

**Plant Gene Register**

# Cloning and Nucleotide Sequence of a S-Adenosylmethionine Synthetase cDNA from Carnation<sup>1</sup>

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SAM<sup>2</sup> serves as a methyl donor in many transmethylation reactions involving a variety of methyl acceptor molecules such as proteins, lipids, polysaccharides, and nucleic acids. In addition, SAM is a precursor in the synthesis of polyamines and ethylene (8). It has been suggested that the dynamic equilibrium between polyamines and ethylene in cells is regulated through the availability of SAM (1, 4). The genes for SAM synthetase which catalyzes the conversion of methionine to SAM have recently been isolated and cloned from *Arabidopsis thaliana* (6, 7). Using a cDNA probe for the SAM synthetase mRNA, Peleman *et al.* (6) showed strong cellular preference in the expression of these genes. An increase in the rate of ethylene production has not generally been considered to be dependent on increased availability of SAM (10); however, this has not been critically examined. Carnation floral tissues, and particularly styles and petals, produce ethylene at very high rates during senescence and thus provide an excellent model to address the regulation of SAM synthetase in relation to ethylene biosynthesis (2). Here we report the nucleotide sequence of a cDNA clone encoding SAM synthetase (EC 2.5.1.6) from carnation (*Dianthus caryophyllus* L., cv White Sim). The nucleotide sequence of cDNA clone pSAM2 is 1632 base pairs and contains an open reading frame encoding a polypeptide of 396 amino acids (Fig. 1). The predicted protein is highly homologous to functionally identified SAM synthetase proteins from rat (3) and yeast (9). In addition, the pSAM2 protein shares extensive homology with the predicted proteins from cloned SAM synthetase genes of *Arabidopsis* (6, 7).

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<sup>2</sup> Abbreviation: SAM, S-adenosylmethionine.

