Plant Gene Register

Nucleotide Sequence of a cDNA Clone Encoding the Precursor of Ribulose-1,5-Bisphosphate Carboxylase Small Subunit from Malus

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rbc (EC 4.1.1.39) is a bifunctional enzyme involved in carbon fixation. It consists of eight chloroplast-encoded large subunits containing the active site and eight nuclear-encoded small subunits required for enzyme assembly and function (Akazawa et al., 1984). We report the isolation and analysis of a cDNA clone for the rbcS from Malus (Table I).

A Malus leaf cDNA library (from an unclassified crab apple cultivar) was screened by in situ plaque hybridization using a heterologous rbcS cDNA clone from Lycopersicon esculentum. Four independent rbcS cDNA clones were obtained, and the nucleotide sequence of the longest clone, pRAPS10, was determined. pRAPS10 encodes an mRNA of 853 bp containing one long open reading frame of 549 bp, with 49 bp of 5' untranslated and 255 bp of 3' untranslated sequence (Fig. 1).

The derived amino acid sequence of the mature protein is 80% homologous to rbcS-3 from L. esculentum (Sugita et al., 1987). The first 60 amino acids make up a putative chloroplastic transit peptide (Keegstra et al., 1989). The 5'-nucleotide sequence of the four rbcS clones, covering the transit peptide-coding region, was determined (data not shown), and the derived sequence of the transit peptide of each has been submitted to the chloroplast transit peptide data base (von Heijne et al., 1991).

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Abbreviations: rbc, ribulose-1,5-bisphosphate carboxylase; rbcS, rbc small subunit precursor.

Figure 1. Nucleotide and deduced amino acid sequence of pRAPS10.

Table I. Characteristics of pRAPS10

| Organism: | Unclassified crab apple cultivar (Malus). |
| Function: | Small subunit of rbc (EC 4.1.1.39). |
| Techniques: | Double-stranded plasmid sequencing; restriction fragment subcloning andideoxy sequencing of both strands. |
| Method of Identification: | Isolated from a cDNA library constructed from mRNA from young leaves. Library probed with pTSS 1-91 (cDNA clone for rbcS of L. esculentum). Derived amino acid sequence shares 80% homology with that of L. esculentum rbc-3. |
| Characteristics of Deduced Protein: | Open reading frame of 183 amino acids consisting of a transit peptide of 60 amino acids and a mature protein of 123 amino acids. Predicted molecular mass of the preprotein is 20,502 D. |
| Antibodies: | Not available. |
| Subcellular location: | Chloroplast; assembled with large subunit. |
LITERATURE CITED


