

A Study on Transcriptome Analysis Using de novo RNA-sequencing to Compare Ginseng Roots Cultivated in Different Environments

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Ginseng (*Panax ginseng* C.A. Meyer), one of the most widely used medicinal plants in traditional oriental medicine, is used for the treatment of various diseases. It has been classified according to its cultivation environment, such as field cultivated ginseng (FCG) and mountain cultivated ginseng (MCG). However, little is known about differences in gene expression in ginseng roots between field cultivated and mountain cultivated ginseng. In order to investigate the whole transcriptome landscape of ginseng, we employed High-Throughput sequencing technologies using the Illumina HiSeqTM2500 system, and generated a large amount of sequenced transcriptome from ginseng roots. Approximately 77 million and 87 million high-quality reads were produced in the FCG and MCG roots transcriptome analyses, respectively, and we obtained 256,032 assembled unigenes with an average length of 1,171 bp by de novo assembly methods. Functional annotations of the unigenes were performed using sequence similarity comparisons against the following databases: the non-redundant nucleotide database, the InterPro domains database, the Gene Ontology Consortium database, and the Kyoto Encyclopedia of Genes and Genomes pathway database. A total of 4,207 unigenes were assigned to specific metabolic pathways, and all of the known enzymes involved in starch and sucrose metabolism pathways were also identified in the KEGG library. This study indicated that alpha-glucan phosphorylase 1, putative pectinesterase/pectinesterase inhibitor 17, beta-amylase, and alpha-glucan phosphorylase isozyme H might be important factors involved in starch and sucrose metabolism between FCG and MCG in different environments.

Key words: *Panax ginseng* C.A. Meyer, de novo RNA sequencing, transcriptome, Differential gene expression