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Expressed sequence tags(EST) analysis in *Glycyrrhiza ularensis*

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Objectives

We present the results of expressed sequence tags analysis from cultivated roots and in vitro cultured seedling root of *Glcyrrhiza ularensis*. We identified 2341 known sequences, including several candidate sequences having significant sequence homology with the glycosyltransferase genes involved in licorice biosynthesis.

Materials and Methods

Two cDNA libraries were constructed from 4-years-old cultivated roots(from rural development administration, suwon, south korea) and in vitro cultured seedling roots of *glycyrrhiza ularensis*. Construction of licorice cDNA libraries used total RNAs prepared from plant tissues using Trizol reagent according to the procedures of Invitrogen.

Results and Discussion

Licorice (*Glycyrrhiza ularensis*) is a medicinal plant that accumulates glycyrrhizin in the roots and stolons. We sequenced 4,036 ESTs from two licorice libraries in order to create a gene resource for biosynthesis of glycyrrhizin, which ate thought to be the major active compound in roots and stolons. Only 58% of the licorice ESTs exhibited significant homology to previously known polypeptide sequences. Information storage and processing proteins were most abundant in 4-year-old licorice roots and *in vitro* cultured seedling root. Information storage and processing proteins represent 36%, 41% of the total number of transcripts in 4-year-old licorice roots and *in vitro* cultured seedling root, respectively. We identified 5 glycosyltransferase candidates, which may be involved in modification of the triterpene backbone.

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