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인삼 cDNA로부터 glutamate decarboxylase (GAD)의 molecular cloning과 스트레스 반응에 의한 다른 발현

경희대학교 고려인삼명품화사업단 및 인삼유전자원소재은행
이정혜*, 라마 크리시나풀라, 김유진, 정대영, 민진우, 김세화, 양덕춘

Molecular cloning of Glutamate decarboxylase (GAD) cDNA from *Panax ginseng* and their differential expression in response to stresses

Korean Ginseng Center for Most Valuable Products & Ginseng Genetic Resource Bank, Kyung Hee University, Suwon 449-701, Korea
Jung-Hye Lee*, Rama Krishna Pulla, Yu-Jin Kim, Dae-Young Jeong, Jin-Woo Min, Se-Hwa Kim, Ju-Sun Shim, Deok-Chun Yang

Objectives

This study was aimed to confirm the existence of a GAD gene in *Panax ginseng* C.A. Meyer, to determine the base sequence of the gene, predict the amino acid sequence, and to determine the GAD involvement in mediating stress responses.

Materials and Methods

○ Material

Fourteen-year old Panax ginseng plants grown at field were used for cDNA library construction. This material and cDNA were provided by Ginseng Genetic Resource Bank.

○ Methods

1) RNA purification and construction of a cDNA library
2) Nucleotide sequencing and sequence analysis
3) Stress treatment : Salt, Chilling, SA, Wounding, 2,4-D
4) Semi-quantitative RT-PCR Analysis

Results

A full-length cDNA encoding GAD (designated as *PgGAD*) was isolated and characterized from the root of *Panax ginseng* C.A. Meyer. The length cDNA of *PgGAD* was 914 bp and contained a 588 bp open reading frame (ORF) encoding a glutamate decarboxylase protein of 195 amino acids. RT-PCR analysis revealed that GAD gene has diverse expression patterns in hairy roots and adventitious roots of *P.ginseng*. In salt and chilling treatment in both of roots, the expression of *PgGAD*

*Corresponding author: Lee Jung-hye Tel: 031-201-2688, E-mail: dcyang@khu.ac.kr

was gradually decreased with time. By contrast, GAD mRNA levels significantlyincreased in response to salicylic acid (SA), wounding, and 2,4-D stress treatment.

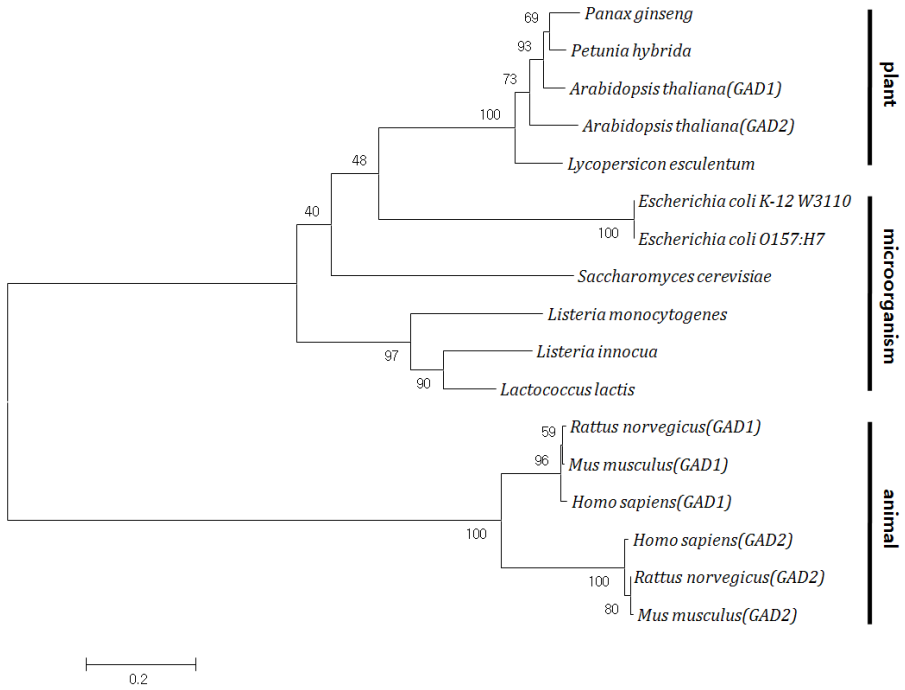

Fig. 1. Phylogenetic relationship of GAD from *P. ginseng* and other species.

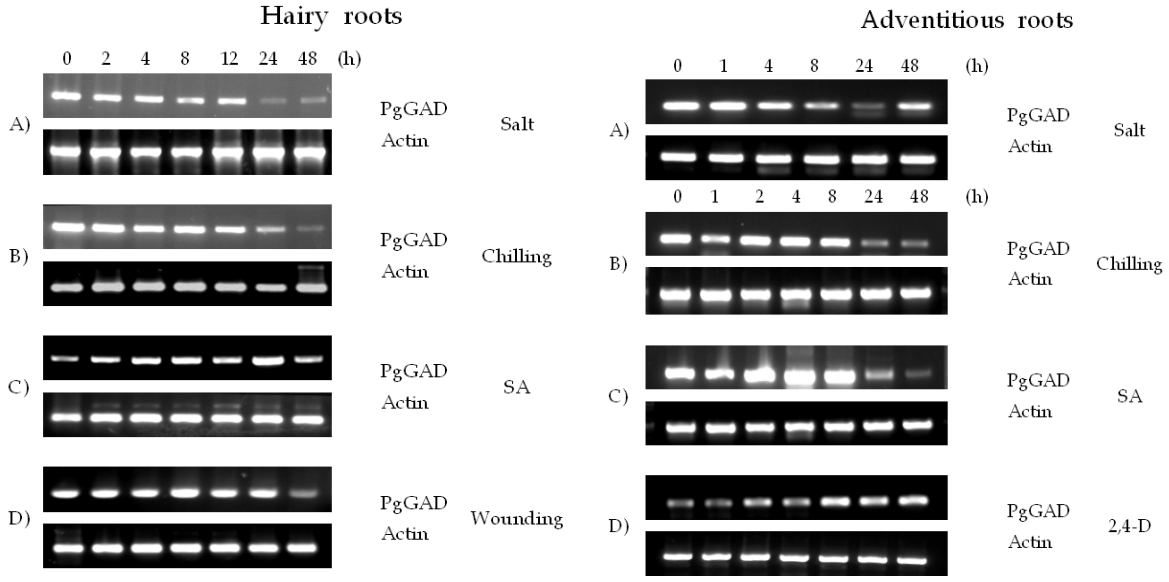

Fig. 2. RT-PCR analysis of the expression pattern of the *PgGAD* under various stress signals in hairy roots and adventitious roots.