

**Plant Gene Register**

# Nucleotide Sequence of a Rice Acidic Ribosomal Phosphoprotein P0 cDNA<sup>1</sup>

Yukako Hihara\*, Masaaki Umeda, Chikage Hara, Kinya Toriyama, and Hirofumi Uchimiya

Institute of Molecular and Cellular Biosciences, University of Tokyo, Bunkyo-ku, Tokyo 113, Japan (Y.H., M.U., C.H., H.U.); and Faculty of Agriculture, Tohoku University, Sendai 981, Japan (K.T.)

The eukaryotic 38-kD acidic ribosomal protein P0 is localized to the stalk of the 60S ribosomal subunit, forming a pentameric complex with dimers of 13-kD acidic ribosomal proteins P1 and P2 (Rich and Steitz, 1987). P1 (P2) and P0 are analogous to *Escherichia coli* ribosomal protein L7/L12, and L10, respectively, and are thought to have the same functions as their prokaryotic counterparts, i.e. binding to 28S rRNA, interaction with translation factors, promotion of aminoacyl-tRNA binding, and association with GTP-binding activity (Sanchez-Madrid et al., 1979; MacConnell and Kaplan, 1982). The P0 gene has been cloned from many species such as human (Rich and Steitz, 1987), yeast (Mitsui et al., 1989), rat (Wool et al., 1991), *Drosophila* (Grabowski et al., 1991), *Trypanosoma* (Schijman and Levin, 1992), and the dicotyledonous plant *Chenopodium rubrum* (Kaldenhoff and Richter, 1990). However, no reports have been presented of P0 gene isolated from a monocotyledonous plant.

We have carried out the random sequencing of cDNA clones derived from the anther-specific cDNA library of the graminaceous monocot rice (*Oryza sativa* L.) (Tsuchiya et al., 1992). By comparing partial sequences of cDNA clones to the GenBank data base, we found one clone (YK704) that is similar to the P0 protein gene. Thus, we were prompted to determine the complete nucleotide sequence of YK704 (Table I). The cDNA is 1220 bp in length, and the deduced open reading frame encodes a 34-kD protein of 319 amino acid residues. The nucleotide sequence shows 70% identity with that of *Chenopodium*, 60% with *Drosophila* and human, and 54% with yeast. The GC contents in the coding region and the third position of the codon are 55 and 70%, respectively. In the case of the dicotyledonous plant *Chenopodium*, the GC content in the coding region is 48%, and the third position of the codon shows 49% GC. Thus, the rice P0 gene has an apparent GC bias at the third position of the codon. As reported for other acidic ribosomal P0 proteins (Rich and Steitz, 1987; Mitsui et al., 1989; Wool et al., 1991), rice P0 protein appears to be hydrophobic because of the high content of hydrophobic amino acid residues such as Ala (9.7%), Val (10.3%), and Leu (9.7%).

The deduced amino acid sequence of rice P0 shows 68%

**Table I.** Characteristics of the acidic ribosomal phosphoprotein P0 cDNA from rice

Organism:	Rice ( <i>Oryza sativa</i> L. cv Hayayuki).
Source:	λZAP cDNA library constructed from poly(A) <sup>+</sup> RNA of rice anthers at the uninucleate microspore stage.
Techniques:	Double-strand plasmid sequencing of cDNA-library; dideoxy sequencing of restriction fragment subclones.
Method of Identification:	Deduced amino acid sequence shows 70% identity with that of <i>C. rubrum</i> .
Feature of the cDNA:	1220 nucleotides in length, consisting of a 111-nucleotide 5' untranslated region, a 960-nucleotide open reading frame, and a 149-nucleotide 3' untranslated region.
Feature of the Protein:	319 amino acid residues with a calculated <i>M<sub>r</sub></i> of 34,377.
(G + C) Content:	Coding region 55%.

