Transcriptome analysis of postharvest pear (*Pyrus pyrifolia* Nakai) in response to *Penicillium expansum* infection

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Abstract

In pears, blue mold decay caused by *Penicillium expansum*, is a destructive postharvest disease around the world, which leads to stasis of the pear industry and creates huge economic losses. Our previous research work proved that *P. expansum* mainly secretes cell wall degrading enzymes (CWDEs) to infect pears. To further understand the molecular basis of *P. expansum* infection and disease progression, in the present study we have tried to investigate the transcriptome of pears infected with *P. expansum*. The differentially expressed genes (DEGs) identified from the RNA-seq results were clustered into 2 upward trends and 6 downward trends according to their gene expression patterns. Comparison of Gene ontology (GO) terms in downward and upward trend profiles evidenced that the enriched GO terms (included metabolic processes for l-phenylalanine, aromatic amino acid family and ethylene, etc.), found in upward trend profiles were more relevant to pear defense. Moreover, the Kyoto Encyclopedia of Genes and Genomes (KEGG) results revealed that pears can produce a complex defense response against *P. expansum* infection. Briefly, *P. expansum* produced CWDEs to establish infection, which triggers relevant transduction pathways in pear. These pathways led to further activation of the secondary regulatory networks. Finally, some metabolites were synthesised to defense against *P. expansum*. In general, the information obtained in this study will be supportive to develop new strategies to control fungal diseases.