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Plant Gene Register PGR 98–190

Cloning, Expression, and Mapping of a Second Tomato Sucrose Synthase Gene, *Sus3* (Accession Nos. AJ011319 and AJ011534).

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Plant Gene Register PGR 98–191

cDNA Isolation of Two Serine/Threonine Phosphatases (PP1 and PP2A) from *Catharanthus roseus* (Accession Nos. AJ007332 and AJ007333).

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Plant Gene Register PGR 98–192

Nucleotide and Deduced Amino Acid Sequences of the Pyruvate Dehydrogenase Kinase from *Arabidopsis* (Accession No. AF039406).

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Plant Gene Register PGR 98–193

Genomic Nucleotide Sequence of a NADP Sorbitol-6-Phosphate Dehydrogenase Gene from Apple (Accession No. AF057134).

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Plant Gene Register PGR 98–194

Soybean Gene Coding for a Nodule-Specific Glutamine Synthetase (Accession No. AF091456).

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Plant Gene Register PGR 98–195

Identification of a Putative Chloroplastic Fructose-1-6-Bisphosphate Aldolase (Accession No. AJ011516) of *Scherffelia dubia* (Chlorophyta).

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Plant Gene Register PGR 98-212

The cDNA Sequence of *AtSIG4*, a New Member of the Nuclear-Encoded Σ -Like-Factor Gene Family in *Arabidopsis* (Accession No. AF101075).

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Plant Gene Register PGR 98-213

Characterization of a Drought-Induced Soybean cDNA Encoding a Plant Defensin (Accession No. U12150).

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Plant Gene Register PGR 98-214

Cloning of a Plant Isochorismate Synthase (Accession No. AF078080).

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Plant Gene Register PGR 98-215

cDNA Sequence Encoding an Histone H2A from *Cicer arietinum* (Accession No. AJ006768).

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Plant Gene Register PGR 98-216

Isolation and Sequence Analysis of a cDNA Encoding a Ribosome-Associated p40 Protein from a Cell-Suspension Culture of *Brassica napus* L. cv Jet Neuf (Accession No. AF097522).

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Plant Gene Register PGR 98-217

Isolation and Sequence Analysis of a Gene from *Cucurbit* (Accession No. AF099501) Encoding the Carotenoid-Associated Protein CHRC.

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Plant Gene Register PGR98-215

Berta Dopico, Rocio Esteban and Emilia Labrador (1998) cDNA Sequence Encoding an Histone H2A from *Cicer arietinum* (Accession No. AJ006768) (PGR98-215) Plant Physiol. **118**: 1536

cDNA Sequence Encoding an Histone H2A from *Cicer arietinum* (Accession No. AJ006768)

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Histones, a family of basic proteins found in all eukaryotic nuclei, are a major component of eukaryotic chromatin in association with DNA and nonhistone chromosomal proteins. There are five major types of histone chains, these are termed H1, H2A, H2B, H3 and H4. The synthesis of chromatin is not a continuous process but occurs in the late G1 and S phases of the cell cycle or during DNA endoduplication. The core histones H2A, H2B, H3 and H4 are among the most abundant and highly conserved proteins in eukaryotic organism (Stein *et al.*, 1984). The amino acid sequences of these four histones are now known for a wide variety of organism. These proteins and their mRNAs are usually synthesized in a cell cycle-dependent fashion at the beginning of S phase (Maxon *et al.*, 1983). This mode of synthesis is necessary to allow nucleosome formation on the duplicated DNA. Some histones are expressed in a non-cell cycle-dependent manner.

We have isolated a cDNA clone corresponding to a histone H2A gene from *Cicer arietinum*. The identification of the clone was based on the high degree of nucleotide sequence identity (89-70%) to a range of histone H2A genes and the presence of a 9 amino acids long sequence identical to the conserved H2A box in the deduced amino acid sequence.

The nucleotide sequence of the cDNA clone CanH2A contains an open reading frame with the start codon at position 83. The ORF encodes a putative protein of 139 amino acids with a calculated molecular weight of 14.607 and a pI of 10.34. The nucleotide sequence shows identity to the sequences of *Pinus taeda* H2A (75%), wheat H2A (69.9%), pea H2A (69.1%), *Chlamydomonas* (66.05%). The deduced amino acid sequence of the chickpea protein is highly similar to *Picea* H2A (89.1% identity) (Sundas *et al.*, 1993) a gymnosperm species. Also present high identity to *Volvox* and *Chlamydomonas* (78.3 and 77.5% respectively). Lower homology was found as we compare with other angiosperms as *Phaseolus* (72.7%) (Guo *et al.*, 1994) or *Triticum* (74.1%) (Huh *et al.*, 1995). The chickpea histone H2A sequence AGLQFPVGR (amino acids 26 to 34) is identical to the highly conserved "H2A box", described in every H2A histone sequences investigated so far (van Daal *et al.*, 1988)

All histone H2A share a typical central core region but their amino and carboxy terminal regions differ. However, due to the high homology to *Picea*, the histone H2A from chickpea also share the carboxy terminal with *Picea* H2A.

Acknowledgements

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Table I. Characteristics of CanH2A from *Cicer arietinum*

Organism:

Cicer arietinum L cv. castellana

Clone Type, Designation:

cDNA, full length, CanH2A

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 Swall data bases respectively.

Feature of the cDNA

The clone is 685 bp in length, including a complete ORF of 417 bp. Untranslated 5' and 3' regions of 82 and 186 nucleotides, respectively.

Features of deduced protein:

The ORF encodes a 139 amino acid polypeptide. The encoded protein has a predicted molecular mass of 14.607 kD, and an isoelectric point of 10.34.

Gene product:

A histone H2A protein.

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