identity with that of *Chenopodium*, 54% with *Drosophila*, 53% with human, 46% with yeast, and 38% with *Trypanosoma*. Among rice and the others, there are a lot of conserved amino acid residues that are not evenly dispersed but rather clustered, in areas of various length, throughout the polypeptide. Although the functions of these residues are unclear, there is one hydrophilic segment recognized as the putative 28S rRNA-binding site (Mitsui et al., 1989), which locates within amino acid positions 45 to 67 of rice P0. This region is Lys and Arg rich, and the positions of basic amino acids are well conserved. In the carboxy-terminal sequences, we found the characteristic segments such as an Ala-rich region in positions 279 to 296, an acidic amino acid-rich hydrophilic region in positions 298 to 312, and a hydrophobic terminus in positions 313 to 319. Each organism has these three segments, but they are not strictly conserved. Rice P0 possesses a putative casein kinase I phosphorylation site (XEXXSX) (Chan et al., 1986) in the Ser residue at position 309, which may have some role in regulating the protein activity. In the case of human, rat, and yeast, the carboxy-terminal segment (amino acid position 304–319) is well conserved among P0, P1, and P2, causing their immunological cross-reactivity (Rich and Steitz, 1987;

<sup>1</sup> This research was supported by Grant-in-Aid for Scientific Research, Ministry of Education, Culture and Science, Japan, and a grant from the Rockefeller Foundation.

\* Corresponding author; fax 81-03-3812-2910.

Mitsui et al., 1989; Wool et al., 1991). It will be intriguing to investigate the carboxy termini of rice P1 and P2 proteins.

Received January 3, 1994; accepted January 17, 1994.

Copyright Clearance Center: 0032-0889/94/105/0753/02.

The DDBJ/EMBL/GenBank accession number for the sequence reported in this article is D21130.

#### LITERATURE CITED

- Chan PK, Aldrich M, Cook RG, Busch H** (1986) Amino acid sequence of protein B12 phosphorylation site. *J Biol Chem* **261**: 1868–1872
- Grabowski DT, Deutsch WA, Derda D, Kelley MR** (1991) *Drosophila* AP3, a presumptive DNA repair protein, is homologous to human ribosomal associated protein P0. *Nucleic Acids Res* **19**: 4297
- Kaldenhoff R, Richter G** (1990) Light induction of genes preceding chloroplast differentiation in cultured plant cells. *Planta* **181**: 220–228
- MacConnell WP, Kaplan NO** (1982) The activity of the acidic phosphoproteins from the 80S rat liver ribosome. *J Biol Chem* **257**: 5359–5366
- Mitsui K, Nakagawa T, Tsurugi K** (1989) The gene and the primary structure of acidic ribosomal protein A0 from yeast *Saccharomyces cerevisiae* which shows partial homology to bacterial ribosomal protein L10. *J Biochem* **106**: 223–227
- Rich BE, Steitz JA** (1987) Human acidic ribosomal phosphoproteins P0, P1, and P2: analysis of cDNA clones, in vitro synthesis, and assembly. *Mol Cell Biol* **7**: 4065–4074
- Sanchez-Madrid F, Reyes R, Conde P, Ballesta JPG** (1979) Acidic ribosomal proteins from eukaryotic cells. *Eur J Biochem* **98**: 409–416
- Schijman AG, Levin MJ** (1992) Nucleotide sequence of a cDNA encoding a *Trypanosoma cruzi* acidic ribosomal P0 protein: a novel C-terminal domain in *T. cruzi* ribosomal P proteins. *Nucleic Acids Res* **20**: 2894
- Tsuchiya T, Toriyama K, Nasrallah M, Ejiri S** (1992) Isolation of genes abundantly expressed in rice anthers at the microspore stage. *Plant Mol Biol* **20**: 1189–1193
- Wool IG, Chan YL, Glück A, Suzuki K** (1991) The primary structure of rat ribosomal proteins P0, P1, and P2 and a proposal for a uniform nomenclature for mammalian and yeast ribosomal proteins. *Biochimie* **73**: 861–870