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Comprehensive Expression Analysis of Triterpenoid Biosynthesis Genes Using Pac-Bio Sequencing and rnaSPAdes assembly in *Codonopsis lanceolata*

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[Abstract]

Codonopsis lanceolata (*C. lanceolata*) has been widely used in East Asia as a traditional medicine to treat various diseases such as bronchitis, convulsions, cough, obesity, and hepatitis. *C. lanceolata* belonging to Campanulaceae contains bioactive compounds such as polyphenols, saponins, and steroids. However, despite the pharmacological significance of *C. lanceolata*, the genetic information of this plant is limited and there are few studies of its transcriptome. In this study, we constructed a unigene set of *C. lanceolata* using Pac-Bio sequencing. Furthermore, the reads generated from Pac-bio and Illumina sequencing were mixed and assembled using rnaSPAdes. All genes involved in the triterpenoid pathway, a major bioactive compounds of *C. lanceolata*, were searched from the two unigene sets and the expression profiles of these genes were analyzed. The results showed that lupeol, beta-amyrin, and dammarenediol synthesis genes were activated in the leaves and roots of *C. lanceolata*. In particular, the expression of genes related to lupeol synthesis was relatively high, suggesting that the main triterpenoid of *C. lanceolata* is lupeol. Transcriptome studies related to lupeol synthesis in *C. lanceolata* have been rarely reported. Lupeol has been reported to have pharmacological effects such as anti-inflammatory, anti-cancer, and anti-bacterial. This study suggests the importance of *C. lanceolata* as a lupeol producing plant.

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