Eukaryotic cytosolic ribosomes are composed of four RNA species and about 80 ribosomal proteins. The assembly of a functional ribosome requires the coordinate expression of genes for all constituent ribosomal proteins as well as rRNAs (Amaldi et al., 1989). Molecular dissection of animal ribosomal protein genes revealed that sequence elements embedded in the promoters and the 5' end of mature transcripts play critical roles in transcriptional and translational control of their expression (Harharian and Perry, 1990). Relatively little is known about the regulation of plant ribosomal protein gene expression. Over the last few years, an increasing number of plant ribosomal protein genes have been cloned and sequenced (Taylor and Davies, 1994, and refs. therein). Such structural information is an essential early step in exploring the function of the genes.

In the course of studying developmental and environmental regulation of the rice (Oryza sativa L.) 4'-coumarate CoA ligase gene, we isolated a cDNA clone that was expressed constitutively in various tissues and in different physiological contexts (Table I). A partial sequence of the cDNA clone showed high homology with human ribosomal protein S16 (Batra et al., 1991), a component of the 40S subunit of the cytosolic ribosome. Our interest in characterizing this clone further includes the fact that in gene regulation experiments involving RNA quantification, such as RNA gel blotting or run-on assays, an invariant internal control is often required. Although there were observations that the transcript levels of certain ribosomal protein genes vary among different tissues (Larkin et al., 1989), the use of ribosomal protein S26 and L27 genes as the internal controls had been successful (Lebeau et al., 1991; Vincent et al., 1993). We were curious if the rice S16 sequence could possibly serve as an internal standard in our studies on rice genes. Also, although S16 genes have been characterized from human, rat, mouse, and Lupinus polyphyllus (Batra et al., 1991; Warskulat et al., 1991), no information was available from any monocot plant. It would be useful to add the rice S16 data for comparative and evolutionary studies.

Yan Zhao, John C. Watson, Shain-dow Kung, and Paul J. Bottino*  
Department of Botany, University of Maryland, College Park, Maryland 20742–5815

**Characterization of a cDNA Encoding Ribosomal Protein S16 in Rice**

![Eukaryotic cytosolic ribosomes are composed of four RNA species and about 80 ribosomal proteins.](image)

**Table I. Characteristics of a cDNA encoding ribosomal protein S16 in rice**

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Organism:</strong></td>
<td>Rice (Oryza sativa cv IR36).</td>
</tr>
<tr>
<td><strong>Source:</strong></td>
<td>cDNA library in AZAPII, constructed from poly(A) RNA of etiolated seedlings.</td>
</tr>
<tr>
<td><strong>Function:</strong></td>
<td>Encoding ribosomal protein S16 of the 40S subunit.</td>
</tr>
<tr>
<td><strong>Method of Identification:</strong></td>
<td>Comparison of the deduced amino acid sequence with the ribosomal protein S16 from human, rat, mouse, and Lupinus polyphyllus.</td>
</tr>
<tr>
<td><strong>Structural Features of the cDNA:</strong></td>
<td>Full-length cDNA with an oligopyrimidine tract at the 5' end and a poly(A) tail at the 3' end; a putative translational initiation site at nucleotide 70 and a termination site at nucleotide 517.</td>
</tr>
<tr>
<td><strong>Features of the Encoded Protein:</strong></td>
<td>A protein of 149 amino acids with a calculated molecular mass of 16.9 kD and a pl of 11.22; high content of hydrophobic amino acids (44.3%) and basic amino acids (23.5%).</td>
</tr>
<tr>
<td><strong>Expression Pattern:</strong></td>
<td>Expressed constitutively in various tissues and under the different physiological conditions examined.</td>
</tr>
</tbody>
</table>

The full-length rice S16 cDNA contains 702 nucleotides. The first 10 nucleotides of the 5' untranslated region of the cDNA are pyrimidines (CCCTCTCTCC). The oligopyrimidine tract has been reported to be present at the 5' end of many eukaryotic ribosomal protein mRNAs and is required for their translational control (Levy et al., 1991). The open reading frame starts at nucleotide 70 and the sequence context surrounding the initiation codon (GCCGCAACCATGG) matches the consensus sequence for translation initiation in higher eukaryotes (Kozak, 1989). A poly(A) tail is present 169 nucleotides downstream of the translation termination codon. The 447-nucleotide open reading frame specifies a protein of 149 amino acids with a calculated molecular mass of 16.9 kD. In the polypeptide, basic amino acids (23.5%) dominate over acidic amino acids (8.1%), resulting in a high calculated pl value of 11.22. The basic amino acids are not evenly distributed, but rather are relatively concentrated in three regions; for example, 10 of the 22 amino acids at the C terminus are basic. Another notable feature of the protein is its high content of hydrophobic amino acids (44.3%), with many of these grouped into uninterrupted blocks of four to five residues. A FASTA

---

1 Y.Z. is a recipient of a fellowship from the Center for Agricultural Biotechnology, University of Maryland.

2 Present address: Department of Biology, Indiana University-Purdue University at Indianapolis, Indianapolis, IN 46202–5132.

* Corresponding author; e-mail pb230@umail.umd.edu; fax 1-301-314–9082.
search of current data bases (Protein Information Resource and SwissProt) revealed the greatest sequence identities between the rice S16 and the S16 from human (68% over 144 amino acids), rat (68% over 144 amino acids), mouse (67% over 144 amino acids), and *L. polyphyllus* (83% over 117 amino acids).

To estimate the number of the S16 genes in the rice genome, DNA gel blot analysis was carried out using the full-length cDNA as a probe. Three to four bands were hybridized when the genomic DNA was digested with BamHI, EcoRI, or HindIII. The hybridization patterns suggested that there might exist a small multigene family encoding S16. To assess the steady-state levels of the S16 transcripts, total cellular RNA was isolated from roots and shoots of young seedlings and cultured rice suspension cells grown in dark or light and treated with UV-B, fungal elicitor, or exogenous cAMP or cGMP. The results of RNA protection assays showed that the transcript levels were essentially the same in the different tissues and physiological contexts examined.

**ACKNOWLEDGMENTS**

We are grateful to Dr. Gideon Schaeffer (U.S. Department of Agriculture, Agricultural Research Service, Beltsville, MD) for providing rice suspension cells.

Received September 29, 1994; accepted October 11, 1994. Copyright Clearance Center: 0032-0889/95/107/1471/02.

The GenBank accession number for the sequence reported in this article is L36313.

**Literature Cited**


The GenBank accession number for the sequence reported in this article is L36313.