IDENTIFICATION OF AN EST-SSR MARKER WITH COMPLETE LINKAGE TO THE LIGON LINTLESS-2 GENETIC LOCUS IN COTTON (*Gossypium hirsutum* L.)

Doug J. Hinchliffe  
USDA-ARS-SRRC  
New Orleans, LA  
Rickie B. Turley  
USDA-ARS-MSA  
Stoneville, MS  
Marina Naoumkina  
Hee Jin Kim  
USDA-ARS-SRRC  
New Orleans, LA  
Yuhong Tang  
The Samuel Roberts Noble Foundation  
Ardmore, OK  
Kathleen M. Yeater  
USDA-ARS-SPA  
Williamsburg, VA  
Ping Li  
David Fang  
USDA-ARS-SRRC  
New Orleans, LA

Abstract

Cotton fiber length is an important quality attribute to the textile industry and longer fibers can be more efficiently spun into yarns to produce superior fabrics. There is typically a negative correlation between yield and fiber quality traits such as length. An understanding of the regulatory mechanisms controlling fiber length can potentially provide a valuable tool for cotton breeders to improve fiber length while maintaining high yields. The cotton (*Gossypium hirsutum* L.) fiber mutation Ligon lintless-2 is controlled by a single dominant gene (*Li2*) that results in significantly shorter fibers than a wild-type. In a near-isogenic state with a wild-type cotton line, *Li2* is a model system with which to study fiber elongation.

Two near-isogenic lines of Ligon lintless-2 (*Li2*) cotton, one mutant and one wild-type, were developed through five generations of backcrosses (BC5). An F2 population was developed from a cross between the two *Li2* near-isogenic lines and used to develop a linkage map of the *Li2* locus on chromosome 18. Five simple sequence repeat (SSR) markers were closely mapped around the *Li2* locus region with two of the markers flanking the *Li2* locus at 0.87 and 0.52 centimorgan. No apparent differences in fiber initiation and early fiber elongation were observed between the mutant ovules and the wild-type ones. Gene expression profiling using microarrays suggested roles of reactive oxygen species (ROS) homeostasis and cytokinin regulation in the *Li2* mutant phenotype. Microarray gene expression data led to successful identification of an EST-SSR marker (NAU3991) that displayed complete linkage to the *Li2* locus on chromosome 18 and resided in a gene with similarity to a putative pectin-related protein. The complete linkage suggests that this expressed sequence may be the *Li2* gene.