Plant Gene Register

Characterization of a S-Adenosylmethionine Synthetase Gene in Rice

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SAM-S (EC 2.5.1.6) catalyzes the biosynthesis of SAM (Adomet) from Met and ATP. Adomet is a universal methyl group donor in several transmethylation reactions and is involved in the regulation of the biosynthesis of Met and other Asp-derived amino acids. In plants, Adomet also functions as a precursor in the biosynthesis of the phytohormone ethylene and serves after decarboxylation as a propylamine group donor in the biosynthesis of polyamines (Goodwin and Mercer, 1983). SAM-S genomic and cDNA clones have been isolated and characterized from a variety of species, including Escherichia coli, Saccharomyces cerevisiae, parsley, Arabidopsis thaliana, carnation, poplar, rat, and human (Horikawa and Tsukada, 1991; Larsen and Woodson, 1991; Van Doorselaere et al., 1993, and refs. therein).

In Arabidopsis, the sam1 gene is expressed primarily in the vascular tissue (Peelman et al., 1989a). This phenomenon probably reflects the enhanced need for Adomet in the synthesis of structural components of these tissues. Xylem, sclerenchym, and, to a lesser extent, phloem are highly lignified, and biosynthesis of lignin consumes Adomet (Higuchi, 1981). In parsley and alfalfa cells, sam gene expression is induced by exposure to a fungal elicitor (Kawalleck et al., 1992) and yeast cell walls, respectively (Gowri et al., 1991).

We report the isolation and sequencing of a rice (Oryza sativa) genomic clone coding for SAM-S and the expression characteristics of this gene in rice (Table I). The rice sam gene shows 80% similarity with the sam1 and sam2 genes of Arabidopsis. There is an AATAAT polyadenylation signal 119 bp downstream from the stop codon. Nineteen base pairs downstream of the polyadenylation signal a second sequence motif implicated in 3' mRNA processing is present: TGTGTTT (McDevitt et al., 1986).

The deduced SAM-S polypeptide from rice shows 90% identity with the SAM1 and SAM2 Arabidopsis polypeptides. A conserved amino acid sequence motif involved in ATP binding (Kamps et al., 1984) is represented in the rice SAM-S protein as the peptide GAGDQG (position 121-126), followed by a Lys residue 19 amino acids downstream of this motif.

Table I. Characteristics of a sam gene from rice

| Organism: Rice (Oryza sativa, Taichung Native 1). |
| Clone, Source, Method of Identification: pRSAM1, isolated from a genomic cosmid library by probing with the Arabidopsis thaliana sam2 cDNA clone (Peelman et al., 1989b). |
| Features of Sequence: A total of 2183 bp, including 787 bp upstream and 204 bp downstream of the coding region. No introns. Polyadenylation site 120 bp downstream of the stop codon. Rice sam gene shows 80% sequence homology with the sam1 and sam2 genes of Arabidopsis and the deduced amino acid sequence is 90% identical with both Arabidopsis genes. Putative ATP-binding site at amino acid positions 121 to 126, with a Lys residue 19 amino acids downstream of this motif. |
| Expression Characteristics: Similar steady-state sam mRNA levels in roots, lamina, leaf, and cell suspension. Relatively high sam mRNA levels in early stage of development in leaf and root tissue. Steady-state sam mRNA level remains constant during further leaf development and declines in older roots. Drought stress elevates sam mRNA levels 2- to 4-fold. |
| Gene Copy Number: Small multigene family (two or three genes). |

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Abbreviations: SAM, S-adenosylmethionine; SAM-S, S-adenosylmethionine synthetase.
Drought stress (imposed by removing plants from their growth medium for 15-180 min) was correlated with 2- to 4-fold increases in steady-state levels of \textit{sam} transcript. Southern analysis of genomic rice DNA revealed that the \textit{sam} gene belongs to a small gene family (two or three copies). Northern hybridization experiments with \textit{sam} gene-specific probes will show whether there is a differential contribution of the genes to the observed mRNA levels.

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LITERATURE CITED


McDevitt MA, Hart RP, Wong WW, Nevins JR (1986) Sequences capable of restoring poly(A) site function to define two distinct downstream elements. EMBO J 5: 2907–2913

