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Brandenburg SA, Williamson CL, Slocum RD (1998) Characterization of a cDNA encoding the small subunit of Arabidopsis carbamoyl phosphate synthetase (accession no. U73175) (PGR 98–087). *Plant Physiol* **117**: 717.

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Plant Gene Register PGR 98–087

Characterization of a cDNA Encoding the Small Subunit of Arabidopsis Carbamoyl Phosphate Synthetase (Accession No. U73175).

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Plant Gene Register PGR 98–088

Molecular Cloning and Sequencing of a Broccoli cDNA (Accession No. AF047476) Encoding an ETR-Type Ethylene Receptor.

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Plant Gene Register PGR 98–090

Nucleotide Sequence of a cDNA Clone (Accession No. AF047694) for Glutaredoxin from *Aleurites fordii* Seeds.

Fuqiang Tang*, John M. Dyer, Alan R. Lax, Ding S. Shih, Dorselyn C. Chapital, and Armand B. Pepperman.

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Plant Gene Register PGR 98–089

cDNA Cloning of Aquaporin (Accession No. AF047173) from *Aleurites fordii* Seeds.

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Plant Gene Register PGR 98–091

Isolation of a Novel Gene Coding for a Putative Arginine/Serine-Rich Splicing Factor Homologous to PR264/SC35 (Accession No. Y16672) from Alfalfa.

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Plant Gene Register PGR 98–092

Ribosomal Protein L24 Homolog (Accession No. AJ225027) Is Expressed in *Cicer arietinum* L. Epicotyls.

etale, 234 Av du Brezet, Domaine de Crouelle, 63039 Clermont-Ferrand cedex 2, France (D.T.).

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Plant Gene Register PGR 98-109

Cloning and Expression Analysis of a cDNA for Carrot Ubiquitin Carboxyl Extension Protein (Accession No. U68751).

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Plant Gene Register PGR 98-110

cDNA and Deduced Amino Acid Sequence of a Cytosolic Aldolase (Accession No. AJ005041) from *Cicer arietinum* L. Epicotyls.

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Plant Gene Register PGR 98-111

Molecular Cloning of Two cDNAs Encoding Novel Myb Homologs from *Arabidopsis* (Accession Nos. AB005888 and AB005889).

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Plant Gene Register PGR 98-112

PEP2, a Second bHLH Protein Binding to the E-box Motif of the Bean Seed-Storage Protein Beta-Phaseolin Bene (Accession No. U18349).

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Plant Gene Register PGR98-110

Berta Dopico, Francisco J. Muñoz and Emilia Labrador (1998) cDNA and Deduced Amino-acid Sequence of a Cytosolic Aldolase (Accession No. AJ005041) from *Cicer arietinum* L. epicotyls. (PGR98-110) Plant Physiol. 117: 720

cDNA and Deduced Amino-acid Sequence of a Cytosolic Aldolase (Accession No. AJ005041) from *Cicer arietinum* L. epicotyls

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Fructose-1,6-bisphosphate aldolase (EC 4.1.2.13) catalyzes the reversible aldol cleavage of fructose-1,6-bisphosphate into D-glyceraldehyde 3-phosphate and dihydroacetone phosphate. Aldolase is a prerequisite for both the glycolytic/gluconeogenic pathway and the pentose phosphate cycle and Calvin cycle in plants, and at least two isozyme forms differing in their cellular location, cytoplasm and chloroplast, are known (Anderson and Levin, 1970). The chloroplastic and cytosolic aldolases of higher plants are class-I type enzymes forming a Schiff base with the substrate as intermediate.

We report here the nucleotide sequence of a full-length cDNA encoding a cytosolic fructose-1,6-bisphosphate aldolase from chickpea epicotyls (*Cicer arietinum* L cv castellana). This AldC cDNA sequence has an open reading frame consisting of 1077 bp. The encoded protein contains 359 aminoacids residues from which a molecular mass of 38,45 kDa can be estimated.

Comparison of the amino acid sequences of chickpea aldolase with other plant cytosolic aldolases revealed a high homology among them. The highest homology is with *Pisum sativum* aldolase cytoplasmic isozyme 2, Aldcyt-2 (90,3%) and with *Oryza sativa* AldC-2 (79,3%) (Hidaka *et al.* 1990). Also high homology present to cytosol aldolase from *Zea mays* (77,7%) (Kelley and Tolan, 1986), *Spinacia oleracea* (76,2%) (Pelzer-Reith *et al.* 1993) and *Pisum* aldolase isozyme 1 (77%).

The active site of chickpea aldolase (by similarity) is located in a highly conserved region of the protein that includes the amino acid Lys-226, which forms a Schiff base with the substrate (Kelly and Tolan, 1986). This lysine residue is conserved in all cytosolic aldolases of plants, ranging from Lys-225 in corn and pea aldolase 1 to Lys-226 in pea aldolase 2. In chickpea aldolase, by homology to other cytoplasmic aldolases described (Kelly and Tolan, 1986), the residues Arg-52 and Lys-142 seem to interact with the C1 phosphate group of fructose 1,6-bisphosphate and residue Lys-103 with the C6 phosphate group. These residues are also found in chloroplast aldolase (Arg-47, Lys-137 and Lys-98), within conserved domains of the protein (Pelzer-Reith *et al.* 1993). The C-terminal tyrosine residue is conserved in plant aldolases, and have been described that is essential for enhanced activity of the enzyme toward fructose 1,6-bisphosphate as compared with fructose 1-phosphate.

Acknowledgements

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Table I. Characteristics of CanAldC from *Cicer arietinum*

Organism:

Cicer arietinum L cv. castellana

Clone Type, Designation:

cDNA, full length, CanAldC

Source:

cDNA library in lambda-ZAP constructed from poly A+ RNA from *Cicer arietinum* 5-day-old epicotyls.

Gene identification:

Nucleotide and amino acid sequence comparisons to published sequences in GenBank and EMBL data bases and Swiss-Prot and Blitz data bases respectively.

Feature of the cDNA:

The clone is 1370 bp in length, including a complete ORF of 1077 bp, 39-bp 5' untranslated sequence and 254-bp 3' untranslated sequence.

Features of deduced protein:

The ORF encodes a 359 amino acid polypeptide. The encoded protein has a predicted molecular mass of 38,45 kD and an isoelectric point of 6,47. Ala (11,70 %) and Leu (10,86 %) present the highest percentage.

Gene product:

A cytosolic fructose-1,6-bisphosphate aldolase.

Literature cited

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Hidaka S, Kadowaki K, Tsutsumi K, Ishikawa K (1990) Nucleotide sequence of the rice cytoplasmic aldolase cDNA. *Nucl. Acid. Res.* **18**: 3991

Kelley PM, Tolan DR (1986) The complete amino acid sequence for the anaerobically induced aldolase from maize derived from cDNA clones. *Plant Physiol.* **82**:1076-1080

Pelzer-Reith B, Penger A, Schnarrenberger C (1993) Plant aldolase: cDNA and deduced amino-acid sequences of the chloroplast and cytosol enzyme from spinach. *Plant Mol. Biol.* **21**: 331-340



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