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The Electronic Plant Gene Register

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Plant Gene Register PGR 99–025

Sequence Analysis of a cDNA Encoding Pex10p, a Zinc-Binding Peroxisomal Integral Membrane Protein from Arabidopsis (Accession No. AF119572).

Uwe Schumann, Christine Gietl*, and Markus Schmid.
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Plant Gene Register PGR 99–026

Nucleotide Sequence of a Caffeic Acid *O*-Methyltransferase Gene (Accession No. F119225) from *Pinus radiata*.

Richard Moyle*, Armin Wagner, and Christian Walter.
New Zealand Forest Research Institute Limited, Sala Street, Private Bag 3020, Rotorua, New Zealand.
* Corresponding author; e-mail moyler@fri.cri.nz; fax 64–7–347–5444.

Plant Gene Register PGR 99–027

A mRNA (Accession No. AF109156) from Symbiotic Root Nodules of *Datisca glomerata* with Homology to Thiosulfate Sulfurtransferase Genes.

Patricia A. Okubara[1] and Alison M. Berry*.
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Plant Gene Register PGR 99–028

Sequence Analysis of a Vacuole-Associated Annexin (Accession No. AF113545) from Tobacco.

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Dartmouth Medical School, Department of Biochemistry, 1700 Vail Building, Hanover, New Hampshire 03755 (D.F.S.); and Indiana University-Purdue University at Indianapolis, Department of Biology, 723 West Michigan Street, Indianapolis, Indiana 46202 (S.K.R.).
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Plant Gene Register PGR 99–029

The Nucleotide Sequence of a Tobacco Homolog of *Pftf* (Accession No. AF117339). Evidence for Two Plastid-Localized AAA-Family Proteins in Higher Plants.

Elizabeth J. Summer and Kenneth Cline*.
Horticultural Sciences Department and Plant Molecular and Cellular Biology Program, University of Florida, Gainesville, Florida 32611–0690.
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Plant Gene Register PGR 99–030

Cloning of a Wound-Induced Gene WI12 from *Mesembryanthemum crystallinum* (Accession No. AF117224).

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Plant Gene Register PGR 99–040

An S-Like Ribonuclease Is Expressed in *Cicer arietinum* Epicotyls (Accession No. AJ012689).

Rocio Esteban, Berta Dopico, and Emilia Labrador*.
Departamento de Fisiología Vegetal, Facultad de Biología, Universidad de Salamanca, E-37007, Salamanca, Spain.
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Plant Gene Register PGR 99–041

Characterization of a cDNA Encoding a Thaumatin-Like Protein from *Pseudotsuga menziesii* (Accession No. AJ131731).

Roberto G. Iglesias*, Gregorio Nicolás, and Maria J. Babiano.
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Plant Gene Register PGR 99–042

A Rice Transposon Protein-Like cDNA Is Induced by *Magnaporthe grisea* (Accession No. AF121139).

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Plant Gene Register PGR 99–043

An mRNA (Accession No. AF119050) from Symbiotic Root Nodules of *Datisca glomerata* with Homology to Zinc Finger Transcription Factor Genes.

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PLANT GENE REGISTER PGR99-040

Rocio Esteban, Berta Dopico and Emilia Labrador (1999) An S-like Ribonuclease is Expressed in *Cicer arietinum* Epicotyls (Accession No. AJ012689). (PGR99-040) Plant Physiol. 119: 1149

An S-like Ribonuclease is Expressed in *Cicer arietinum* Epicotyls (Accession No. AJ012689)

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REPORT

In plants, several RNase families have been characterized biochemically (for review see Green 1994), but only one has been shown to have members with functions in RNA degradation. This group, the T2/S superfamily has also been identified in other organisms as fungal (Kawata et al. 1988) or animal systems (Watanabe et al. 1993). In plants T2/S type Rnases have a specialized function:involvement in self-incompatibility (SI) a genetic barrier to self fertilization.These RNases are referred to as S-RNases. Related RNases (S-like RNases) have been identified in self-compatible species, indicating that RNases in the T2/S family likely exist in a broad range of plants.

We reported here the isolation and characterization of a cDNA expressed in chickpea epicotyls, whose deduced amino acid sequence showed high similarity with RNases. The highest homology is with the RNS1 (69.4 % similarity) and RNS3 (63.1 %) from *Arabidopsis thaliana* (Bariola et al. 1994) and with RNLE (62.9%) and RNLX (58.5%) from *Lycopersicum esculentum* (KÖck et al. 1995), all of them classified as S-like RNases because they exhibit sequence homology to the S- and the fungal T2-type RNases. Lower homology presents with plant S-RNase sequences as RNS2 of *Solanum tuberosum* (21.1 %) (A No. Q01796) or RNS3 of *Petunia hybrida* (18.5 %) (A No. Q40875).

S and S-like RNases are distinct subclasses within the same RNase superfamily. This type of enzyme represents a major class of RNase in the Angiosperms and probably in the plant kingdom. Each subclass contains highly conserved residues that are not conserved among members of the other subclasses (Taylor et al. 1993). The residues that distinguish the S-like RNases from the S-RNases are located primarily between the active-site histidines, where most of the residues common to the fungal enzymes are located, and at the N-terminus. A cluster of amino acids that are conserved only in the S-RNases is located between positions 143 and 156

The chickpea RNase cDNA contains a 687 bp open reading frame encoding a polypeptide of 229 amino acid residues. The three active site histidine residues that are required for the catalytic activity of RNase are located at positions 64, 117 and 122, being these positions similar to other S-like RNases (64, 118, 122 for RNLE or 65, 119, 123 for RNS1 of Arabidopsis). Chickpea RNase, as most of the S-like RNases, have a signal sequence and, therefore enter the secretory pathway. RNase LE is secreted into the medium in cultured tomato cells, and its high structural similarity with CanRN indicate that this enzyme is also extracellular, as have been postulated for RNS1 and RNS3, with a high similarity also.

The finding that some of these S-like RNases are induced by phosphate (Pi) starvation (Nürnberger et al. 1990, Bariola et al. 1994) indicates that the S-like RNases could play a role in the remobilization of Pi from RNA under conditions of Pi deficiency.

ACKNOWLEDGMENTS

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TABLE I

Characteristics of CanRN from Cicer arietinum

Organism:
Cicer arietinum L cv. castellana

Clone Type, Designation:
cDNA, full length,CanRN

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 935 bp in length, including a complete ORF of 687 bp. Untranslated 5' and 3' regions of 43 and 205 nucleotides, respectively.

Features of deduced protein:
The ORF encodes a 229 amino acid polypeptide. The encoded protein has a predicted molecular mass of 25.291 kD, and an isoelectric point of 4.56.

Gene product:
A S-like ribonuclease T2 protein. Similarity to fungal Ribonuclease of the T2/RH/M family and to plants self-incompatibility ribonucleases.

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