

Characterization of the 19 Novel Cotton *FLA* Genes and Their Expression Profiling in Fiber Development and in Response to Phytohormones and Salt Stress

HUANG Geng-qing, XU Wen-liang, GONG Si-ying, WANG Xiu-lan, LI Xue-bao
(College of Life Sciences, Huazhong Normal University, Wuhan 430079, China)

Fasciclin-like arabinogalactan proteins (FLAs), a subclass of arabinogalactan proteins (AGPs), are usually involved in cell development in plants. To investigate the expression profiling as well as the role of *FLA* genes in fiber development, nineteen *GhFLA* genes (cDNAs) were isolated from cotton (*Gossypium hirsutum*). Among them, fifteen are predicted to be glycosylphosphatidylinositol-anchored to the plasma membranes. The isolated cotton *FLAs* could be divided into four groups. Real-time quantitative RT-PCR results indicated that the *GhFLA* genes are differentially expressed in cotton tissues. Three genes (*GhFLA1/2/4*) were specifically or predominantly expressed in 10 DPA fibers, and the transcripts of the other four genes (*GhFLA6/11/14/15*) were accumulated at relatively high levels in cotton fibers. Highest levels of *GhFLA5*, *GhFLA8*, and *GhFLA9* transcripts were detected in leaves, whereas the other cotton *FLA* genes were preferentially expressed in hypocotyls. Furthermore, expressions of the *GhFLA* genes are regulated in fiber development and in response to phytohormones and NaCl. The identification of cotton *FLAs* will facilitate to study their roles in cotton fiber development and cell wall biogenesis.