

GENE EXPRESSION ANALYSIS IN ORANGE LEAVES IN RESPONSE TO THE
CITRUS CANKER PATHOGEN *XANTHOMONAS PV CITRI*

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The Citrus canker disease, caused by the bacterial pathogen *Xanthomonas axonopodis* pv *citri* (Xac), is considered a threat to the Brazilian citriculture because of its easy dissemination and absence of commercial resistant cultivars. Host cell hypertrophy and hyperplasia are the first microscopic symptoms of the disease. We have conducted a systematic gene expression analysis in orange (*Citrus sinensis*) leaves after 6 and 48hs of infection with Xac and *Xanthomonas axonopodis* pv *aurantifolii* (Xaa). Notably, Xaa is not pathogenic to orange but causes canker in Mexican lime (*Citrus aurantifolia*), indicating an ongoing host defense response in orange. Differentially expressed genes were identified by suppression subtractive hybridization (SSH), differential display (DD) and microarray analysis, and confirmed by northern blot and quantitative qPCR. The genes were grouped into functional categories i.e., cell wall proteins, vesicle trafficking, hormone signaling, and defense response, among others. Cell wall remodeling and organ development genes were strongly induced by Xac, which is consistent with the phenomenon of cell division and enlargement that lead to the rupture of the epidermis. On the other hand, genes related to cell wall thickening, ethylene signaling and defense responses were specifically induced by Xaa. We expect that these analyses will provide us with clues to better understand the molecular mechanisms underlying the citrus-Xanthomonas interaction.