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Plant Gene Register

Ribosomal Protein S11 Genes from *Arabidopsis* and Soybean

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Ribosomes found in the eukaryotic cytosol are composed of four rRNAs and more than 70 different ribosomal proteins. Hariharan and Perry (1990) have demonstrated that several mouse ribosomal protein genes are transcribed at nearly equal rates, that these unrelated mouse genes have a remarkably similar promoter architecture, and that in some instances these genes appear to bind common *trans*-acting factors. Although a number of cDNA clones encoding plant cytosolic ribosomal proteins have been isolated and used to explore gene expression, the structure of very few plant ribosomal protein genes has been examined and little sequence information has been determined outside transcribed regions.

The level of ribosomal protein mRNA is typically proportional to the cellular growth rate and consequently is high in plant meristems (Lebrun and Freyssinet, 1991). The abundance of these transcripts can also be induced by a variety of treatments that lead to cellular proliferation (Gantt and Key, 1985). Clearly, expression of plant ribosomal protein genes is influenced by a large number of factors and virtually nothing is known about the mechanisms controlling the expression of these genes.

To begin a search for *cis*-acting elements that might be important for ribosomal protein gene regulation, we determined the sequences of one of two or more genes (*rps11*) encoding ribosomal protein S11 in *Arabidopsis thaliana* (Gantt and Thompson, 1990; Lu et al., 1993) and a homologous soybean gene (Table I). The 5′ ends of the *A. thaliana rps11* transcripts were mapped by primer extension and RNase protection analyses; results from both procedures suggest that transcripts are initiated at several closely spaced sites. We also observed two different primer extension products when soybean S11 RNAs were examined. Little sequence similarity is found when *A. thaliana* and soybean *rps11* genes are compared. In the 5′ untranslated region, the sequence TTTGCCTACAA starts at positions 42 and 62 in the *A. thaliana* and soybean genes, respectively. In the 5′ flanking region, the sequence AAAAAGTAAAA is found at −185 (*A. thaliana*) and −239 (soybean). The sequence TTAGGGTTTT is also found in both genes: at −10 in *A. thaliana* and +16 in soybean. This sequence is notable because it is also found in the *A. thaliana* gene encoding ribosomal protein S15 (at +52), and a similar sequence has been noted in the promoter region of an *A. thaliana* gene encoding the translation elongation factor EF-1α (Curie et al., 1991). Additionally, the sequence is similar to the *Arabidopsis* telomere repeat sequence (TTAGGGT; Richards and Ausubel, 1988). In yeast, a telomere-binding protein (RAP1) plays an important role in ribosomal protein gene regulation (Raué and Planta, 1991).

Table I. *Characteristics of the Arabidopsis and soybean genes encoding cytosolic ribosomal protein S11*

Organisms:
- *Arabidopsis thaliana*, race Columbia.
- *Glycine max*, race Wayne.

Location of Genes:
- Nucleus.

Gene Function:
- The *Arabidopsis Ath-n-erps11A* and soybean *Gma-n-erps11* genes encode cytosolic 40S ribosomal subunit proteins homologous to rat S11.

Method of Identification:
- Sequence comparisons with *Arabidopsis* and soybean S11 cDNAs (Gantt and Thompson, 1990).

Characteristics of Transcribed Regions:
- Both genes have five introns that are located in identical sites in the protein coding region and encode polyadenylated transcripts.

Characteristics of Putative Promoters:
- Both genes contain a telomere repeat sequence (TTAGGGT) located near the site of transcriptional initiation.

Expression Characteristics:
- The abundance of soybean S11 mRNA is known to be elevated following treatment of seedlings with 2,4-D (Gantt and Key, 1985).

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The GenBank accession numbers for the sequences reported in this article are L28831 (soybean) and L28828 (*Arabidopsis*).

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