

# Analysis of differentially expressed genes and differentially abundant metabolites associated with the browning of Meihong red-fleshed apple fruit

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## Abstract

Enzymatic browning affects the quality of fresh-cut produce. To elucidate the mechanism regulating the browning of red-fleshed apple, we analyzed the transcriptome and metabolome of freshly cut Meihong apple samples collected at 0, 0.5, and 4 h after cutting. The main differentially abundant metabolites during the browning process were phenols, amino acids and fatty acids. Phenols are substrates for enzymatic browning and most of them are negatively correlated with browning. Amino acids and their derivatives are associated with non-enzymatic browning and most of them are positively correlated with browning. A transmission electron microscopy analysis revealed the degradation of the cell membrane of cut fruit samples, which significantly affected the fatty acid content. The differentially expressed genes were mainly related to plant–pathogen interactions. Polyphenol oxidase (PPO) plays a major role during the early browning stage, but PPO gene expression was not higher than WRKY, AP2 and MYB transcription factor.