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 30S and 60S ribosomal subunits, forming a 70S ribosome (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 the rice 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% 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.

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

| Organism: Rice (*Oryza sativa* L. cv Hayayuki). | Source: λAZAP cDNA library constructed from poly(A)+ RNA of rice anthers at the uninucleate microspore stage. |
| Feature of the cDNA: | Techniques: Double-strand plasmid sequencing of cDNA library; dideoxy sequencing of restriction fragment subclones. |
| Feature of the Protein: | Method of Identification: Deduced amino acid sequence shows 70% identity with that of *C. rubrum*. |
| (G + C) Content: Coding region 55%. | Feature of the Protein: 319 amino acid residues with a calculated M, of 34,377. |

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

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