

## FINE MAPPING FOR FIBER LENGTH ON CHROMOSOME 1 IN COTTON

Peng W. Chee<sup>1</sup>, Xinlian Shen<sup>1</sup>, Edward L. Lubbers<sup>1</sup>, and Andrew H. Paterson<sup>2</sup>

<sup>1</sup>Crop and Soil Sciences, University of Georgia, Tifton, GA

<sup>2</sup>Plant Genome Mapping Laboratory, University of Georgia, Athens, GA

### Introduction

Cotton is an important cash crop in the world. A long-term challenge facing a cotton breeder is the simultaneous improvement of yield and fiber quality to meet the demands of the cotton producer as well as the textile industry. In the recent years, improvement of cotton fiber quality has been extremely important because of changes in spinning technology. Cotton fiber quality is defined by physical properties. One of the most important aspects of fiber quality is fiber length. Fiber length was the initial property used to assess cotton quality and its suitability for certain end uses. Longer fiber length is desirable for the production of fine yarns and low twist yarns.

The development of DNA markers linked to the fiber quality QTLs would allow cotton breeders to trace this very important trait in early plant-growing stages or early segregating generations. The use of these DNA markers increases the prospect for streamlining the cotton breeding programs to improve fiber quality while maintaining fiber yield. In an earlier study, 24 BC<sub>3</sub>F<sub>2</sub> families were developed from a cross by *Gossypium hirsutum* cv. Tamcot 2111 and *G. barbadense* cv. Pima S6 with three backcrosses to Tamcot 2111. Twenty eight non-overlapping QTLs for fiber length were identified in these families. The fiber length QTL on chromosome 1 was detected in three different families which explained 12-24% of phenotypic variance (PV) (Chee et al, 2005). These results suggest that this fiber length QTL can be expressed stably and have less interaction effect with other loci, making it a valuable target for genetic analysis and also for further application in cotton quality breeding.

### Materials and Methods

In an earlier study, 28 non-overlapping QTLs for fiber length were identified in BC<sub>3</sub>F<sub>2</sub> families developed from a cross by *G. hirsutum* cv. Tamcot 2111 and *G. barbadense* cv. Pima S6. The fiber length QTL on chromosome 1 near RFLP marker A1686a was detected in three different families. In this study, three BC<sub>3</sub>F<sub>2</sub> plants, R01-40, R03-02, and R05-17, with a Pima S-6 introgression in the target region had significantly longer fiber and relatively few non-target background introgressions, were selected to develop three BC<sub>3</sub>F<sub>3</sub> populations to fine map the target fiber length QTL.

Thirty eight SSR markers from chromosome 1 that were based on the cotton genetic linkage maps of Rong et al. (2004), Nguyen et al. (2004), and Han et al. (2005) along with 16 STS markers were selected to genotype three BC<sub>3</sub>F<sub>3</sub> families. Mapping and statistical analysis were performed based on three sets of data from three separate populations and one combined population (combined Pop). Linkage maps were constructed using the MAPMAKER/Exp Version 3.0b Software. QTLs were identified by composite interval mapping (CIM) using Windows QTL Cartographer 2.5.

## Results and Discussion

Composite interval mapping for fiber length on chromosome 1 was carried out based on three separate populations and a combined population from two environments. Figure 1.A shows the log-likelihood (LOD) score plot in the introgression segment. The maximum LOD score was observed between BNL2921 and JESPR56 in all populations. In the combined population, this QTL had a LOD score of 3.7 in the BC<sub>3</sub>F<sub>4</sub> and 4.5 in the BC<sub>3</sub>F<sub>5</sub>, which explained an R<sup>2</sup> of 12.14% in the BC<sub>3</sub>F<sub>4</sub> and 14.48% in the BC<sub>3</sub>F<sub>5</sub>. The allele from long fiber length parent *G. barbadense* can increase fiber length by 0.0179-0.0211 inch.

