

Omics provide insights to understand cotton responsive to *Verticillium dahliae* and application (Abstract)

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ABSTRACT

Due to no high resistant germplasm in upland cotton (*Gossypium hirsutum*), *Verticillium* wilt has become the most serious disease for cotton production in China. Through whole genome gene expression analysis by RNA sequence, we found the expression level of lignin synthesis-related genes and the activity of corresponding enzymes induced more quickly in resistant cultivar '7124' (*G. barbasense*) [1]. Recently, an ethylene response-related factor, GbERF1-like, from '7124' was proved as a positive regulator in lignin synthesis and contributed substantially to resistance to *V. dahliae* [2]. And suppression the expression level of a cotton P450 gene, SILENCE-INDUCED STEM NECROSIS (*SSN*), causes a lesion mimic phenotype in cotton. Further study shows that *SSN* silencing causes an imbalance in LOX (lipoxygenase) expression and excessive hydroperoxide fatty acid accumulation. We also show that an unknown oxylipin-derived factor is a putative mobile signal required for systemic cell death [3]. Complex phytohormones interaction was also found involving in cotton responsive to *V. dahliae* [4]. BR and JA signal pathways play essential roles in interaction of cotton and *V. dahliae* [4, 5]. Furthermore, we identify the key data from genomics and proteomics with a data-mining strategy accompanied by VIGS and heterologous expression [6]. GbWRKY1 is one of the key candidate genes and has been proved with as a critical regulator mediating the plant defense-to-development transition during *V. dahliae* infection by activating JAZ1 expression [7]. Overall, our study provides highlights to understand the mechanism of cotton resistance to *V. dahliae* at molecular level.

Keywords: Omics, cotton, *verticillium dahliae*.

