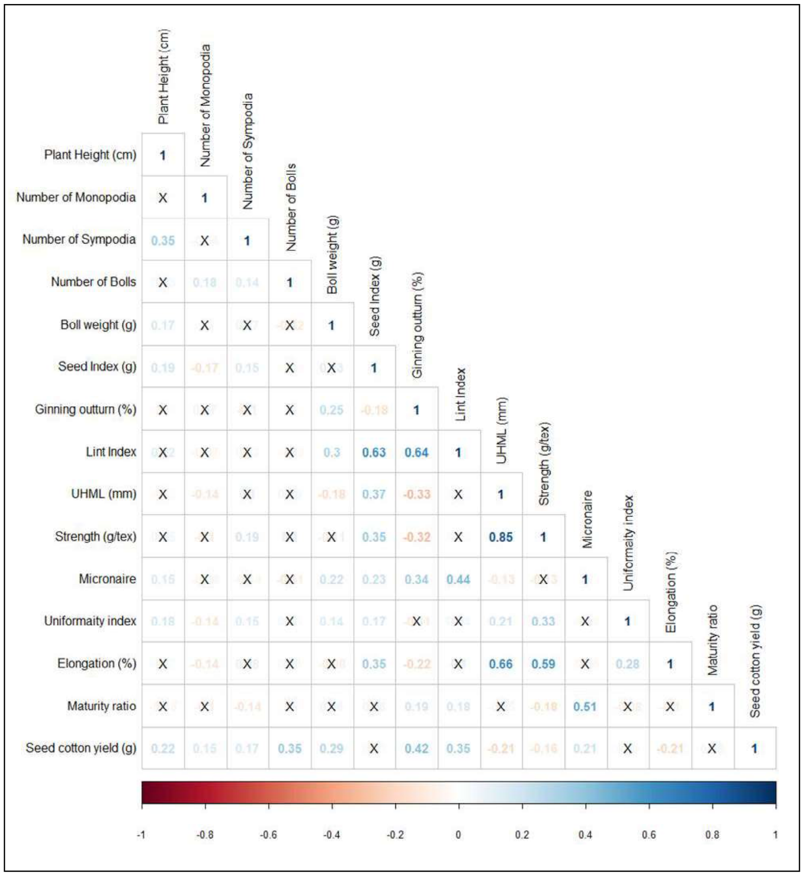

Fig. 3. Correlation analysis between various traits under study in the *G. hirsutum* cv DS-28 x *G. barbadense* cv SBYF-425 RIL mapping population

The augmented ANOVA of two years *i.e.,* 2017-18 and 2018-19 indicates that all the traits were differing significant at least at 0.05 level of confidence in the RILs. The coefficient of variation for all the traits was less than 20% (Table 1 & 2) indicates the less influence of other factors on the experiment. The range for the mean of two-season data indicates that the fiber quality traits such as UHML (24.74-33.71 mm), FS (23.55-33.75 g/tex), Mic. (2.92-4.63), FU (74.29-95.61) and FEL (5.17-6.47) had very high variability. The core important yield attributing traits such as BWT (2.04-5.89 g), BN (2.90-30.74) and LP (27.83-43.91 %) along with the SCY (7.61-64.44 g) had high variability (Table 3). Traits such as MON (0.89), BN (0.67), SI (0.69), SCY (0.65), FS (0.62) and FEL (0.73) showed high broad sense heritability (>60%). However, moderate broad-sense heritability (30-60%) was noted for traits such as PH (0.49), SYM (0.48), BWT (0.56), LP (0.52), LI (0.50), UHML (0.59), MIC (0.59), FU (0.38) and FM (0.53) (Table 3). The PCA analysis showed that six components out of 15 had a standard deviation of one and above with a cumulative proportion of 72%. PC_1 explained 21 % of the total variation, the major contribution *i.e.,* Major Eigenvectors in the PC_1 were UHML (-0.47), FS (-0.47) and FEL (-0.41). The major Eigenvectors in PC_2 were SI (0.42) and LI (0.52) (Table 4). The scatter biplot of PC_1 vs PC_2 depicts

Table 5. Best performing RIL in two seasons for yield, its component and fiber quality traits, in the *G. hirsutum* cv DS-28 x *G. barbadense* cv SBYF-425 RIL mapping population

