Sequence of the rbcL gene for the large subunit of ribulose bisphosphate carboxylase-oxygenase from alfalfa

Jane Aldrich1, Barry Cherney2, Ellis Merlin3 and Jeff Palmer*

Standard Oil, 4440 Warrensville Center Road, Cleveland, OH 44128 and *Division of Biological Sciences, University of Michigan, Ann Arbor, MI 48109, USA

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The sequence of the chloroplast-genome encoded rbcL gene from Medicago sativa cv. Regen S is shown compared to pea (1). Alfalfa shares 99.9% nucleotide sequence homology with pea for 1728 of 1788 bases spanning the gene beginning 213 bases upstream of the coding sequences through 63 bases into the 3' flanking region ending at position 1588. Pea sequences are highly divergent from alfalfa after this point. The deduced amino acid sequence is also 99.9% homologous to that of pea, with 68% (18/27) of the substitutions non-conservative. The second ATG codon (+1) in the open reading frame is the probable translation start site (2,3).

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