

A difference of enzymatic browning unrelated to PPO from physiology, targeted metabolomics and gene expression analysis in Fuji apples

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Abstract

Browning is an important factor affecting the quality of fresh-cut apples, and studying this factor is valuable. Previous research has found that apple browning is due to an enzymatic reaction caused by polyphenol oxidase (PPO), which results in the darkening of apples through the oxidation of polyphenols to quinones. We screened two Fuji apple types, “flushed-skin color pattern” (Type P) and “striped-skin color pattern” (Type T) from bud mutation cultivars. Type P has slower browning rate than type T. Using physiology, targeted metabolomics and real-time quantitative PCR, we found that polyphenol-related parameters including PPO activities, total phenol contents and expression of five genes (*MdF3H*, *MdPPO*, *MdUGT88F1/4*, *MdLAR* and *MdC4H*) did not change during browning in both apple types. However, levels of hyperoside, peroxidase (POD), superoxide dismutase (SOD), hydrogen peroxide (H₂O₂), ascorbic acid (AsA) and expression of nine genes (*MdPAL*, *MdCHS*, *MdCHI*, *MdANS*, *MdFLS*, *MdANR*, *MdUGT71K1s*, *MdTTG1* and *MdMYB1*) were higher levels in type P apples. Correlation analysis indicated that the browning was unrelated to total phenol and PPO activities. Browning index (BI) was negatively correlated with hyperoside, whilst malondialdehyde (MDA) and nine up-regulated genes were positively correlated. We therefore conclude that hyperoside may be the most critical indicator in apple browning. In summary, we found a difference of enzymatic browning unrelated to in Fuji apples. This research provides new insight into the phenomenon of fruit browning.