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Plant Gene Register

Cloning and Sequencing of a cDNA Clone Encoding the Cytosolic Triose-Phosphate Isomerase from *Arabidopsis thaliana*[1]

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Photosynthesis, which converts solar energy and CO_2 into carbohydrates, is one of the most important metabolic pathways in plants. The fixation of CO_2 is carried out inside chloroplasts by a set of enzymes encoded mainly by nuclear genes (Weeden and Gottlieb, 1980; Cerff, 1982; Shih et al., 1986). In addition to photosynthetic carbon fixation enzymes, higher plants possess a set of similar enzymes that function in cytosolic glycolysis. Although the enzymic functions of the two pathways are quite similar, they are involved in the opposite directions of carbon metabolism. Expression of the photosynthetic carbon fixation genes and the glycolytic genes is affected differently by environmental conditions (Yang et al., 1993). Therefore, the two sets of genes can be used as model systems for studying how changing environmental conditions, such as light, carbon source, and temperature, affect plant growth and development at the molecular level.

The five steps in the conversion of 3-phosphoglycerate into Fru-6-P are identical for the two pathways except that the reactions flow in opposite directions. The chloroplast enzymes involved, phosphofructokinase, aldolase, TPI, glyceraldehyde-3-P dehydrogenase, and phosphoglycerate kinase, are structurally and functionally very similar to their cytosolic counterparts (Weeden and Gottlieb, 1980; Gottlieb, 1982). Therefore, the genes encoding these enzymes present very interesting models for studying not only the evolution of nuclear genes encoding chloroplast proteins but also how genes involved in two primary carbon metabolic pathways are regulated under different physiological conditions.

The genes and cDNA clones for cytosolic TPI have been obtained from several plant species, including maize (Marchionni and Gilbert, 1986) and rice (Xu and Hall, 1993; Xu et al., 1993). I report here the cloning and characterization (Table I) of the cDNA clone encoding cytosolic TPI from *Arabidopsis thaliana*. A maize TPI cDNA fragment was obtained by PCR amplification and used to screen an *Arabidopsis* leaf cDNA library. Partial sequence analysis and restriction mapping indicated that isolated clones belong to the same cDNA. The complete nucleotide sequence for the longest clone was determined.

The putative *Arabidopsis* cytosolic TPI clone contains an open reading frame of 254 amino acids. The deduced amino acid sequence of the *Arabidopsis* TPI contains features characteristic of TPI that are conserved throughout evolution (Marchionni and Gilbert, 1986). It has 82% identity with that of maize and rice clones. In contrast, the deduced amino acid of all three plant cytosolic TPIs shows only about 60% identity with that of chicken TPI.

Table I. *Characteristics of an Arabidopsis cytosolic cDNA clone*

Organism:	*Arabidopsis thaliana* L. (Heynh.) ecotype Columbia.
Function:	Encodes glycolytic enzyme TPI (EC 5.3.1.1).
Techniques:	Screening of an *Arabidopsis* λgt11 leaf cDNA library using maize cytosolic TPI (Marchionni and Gilbert, 1986) as the hybridization probe. Nucleotide sequence was determined by the dideoxy chain termination method, using double-stranded DNA as templates.
Confirmation:	Deduced amino acid sequence identity with TPI from maize (Marchionni and Gilbert, 1986) and rice (Xu and Hall, 1993).
Location of the Gene:	Nuclei.
Expression Pattern:	The corresponding mRNA can be detected in leaves, stems, and roots.
Features of Protein Sequence:	254 amino acids, 82% identity was TPI from maize and rice and 61% identity with chicken TPI.
Subcellular Location:	Cytosol.

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Abbreviation: TPI, triose-phosphate isomerase.

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