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Plant Gene Register

Serine Hydroxymethyltransferase from *Solanum tuberosum*[1]

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SHMT, EC 2.1.2.1, catalyzes the interconversion of Ser and Gly accompanied by the production or consumption of one-carbon units. In leaves it is a component of the photorespiratory pathway (Keys et al., 1978). The main function of that pathway is the salvage of reduced carbon and nitrogen withdrawn from the Calvin cycle by the oxygenation of ribulose 1,5-bisphosphate. By the cooperation of SHMT with the mitochondrial Gly cleavage system two molecules of Gly are converted into Ser, CO_2, and NH_3. This reaction is considered to be the exclusive source of photorespiratory CO_2 release (Somerville and Ogren, 1981).

The enzyme was first isolated from rabbit liver (Schirch and Mason, 1963) and, since then, has been studied in a variety of organisms and tissues. From human, cDNAs of both the cytosolic and the mitochondrial iso-SHMT were cloned (Garrow et al., 1993). In addition, the cloning of SHMT (*glyA*) genes from prokaryotes and *Neurospora crassa* has been reported (Plamann et al., 1983; Chan and Bingham, 1991; Rossbach and Hennecke, 1991; McClung et al., 1992).

Among plants, two immunologically indistinguishable forms of SHMT have been purified from pea leaf mitochondria, and the cDNA of one of them has been sequenced. Immunoinhibition experiments showed that a third, nonmitochondrial isoenzyme contributes to 30% of the total activity in leaves and is the only SHMT species present in roots (Turner et al., 1992). There is limited evidence that at least one form of SHMT is located in the plastids (Walton and Woolhouse, 1986).

Using a cDNA probe from pea we have isolated a full-length SHMT clone from a potato leaf cDNA library (Table I). Its sequence shares the highest degree of homology in comparison with the cDNA from pea (80.9%). It is much less similar to the corresponding cDNA sequences from *N. crassa* and the different (mitochondrial and cytosolic) isoforms from human with homologies of 68.7, 61.4, and 60.1%, respectively. On the protein level there is 42 to 45% homology to the enzymes from prokaryotes, 57% homology to the cytosolic SHMT from *N. crassa* and human, and 60% homology to the mitochondrial isoenzyme from human. The homology to pea mitochondrial SHMT is 89%. Several highly conserved regions are shared by all of the SHMTs from different cellular compartments and organisms.

Table I. *Characterization of the cDNA for SHMT from S. tuberosum*

Organism:	
	Solanum tuberosum cv Desiré.
Isolation:	
	Screening of a total leaf cDNA library in λ Uni-ZAP-XR with a cDNA clone from pea.
Sequencing:	
	Both strands by nested deletions.
cDNA:	
	1745 bp; open reading frame from position 6 to 1562.
Protein:	
	cDNA encodes a 518-amino acid precursor protein of *M*, 57,146. The mature protein probably consists of 487 amino acids and has a molecular mass of 53.7 kD.
Cellular Localization:	
	Mitochondrial matrix.
Gene Localization:	
	Nuclear encoded.

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Abbreviation: SHMT, Ser hydroxymethyltransferase.

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The EMBL accession number for the sequence reported in this article is Z25863.

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