

Transcriptome profiling for pericarp browning during long-term storage of intact lotus root (*Nelumbo nucifera*)

Kanjana Worarad, Tomohiro Suzuki, Haruka Norii, Yuya Mochizuki, Takashi Ishii, Keiko Shinohara, Takao Miyamoto, Tsutomu Kuboyama and Eiichi Inoue

Plant Growth Regulation 95: 207–221. (2021)

Abstract

Lotus root (*Nelumbo nucifera*) is an edible rhizome that the consumption/production has continuously increased as more consumers demand convenient and ready-to-eat foods. However, the processing, storage, and transportation of fresh-cut fruits and vegetables promotes physiological deterioration, such as browning, which leads to a reduction in the value of the product. This study aimed to reduce the browning of lotus root pericarps during long-term storage and long-distance transport, and to clarify the functions of unigenes and browning-associated metabolic pathways using RNA-sequencing techniques. Intact lotus root cv. 'Kanasumi No.34' browning decreased after the roots were packed along with an anti-browning solution. Over 200 million short single-end reads were mapped onto the *N. nucifera* consensus coding sequence set. The significantly differentially expressed genes (DEGs) were identified. Based on the Uniprot, GO, and KEGG databases, secondary metabolism, lipid metabolism, and redox state genes were significantly upregulated in the un-packed and packed with water treatments compared to after harvest sample. Additionally, 16 expected DEGs (e.g., *PPO*, *PAL*, *POD*, *CHS*, *PDCR*, and *SOD*), which are affected by browning development, were differentially regulated in lotus root pericarp. The gene expression data presented in this study will help elucidate the molecular mechanism underlying browning development in intact lotus root during long-term storage. The results may also inform future research on improving the post-harvest shelf life of lotus roots'.