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Transcriptional changes involved in kumquat (*Fortunella* spp) defense response to *Xanthomonas citri* subsp. *citri* in early stages of infection

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Highlights

- The transcriptional response of kumquat plants (*Fortunella* spp) against *Xanthomonas citri* subsp. *citri* (Xcc) infection was investigated using RNA-seq.
- The DEGs in kumquat were related to pathogen recognition receptors (PRR and NLR), ROS production and oxidative burst, cell wall reinforcement, pathogenesis-related (PR) proteins and synthesis of secondary metabolites (phytoalexins).
- Enriched metabolic pathways included the biosynthesis of phenylpropanoids, diterpenoids, and alkaloids.
- 3 disease resistance genes (R) with NLR domains were found to be significantly induced in plants infected with Xcc.
- Some genes related to Systemic Acquired Resistance (SAR) and Hypersensitive Response (HR) were also significantly induced in infected plants.

defense are not fully understood. In this study, using RNA-seq approach, the transcriptional responses of kumquat leaves at 24 h after water (controls) and Xcc inoculation were analyzed. A total of 1439 Differentially expressed genes (DEG) with statistical significance (p-value<0.025) were identified, with 444 being upregulated. These genes were found to be involved in pathogen recognition, cell wall remodeling and reinforcement, lignin biosynthesis, reactive oxygen species (ROS) production, pathogenesis-related proteins (PR) and biosynthesis of secondary metabolites including phenylpropanoids, terpenoids and alkaloids. Genes related to disease resistance (R genes) and salicylic acid (SA)-dependent systemic acquired resistance (SAR) were also induced. In turn, the 995 downregulated genes were mainly associated with photosynthesis, photorespiration, chlorophyll synthesis and cell growth. This suggest that, once the pathogen is detected, the plant generates a strong oxidative burst and its cellular machinery is directed towards the synthesis of secondary metabolites and defense proteins while its own growth is inhibited. Overall, these transcriptional changes provide valuable information about the molecular basis of the defense in kumquat plants, which may be useful in the design of new control methods for citrus canker.

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Keywords

Citrus canker; Differentially expressed genes (DEG); Plant immunity; Plant-pathogen interaction; RNA-seq

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