To more finely map this QTL location, the phenotypic means for different recombinants were compared to recurrent parent Tamcot 2111. Five of the six recombinants which carried any Pima S-6 introgression segments between BNL1350-JESPR56 had significantly longer fiber lengths than that of recurrent parent Tamcot 2111; the sixth recombinant, R03-02-14, was also longer but not significantly longer. One of the recombinants, R05-17-67, only contained PimaS-6/Tamcott 2111 heterozygous segment between BNL2921-JESPR56, but the mean of fiber length was still significantly longer than the recurrent parent Tamcot 2111, thus indicating that this QTL was most likely located in a 1.5 cM interval flanked by BNL2921-JESPR56. This finding was also supported by the phenotype of the recombinant R-5-17-54, with an introgression between BNL1350-NAU422, which was not significantly different from the control Tamcot 2111.

In our original advanced backcross QTL study, a QTL on chromosome 1 associated with fiber length was detected in three BC<sub>3</sub>F<sub>2</sub> families by ANOVA analysis. Here we used three populations derived from three pre-NILs (Near Isogenic Introgression Line) for the target region to confirm the positive phenotypic effect of the *G. barbadense* allele at this QTL. Our experiments verified that this region is strongly associated with fiber length. Composite interval mapping and comparing different recombinants with stable phenotype confirmed the chromosome position of this QTL was located at a 1.5 cM interval flanked by SSR markers BNL2921 and JESPR56.

## References

- Chee P, Draye X, Jiang CX, Decanini L, Delmonte T, Bredhauer R, Smith CW, Paterson AH (2005) 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
- Han ZG, Guo WZ, Song XL, Zhang TZ (2004) EST-derived microsatellites from diploid A-genome *Gossypium arboreum* and their genetic mapping in AD allotetraploid cotton. *Mol Gen Genet* 272:308-327
- Nguyen TB, Giband M, Brottier P, Risterucci AM, Lacape JM. (2004) Wide coverage of the tetraploid cotton genome using newly developed microsatellite markers. *Theor Appl Genet* 109:167-175
- Rong JK, Abbey C, Bowers JE, Brubaker CL, Chang C, Chee PW, Delmonte TA, Ding X, Garza JJ, Marler BS, Park C, Pierce GJ, Rainey KM, Rastogi VK, Schulze SR, Tronlinde NL, Wendel JF, Wilkins TA, Wing RA, Wright RJ, Zhao X, Zhu L and Paterson AH (2004) A 3347-locus genetic recombination map of sequence-tagged sites reveals features of genome organization, transmission and evolution of cotton (*Gossypium*). *Genetics* 166:389-417.

**Table1.** Phenotype values for fiber length (inch) of parents, original BC<sub>3</sub>F<sub>2</sub> individuals and their BC<sub>3</sub>F<sub>4</sub>/BC<sub>3</sub>F<sub>5</sub> family.

Populations/ parents	Population Size	BC <sub>3</sub> F <sub>4</sub> Family (2004)				BC <sub>3</sub> F <sub>5</sub> family (2005)			
		Max	Min	Mean	Skew	Max	Min	Mean	Skew
R-01	24	1.22	1.06	1.16	-0.56	1.26	1.02	1.16	-0.53
R-03	53	1.19	1.06	1.13	-0.14	1.19	1.06	1.11	0.29
R-05	63	1.21	1.05	1.15	-0.91	1.22	1.07	1.15	-0.26
Combined Pop	140	1.22	1.05	1.14	-0.42	1.26	1.02	1.14	0.04
Pima S-6		1.30				1.33			
Tamcot 2111		1.1				1.12			

