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IDENTIFICATION OF AN APOPLASTIC CU/ZN SUPEROXIDE DISMUTASE IN DEVELOPING COTTON FIBERS

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Abstract

Cotton fibers are unicellular trichomes originating from the ovule epidermis. The thick secondary wall of mature cotton fibers is composed of almost pure cellulose. During the transition from fiber cell expansion to secondary wall synthesis, the rate of cellulose synthesis in cotton fibers is estimated to rise nearly 100-fold.

Hydrogen peroxide is a key regulator for a broad range of physiological processes in plants. In cotton fibers, the levels of hydrogen peroxide can influence the rate of cellulose biosynthesis by controlling both transcription and post-translational modification of cellulose synthase complexes. However, little is known about how hydrogen peroxide is generated in plant cell walls because apoplastic forms of hydrogen peroxide producing enzymes have not been identified from cotton nor Arabidopsis, a model plant.

We found high CuZn-superoxide dismutase (CSD) activities in developing cotton fibers and isolated three different types (GhCSD1, GhCSD2a / 2b, GhCSD3) of CSD genes from cotton fibers. In silico analyses showed that none of them were expected to localize to the cell walls because all three types were missing a classical signal peptide for the secretory pathway. When GhCSDs as GFP fusion proteins were over-expressed in Arabidopsis, we discovered that GhCSD3 was an apoplastic form of CSD. In contrast, GhCSD1 localized to the cytoplasm, and GhCSD2a and GhCSD2b that contained a transit peptide were in plastids.

A model will be proposed for the involvement of apoplastic GhCSD3 in concert with other reactions important for the dynamic changes that take place in the cell wall during cotton fiber development.