

Transcriptome analysis provides strategies for postharvest lotus seeds preservation

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Abstract

The rapid deteriorative quality is a major factor that currently limits storage and transport of fresh lotus seeds. However, the physiological changes and molecular mechanisms of lotus seeds during postharvest storage remains poorly understood. Here, physiological and RNA-sequencing analyses were conducted on the postharvest seeds of seed-lotus cultivar ‘Jianxuan 17’. A rapid increase in starch and protein content was observed, while soluble sugar content was continuously decreased during postharvest storage, which could explain increased hardness and reduced sweetness of lotus seeds. Transcriptome analysis identified a total of 3148 differentially expressed genes (DEGs), and functional enrichment analysis showed six pathways that included starch and sucrose metabolism were commonly enriched in all comparison groups. Most DEGs involved in energy metabolic pathways, such as glycolysis and tricarboxylic acid cycle were down-regulated. Altered starch and soluble sugar contents were associated with significant changes in activity of enzymes involved in starch and sucrose metabolism. In addition, the content of plant hormones including, auxin (IAA), jasmonoyl-isoleucine (JA-Ile) and salicylic acid (SA), increased in lotus seeds during postharvest storage, and the activation of signaling transduction pathways were demonstrated at transcriptional level. These results provide not only valuable gene expression dataset for investigating molecular mechanism underlying changes during postharvest storage, but also is a useful reference for developing further preservation technology of fresh lotus seeds.