Gossypium herbaceum Negative Mutant for Fiber Elongation a Useful Isoline for Identification of Genes for Fiber Elongation

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Actin cytoskeleton plays an important role in cell morphogenesis in plants as demonstrated by pharmacological, biochemical, and genetic studies. The actin cytoskeleton may be involved in the transportation of organelles and vesicles carrying membranes and cell wall components to the site of cell growth as in root hairs, trichome cells, and pollen tubes. Actins in plants are encoded by a multigene family that comprises dozens or even hundreds of actin genes. In *Arabidopsis*, the actin gene family contains 10 distinct members, of which eight are functional genes and two are pseudo genes. In other plant species, the actin gene family also appears to have dozens of members. Studies on actin sequences revealed that structural and functional divergence occurred within the gene family during evolution. Members of the actin gene family are divergent and differentially expressed during plant development. *Arabidopsis* contains two major actin gene classes: a vegetative class that is expressed predominantly in leaves, stems, roots, petals, and sepals and a reproductive class that is strongly expressed in pollen, ovules, and embryonic tissues. The soybean (*Glycine max*) actin gene family includes at least three divergent classes: m-, k-, and l-actin. The m-actin transcripts are differentially accumulated in leaves, roots, and hypocotyls. The k- and l-actin proteins are preferentially localized in roots. In other plant species, such as rice (*Oryza sativa*) and tobacco (*Nicotiana tabacum*), actin genes also appear to be expressed in a tissue-specific manner. Although actin genes in a few plant species such as *Arabidopsis* have been well characterized, our knowledge of cotton actin genes, especially its role in fiber development, needs to be explored. A unique feature of cotton seed development is that 30% of the ovule epidermal cells initiate into fibers from the outermost layer of integument at anthesis. Each cotton fiber is a single cell and elongates from 10 to 15 mm up to 2.5 to 3.0 cm by 16 days after anthesis (DAA) before it switches to secondary cell wall cellulose synthesis. The rate of fiber elongation and the final length attained are well above that commonly seen for plant cells, and render it perhaps the longest single cell in higher plants. Thus, the cotton fiber represents a unique system in which to study not only carbon partitioning to cellulose synthesis, but also the control of cell elongation without the complication of cell division and multicellular development. Apart from its significance in understanding basic cell biology, elucidating the cellular and molecular basis of fiber elongation could also identify potential targets for genetic manipulation of fiber length, a key determinant of fiber yield and quality. The study on fiber development not only provides the basic understanding of cell differentiation and elongation, but also identifies potential target genes for genetic manipulation of cotton fiber. Here we reported a negative mutant for elongation in *G. herbaceum*. The mutant is normal in flowering and fruiting except it has no elongation. Identification of *G. herbaceum* specific actins is under study with this mutant and its normal isogenic line. Molecular tagging for fiber elongation using F_2 and $F_{2:3}$ also is under progress.