Plant Genes Register

Nucleotide Sequence of a cDNA for a P2 60S Acidic Ribosomal Protein from Parthenium argentatum

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In screening a stem-bark cDNA library from guayule (Parthenium argentatum), we isolated a full-length gene for a P2 60S acidic ribosomal protein that shows sequence similarity to vertebrate, invertebrate, and yeast proteins (Table I). The guayule P2 sequence is a full-length cDNA; a partial cDNA has been described for P2 sequence to the human LA2 protein (Rich and Steitz, 1987). The guayule P2 sequence shows nearly the same identity, 52.7 versus 59.0%, respectively, making it difficult to classify the guayule P2 sequence with both the P2 subunits. Comparison of the P2 Parthenium sequence with both the P2 subunits (Beltrame and Bianchi, 1987) and P2 subunits of fission yeast shows nearly the same identity, 52.7 versus 50.9%, respectively, making it difficult to classify the guayule P2 protein as P2 or P2. Comparison of the P2 Parthenium sequence to the human LA2 protein (Rich and Steitz, 1987) shows 59.0% identity at the nucleic acid level and 54.5% identity and 79.5% similarity at the amino acid level. Our interest in this gene extends to its potential use in experimental studies of Parthenium, from which few genes are at present available. Being a ribosomal protein, it should display minimal variations in expression and thus serve as a suitable internal control for gene expression studies in this species.

The P2 60S acidic ribosomal protein plays a crucial role in the elongation step of protein synthesis. The P2 proteins exist as heterodimers composed of α and β subunits. Comparison of the P2 Parthenium sequence with both the α and β subunits shows sequence similarity to vertebrate, invertebrate, and yeast (Beltrame and Bianchi, 1987, 1990; Remacha et al., 1988) 60S acidic ribosomal proteins (Table I). The guayule P2 sequence is a full-length cDNA; a partial cDNA has been described for Arabidopsis (C. Bardet, M. Axelos, D. Tremouays, W. Lebas, T. Lagravere, and B. Lescure, unpublished data; EMBL accession number X17464) with 65.5% identity at the nucleic acid level and 54.5% identity and 74.5% similarity at the amino acid level. Our interest in this gene extends to its potential use in experimental studies of Parthenium, from which few genes are at present available. Being a ribosomal protein, it should display minimal variations in expression and thus serve as a suitable internal control for gene expression studies in this species.

The P2 60S acidic ribosomal protein plays a crucial role in the elongation step of protein synthesis. The P2 proteins exist as heterodimers composed of α and β subunits. Comparison of the P2 Parthenium sequence with both the α subunits (Beltrame and Bianchi, 1987) and β subunits (Beltrame and Bianchi, 1990) subunits of fission yeast shows nearly the same identity, 52.7 versus 50.9%, respectively, making it difficult to classify the guayule P2 protein as P2 or P2. Comparison of the P2 Parthenium sequence to the human LA2 protein (Rich and Steitz, 1987) shows 59.0% identity at the nucleic acid level and 54.5% identity and 79.5% similarity at the amino acid level, with a similar level of identity for the Drosophila gene (Qian et al., 1987).

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**LITERATURE CITED**


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Table I. Characteristics of a P. argentatum P2 60S acidic ribosomal protein cDNA

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<thead>
<tr>
<th>Organism:</th>
<th>Parthenium argentatum Gray, line 11591, Asteraceae.</th>
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<tr>
<td>Protein, Function:</td>
<td>Plays an important role in the elongation step of protein synthesis.</td>
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<tr>
<td>Method of Identification:</td>
<td>Comparison of the coding region with the published sequence data from Homo sapiens (59.0% identity in DNA sequence and 50.9% identity in amino acid sequence).</td>
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<td>Techniques:</td>
<td>Screening from a stem-bark cDNA library in λZAP, cloning into pBluescript phagemid, dideoxynucleotide sequencing of both strands using standard sequencing primers.</td>
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<td>Structural Features of the cDNA:</td>
<td>The cDNA was 570 bp long and contained a 5' untranslated region of 30 bp, a eukaryotic start codon at 31 bp, and a 3' untranslated region of 165 bp.</td>
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<td>Structural Features of the Protein:</td>
<td>The open reading frame indicates a protein of 114 amino acids with a mol wt of 11,502 and an isoelectric point of pH 3.96. The sequence analysis software of the Genetics Computer Group, University of Wisconsin, was used to analyze the cDNA and deduced peptide sequence.</td>
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