

DNA hypermethylation associated with the development of temperature-dependent postharvest chilling injury in peach fruit

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Abstract

Peach fruit is often subjected to postharvest chilling injury (CI) during long-term cold storage and the degree of CI is related to the storage temperature. Analysis of the data on softening, ethylene production and internal browning (IB) showed that CI occurred in fruit stored at or below 12 °C. Impairment of ethylene production and softening was greater in fruit stored at 0 and 5 °C and was consistent with lower expression of related critical genes. Lower malondialdehyde and hydrogen peroxide contents and enhanced hydroxyl radical contents were observed in fruit stored at 0 and 5 °C. These changes were associated with higher transcript levels of *polyphenol oxidases* and *peroxidase*, but lower expression levels of *lipoxygenase*, *superoxide dismutase* and *catalase*. To investigate whether DNA methylation is involved in the CI development in peach fruit, single-base resolution DNA methylome and transcriptome analysis was carried out. The DNA methylation level was higher in CI fruit and a close positive correlation was observed between the methylation level and IB index. Furthermore, for most genes involved in softening, ethylene biosynthesis and signal transduction, IB and reactive oxygen species metabolism, the expression level was found to be well correlated with low temperature-induced DNA hyper- or hypo-methylation in promoter, genebody or downstream regions. It was concluded that changes in DNA methylation in different genomic regions regulate CI associated gene expression and contribute to the development of temperature-dependent CI in postharvest peach fruit.