

Title Genes differentially expressed in quercetin-treated apples and associated with resistance to blue mould caused by *Penicillium expansum*

Author Simona M. Sanzani, Leonardo Schena, Annalisa De Girolamo, Franco Nigro, Antonio Ippolito and Luis Gonzalez Candelas

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Abstract

The fungus *Penicillium expansum* is the causal agent of blue mould of apples. This disease is of economic concern not only to the fresh-fruit industry but also to the fruit-processing industry since some strains of *P. expansum* produce the mycotoxin patulin, which has negative effects on human health. When permitted, control of this Postharvest pathogen is performed with fungicides. However, the appearance of resistant strains and concern about food and environment safety have increased the demand for safe and sound control means. In previous trials the flavonoid quercetin proved to be effective in reducing both disease incidence and severity, together with toxin accumulation. Since quercetin resulted more effective in in vivo than in in vitro trials, a possible role of this substance in enhancing host resistance was hypothesized. To verify this hypothesis, a cDNA library of genes differentially expressed in response to quercetin application was constructed by using the suppression subtractive hybridization (SSH) approach. A total of 89 unique sequences were obtained. By Homology search and functional analysis the identified sequences were putatively categorized as belonging to “metabolism”, “subcellular localization” and “protein with binding functions or cofactor requirement” classes. Similarity was also found with genes coding for proteins whose role in defence mechanisms is still unknown. Further studies, performed by quantitative reverse transcription amplification (qRT-PCR) to validate SSH results, confirmed the differential expression of 14 analysed genes. For five of the most interesting genes an expression profile was built and revealed distinct kinetic of up-regulation.