

iTRAQ-based quantitative proteomic analysis of peach fruit (*Prunus persica* L.) at different ripening and postharvest storage stages

Li Jiang, Ruoyi Kang, Li Feng, Zhifang Yu and Haibo Luo

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Abstract

To better understand the global and dynamic changes in peach (*Prunus persica* L. cv. Xiahui 8) fruit protein expression, an efficient and reliable proteomic technique, iTRAQ, was used to investigate peach fruit proteome from day -7 to day 8 during storage period at 25 ± 1 °C. A total of 387 proteins with more than 1.2-fold abundance changes were observed. These differentially expressed proteins (DEPs) are mainly related to 17 functional categories. DEPs in day -7 were mainly responsible for sugar and carbohydrate syntheses, protein translation, expression and modification, and maintenance of osmotic balance in high ion and material transport capacities and strong redox reaction environment. Harvesting induced the increase of (small) heat shock protein. Upon harvest, the increased level of respiration rates on day 4 reached the highest level. polygalacturonase (PG), pectase lyase (PL), pectinesterase (PE), chorismate mutase (CM), peptidyl-prolyl isomerase (PPIase) and phytoene synthase (PSY) showed increased abundances and reached a peak at day 6, which significantly positive correlation with 9-cis-epoxycarotenoid dioxygenase (NCED) protein, accelerated fruit softening and metabolism of protein, amino acid and lipid. The emergence of eukaryotic translation initiation factor 5A (EIF5A) on day 8 signified the intensification of apoptosis. Our study facilitated a comprehensive understanding of the complex proteomic reprogramming and ripening-associated mechanisms that could be used for endeavors of breeding and postharvest processing to improve peach fruit quality.