

Plant Gene Register

Nucleotide Sequence of a cDNA Encoding Malic Enzyme from Poplar¹

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NADP-dependent ME³ (EC 1.1.1.40) catalyzes the oxidative decarboxylation of malate to pyruvate-generating reducing equivalents (NADPH + H⁺) and CO₂. In plants, both cytosolic and chloroplastic NADP-ME have been found (6).

A leaf cDNA library from a poplar hybrid (*Populus deltoides* × *P. trichocarpa* clone 064) constructed in the vector pUC18 was screened with an NADP-ME cDNA clone from *Phaseolus vulgaris* (7, 8) (Table I). Figure 1 shows the nucleotide sequence of the 2071-bp cDNA insert and the derived amino acid sequence. The cDNA contains one continuous open reading frame corresponding to a protein of 589 amino acid residues (calculated *M_r*, 64,900). The translation initiation codon is preceded by an in-frame stop codon. The polypeptide is 79 and 73% homologous with the NADP-ME from bean (8) and maize (4), respectively. Neither the poplar nor the bean NADP-ME polypeptides contain an apparent transit sequence for translocation to the chloroplasts, suggesting that they are located in the cytosol. Northern hybridizations revealed that the amounts of steady-state NADP-ME mRNA is twofold higher in leaves and stems of *in vitro* grown poplar plants as compared to the levels found in roots (data not shown).

ACKNOWLEDGMENTS

We thank Dr. M. H. Walter for providing the bean pCAD4a clone. J. V. D. is indebted to the Instituut ter aanmoediging van het Wetenschappelijk Onderzoek in Nijverheid en Landbouw for a predoctoral fellowship.

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¹ This work was supported by a grant from the Commission of the European Communities (ECLAIR-OPLIGE No. AGRE-0021-C[EDB]).

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³ Abbreviation: ME, malic enzyme.

Table I. Characteristics of cDNA pPOPCAD1 from Poplar

Organism: *Populus deltoides* × *Populus trichocarpa*, clone 064 (Afocel, France).

Location on chromosome: Unknown.

Gene product; pathway: NADP-dependent ME (EC 1.1.1.40); Calvin cycle and other metabolic pathways (1, 4).

Techniques: Plasmid sequencing (5); RNA preparation (2); northern analysis (3).

Method of identification: Sequence comparison with a chloroplastic NADP-dependent ME from maize (73% homology) and a cytosolic NADP-dependent ME from bean (79% homology) (4).

Expression characteristics: Transcript of about 2200 nucleotides; transcript termini not determined.

Regulation: Unknown.

Features of cDNA structure: Putative polyadenylation signal (AATAAA at position 2008).

Codon usage: No significant differences in codon usage.

(G + C) content: 44.5%.

Structural features of protein: ORF 589 amino acids; *M_r*, 64,900; protein expression not tested; putative charge at pH 7 = 6.36; proposed NADP-binding site VYPTVG (positions 138–144); proposed NAD-binding site ILGLGDLG (positions 193–200); the proposed NAD- and NADP-binding sites are each followed by a cysteine (6, and references therein).

Antibodies: None available.

Subcellular location: Not tested, most probably cytosolic.

EMBL accession No.: X56233.

