

Molecular Cloning and Characterization of Genes Involved in Cotton (*Gossypium barbadense* L.) Response to *Verticillium dahliae*

XU Li, ZHANG Xian-long, ZHU Long-fu, TU Li-li

(National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, Hubei 430070, China)

Verticillium dahliae Kleb. is a necrotrophic plant pathogen which causes serious soil borne vascular disease in cotton. The molecular basis the defense response of cotton to this pathogen is poorly understood. To capture a wide spectrum of differentially expressed genes in cotton defense response, PCR-Select Subtractive Hybridization (SSH) was performed to generate highly enriched transcripts. Tester and driver cDNAs were reverse transcribed from the mRNA of pathogen infected and control cotton. A total of 405 ESTs were sequenced after selected for differential expression by reverse Northern blot among more than 1400 clones in the SSH cDNA library. After processing the sequences and doing blast, a total of 306 different genes were identified. More than one-third of the genes in the EST collection have not been identified as defense response genes in previous studies, and about 20% had not been reported previously to GenBank or were expected to be unknown or newly identified genes. RT-PCR and Realtime PCR were performed to confirm some representative genes expression patterns and study the role that some signal molecules (ET, JA, and SA) play in the cotton defense response. Our results suggested that a complicated and concerted mechanism involving multiple pathways is responsible for cotton defense response. This report represents a set of disease related genes involved in the process of the response and ethylene signaling pathways that may greatly contribute to the defense response.