

Title Transcriptomic and metabolomic analyses of induced resistance in citrus fruit against *Penicillium digitatum*

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Abstract

Penicillium digitatum is one of the major postharvest pathogenic fungi of citrus fruit. Although control is achieved by chemical fungicides, new and safer alternatives, such as induced resistance, are being developed. When citrus fruits are inoculated with the pathogen and then subjected to heat treatment, disease does not progress and fruits become more resistant to a subsequent pathogen attack. Using this system as a model we have analyzed global changes in gene expression at different times during the induction of resistance. To examine transcript accumulation in the flavedo and albedo tissues (outer coloured and inner white part of the rind, respectively), a cDNA microarray containing 12,000 unigenes generated by the Spanish 'Citrus Functional Genomics Project' was used. Analysis of three independent biological replicates for each time point revealed major changes in expression of genes related to the metabolism of aromatic compounds and phenylpropanoids; these were more noticeable in the inner issue. To gain a deeper insight into this latter pathway we studied changes in the expression of genes coding for PAL, 4CL, F3H, IRL, CADs, SAD and OMTs by Northern blot hybridization. Most of these genes are up-regulated by the induction treatment, but to a higher level in the albedo. We have also performed a metabolic profile analysis of phenolic compounds by HPLC. Scoparone, a hydroxycinnamic acid, showed the highest induction. However, the largest number of changes was observed in benzoic acid derivatives.