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Isolation and Characterization of Dehydrin Gene from *Codonopsis Lanceolata*

Kang Lee[1], Jun Gyo In[1], Bum Soo Lee[1], Jong Hak Kim[1], Deok Chun Yang[2]*

[1] *BioPia Co., Ltd., Kyunghee University Oriental Medicine Material and Processing Center*
[2] *Department of Oriental Medicine Material and Processing, Kyunghee University*

Objectives

For the study in the defense mechanism against various stresses, a cDNA clone encoding a dehydrin gene was isolated from a cDNA library prepared from tab root mRNAs of *Codonopsis lanceolata* and characterized.

Materials and Methods

1. Material

4-year root of Codonopsis lanceolata cultivated in field

2. Methods:

We constructed cDNA library from root of *Codonopsis lanceolata*. It was recovered greater than 500bp and this library was amplified once to yield a final titre of 2×10^9pfu/ml. The 5' ends of randomly selected cDNA inserts were sequenced using the specific sequencing primer(Clontech) with an automatic DNA sequencer. Nucleotide and amino acid sequence analyses were performed using DNASIS program (Hitachi). EST were annotated using the BLAST algorithm of Altschul et al. (1990).

Results and Discussion

A cDNA clone encoding a dehydrin gene was isolated from a cDNA library prepared from tab root mRNAs of *Codonopsis lanceolata*. The cDNA, designated *ClDhn1*, is 893 nucleotides long and has an open reading frame of 480 bp with a deduced amino acid sequence of 159 residues. The *ClDhn1* amino acid sequence is highly hydrophilic and possesses two conserved repeats of characterized lysine-rich K-segment (KIKEKLPG), and a 7-serine residue stretch prior to the first lysine-rich repeat that is common to many dehydrins. The DEYGNP conserved motif is, however, absent in the sequence of *ClDhn1* gene. The deduced amino acid sequence of *ClDhn1* was compared with other plant dehydrin1s and showed high homology with *Solanum commersonii* (Commerson's wild potato; Y15813 ; 57% identity).

* Corresponding author : Tel: 031-201-2688, e-mail : dcyang@khu.ac.kr