

RNA-seq based transcriptomic analysis uncovers α -linolenic acid and jasmonic acid biosynthesis pathways respond to cold acclimation in *Camellia* *japonica*

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Abstract

Camellia is a well-known ornamental flower native to Southeast of Asia, including regions such as Japan, Korea and South China. However, most species in the genus *Camellia* are cold sensitive. To elucidate the cold stress responses in camellia plants, we carried out deep transcriptome sequencing of 'Jiangxue', a cold-tolerant cultivar of *Camellia japonica*, and approximately 1,006 million clean reads were generated using Illumina sequencing technology. Overall, 28,038 differentially expressed genes were identified during cold acclimation. Detailed elucidation of responses of transcription factors, protein kinases and plant hormone signalling-related genes described the interplay of signal that allowed the plant to fine-tune cold stress responses. On the basis of global gene regulation of unsaturated fatty acid biosynthesis- and jasmonic acid biosynthesis-related genes, unsaturated fatty acid biosynthesis and jasmonic acid biosynthesis pathways were deduced to be involved in the low temperature responses in *C. japonica*. These results were supported by the determination of the fatty acid composition and jasmonic acid content. Our results provide insights into the genetic and molecular basis of the responses to cold acclimation in camellia plants.