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Analysis of Expressed Sequence Tags from the Flower Bud of Korean Ginseng (*Panax ginseng* C.A. Meyer)

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Objectives

Expressed sequence tags (ESTs) 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 flower bud of Korean ginseng.

Materials and Methods

1. Materials: Korean ginseng (*Panax ginseng* C. A. Meyer) flower bud
2. Methods: mRNA purification, cDNA library construction, 5' single pass sequencing, Sequence processing and functional classification

Results and Discussion

In order to study gene expression in a reproductive organ, we constructed a cDNA library of flower buds in Korean ginseng and generated expressed sequence tags (ESTs) of 3,360 clones randomly selected. The ESTs could be clustered into 1,844 non-redundant groups. Similarity search of the non-redundant ESTs against public non-redundant databases of both protein and DNA indicated that 1,254 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 unknown protein (72), chlorophyll a/b-binding protein (48), and stylar glycoprotein. There are no useful informations of gene expression during the development of flower bud in Korean ginseng. These results could help to understand the development of flower bud in Korean ginseng.

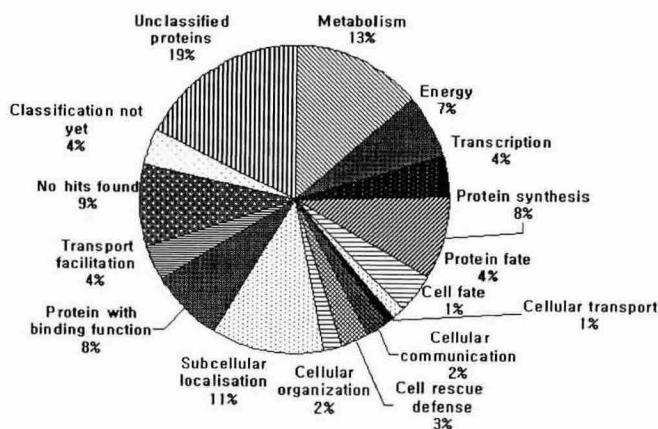


Figure 1. Functional classification of Korean ginseng flower bud ESTs.

Table 1. Most abundant mRNA.

Functional classification	No. of ESTs	Percent of total (%)
Unknown protein 1	72	2.33
Chlorophyll a/b-binding protein	48	1.55
Stylar glycoprotein 3	45	1.46
Unknown protein	42	1.36
Cyclophilin	36	1.16
Clone mubg1 ubiquitin gene	26	0.84
Calmodulin	22	0.71
Chlorophyll a/b binding protein of LHCII type I	20	0.64
Unknown protein 2	18	0.58
Ribosomal protein small subunit 28 kda	16	0.51
Metallothionein	15	0.48
Unknown protein 3	14	0.45

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