Differential Expression of Genes in Buds of Apple Trees Exposed to Low Temperatures at an Early Growing Stage

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Abstract

A transcriptome from growing buds of 'Fuji' and 'Hongro' apple trees exposed to low temperatures (-4°C) for 3 hours was analyzed to select differentially expressed genes (DEGs) in each cultivar. A total of 54,703,738 and 78,572,320 paired-end reads for samples of 'Fuji' and 'Homgro' apple tree leaves were obtained, respectively. The average read-length ranged from 148,77 bp and the analyzed reads were found to cover 91.47% of the raw data. DEGs were divided into 12, 4, and 10 main functional categories of molecular functions, cellular components, and biological processes with different degrees at level 3, respectively. The major up-regulated genes included GDSL-like Lipase/Acylhydrolase superfamily protein, ARM repeat superfamily protein, plant U-box 18, ARM repeat superfamily protein, C-repeat-binding factor 4, while the major down-regulated genes included beta glucosidase 17, Chalcone and stilbene synthase family protein, cytochrome P450, cellulose synthase like E1, Glucose-methanol-choline (GMC) oxidoreductase family protein, Leucine-rich repeat protein kinase family protein, ethylene response factor 1, Ribosomal protein L19e family protein, osmotin 34, Pathogenesis-related thaumatin superfamily protein gene in apple tree buds exposed to low temperatures. The selected DEGs were confirmed to be differentially expressed by high temperatures in a quantitative real time-PCR analysis with gene-specific primers. Transcriptome data can provide meaningful information to be used for the discovery of specific gene and can elucidate the mechanism in apple trees responding to extreme temperatures, and selected DEGs can be used as genetic resources in the molecular breeding of apples tolerant to foreign stress sources in the future.

Keywords

Apple, Buds, DEGs, Low temperature, Transcriptome.