

The Korean Ginseng Root Transcriptome : Analysis of 6816 Expressed Sequence Tags

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Korean ginseng (*Panax ginseng* C. A. Meyer) is an representative medicinal herb. It is classified as an adaptogen, helping the body to adapt to stress, improving stamina and concentration, and providing a normalizing and restorative effect. However, cultivation and breeding of the plant is very difficult because it requires at least 4-year cultivation from seed germination to root harvest.

Recent rapid progress in genetic engineering and the availability of various automated genetic analysis instruments have made it possible to perform large-scale isolation and partial sequencing of anonymous cDNA clones. Expressed sequence tags (ESTs) are short sequences, a few hundred base pairs in length, which are derivated by partial, single pass sequencing of the inserts of randomly selected cDNA clones. The ESTs analysis is now a widely used tool in genome research. ESTs help to quickly identify functions of expressed genes and to understand the complexity of gene expression.

In order to study gene expression in root used as medicinal material in Korean ginseng, we constructed two cDNA libraries of 4-year root and 14-year root. We analyzed expressed sequence tags (ESTs) of 2,975 from 4-year root and 3,841 from 14-year root. These ESTs could be clustered into 2,056 (64%) and 1,991 (70.2) non-redundant groups, respectively. Similarity search of the non-redundant ESTs against public non-redundant databases of both protein and DNA indicated that 1,498 and 1,553 groups show similarity to genes of known function, respectively. These ESTs clones were divided into sixteen categories depending upon gene function. The most

abundant transcripts were major latex protein (41) in 4-year root and ribonuclease 1 (67) in 14-year root. There are few useful informations of gene expression during the development of root in Korean ginseng. These results could help to understand the root used as medicinal material in Korean ginseng. Also, our extensive EST analysis of genes expressed in 4-year and 14-year ginseng root not only contributes to the understanding of the dynamics of genome expression patterns in root organ but also adds data to the repertoire of all genomic genes.