Title Characterization of genes associated with induced resistance against *Penicillium expansum* in apple fruit treated with quercetin

Author Simona Marianna Sanzani, Leonardo Schena, Annalisa De Girolamo, Antonio Ippolito and Luis González-Candelas

Citation Postharvest Biology and Technology, Volume 56, Issue 1, April 2010, Pages 1-11

Keywords Induced disease resistance; Quercetin; *Penicillium expansum*; *Malus domestica*; Quantitative real-time PCR; Suppression subtractive hybridization

Abstract

Penicillium expansum causes blue mould, a serious postharvest disease of apples, and is the main producer of the mycotoxin patulin. Since control by synthetic fungicides is less accepted by consumers, the demand for alternative means is pressing. In a recent study, the flavonoid quercetin, although scarcely effective in *in vitro* assays against *P. expansum* growth, significantly reduced blue mould rots on 'Golden Delicious' apples, suggesting an enhancement of host disease resistance. To confirm or reject this hypothesis, genes differentially expressed in quercetin-treated 'Golden Delicious' apples were identified by suppression subtractive hybridization (SSH). A pool of 88 unique gene transcripts was obtained. Several sequences revealed high similarities with different classes of pathogenesis-related proteins (RNase-like PR10 and PR8), or with proteins expressed under stress conditions. Other transcripts had high similarity to genes of unknown function or genes coding for proteins having a role in pathogen recognition and in signalling pathways. SSH data were validated by analysing the expression of 14 genes by quantitative real-time PCR (qPCR). Eleven genes proved to be up-regulated at a medium-high level in freshly harvested apples. Among these, 5 genes selected for temporal expression profiling revealed the existence of a combined effect, particularly at 24 or 48 h, between wounding and phenolic treatment. These results provide evidence that quercetin induces resistance to *P. expansum* in apples, by acting on the transcription level of genes involved in several distinct metabolic processes.