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Plant Gene Register

RNA-Binding Protein from *Arabidopsis*[1]

Alice J. DeLisle*

Department of Biochemistry, University of Nevada, Reno, Nevada 89557

In chloroplasts, the majority of gene regulation occurs at posttranscriptional levels, mainly by RNA processing and control of RNA stability in higher plants (Deng et al., 1987; Mullet and Klein, 1987; Deng and Gruissem, 1988). Nuclear mutants in *Chlamydomonas* have been isolated that are deficient in the posttranscriptional regulation of chloroplast mRNA-processing events, suggesting that nuclear-encoded regulatory genes are required for posttranscriptional regulation of chloroplast genes (Kuchka et al., 1989; Sieburth et al., 1991). In addition, a spinach nuclear-encoded RBP has been purified from chloroplasts and the corresponding cDNA cloned. Depletion of that spinach protein from an in vitro chloroplast pre-mRNA-processing extract abolishes 3′-end processing, strongly suggesting that the RBP is involved in the reaction (Schuster and Gruissem, 1991).

In this report an *Arabidopsis thaliana* L. (Heyn) cDNA is described that was isolated by screening a λgt11 expression library for clones encoding proteins that bind to single-stranded DNA, a characteristic of RBPs (Table I). A 1050-bp clone, *Atrbp31* (*A. thaliana* RBP, approximately 31 kD), was isolated. Subsequently, a longer *Atrbp31* cDNA of 1208 bp was isolated that potentially encoded two polypeptides of 330 and 326 amino acids, both in the same reading frame. Each start codon was in a good consensus sequence. Data bank searches demonstrated that the encoded protein, ATRBP31, was homologous to the spinach RBP described above (Schuster and Gruissem, 1991), to three tobacco chloroplast-localized RBPs (Li and Sugiura, 1990), and to a maize RBP (Cook and Walker, 1992). The organization of polypeptide domains is the same in all of these proteins. Each contains a putative chloroplast transit peptide, a near-amino-terminal acidic domain, and two RNA-binding domains (Bandziulis et al., 1989) in the carboxyl two-thirds of the molecule. ATRBP31 was 37 to 76% identical with the chloroplast RBPs in the RNA-binding domains. Based on the degree of similarity between ATRBP31 and the known chloroplast RBPs, it is likely that ATRBP31 is part of this family of nuclear-encoded chloroplast regulatory proteins.

Table I. *Characteristics of an Arabidopsis cDNA encoding a putative chloroplast RBP*

Organism:
  Arabidopsis thaliana L. (Heyn) Columbia.
Source of Clone:
  cDNA library (leaves and stems) in λgt11 (Clonetech).
Techniques:
  cDNA expression library screening for binding to single-stranded DNA, followed by hybridization screening to obtain entire coding region. Both strands of cDNAs were sequenced using the dideoxy method on double-stranded plasmid DNA.
cDNA Characteristics:
  cDNA of 1208 nucleotides encoding two potential open reading frames, both in the same frame, one from 96 to 1082 and the other from 138 to 1082.
Structural Features of Deduced Polypeptides:
  First reading frame: 330 amino acids (M_r 35,785); isoelectric point 4.4; putative chloroplast transit peptide, 1 to 82; acidic domain with seven repeats of SEGDX or SEGXX, 108 to 138; RNA-binding domain I, 142 to 228; RNA-binding domain II, 237 to 330; ribonucleoprotein consensus sequence 1 (two copies), 191 to 198, 285 to 292; ribonucleoprotein consensus sequence 2 (two copies), 152 to 156, 246 to 250 (Bandziulis et al., 1989); RNA-binding domains are 37 to 76% identical with chloroplast RBPs from spinach (Schuster and Gruissem, 1991), tobacco (Li and Sugiura, 1990), and maize (Cook and Walker, 1992).
  Second reading frame: Identical with first reading frame except that it lacks 14 amino acids at the amino terminus.
Function:
  Function not tested.
Antibodies:
  Not available.

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* Fax 1-702-784-1650.

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The GenBank accession number for the sequence reported in this article is M94554.

Abbreviation: RBP, RNA-binding protein.

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