Transcriptomic analysis reveals a role of phenylpropanoid pathway in the enhancement of chilling tolerance by pre-storage cold acclimation in cucumber fruit

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Abstract

Cucumber fruits are susceptible to chilling injury, which can cause severe quality losses. In this study, pre-storage cold acclimation (PsCA, 10°C for 72 h) significantly induced chilling tolerance in cucumber fruits. To gain insight into the induction mechanisms of PsCA, comparative transcriptome analysis of fruit samples at 0 h, 12 h and 72 h during cold treatments were conducted. High-throughput transcriptome sequences were de novo assembled into 24878 unique transcripts. A total of 10164 differentially expressed genes (DEGs) were identified during cold stress, and 6205 DEGs were identified during cold acclimation, and 7976 DEGs were identified in cold acclimation compared to cold stress. Large numbers of DEGs were commonly detected between cold stress and cold acclimation, suggesting that these DEGs are related to cold response. Twelve DEGs were selected for qRT-PCR validation, and confirmed the credibility and accuracy of transcriptome data. Gene ontology (GO) enrichment and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of DEGs indicated that biological processes or pathways such as plant hormone signal transduction, carbon metabolism, and biosynthesis of amino acids were commonly affected by cold stress and acclimation treatments when compared to fruits just harvested. However, compared with cold stress, cold acclimation-affected DEGs were most enriched in phenylpropanoid pathway. Moreover, PsCA upregulated the expression of six DEGs in phenylpropanoid pathway in cold-stored cucumbers. These results suggest that phenylpropanoid pathway may play a role in PsCA-enhanced chilling tolerance. These findings provide novel insights into understand the induction mechanisms underlying PsCA-induced chilling tolerance in cold-stored cucumbers.