The Electronic Plant Gene Register

Plant Gene Register titles for PGR 99–014 to PGR 99–024 appear below. The sequences have been deposited in GenBank and the articles listed online through the World Wide Web.

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Duff RJ, Oliver MJ, Wood AJ (1998) Nucleotide sequence of a truncated cDNA (accession no. AF093108) encoding a H3-like histone protein from the bryophyte *Tortula ruralis* (PGR 99–014). Plant Physiol **119**: 805.

To access the Plant Gene Register through the World Wide Web, use the URL:

http://www.tarweed.com/pgr/

Plant Gene Register PGR 99-014

Nucleotide Sequence of a Truncated cDNA (Accession No. AF093108) Encoding a H3-Like Histone Protein from the Bryophyte *Tortula ruralis*.

R. Joel Duff, Melvin J. Oliver, and Andrew J. Wood*.

Department of Plant Biology, Southern Illinois University-Carbondale, Carbondale, Illinois 62901–6509 (R.J.D., A.J.W.); and Plant Stress and Water Conservation Unit, United States Department of Agriculture-Agricultural Research Service, Route 3, Box 215, Lubbock, Texas 79401 (M.J.O.).

*Corresponding author; e-mail wood@plant.siu.edu; fax 1–618–453–3441.

Plant Gene Register PGR 99-015

Isolation of a cDNA Clone Encoding 1-Aminocyclopropane-1-Carboxylate Oxidase from *Dendrobium crumenatum* (Accession No. AF038840).

Xiao-Hui Yang, Eng-Chong Pua, and Chong-Jin Goh*. Department of Biological Sciences, Faculty of Science, National University of Singapore, 10 Kent Ridge Crescent, Singapore 119260.

* Corresponding author; e-mail dbsgohcj@nus.edu.sg; fax 65–779–5671.

Plant Gene Register PGR 99-016

Nucleotide Sequence of a cDNA Encoding Ethylene Receptor from Banana Fruits (Accession No. AF113748).

Houng-Ta Wu, Yi-Yin Do, and Pung-Ling Huang*. Department of Horticulture, National Taiwan University, Taipei, Taiwan 106, Republic of China.

* Corresponding author; e-mail pungling@ccms.ntu.edu. tw; fax 886–2–2362–7053. Plant Gene Register PGR 99-017

Isolation, Sequence Analysis, and Expression of the Late-Embryogenesis-Abundant Protein of *Fagus sylvatica* L. Seeds (Accession No. AJ130888).

Oscar Lorenzo, Angel P. Calvo, Carlos Nicolás, Gregorio Nicolás, and Dolores Rodríguez*.

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Plant Gene Register PGR 99-018

Identification of Two Putative Nitrate Transporters Highly Homologous to CHL1 from Arabidopsis (Accession Nos. AJ011604 and AJ131464).

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* Corresponding author; e-mail ksaito@p.chiba-u.ac.jp; fax 81–43–290–2905.

Plant Gene Register PGR 99-019

Nucleotide Sequences of cDNAs Encoding Three Types of Metallothionein-Like Protein (Accession Nos. AF017366, U77284, AF017365, AF009959, and AF001396) from Rice.

Yong Hwan Kim, Myung Chul Lee*, Doh Won Yun, and Moo Young Eun.

Cytogenetics Division, National Institute of Agricultural Science and Technology, RDA, Suwon, 441–707, Korea.

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Plant Gene Register PGR 99-020

cDNA Sequence Encoding a Lysine-Rich H1 Histone of *Cicer arietinum* (Accession No. AJ006767).

Berta Dopico and Emilia Labrador*.

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Plant Gene Register PGR 99-021

Isolation and Characterization of a cDNA Encoding a Late-Embryogenesis-Abundant Protein (Accession No. AJ012483) from *Pseudotsuga menziesii* Seeds.

Roberto G. Iglesias* and J. Babiano.

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Plant Gene Register PGR 99-022

Nucleotide Sequence of a Tobacco cDNA Clone Encoding a Homolog of Proliferating Cell Nuclear Antigen (Accession No. AF038875).

Sun-Chung Park, Eun-Ha Park, and Jeong Woo Cho*. Kumho Life and Environmental Science Laboratory, 572 Sangamdong Kwangsanku, Kwangju 506–712, Korea. * Corresponding author; e-mail jwcho@ksc.kumho.co.kr; fax 82–62–972–5085.

