

Plant Gene Register

The *Arabidopsis thaliana* myo-Inositol 1-Phosphate Synthase (EC 5.5.1.4)¹

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Inositol has been recognized as an essential growth factor for plants, animals, yeast, and some microorganisms since the earliest recording of its occurrence in plant materials. Metabolic products of inositol have been shown to play a vital role in signal transmission for a wide variety of hormones, growth factors, and neurotransmitters (Loewus and Loewus, 1983; Berridge and Irvine, 1989; Boss, 1989).

Because inositol's mechanistic role in most cellular processes of plants and animals remains to be elucidated, we necessarily began our initial studies of the regulation of inositol biosynthesis and metabolism in the higher plant *Arabidopsis* by isolating and studying the gene that encodes the pivotal biosynthetic enzyme, MI-1-P synthase. This enzyme is known to catalyze a complex series of reactions that involve at least three partial reactions (Loewus and Loewus, 1983; Loewus, 1990). A mechanism based on experimental observations has been proposed (Kiely and Sherman, 1975; Sherman et al., 1977; Wong and Sherman, 1985). An *Arabidopsis thaliana*, ecotype Columbia, full-length cDNA sequence encoding a protein with MI-1-P synthase activity has been isolated and used to study the regulation of inositol biosynthesis in *Arabidopsis* (M.D. Johnson and I. Sussex, unpublished data).

Here we report the characteristics of the cDNA clone as determined by DNA sequencing (Table I). Sequence data base searches were performed using programs based on the BLAST algorithm (Altschul et al., 1990). The BLASTP program was used to screen the amino acid sequence version of the Non-Redundant DataBase (National Center for Biotechnology Information, National Institutes of Health, Bethesda, MD). The data base search revealed two proteins that produced high-scoring segment pairs. The highest score, 740, was generated from GenBank entrant # (gp!Z11693!SPMIPHSYM), D-myoinositol 3-phosphate synthase from *Spirodela polyrrhiza* (Smart and Fleming, 1993). The second highest score, 549, resulted from the comparison of entrant # (gp!L23520!YSCINO1A), myo-inositol 1-phosphate synthase from the yeast *Saccharomyces cerevisiae* (Johnson and Henry, 1989). These results suggest that inositol synthases are highly conserved. High-scoring segment pairs

Table I. Characteristics of a cDNA clone encoding MI-1-P synthase

Organism:	<i>Arabidopsis thaliana</i> ecotype Columbia.
Source:	cDNA library (λ YES-R) in λ YES constructed from poly(A) ⁺ RNA of vegetative and flowering whole plants of <i>Arabidopsis</i> .
Isolation:	Complementation of a yeast inositol mutant.
Sequencing Technique:	cDNA was subcloned into pBluescript; both strands sequenced using double-stranded plasmid minipreps with Sequenase and synthetic oligonucleotides.
Method of Identification:	Genetic complementation, enzyme assays, and regulatory studies of the corresponding gene.
Feature of cDNA Structure:	The clone consists of 1902 bp; translation starts at nucleotide +50 with an open reading frame of 471 amino acids, a predicted molecular weight of 52,541, net charge of -4 at pH 7.0, and an amino acid composition containing 40% hydrophobic residues.
Antibodies:	Yeast polyclonal antibody to MI-1-P synthase.
Subcellular Location:	To be reported.
Function:	Converts Glc 6-phosphate to inositol 1-phosphate.

will be used to define conserved sequence motifs. These motifs will be used to delineate domains that are responsible for the inositol synthase activities.

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Abbreviation: MI-1-P synthase, myo-inositol 1-phosphate synthase.

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