

Metabolite changes of apple *Penicillium expansum* infection based on a UPLC-Q-TOF metabonomics approach

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Postharvest Biology and Technology, Volume 181, November 2021, 111646

Abstract

The *Penicillium expansum* (*P. expansum*) infection causes apple postharvest deterioration and declines the quality of apple derived products. Investigation into the metabolic process of apple *P. expansum* infection will help to illustrate the mechanism of pathology and discover the biomarkers for quality control. Here, the changes of metabolite during the apple *P. expansum* infection were explored by ultra performance liquid chromatography and the quadrupole-time of flight mass spectrometry (UPLC-Q-TOF/MS) based metabonomics. Between four group of 32 samples, average 1720 positive and 1761 negative peaks were obtained, which aligned into comparable peaks of 5048 and 4945. Significantly metabonomic differences were observed between the control and *P. expansum* infected samples. A total of 485 differential metabolites were screened. In these different metabolites, the majority of sugars were decreased during *P. expansum* infection, whereas the majority of organic acids, amino acids and peptides were increased. Changes in the profile of phenolics and fatty acids were diverse, and major of them were increased for disease resistance. Disturbed metabolic pathways in early infection were mainly secondary metabolite biosynthesis, ATP-binding cassette transporters, amino acid and carbon metabolism. The intergroup comparison obtained 140 differential metabolites to represent the core metabolic changes during infection. And 27 metabolites were strongly increased along with the disease process, which could aid the biomarker discovery. This study highlights the differential metabolites during the apple *P. expansum* infection, and provide a basis for further investigation.