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1  AATCTTTTTTTTTTCTTGCTGTCTCTCTCTTTTTTTGTTCCCTCGGGATTCCCAGATT 60
61  AAGAAACAAAATGGCAGCTGCAGCGGACACTTTCCTATTACATCTGAGTCCGTGAATG 120
    M A A A A D T F L F T S E S V N E
121  AGGGACACCCCGACAAGCTCTGCGATCAGATCTCTGATGCGGTGCTTGACGCTTGCCCTAG 180
    G H P D K L C D Q I S D A V L D A C L A
181  CGCAAGATGCTGAGAGCAAGGTTGCTTGAGACATGCACCAAGACCAACTTGGTCATGG 240
    Q D A E S K V A C E T C T K T N L V M V
241  TCTTTGGTGAGATCACCACCAAGGTAACGTTGACTACGAGAAGATCGTGGCTGACACAT 300
    F G E I T T K A N V D Y E K I V A D T C
301  GCCGTGAGATGGCTTCGTGTCCCTGATGTGCGGTCTTGATGCTGACAACCTGCAAGGTCT 360
    R E I G F V S P D V G L D A D N C K V L
361  TGGTCTACATTGAGCAGCAAAGCCCGACATGCTCAGGGTGTCCACGGTCAACCA 420
    V Y I E Q Q S P D I A Q G V H G H L T K
421  AGCGCCCTGAGGATATTGGTGCCGGTGACCAGGGTCACATGTTCCGGCTATGCCACCGACG 480
    R P E D I G A G D Q G H M F G Y A T D E
481  AGACTCCCGAGTTGATGCCTTTGAGTCACGTCCTTGCTACCAAGCTTGGTGCCCGTTTGA 540
    T P E L M P L S H V L A T K L G A R L T
541  CTGAGGTCCGCAAGAACGGAACCTGCGCGTGGTTGAGGCCTGATGGCAAGCCCAAGTCA 600
    E V R K N G T C A W L R P D G K T Q V T
601  CGGTGAGTACTACAATGAGAACGGTGCCATGGTTCCCATCCGTGTCCACACCGTCCTCA 660
    V E Y Y N E N G A M V P I R V H T V L I
661  TCTCTACTCAGCACGATGAGACCGTCACCAATGATGAGATTGCTGCTGACTTGAAGGAGC 720
    S T Q H D E T V T N D E I A A D L K E H
721  ACGTGATCAAGCCAGTACCCCCGAGAAGTACCTCGACGAGAACCACATCTCCACCTTA 780
    V I K P V I P E K Y L D E N T I F H L N
781  ACCCATCTGGCCGATTGTGATCGGTGGCCACACGGTGATGCTGGTTTGACCGCCGTA 840
    P S G R F V I G G P H G D A G L T G R K
841  AGATTATCATCGACACCTACGGAGGTTGGGGTGCCACGGTCTGGTGCCTTCTCCCGAA 900
    I I D T Y G G W G A H G G G A F S R K
901  AGGACCCGACCAAGGTCGACAGGAGTGGGCATACATTGCCAGGCAGGCGCCAAAGAGCA 960
    D P T K V D R S G A Y I A R Q A A K S I
961  TTGTTGCCAGCGCCTTGCGCGCAGGTGCATTGTCCAGATCTCGTATGCTATCGGTGTCC 1020
    V A S G L A R R C I V Q I S Y A I G V P
1021  CTGAGCCCTTGTGCGGTGTTTGTGACACGTACGGAACAGGAAAGATCCACGACAGGGAGA 1080
    E P L S V F V D T Y G T G K I H D R E I
1081  TCCTCAAGATCGTGAAGGAGAACTTCGACTTCAGGCTGGTATGATCGCCATTGCCCTCG 1140
    L K I V K E N F D F R P G M I A I A L D
1141  ACCTCAAGAAGGGTGGGAACAGGTAAGACAGCCGCGTATGGACACTTTGGACGTG 1200
    L K K G G N R Y L K T A A Y G H F G R E
1201  AAGACCCGACTTCACGTGGGAGGCTGCAAAGACCCTCAAGTGGGAGAAGCCGCAAGCGT 1260
    D P D F T W E A A K T L K W E K P Q A *
1261  AAATGAAAGTGGCAGAGACGCATATGAGATAATTCATTGATTAATAATTGGGGACAAATTA 1320
1321  GATGAAAATGTGAGGGTATTCTACAGACAAACAGTTGCTCTCTATAACACCAGTGATGC 1380
1381  AATGCACTTGTGTCTTATGTATGTCTTTTTTCTGTTTTTTTTTTTTGGGTAAATTTGTT 1440
1441  TAGTTGTTTTTAATTGGTAGCAAAGAAGCAGCAGACTTGGTAGACAAAGGAGCTGCATG 1500
1501  TTATGGTTTTTATGTATGTGTTTGACAGAAACAGAAATGGGTTGTAGCTGCTTAGC 1560
1561  ACAGACCCTACAGTATGTAATTTGTTCTTTTTATAACAATCCTATGTTCTTTGCAAAAA 1620
1621  AAAAAAAAAAAAA 1632

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Figure 1. Nucleotide and deduced amino acid sequence of pSAM2.

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**Table 1. Characteristics of pSAM2 from *Dianthus caryophyllus* L. cv White Sim**

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**Organism:**

Carnation (*Dianthus caryophyllus* L. cv White Sim) cDNA.

**Function:**

pSAM2; S-adenosylmethionine synthetase (EC 2.5.1.6)

**Techniques:**

Double-stranded plasmid sequencing; exonuclease III deletion subcloning and dideoxy sequencing of both strands.

**Method of Identification:**

Isolated from cDNA library of senescing petal transcripts (5). Library probed with pATCC9A1-2 (7). Nucleotide sequence shares 68% homology with pATCC9A1-2, a cDNA clone for S-adenosylmethionine synthetase from *Arabidopsis thaliana*.

**Characteristics of Deduced Protein:**

ORF 396 amino acids; *M<sub>r</sub>* 43,560; 88, 61, and 63% identical with S-adenosylmethionine synthetase proteins from *Arabidopsis* (7), yeast (9), and rat (3), respectively.

**Expression characteristics:**

1700-base pair transcript detected in vegetative and reproductive tissues. Senescence of petals is associated with a reduction in pSAM2 transcript levels.

**Gene Copy No.:**

DNA gel blots and genome reconstructions indicate S-adenosylmethionine synthetase is encoded by two to three genes in carnation.

**Antibodies:**

None available.

**Subcellular Location:**

Not determined.

GenBank Accession No.: M61882

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