

Expression Analysis of ESTs Derived from the Four-Year Root of Chunpoong (*Panax ginseng* C.A. *Meyer*)

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Expressed sequence tags (EST) are help to quickly identify functions of expressed genes and to understand the complexity of gene expression. To assist genetic study of the root development in *Panax ginseng*, which is one of the most important medicinal plant, expressed sequence tags (EST) analysis was carried out. We constructed a cDNA library using the 4-year Chunpoong root. Partial sequences were obtained from 3,841 clone. The ESTs could be clustered into 2,056 (64%) non-redundant groups. Similarity search of the non-redundant ESTs against public non-redundant databases of both protein and DNA indicated that 1,498 groups show similarity to genes of known function. These ESTs clones were divided into eighteen categories depending upon gene function. The most abundant transcripts were major latex protein (41), ribonuclease 2 (36), metallothionein 2(35). Our extensive EST analysis of genes expressed in 4-year Chunpoong root not only contributes to the understanding of the dynamics of genome expression patterns in root organ development but also adds data to the repertoire of all genomic genes.