	MON-1	MON-2	MON-M	BWT-1	BWT-2	BWT-M	SCY-1	SCY-2	SCY-M	UHML-1	UHML-2	UHML-M	FS-1	FS-2	FS-M	MIC-1	MIC-2	MIC-M
RILs with superior architectural traits																		
RIL-117	0.23	0.19	0.21	4.08	3.75	3.91	12.19	36.37	24.28	28.08	28.98	28.53	28.54	27.31	27.93	4.08	3.65	3.87
RIL-167	0.22	0.18	0.20	3.79	4.51	4.15	27.26	50.37	38.82	26.71	24.48	25.59	27.17	24.54	25.86	4.24	4.20	4.22
RILs with higher seed cotton yield and fiber quality																		
RIL-77	0.93	1.92	1.42	3.67	3.00	3.34	36.79	33.64	35.21	30.76	32.63	31.69	31.25	31.43	31.34	3.52	3.53	3.52
RIL-88	0.00	1.92	0.96	4.37	5.30	4.84	30.91	65.84	48.37	29.76	31.53	30.64	30.05	31.03	30.54	3.47	3.60	3.53
RIL-93	0.42	0.97	0.69	4.61	4.16	4.39	40.46	31.60	36.03	28.76	32.75	30.75	29.14	29.03	29.09	4.22	3.86	4.04
RIL-133	0.42	1.35	0.89	3.41	3.83	3.62	22.24	53.84	38.04	30.03	31.98	31.00	30.76	29.96	30.36	3.64	3.65	3.65
RILs with higher seed cotton yield																		
RIL-98	0.42	2.57	1.49	3.93	1.86	2.90	38.23	72.60	55.42	27.26	26.25	26.75	28.04	22.83	25.44	4.02	3.33	3.67
RIL-135	0.22	0.95	0.59	4.01	3.83	3.92	40.63	74.44	57.54	28.73	29.18	28.95	29.26	27.26	28.26	4.10	3.68	3.89
RILs with higher fiber quality																		
RIL-149	1.64	0.15	0.90	3.22	3.83	3.53	38.65	23.24	30.94	33.50	34.68	34.09	33.00	32.46	32.73	3.62	3.35	3.48
RIL-189	2.07	0.16	1.12	2.83	2.67	2.75	28.69	36.47	32.58	34.60	34.80	34.70	32.00	34.04	33.02	4.12	3.12	3.62
RIL-206	2.07	0.82	1.45	5.13	2.80	3.96	22.58	27.07	24.83	34.40	34.36	34.38	30.90	32.96	31.93	4.04	3.08	3.56
Checks																		
DS-28	1.19	1.22	1.21	4.65	3.78	4.21	35.80	31.58	33.69	29.86	28.78	29.32	29.93	25.78	27.86	4.00	3.88	3.94
SBYF-425	0.21	0.60	0.40	2.81	2.88	2.84	16.64	26.38	21.51	31.63	34.63	33.13	32.42	34.57	33.49	3.97	3.31	3.64
MCU-5	0.52	1.20	0.86	3.91	3.72	3.81	23.79	37.68	30.73	31.16	33.03	32.10	31.80	30.20	31.00	3.55	3.50	3.53
Sahana	0.71	1.55	1.13	3.92	3.95	3.94	40.53	37.56	39.04	27.21	28.64	27.93	27.54	27.47	27.51	4.20	3.90	4.05
CNH120MB	0.71	1.22	0.96	3.83	3.75	3.79	32.15	62.94	47.55	26.64	26.94	26.79	27.12	25.52	26.32	4.34	4.30	4.32
Suraj	0.62	1.14	0.88	4.16	4.14	4.15	31.75	44.48	38.12	29.34	31.25	30.30	29.88	30.42	30.15	4.00	4.01	4.00
CV	19.54	18.9	-	17.28	11.8	-	19.93	18	-	6.77	5.3	-	7.83	4.9	-	9.95	6.8	-
C.D.@5%	1.029	0.72	-	1.50	1.33	-	19.51	23.36	-	0.019	4.59	-	0.007	4.01	-	0.002	0.76	-

Note: -1 in row one indicates evaluation during 2017-18, -2 indicates evaluation during 2018-19, and -M indicates mean of two seasons.

