Analysis of upland cotton (*Gossypium hirsutum*) response to *Verticillium dahliae* inoculation by transcriptome sequencing


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**ABSTRACT.** Verticillium wilt is one of the main diseases in cotton (*Gossypium hirsutum*), severely reduces yield and fiber quality, and is difficult to be controlled effectively. At present, the molecular mechanism that confers resistance to this disease is unclear. Transcriptome sequencing is an important method to detect resistance genes, explore metabolic pathways, and study resistance mechanisms. In this study, the transcriptome of a disease-resistant inbred cotton line inoculated with *Verticillium dahliae* was sequenced. A total of 126,402 unigenes were obtained using *de novo* assembly and data analysis, 99,712 (78.88%) of which were annotated into the Nr, Nt, Swiss-Prot, KEGG, COG, and GO databases. The expression patterns of 16 candidate disease-resistance genes showed that some genes were upregulated soon after *V. dahliae* inoculation and others were upregulated later, which may indicate instantaneous basal defense and lagged specific defense, respectively. We conducted a preliminary analysis of the transcriptome database, which will contribute to further research regarding the cloning of disease-resistance genes.

**Key words:** Cotton; Verticillium wilt; Transcriptome sequencing; Disease-resistance gene