

Plant Gene Register**Sequence of a cDNA from *Linum usitatissimum* Encoding the Stearoyl-Acyl Carrier Protein Desaturase**

Surinder Singh*, Susan McKinney, and Allan Green

Commonwealth Scientific and Industrial Research Organization, Division of Plant Industry, Canberra, ACT, Australia

The soluble plastid enzyme SAD (EC 1.14.99.6) introduces a double bond into the C18 fatty acid stearic acid between carbons 9 and 10 to produce the monounsaturated oleic acid. We report here the isolation and sequence characterization of a cDNA clone isolated from flax that encodes a precursor to SAD (Table I). This clone was isolated by screening a pGEM3Z cDNA library, constructed from mRNA isolated from mid-maturity (18–22 d after fertilization) flax embryo tissue, with a castor bean SAD probe (Shanklin and Somerville, 1992). The 1447-bp cDNA contained a 1188-bp open reading frame, with the putative initiation of translation beginning at ATG residing within an exact 9-bp copy of the proposed consensus sequence for initiation of translation in plants, AACAAUGGC (Lutcke et al., 1987). The open reading frame encodes a polypeptide of 396 amino acid residues, exactly the same size as described for castor bean, cucumber, and safflower desaturases (Gregory et al., 1991; Shanklin et al., 1991; Shanklin and Somerville, 1992). Most of the amino acid residues are generally hydrophilic, and there is a lack of hydrophobic clusters commonly found in membrane-associated proteins. This is consistent with SAD being a soluble plastidic protein. A putative transit peptide cleavage site could be identified by homology to the safflower SAD cleavage site (Gregory et al., 1991), resulting in a mature peptide of 366 amino acid residues. A high degree of conservation was observed between the flax SAD and the SAD from castor, cucumber, and safflower. Greater than 80% identity exists at the amino acid level within the mature SAD peptides of flax and the above-mentioned species (Gregory et al., 1991; Shanklin et al., 1991; Shanklin and Somerville, 1992).

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* Corresponding author; fax 61-6-246-5255.

Abbreviation: SAD, stearoyl-acyl carrier desaturase.

Table I. Characteristics of pDs1, a cDNA from flax encoding the SAD

Organism:	<i>Linum usitatissimum</i> L. (Flax, cv Glenelg).
Location of Gene:	Nuclear encoded.
Function:	Introduction of a <i>cis</i> double bond between carbons 9 and 10 of stearoyl-acyl carrier protein.
Clone Type, Designation:	cDNA, full-length, pDs1.
Method of Identification:	Sequence comparison (greater than 80% amino acid identity in the mature peptide) to cDNA encoding the SAD from castor, cucumber, and safflower.
Gene Copy Number and Expression:	Southern blot data suggested that the flax SAD is encoded by a single-copy gene, and northern analysis indicated that the transcript was abundant in the developing cotyledons.
Structural Features of the Protein:	The 1188-bp open reading frame encodes a 396-amino acid preprotein. A putative transit peptide of 30 amino acids could be identified by homology to the safflower preprotein resulting in a mature peptide of 366 amino acids.
Subcellular Location:	Soluble plastid enzyme.

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