

Proteomic and physiological analysis of 'Korla' fragrant pears (*Pyrus x brestschneideri* Rehd) during postharvest under cold storage

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Abstract

Low-temperature storage is widely used to maintain the quality of postharvest fruit and prolong the shelf-life. Although the biochemical and physiological changes occurring during pear during storage have been explored in previous studies, the underlying mechanisms remain unclear. Herein, protein expression profiles of pears during cold storage were investigated by two-dimensional electrophoresis (2-DE). Proteomic analysis revealed 22 significantly differentially expressed proteins, 21 of which were identified by matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF-MS). Functional annotation of the differentially expressed proteins (DEP) revealed that many were involved in carbohydrate and energy metabolism, signal transduction and transcriptional regulation, stress response and antioxidants, and protein metabolism. An increase in the activity of ethylene synthesis-related enzymes and a decrease in protein synthesis capacity indicate that fruit senescence remained normal during cold storage. Two pathogenesis-related proteins (β -1,3-glucanase and Pyr c1) in the glycosyl hydrolyse pathway were up-regulated, which may increase the resistance of pears to low temperature or pathogen stress. Our results presented some useful information on the changes of protein during senescence of fragrant pear that will help to better understand cellular events in pears during cold storage, and minimize postharvest losses.