Cloning *GhSCFP* Gene and Its Function in Cotton Fiber Development

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As a major raw material for the textile industry and the most important fiber crop in the world, cotton is of great significance in Chinese economy. The development of cotton fiber can be divided into initiation, elongation, secondary wall synthesis, and maturation stages. The initiation and elongation stages of fiber, which determine the number of fibers on each seed and the final length of fiber, directly affect the yield and quality of cotton fiber. To reveal the molecular mechanism of cotton fiber development and therefore provide useful genes for cotton breeding, a fiber cDNA clone, *GhSCFP* (Seed Coat and Fiber specific Protease), which has tissue specific expression in ovule epidermal cells and fibers, was selected from the cDNA library, and its function was further investigated. The expression of *GhSCFP* was not observed in young stems, leaves, and flowers, and a very low transcriptional level was detected in roots. However, its transcripts accumulated abundantly in ovules and in fibers. The expression of *GhSCFP* reached a maximum at 8 DPA and ended at 18 DPA. To confirm the expression specificity of the *GhSCFP* gene and to isolate seed coat- and fiber-specific gene promoters, a fragment of 1037 bp up stream the first initiation code was cloned by YADE method. To test whether the fragment contained the promoter activity in a tissue-specific manner, transgenic tobacco and cotton plants harboring pGhSCFP-GUS were generated. In tobacco transformants, the GUS gene was preferentially expressed in developing seeds (0-15 DPA), but not in roots, leaves, and stems. Microscopic observation indicated that the GUS gene was specifically expressed in the outermost layer of epidermal cells in the developing seed coat. In transgenic cottons, GUS activity was detected only in fiber cells. These results indicate that the cloned *GhSCFP* promoter can drive the down stream gene to express in a fiber-specific manner. To genetically analyze the biological function of *GhSCFP*, two suppression vectors (pSCFP-RNAi and p5-anti-*GhSCFP*) were constructed and introduced into cotton. Twenty pSCFP-RNAi and 46 p5-anti-*GhSCFP* transgenic plants were obtained. With the lowered expression of *GhSCFP*, the boll growth in transgenic cottons was inhibited, which resulted in a decrease of boll size. Compared to untransformed cottons, the transgenic cotton produced fibers with increased micronaire values and decreased fiber strength, while no significant difference in fiber length uniformity and fiber elongation. Microscopic observation showed that the density of fiber initials on the surfaces of ovules at 6 h after flowering was lower in the transgenic cottons than in wild type. Fiber counting revealed that the fiber numbers on transgenic ovules at 2 DPA were significantly reduced (41.1% to 70.6%), while on mature seeds, the fiber number of the transgenic plants decreased by 32.8% of the control. In conclusion, *GhSCFP* is a fiber-specific gene influencing fiber number, and its upstream sequence can be used in the study on cotton fiber development or in cotton improvement as a fiber-specific promoter.

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