\* See Chee et al. 2005

**Table 2.** QTL mapping for fiber length by composite interval mapping

Populations	Year	LOD	Additive	Dominance	R <sup>2</sup>
R01	2004	1.57	-0.0246	0.0001	24.97
	2005	3.11	-0.04098	0.0102	43.06
	Combined year (04/05)	2.75	-0.0332	0.0035	39.27
R03	2004	2.09	-0.0206	0.0059	18.42
	2005	2.04	-0.0208	0.0040	18.07
	Combined year (04/05)	2.75	-0.0210	0.0013	23.53
R05	2004	2.02	-0.0152	0.0029	13.54
	2005	2.24	-0.016	0.0058	14.88
	Combined year (04/05)	2.5	-0.0152	0.0072	16.53
Combined Pop	2004	3.7	-0.0179	0.0023	12.14
	2005	4.5	-0.0211	0.0016	14.48
	Combined year (04/05)	4.2	-0.0181	0.0001	13.30

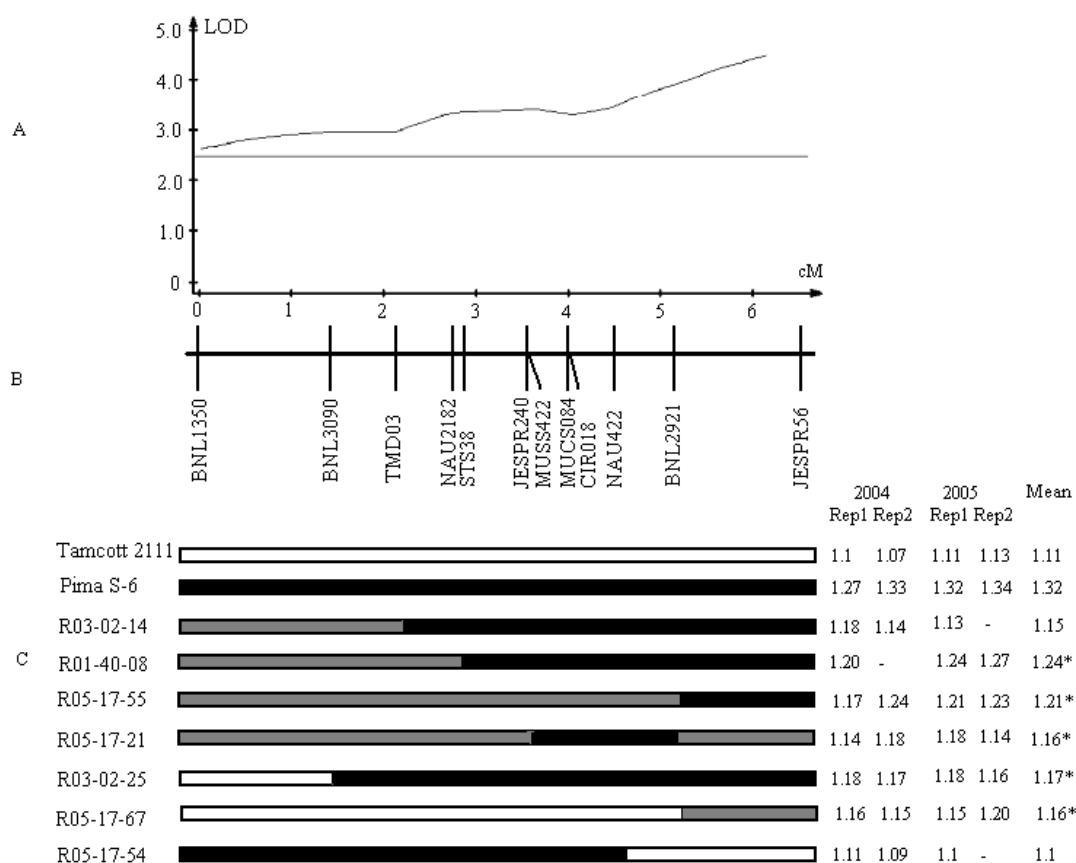


Fig 1 A: Composite interval mapping of fiber length QTL from the combined population in 2005; B: Localized linkage map on chromosome 1; C: Graphical genotypes of recombinant lines and their fiber length (inches). The black, grey, and open boxes indicate homozygous Pima S-6 genotypes, heterozygous genotype and homozygous Tamcot 2111 genotypes. \* indicates significant fiber length differences between recombinants and Tamcot 2111.