

Functional Analysis of ESTs from the 14-year Root of Korean Ginseng

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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 14-year ginseng root. Partial sequences were obtained from 2,975 clone. The ESTs could be clustered into 1,991 (70.2%) non-redundant groups. Similarity search of the non-redundant ESTs against public non-redundant databases of both protein and DNA indicated that 1,553 groups show similarity to genes of known function. These ESTs clones were divided into sixteen categories depending upon gene function. The most abundant transcripts were ribonuclease 1 (67) and ribonuclease 2 (65). Our extensive EST analysis of genes expressed in 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.