

RNA-seq을 이용한 참당귀의 전사체 분석과 꽃 색 관련 유전자 분석

김남수¹, 정대희¹, 박홍우^{2*}, 박윤미², 전권석³, 김만조³

¹국립산림과학원 산림약용자원연구소 석사연구원, ²국립산림과학원 산림약용자원연구소 임업연구사,
³국립산림과학원 산림약용자원연구소 임업연구관

Transcriptome and Flower Color Related Gene Analysis in *Angelica gigas* Nakai Using RNA-Seq

Nam Su Kim¹, Dae Hui Jung¹, Hong Woo Park^{2*}, Yun mi Park²,
Kwon Seok Jeon³ and Mahn Jo Kim³

¹Master's Degree Researcher, ²Researcher, ³Senior Researcher, Forest Medicinal Resources
Research Center, National Institute of Forest Science, Yeongju 36040, Korea

Angelica gigas Nakai (Korean danggui), a member of the Umbelliferae family, is a Korean traditional medicinal plant whose roots have been used for treating gynecological diseases. Transcriptomics is the study of the transcriptome, which is the complete set of RNA transcripts that are produced by the genome, using high-throughput methods, such as microarray analysis. In this study, transcriptome analysis of *A.gigas* Nakai was carried out. Transcriptome sequencing and assembly was carried out by using Illumina Hiseq 2500, Velvet and Oases. A total of 109,591,555 clean reads of *A. gigas* Nakai was obtained after trimming adaptors. The obtained reads were assembled with an average length of 1,154 bp, a maximum length of 13,166 bp, a minimum length of 200 pb, and N50 of 1,635 bp. Functional annotation and classification was performed using NCBI NR, InterprotScan, KOG, KEGG and GO. Candidate genes for phenylpropanoid biosynthesis were obtained from *A.gigas* transcriptome and the genes and its proteins were confirmed through the NCBI homology BLAST searches, revealing high identity with other orthologous genes and proteins from various plants species. In RNA sequencing analysis using an Illumina Next-Seq2500 sequencer, we identified a total 94,930 transcripts and annotated 71,281 transcripts, which provide basic information for further research in *A.gigas* Nakai. Our transcriptome data reveal that several differentially expressed genes related to flower color in *A.gigas* Nakai. The results of this research provide comprehensive information on the *A.gigas* Nakai genome and enhance our understanding of the flower color related gene pathways in this plant.

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*(Corresponding author) E-mail: redrain39@korea.kr, Tel: +82-54-630-5649