A cDNA Clone for 5-Aminolevulinic Acid Dehydratase from Tomato (Lycopersicon esculentum Mill.)

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ALAD (EC 4.2.1.24) catalyzes the condensation of two ALA molecules to form porphobilinogen, a monopyrrole precursor of both heme and Chl (Richards, 1993). In plants, ALAD is synthesized in the cytoplasm and subsequently is associated exclusively with plastids, even in tissues in which synthesis of nonplastic heme is predominant (Smith, 1988). Synthesis of ALAD is amplified by the action of phytochrome (Tchuinmogne et al., 1989), and ALAD may interact with an ALA precursor (4,5-dioxovalerate) to limit Chl synthesis in light (Kotzabasis et al., 1989). We are investigating a possible regulatory role of ALAD in Chl synthesis during tomato (Lycopersicon esculentum Mill.) fruit development and ripening.

cDNAs encoding ALAD have been cloned from pea (Boese et al., 1991), spinach (Schaumburg et al., 1992), and soybean (Kaczor et al., 1994) in addition to those isolated from animal and bacterial species. We report here the complete nucleotide sequence of a cDNA for tomato fruit ALAD (Table I). A AZapII cDNA library constructed from 3- to 8-d fruits (obtained from Dr. Wilhelm Gruissem, University of California at Berkeley) was screened using a pea ALAD cDNA (Boese et al., 1991) insert as a probe. The tomato cDNA is 1775 nucleotides long and comprises an 18-nucleotide poly(A) tail. Open reading frame of 1290 nucleotides. Untranslated 5' and 3' regions of 51 and 434 nucleotides, respectively. The presence of a stop codon (TGA) six nucleotides upstream from the first ATG codon indicates that this ATG is in fact the initiation codon and that the coding sequence is complete. Tandem polyadenylation signals (AATAAA) are located at positions 1723 and 1729 in the 3' untranslated region. The tomato ALAD cDNA sequence showed 64.6% homology with spinach and 69.2% with pea.

Table I. Characteristics of a cDNA encoding tomato ALAD

| Organism: | Tomato (Lycopersicon esculentum Mill. cv VFNT Cherry). |
| Genome Location: | Nuclear genome. |
| Gene Product, Function: | ALAD (EC 4.2.1.24) catalyzes the conversion of two ALA molecules into one porphobilinogen molecule. |
| Source: | cDNA library in AZAPII constructed from 3- to 8-d fruits. |
| Techniques: | Library screened with heterologous probe from pea. Both strands sequenced by automated dideoxy method on an Applied Biosystem (Foster City, CA) 373A system. |
| Method of Identification: | Sequence comparison with published ALAD nucleotide sequences from pea and spinach. |
| Features of cDNA Sequence: | cDNA is 1775 nucleotides, including an 18-nucleotide poly(A) tail. Open reading frame of 1290 nucleotides. Untranslated 5' and 3' regions of 51 and 434 nucleotides, respectively. Tandem polyadenylation signal present in the 3' region. |

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The GenBank accession number for the sequence reported in this article is L31367.

LITERATURE CITED


Schaumburg A, Schneider-Poetsch HAW, Eckerskorn C (1992) Characterization of plastid 5-aminolevulinate dehydratase (ALAD; EC 4.2.1.24) from spinach (Spinacia oleracea L.) by sequencing and comparison with non-plant ALAD enzymes. Z Naturforsch 47c: 77–84