BWT: Boll weight (g)	SCY: Seed cotton yield per plant (g)	MON: Number of monopodial branches
FS: Fiber strength (g/tex)	MIC: Micronaire value	

the magnitude of variability of each trait *i.e.*, Eigenvector as red lines (Fig. 1). Based on the Eigenvectors of the PC_1, hierarchical clustering was done and genotypes were split into three clusters. Imposing these three clusters in the biplot of PC_1 *vs.* PC_2 distributed the population into three well-defined clusters with the continuous link between the clusters. The cluster in pale red color contains high fiber quality lines, clusters in blue were average fiber quality lines and clusters with green had low fiber quality lines (Fig. 2). The dimensionality reduction through principal component analysis suggested that the population structure is explained by traits such as UHML, FS and FEL by their higher Eigenvalues unlike in many studies wherein the population structure is explained by BWT, BN, SCY, or yield attributing traits (Isong*, et al.,* 2017; Rathinavel 2018), inferring that the population is highly suited for mapping fiber quality traits. Correlation analysis indicated that SCY was positively associated with PH (0.22), MON (0.15), SYM (0.17), BN (0.34), BWT (0.29), LP (0.42), LI (0.35) and FM (0.21) (Fig. 3). However, it was negatively associated with UHML (-0.21), FS (-0.16) and FEL (-0.21). UHML, FS, FU and FEL were positively associated with each other but were all negatively associated with FM and MIC. The correlation studies indicate that the association between the fiber quality traits, yield and yield attributing traits were in close agreement with earlier studies (Wang *et al.,* 2015; Zhang*, et al.,* 2019). UHML and FS were negatively associated with SCY hence the precise introgression of the genomic regions of UHML and FS under the background of high yield line would pave a way for breaking the negative association. The presence of higher heritability (Broad sense) with a wider range for seed cotton yield and fiber traits is useful in the commercial utilization of promising RILs of this population.

Promising Lines

a. Plant architecture

Cotton plants have two branching systems, monopodial and sympodial branches. Monopodial branches mainly arise from the bottom of the plant, grows parallelly to the main branch and generally range from 2-5 per plant. They provide balance to the robustly growing plant under very high management conditions beside monopodial sympodia possessing few fruiting bodies. Due to presence of monopodial branches and high noded sympodial branches, genotypes are not amenable for machine harvesting. Suitable genotypes for machine harvesting are need of the hour, genotypes with zero monopodia and short noded sympodia will be of more use in future. Since in the current study RILs were obtained from a parent with normal branching, another with unimodal sympodia and zero monopodia, RIL-117 & RIL-167 (Table 5) with zero monopodia and short noded sympodia having a compact stature were identified which are highly amenable for high-density planting.

b. Higher seed cotton yield with fiber qualities of long staple cotton

As evident from the current study and from literature that there is a strong significant negative association between fiber quality traits such as UHML, FS and FEL with the SCY. Efforts for breeding genotypes with good fiber quality traits and also higher yield is attempted by cotton breeders from at least 40 years using both conventional and molecular techniques. Only partial success with inter-specific hybrid such as Varalaxmi and hybrid derivatives such as MCU-5 are under current cultivation. In the current study RIL-77, RIL-88 and RIL-133 performed well for both fiber quality traits (UHML>30.64 mm & FS>30.54 g/tex) and seed cotton yield (>35.21 g/plant) (Table 4). These lines were on par with the MCU-5 for fiber quality with 14% higher seed cotton yield. These can be put into extensive multi location testing, since there is potentiality to release them as varieties.

c. RILs superior only for higher seed cotton yield and only high fiber qualities

The RILs with only high seed cotton yield or only high fiber quality can be utilized as donors in introgression breeding programs. These lines can also be used in intra-hirsutum hybrid breeding programme. For seed cotton yield the RIL-98 (55.42g/plant) and RIL-135 (57.54g/plant) out performed, 16% more than best check CNH120MB (47.55g/plant), these RILs can be released as varieties after multilocation testing in larger plots. The RIL-149, RIL-189 and RIL-206 (Table 5) performed well for fiber quality where in the UHML and FS were on par with the superior check SBYF-425, these can be used as donor lines of high fiber quality in introgression breeeding programme.

Conclusion

Interspecific hybridization followed by pedigree method of selection is one of the best methods of generating novel source of genetic material. In this study, lines with higher seed cotton yield and fiber quality suitable for long staple cotton and lines suitable for high density planting were isolated.

References

Anonymous I, 2015, Measuring Sustainability in Cotton Farming Systems: Towards a Guidance Framework. Rome (Accessed 05 July 18).

