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Study of Mexican lime genes expression during infection with *Candidatus Phytoplasma aurantifolia*

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Candidatus Phytoplasma aurantifolia causes witches broom disease in acid lime (*Citrus aurantifolia* L.). The molecular basis of compatibility and disease development in this system is poorly understood. We have carried out a cDNA-AFLP analysis to identify acid lime genes associated with the infection process. We carried out cDNA-AFLP analysis on grafted infected lime of the susceptible cultivar at the representing symptoms stage. Selective amplifications with 43 primer combinations allowed the visualization of about 65 transcript-derived fragments (TDFs) in infected leaves, which were differentially expressed. We sequenced all fragments, which were identified as acid lime transcripts after homology searching, while 1 were homologous to sequences in *NCBI* databases and were attributed to *Candidatus Phytoplasma aurantifolia*. Many acid lime genes spanning almost all functional categories were down regulated during infection, especially genes involved in photosystem II, ubiquitin-protein ligase, Alpha-amylase, glycerophosphoryl diester phosphodiesterase, calcium ion binding, RNA binding protein, RNA polymerase beta, Cytochrome b, tubulin beta-4 chain, accumulation and replication of chloroplast, autophagy protein, transducin family protein. In contrast, genes encoding serine-rich protein, ATP synthase, leucine-rich protein, Proline-rich cell, ATP binding protein, Glutamine synthetase, ADP-ribose diphosphatase were primarily up regulated during infection. This study provides the first global catalogue of acid lime genes expressed during infection with their functional annotations. This will help to elucidate the molecular basis of the infection process and identify genes and chemicals that could help to inhibit the pathogen.

Keywords: *Candidatus Phytoplasma aurantifolia*, cDNA-AFLP