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

HUANG Gong-qing, XU Wen-liang, GONG Si-ying, WANG Xiu-lan, Li Xue-bao

(College of Life Sciences, Huazhong Normal University, Wuhan 430079, China)

Fascilin 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 (GhFLA6/11/15) 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.