

IDENTIFICATION OF DIFFERENTIALLY EXPRESSED GENES IN VIRULIFEROUS *BEMISIA TABACI* USING DIFFERENTIAL DISPLAY ACP-RT-PCR

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ABSTRACT

Acquisition of plant viruses has different effects on physiological mechanisms in vector insects and its endosymbionts. *Bemisia tabaci* is the only known vector of *Tomato yellow leaf curl virus* (TYLCV), which is considered to be the most serious virus affecting tomato crop in tropical and subtropical regions. In this study we aimed at studying the expression profile of the non-viruliferous and viruliferous whiteflies reared on TYLCV. We used the annealing control primer (ACP)-differential display RT-PCR method to identify differentially expressed fragments (DEFs) that may contribute in virus translocation, thus transmission of virus *via* its vector whitefly. Using four arbitrary ACP primers, a total of 14 DEFs were identified and sequenced. BLAST searches revealed high homology with some putatively transmission related genes like endosymbionts 16S ribosomal RNA genes, (StAR)-related lipid transfer (START), peptidase and Vitellogenin. Some other fragments have showed a considerable homology with a former studied EST fragments registered in the Genbank. The data obtained were confirmed using real time-PCR analysis and revealed that the expression of all endosymbionts 16S ribosomal RNA gene in case of the viruliferous whiteflies showed a significant down-regulation, while the steroidogenic acute regulatory protein (StAR)-related lipid transfer (START) protein, peptidase and Vitellogenin genes showed up-regulation in case of viruliferous whiteflies.

KEYWORDS: ACP DD-RT-PCR, Differentially Expressed fragments (DEFs), TYLCV, whitefly and endosymbionts bacteria