METABOLITE AND GENE EXPRESSION ANALYSIS OF TWO NEAR-ISOGENIC LINES OF LIGON LINTLESS-2 (*LI_2*) COTTON (*GOSSYPIUM HIRSUTUM* L.)

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Abstract

Cotton fiber is the most prevalent natural raw material used in textile industry. The modern textile industry requires cotton with strong and consistently long fibers in order to produce high quality yarns. Length is one of the most important properties of cotton fibers since longer fibers produce stronger yarns that allow for more valuable end products. Longer fibers also enable higher spinning speeds. Cotton fibers are single-celled trichomes that differentiate from the ovule epidermis. After initiation the fiber cells elongate rapidly and eventually lead to accumulation of a large amount of cellulose. The cotton (*Gossypium hirsutum* L.) fiber mutation Ligon lintless-2 is controlled by a single dominant gene (Li_2) that results in significantly shorter fibers than a wild-type. Li_2 represents a good model system to study fiber elongation because it does not show pleiotropy. Understanding metabolic processes undergoing during fiber elongation can provide valuable information for genetic manipulations to increase the quality and the value of the crop. Here we present GC-MS-based metabolite profiling in combination with gene expression analysis to reveal metabolic changes during fiber elongation in two near isogenic lines of Li_2, wild type and mutant. Principal component analysis of approximately 500 detected metabolites in developing fibers divided samples into 5 groups, separating elongation stage only for wild type samples. Significant changes in the relative abundance of multiple identified metabolites were observed between near isogenic lines which are the result of genetic reprogramming of primary metabolism in response to Li_2 mutation.