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To isolate useful and interesting plant genes in large quantities, random sequencing of cDNA clones from *Panax ginseng* hairy root library induced by *Agrobacterium* was performed. Partial sequences of randomly selected 173 clones with the insert longer than 300 base pairs (bp) have been compared with sequences in DDBJ, EMBL and GeneBank nucleic acid databases and identified 54 (31.2%) expressed sequence tags (ESTs). Out of 54 cDNA clones 15 clones have complete cDNA sequence (CDS). The 54 cDNA clones are related to various aspect of metabolic pathways such as glycolysis, amino acid synthesis, translation mechanism, ribosome synthesis, hormone response, stress response, regulation of gene expression, and signal transduction. Among the 51 ESTs, 3 ESTs (6 cDNA clones) appeared more than once and 48 ESTs appeared once regarded as a solitary group. In order to generate more ESTs from hairy root library we are continuously in progress the nucleotide sequencing.

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