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

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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 (Li_2) that results in significantly shorter fibers than a wild-type. In a near-isogenic state with a wild-type cotton line, Li_2 is a model system with which to study fiber elongation.

Two near-isogenic lines of Ligon lintless-2 (Li_2) cotton, one mutant and one wild-type, were developed through five generations of backcrosses (BC_5). An F_2 population was developed from a cross between the two Li_2 near-isogenic lines and used to develop a linkage map of the Li_2 locus on chromosome 18. Five simple sequence repeat (SSR) markers were closely mapped around the Li_2 locus region with two of the markers flanking the Li_2 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 Li_2 mutant phenotype. Microarray gene expression data led to successful identification of an EST-SSR marker (NAU3991) that displayed complete linkage to the Li_2 locus on chromosome 18 and resided in a gene with similarity to a putative plectin-related protein. The complete linkage suggests that this expressed sequence may be the Li_2 gene.