Analysis of the time-dependent protein changes in wounded apples ('Golden Delicious')

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Acta Horticulturae 1053: 171-176. 2104.

Abstract

Malus × domestica Borkh. 'Golden Delicious' is one of the most important apple cultivars worldwide. However, if damaged, the fruit becomes susceptible to opportunistic infection by postharvest phytopathogens such as *Botrytis cinerea* (gray mould) and *Penicillium expansum* (blue mould) which annually lead to large economic losses worldwide. Therefore, a proteomic study of the fruit response to wounding would contribute to better understanding of the physiological mechanisms underlying fruit stress response. In this study, we provide the first systematic description of time-dependent protein changes in wounded 'Golden Delicious' apples, using 2D-PAGE and MS for protein identification. Publicly available protein and EST databases were used for protein identification and annotation. Proteins that did not change in abundance after wounding were mainly categorized in the biological process of 'metabolism', 'response to stress', and 'oxidation-reduction processes', whereas proteins with changes in abundance after wounding were mainly categorized in 'response to stress'. We suggest that fruits react to mechanical damage by synthesizing a broad range of PR proteins. Increasing our knowledge of apple fruit proteins in wounded fruit tissues will be useful in developing new strategies to minimize postharvest losses.