

# Ultrastructure observation and transcriptome analysis of *Penicillium expansum* invasion in postharvest pears

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## Abstract

Pears are one of the most essential fruit worldwide, they are susceptible to *Penicillium expansum* infection during postharvest storage, which results in high economic losses. Due to the dearth of information involving the mechanisms of infection of *P. expansum* in pear fruit it is very important to clarify its pathogenicity. In this study, the fungus strain was isolated from rotten pears and identified as *P. expansum*, which has strong pathogenicity. The results from SEM revealed that *P. expansum* relies on the growth of spores or the secretion of filamentous materials to degrade the cell wall of infected pear tissues. In addition, it was found that tissues were completely damaged after 24 h of infection. The RNA-seq results of *P. expansum* in infected pear tissue suggested that total differentially expressed genes (DEGs) were grouped into 4 profiles due to an upward trend in their gene expression patterns using the STEM software. The DEGs of the 4 profiles were involved in extracellular enzyme activity, cellular response to reactive oxygen, glutathione metabolic species, and polysaccharide metabolic process particularly the plant cell wall degrading enzyme (CWDEs) synthesis pathway. In summary, this research provides a piece of new information with regards to the infection mechanisms of *P. expansum* on pears, which could be useful in understanding the phenomenon of pathogen -host -fruit interaction and the development of new measures for the control of fungal diseases.