Identification of marker compounds for predicting browning of fresh-cut lettuce using untargeted UHPLC-HRMS metabolomics

Zhihao Liu, Jianghao Sun, Zi Teng, Yaguang Luo, Liangli Yu, Ivan Simko and Pei Chen

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Abstract

Enzymatic browning negatively impacts product quality and shelf-life of packaged fresh-cut lettuce. Metabolite profiles of lettuce are affected by the browning process. The purpose of this study was to identify metabolomic marker compounds to predict lettuce browning, which could be applied to discern accessions suited for commercial production and industrial breeding programs. Romaine lettuce with different browning susceptibilities were evaluated in two independent trials and growing seasons. Metabolites were analyzed using ultra-high-performance liquid chromatography coupled with high-resolution mass spectrometry (UHPLC-HRMS). Principal component analysis (PCA) was performed to visualize clusters, trends, and discriminative ion features. Seven metabolites, including quinic acid, caffeoylquinic acid, 3-hydroxytetradecanedioic, cichorioside B, 8-deacetylmatricarin-8-sulfate, dicaffeoylquinic acid and 9S,12S,13S-trihydroxy-10Z-octadecenoic acid, increased with storage time (day 0 *vs.* day 3) Three metabolites, including lactucopicrin-15-oxalate, tri-4-hydroxyphenylacetyl glucoside and 15-deoxylactucin-8-sulfate, decreased with storage time (day 0 *vs.* day 3). Two additional phenolic metabolites, dicaffeoyltartaric and caffeoyltartaric acids, were identified as potential marker compounds, whose presence on day 0 samples immediately after cutting was negatively correlated with browning development (represented by ΔHue). The identified metabolites help to elucidate the biochemical metabolism and pathways during enzymatic browning and have the potential to serve as marker compounds for predicting browning resistant accessions.