Plant Gene Register PGR 99-023

Histone H3 Gene from *Porteresia coarctata* (Accession No. AF109910).

Padmanaban Senthilkumar, Madasamy Parani, Mukkamala Lakshmi, M.N. Jithesh, and Ajay Parida*.

M.S. Swaminathan Research Foundation, III Cross Road, Taramani Institutional Area, Chennai 600 113, India.

* Corresponding author; e-mail MDSAAA51@giasmd01. vsnl.net.in; fax 91–44–2351–319.

Plant Gene Register PGR 99-024

Molecular Cloning of a cDNA Sequence Encoding the H⁺/Ca²⁺ Antiporter 2 from the Japanese Morning Glory (Accession No. AB018526).

Toshio Yamaguchi, Yoshishige Inagaki, Sachiko Fukada-Tanaka, and Shigeru Iida*.

National Institute for Basic Biology, Division of Gene Expression and Regulation I, Myodaiji, Okazaki 444-8585, Japan.

* Corresponding author; e-mail shigiida@nibb.ac.jp; fax 81–564–55–7685.

▶ PLANT GENE REGISTER PGR99-020

Berta Dopico and Emilia Labrador (1999) cDNA Sequence Encoding a Lysine-Rich H1 Histone of Cicer arietinum (Accession No. AJ006767) (PGR99-020). Plant Physiol. 119: 806

cDNA Sequence Encoding a Lysine-Rich H1 Histone of Cicer arietinum (Accession No. AJ006767)

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REPORT

Histones are the major proteinaceous components of eukaryotic chromatin. In all higher eukaryotes, core histones (H2A, H2B, H3, H4) are encoded by genes whose expression is replication-dependent (Osley, 1991). The expression of the less abundant linker histones, H1, is generally more independent of the cell cycle (Osley, 1991). Unlike core histones, which are structural components of the nucleosomes, H1-type linker histones play a role in the formation of chromatin structure, both at the level of the nucleosome particle itself and in the formation of the higher-order structure of the chromatin fibre.

The biological function of the H1 histones is not yet fully understood. It is generally accepted that H1-type linker histones are parts of a general repressor mechanism affecting gene expression. Accordingly, they are found to be more abundant in condensed chromosomal structures which show little or no gene activity. H1-type histones might also be involved in the transcriptional control of specific genes (Grunstein, 1990, Zlatanova, 1990). The suggested functional versatility of the H1-type histones is accompanied by a structural diversity only characteristic of this class of histones.

Here we present the isolation and characterization of a chickpea cDNA encoding a H1-type histone. This chickpea histone H1 cDNA contains a 564 bp open reading frame encoding a polypeptide of 188 amino acid residues. The coding region is preceded by a 58 bp long 5'-untranslated region, which is in good agreement with the size of other 5'untranslated region observed in full-length plant histone cDNAs. A 198 bp long 3'untranslated region of the isolated cDNA contains a 15 nucleotide long poly (A) tract.

The deduced amino acid sequence of the protein showed the characteristic tripartite structure of H1-type histones. The most conserved domain of the protein, the so-called globular region (aa 61-133) revealed high homology to the analogous part of other plant H1 histones known. The highest homology is with the lysine-rich H1-41 histone from Pisum (67.6 %). Lower homology presents with other plant H1 histones of Pisum (48,9%), Arabidopsis (47.3), tobacco (45.7) and 42% with maize and Triticum H1 genes.

We must point out, that sequences of plant H1 histones show very limited homology outside the most conserved globular region.

Although it have been described that the EMIKDAIV segment represents the longest intact sequence element identical in all known dicot H1 histones (Szekeres et al., 1995), the chickpea H1 histone, in a similar way than H1-41 pea histone present amino acids TE instead KD.



TABLE I

Characteristics of CanH1 histone from Cicer arietinum

Organism:

Cicer arietinum L cv. castellana

Clone Type, Designation:

cDNA, full length, CanH1

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 820 bp in length, including a complete ORF of 564 bp. Untranslated 5' and 3' regions of 58 and 198 nucleotides, respectively.

Features of deduced protein:

The ORF encodes a 188 amino acid polypeptide. The encoded protein has a predicted molecular mass of 19.806 kD, and an isoelectric point of 10.64. Present a high content of amino acid lysine (30.4% by weight) (25% by frequency)

Gene product:

A histone H1 protein.

ACKNOWLEDGMENTS

This research was supported by a grant from the UE N° BIO4-CT97-2224.

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