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Molecular Characterization of cDNA Encoding *S*- Adenosylmethionine decarboxylase from *Panax ginseng*

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Objectives

The enzyme S-Adenosylmethionine decarboxylase (SAMDC; EC 4.1.1.50) produced by S-adenosylmethionine (SAM), which serves as an aminopropyl donor in spermidine and spermine synthesis and it also precursor for the biosynthesis of polyamines (PA). The cellular PAs are ubiquitous in nature and are absolutely required for eukaryotic cell growth. They are basic, small molecules thought to promote plant growth and development by activating synthesis of nucleic acids and proteins. Increases in endogenous amounts of PAs induced by environmental stresses were reported in several plants. Here gene encoding SAMDC from Panax ginseng was cloned and their expression patterns in response to abiotic stresses were studied. The cDNA, designated PgSAMDC which is 721 nucleotides long and has an open reading frame of 594 bp with a deduced amino acid sequence of 197 residues. Under various stress conditions, expression patterns of the PgSAM gene was highly induced in adventitious roots by several abiotic stresses. These results indicated that PgSAM plays protective role against diverse environmental stresses.

Material and methods

① RNA isolation and construction of a cDNA library

② Nucleotide sequencing and sequence analysis

③ Stress treatments

-H_2O_2 (10 mM) , NaCl (100 mM), ABA (100 mM) , Chilling (4) and Heavy metal (Cd- 100 μ M).

④ Quantitative RT-PCR analysis.

Results and discussions

The cDNA, designated *PgSAMDC* which is 594 bp with a deduced amino acid sequence of 197 residues. The deduced amino acid sequence of *PgSAMDC* was compared with other plant SAMDCs and showed high homology with *G. Max*

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A phylogenetic analysis of 16 different plant SAMDCs. In the evolutionary tree of amino acid sequences, SAMDCs separate into groups reflecting their evolution.

We report here the functional characterization of cDNA clones, The *PgSAMDC* gene was highly induced by various abiotic stress. (Fig. 2).

SAMDC gene expression was gradually increased in ABA, Chilling, Salt and Heavy metal treated adventitious roots. (Fig. 2 A-D). gene expression was increased until 12 hrs and then decreased in hydrogen peroxidase treated adventitious root. (Fig.2E) .

Wi et., al. 2006 also find the similar expression pattern against to ABA, Salt, Chilling stresses in transgenic tobacco plant lets.

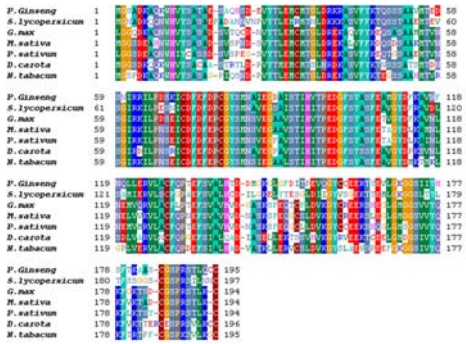

Fig. 1. Multiple alignment of the deduced amino acid sequence of *PgSAMDC* with those of SAMDC genes from other plants; *S.lycopericum* (ABY55855), *G. max* (AAL89723), *M. sativa* (ABO77440), *P. sativum* (BAC81653), *D. carota* (AAR84406) and *N. tabacum* (AAB88854). Sequence data was obtained from GeneBank listed and aligned using DDBJ ClustalW and GeneDoc. Gaps are marked with dashes.

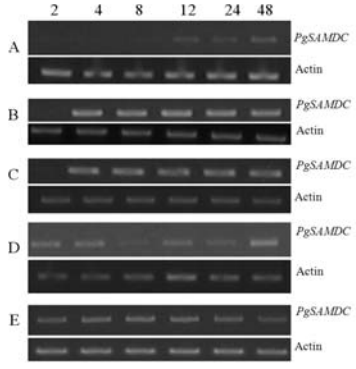

Fig. 2. RT-PCR analysis of the expression of the *PgSAM DC gene* in adventitious roots of *Panax ginseng* under various stress conditions. A, ABA (100mM); B, Chilling (4C); C, 100 mM NaCl D, Heavy metal (Cd -100mM) ; and (E) Hydrogen peroxide stress (100mM).