Choudki V M, Sangannavar P, Savita S G, Khadi B M, Vamadevaiah H M and Katageri I S, 2012b, Genetic improvement of fiber traits in diploid cotton (*G. herbaceum* L.) through interspecific hybridization using *G. barbadense* tetraploid species. *Electronic Journal of Plant Breeding*, 3(1), 686-691

Choudki V M, Sangannavar P, Savita S G, Patil R S, Vamadevaiah H M, Khadi B M and Katageri I S, 2012a, Variability studies in F6 generation recombinant lines of *G. hirsutum* X *G. barbadense* cross. *BIOINFOLET.*, 9(4), 544-553.

Gore M A, Fang D D, Poland J A, Zhang J, Percy R G, Cantrell R G and Lipka A E, 2014, Linkage map construction and quantitative trait locus analysis of agronomic and fiber quality traits in cotton. *The Plant Genome,*7(1): 1-10.

Isong A, Balu P A and Ramakrishnan P, 2017, Association and principal component analysis of yield and its components in cultivated cotton. *Electronic Journal of Plant Breeding,* 8(3): 857-864.

Jackowski T and Frydrych I, 1999, What I learnt in fiber quality: practical experience. Proceedings of the 58th Plenary Meeting of the International Cotton Advisory Committee.

Katageri I S and Kadapa S N, Heterosis and gene action for yield and yield contributing characters in interspecific hybrids (*G. hirsutum* x *G. barbadense*). *Indian Journal of Genetics and Plant Breeding,* 49(1): 107-111, 1989.

Katageri I S, Gowda S A, Prashanth B, Biradar M, Rajeev M and Patil R S, 2021, Prospects for Mole. Breed .in Cotton, Gossypium spp. Plant Breeding - *Current and Future Views*. IntechOpen.

Katarki B, 1972, Varalaxmi hybrid cotton—a valuable import substitute. *Cotton Dev.*

Lacape J M, Gawrysiak G, Cao T V, Viot, C, Llewellyn D, Liu S and de Assunção, J. H., 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 Research*, 144: 256-267.

Nandhini K, Premalatha N, Saraswathi R, Sakthivel N and Kumaravadivel N., 2019, Genetic Studies for Yield and Fiber Quality Related Traits in Upland Cotton (*Gossypium hirsutum* L.) and Identification of Superior Transgressive Segregants. *International Journal of Current Microbiology and Applied Sciences,* 8:1609-1619.

Rathinavel K, 2018, Principal component analysis with quantitative traits in extant cotton varieties (*Gossypium hirsutum* L.) and parental lines for diversity. *Current Agriculture Research Journal,* 6(1): 54.

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* x *Gossypium barbadense*: chromosome organization and evolution in a disomic polyploid genome. *Genetics,* 138(3): 829-847.

Soregaon.C D, Katageri I S, Khadi B M, Narayanan K, Tippeswamy S and Vamadevaiah H M, 2006, Contribution of tetraploid cotton for improving the fiber properties of diploid in Gossypium species, *Journal of Genetics and Breeding.* Vol 60(2):105-118; 2006

Soregaon C D, Veereshgouda R P, Katageri I S and Khadi, B M, 2007, Introgression of fibre traits of *G.barbadense* into *G.hirsutum Indian Journal of Genetics and Plant Breeding*, 67(1); 2007

Wang H, Huang C, Guo H, Li X, Zhao W, Dai B and Lin Z, 2015, QTL mapping for fiber and yield traits in upland cotton under multiple environments. *PloS One,* 10(6): e0130742.

Wu M, Li L, Liu G, Li X, Pei W, Li X and Yu J, 2019, Differentially expressed genes between two groups of backcross inbred lines differing in fiber length developed from Upland× Pima cotton. *Molecular Biology Reports,* 46(1): 1199-1212.

Zhang J and Percy R, 2007, Improving upland cotton by introducing desirable genes from Pima cotton. Paper presented at the *World Cotton Research Conference* - 4, Lubbock, Texas, USA.

Zhang K, Kuraparthy V, Fang H, Zhu L, Sood S and Jones D C, 2019, High-density linkage map construction and QTL analyses for fiber quality, yield and morphological traits using CottonSNP63K array in upland cotton (*Gossypium hirsutum* L.). *BMC* Genom.,20: 889.