

## Expression Profile Analysis of Genes Involved in Brassinosteroid Biosynthesis Pathway in Cotton Fiber Development

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Cotton (*Gossypium hirsutum* L.) is the leading fiber crop and one of the mainstays of the economy in the world. Cotton fibers, as the main product of cotton plants, are unicellular, linear structures derived from the epidermis of the ovule. Cotton fiber development consists of four discrete yet overlapping developmental stages: initiation, elongation, secondary wall deposition, and maturation. Therefore, it is regarded as an ideal experimental model for studying plant cell elongation, cellulose synthesis, and cell wall deposition. Furthermore, the fiber quantity and quality are established during fiber development. The mechanisms controlling cotton fiber initiation and elongation, however, are poorly understood. It is well known that phytohormones play an important role in plant cell growth and development. Brassinosteroids (BRs) are a class of plant steroidal hormones that are involved in a wide variety of physiological and developmental processes, including cell division and elongation, vascular differentiation, reproductive development, senescence, biotic and abiotic tolerance. To understand the role of various brassinosteroids (BRs) in cotton fiber development and further study the mechanism of BR action in plant cell, we determined the expression profile of genes involved in BR biosynthesis pathway by quantitative real-time RT-PCR. The genes in the upstream pathway, namely *GhSMT1*, *GhFK*, *GhHYD1*, *GhSMT2*, *GhDWF5*, *GhDWF7*, *GhDWF1*, and *GhDET2*, shared a similar expression profile. Expression levels of these genes, except *GhDWF7*, peaked at about 10 days post anthesis (DPA), a rapid elongation stage of cotton fibers. Conversely, the transcripts of these genes were lower at  $\sim 0$  DPA, an initiation stage of fiber cell, and at  $\sim 18$  DPA, a stage of biosynthesis of secondary cell wall, than at  $\sim 10$  DPA, except for *GhDWF7*. These results revealed that phytosterols were crucial for the rapid elongation of cotton fibers. On the contrary, the genes involved in downstream of *GhDET2*, including *GhDWF4*, *GhDWF3*, and *GhBR6ox*, shared the lowest expression levels in  $\sim 10$  DPA. Compared with 10 DPA, their expression levels were slightly higher in the early stage of fiber growth and far higher in the stage of secondary cell wall accumulation. These results illuminated that the productions of these enzymes play important roles in secondary cell wall formation of cotton fibers. On the other hand, the BR levels might be very high and be regulated strictly in rapid elongating fiber cell since these genes were sensitive to BR feedback regulation. The *GhDWF7* gene presents a specific expression pattern that increased variably from 0 DPA to 22 DPA. Among all genes detected, the expression level of the *GhDWF1* is highest in 0 DPA. At 8 DPA and 14 DPA, the *GhSMT1*, *GhSMT2*, *GhDWF7*, *GhDWF1*, and *GhDET2* shared higher expression levels. At 18 DPA, the *GhDWF7* transcript maintained high level. These results further indicated that phytosterols play an important role in fiber cell elongation, and there may be a specific phytosterol signal pathway independent on BR signaling. The production of *GhDWF1* may play crucial role in fiber initiation.

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