P 77 Analysis of Expressed Sequence Tags from the 14-year Root of Korean Ginseng (*Panax ginseng* C.A. Meyer)

Jun Gyo In[2], Bum Soo Lee[2], Deok Chun Yang[1,2*]

[1]*Department of Oriental Medicine Material and Processing, Kyung Hee Univ., Gyeonggi-do 449-701, Korea*

[2]*BioPia Co., Ltd., Kyung Hee Oriental Medicine Material and Processing Center, Gyeonggi-do 449-701, Korea*

Objectives

Expressed sequence tags (EST) are help to quickly identify functions of expressed genes and to understand the complexity of gene expression. In this study, we carried out the EST analysis from the 14-year root of Korean ginseng.

Materials and Methods

1. Materials: Korean ginseng (*Panax ginseng* C. A. Meyer) 14-year root
2. Methods: mRNA purification, cDNA library construction, 5′ single pass sequencing, Sequence processing and functional classification

Results and Discussion

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 eighteen 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.

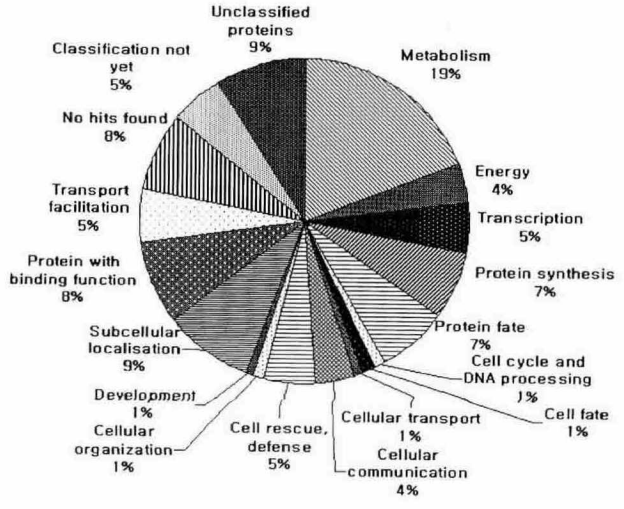

Figure 1. Functional classification of Korean ginseng 14-year root ESTs.

Table 1. Most abundant mRNA.

Functional classification	No. of ESTs	Percent of total (%)
Ribonuclease 1	67	2.3
Ribonuclease 2	65	2.2
Unknown protein 1	25	0.8
Ag13 protein	25	0.8
Unknown protein 2	21	0.7
Proline-rich protein 14K	16	0.5
Beta-amylase	16	0.5
Unknown protein 3	15	0.5
Pearli 1 protein	10	0.3
Catalase	10	0.3
Extensin	10	0.3
60S ribosomal protein L18	10	0.3

*Corresponding author. Tel 031-201-2688 E-mail dcyang@khu.ac.kr