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	ACCAAACCACTACTCCAGAACATTGTATTTAATCTCTATATTTGCTGTTT	
54	CTCCCTTGATTTGAAAGAAGAAAGGTCAGGTTAGGTTCGGTTGGTTAGTTGATATTCAAGATCAGCAGAGAGAGATTAAGTCAGTCAGA	
153	ATGGAGAGCACGCTGAAGGAGATGAGAGACGGAGCTCGGTGCTGCACATGGACCCCAAATCCTACTGTCGGTGGTGGTGGACGTTATGGCGAG	
252	M E S T L K E M R D G A S V L D M D P K S T V G G G V E D V Y G E	33
	GATCGTGCCTACTGAGGACCAGCTGTTACTCCCTGGACCATCTCGTTGCCAGTGGAATATACTTTGTTGAGGGATCCACATCACAAACAAAGGGCTGCT	
D R A T E D Q L V T P W T I S V A S G Y T L L R D P H H N K G L A	66	
351	TTCACTGAGAAAGAAGAGATGCACACTACCTCGCTGGTCTCTCCCTCCAACAACATCTCTCAACAGCTCAGGAAAAGAAATTGATGAACACCATT	
F T E K E R D A H Y L R G L L P P T I S Q Q L Q E K K L M N T I	99	
450	AGACAAATATCAACTCCTCTAAACATACGGCCATGATGGAACCTTGAGGAAGGAAATGAAAGGTTGTTTATAAGCTTTGATCGATAATGTTGAG	
R Q Y Q L P L Q K Y T A M M E L E E R N E R L F Y K L L I D N V E	132	
549	GAATTGCTTCCGGTGTGTTATACACCGACGGTGGGAGCTTGCAGAGATGGAAGTATTTCAGCTCTCAGGGCTATATATAAGTTAAAA	
E L L P V V Y T P T V G E A C Q K Y G S I F K R P Q G L Y I S L K	165	
648	GAGAAGGGAAAGTCTTGATGTGCTGAAAAACTGGCCATGAGAGTATTCAAGTTATTGTGTTACTGATGGTGAAGAATTGGGACTGGGAT	
E K G K V L D V L K N W P Q K S I Q V I V V T D G E R I L G L G D	198	
747	CTTGGCTGTAGGGAAATAGGCATCTCTGTTGGGAGCTGCTCTTACACTGCACTTGGAGGAGTTCGCTCTCAGCTGTTGCCGTAAACCATGAT	
L G C Q G I G I P V G K L S L Y T A L G G V R P S A C L P V T I D	231	
846	GTGGGTACGAAACACGAGCAATTGCTGAAGGATGAATTCTACATTGGACTGAGACAAAGGAGGGCACTGGCCAGGAATACTGAACTTCTCCATGAG	
V G T N N E Q L L K D E F Y I G L R Q R R A T G Q E Y S E L L H E	264	
945	TTCATGACTGCTGAAACAAATTATGGGGAGAAAGTCTGATACAGTTGAAGATTTCGTAACCACAATGCTTTGATCGTCTGCAAAGTATGCC	
F M T A V K Q N Y G E K V L I Q F E D F A N H N A F D L L A K Y G	297	
1044	ACAACCTTTAGTCTCAATGATGATATAACAGGGACGGCTGCTGTTCTGCAGGGCTTATTCAGCACTGAAGTTGCTAGGTGGTCCCTGGCT	
T T H L V F N D I Q G T A A V V L A G L I S A K L I G G S L A	330	
1143	GATCACACTTCTTCTGGTCTGGTGAAGCTGGACTGGTATAGCAGAGCTTAGCTGATGAGATGCAAGACGGTCAAAACACTCTGGAA	
D H T F L F L G A G E A G T G I A E L I A L E M S R R S K T P L E	363	
1242	GAGACTCGAAGAAGATTGGCTGACAGATTCAAAAGGTTGATTGTTAGTCTCGCAAGGGAGTCATTACAACACTCAAGAACCATGGGCTCATGAA	
E T R K K I W L T D S K G L I V S S R K E S L Q H F K K P W A H E	396	
1341	CATGAACCCGTTAAAGGACTCTAGAAGTGTCAAGGAATCAAACCAATAGTCTGATGGAACATCCGGAGTGGAAAAACGTTACTAAGGAAGTG	
H E P V K G L L E V V K A I K P L V L I G T S G V G K T F T K E V	429	
1440	ATTGAGGCATGGCTCTTCAATGAGAAACCTCTAAATTGGCTCTCCAACCCAACCTCACATCTGAATGTCAGCTCAAGAACCTACATTGG	
I E A M A S F N E K P L I L A N S P T S Q S E C T A E E A Y T W	462	
1539	ACTAAGGGCAAAGCAATTGGCTAGTGGAAAGTCCATTGATCTGTTGAGTACGAGGGAAAGTTGTTCTGGCCAGTCAACAAATGCTACATT	
G K G K A I F A S G S P F D P V E Y E G K V F V P G Q S N N A Y I	495	
1638	TTCCCTGGCCTGGGTTGGCATCTCTGGAGCTATTGTTGATGATGATGCTTCTGGCAGCCGCGGAAGCCTGGCTGGCAAATTAAAGAAGAG	
F P G L G L V I S G A I R V H D D M L L A A A E A L A G Q I K E E	528	
1737	TACTTGGCAAAGGGCTGATTAACCCACCTCTATCTAACATCAGAAAAATCTCAGTCCAAATTGCTGCTAACGTAGCTGCAAGGCATATGAACTTGGC	
Y L A K G L I Y P P L S N I R K I S V Q I A A N V A A K A Y E L G	561	
1836	CTGGCTACACGTCTCCCCCGTCCAGAAAACCTTGTGAAGCAGCCAGAGAGTTGCTACAGTCCCGCTATAGATATTACCGGTGAATTGCTGACT	
L A T R L P R P E N L V K H A E S C M Y S P A Y R Y Y R	589	
1935	GTGCTTGTGCAATTATGCTTCTTGGTGTAGAGCAACCGCTAATAAGCAAATAATTGCTGGCTTGTAAATATC	
2034	AGTACCTGTAAACTAGTAAATGGAGCTACATTCTA	

Figure 1. Nucleotide sequence of the 2071-bp cDNA insert and the derived amino acid sequence of pPOPCAD1 from poplar.