

Sequence of the *rbcL* gene for the large subunit of ribulose biphosphate carboxylase-oxygenase from petunia

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Submitted 21 October 1986

The sequence of the chloroplast-encoded *rbcL* gene from *Petunia hybrida* cv. Mitchell is shown compared to tobacco (1). *Petunia* and tobacco share a remarkable 99.97% nucleotide sequence homology in the coding region as well as in the 3' and 5' flanking regions. Of the amino acid changes, (13/477; 99.97% homology) 46% are non-conservative. The second ATG (+1) in the open reading frame is the probable translation start site (2, 3).

Genetic sequence alignment of rbcL gene from Petunia hybrida cv. Mitchell and tobacco. The sequence is presented in a grid format with nucleotide positions (1-1715) indicated at the top. Amino acid translations are shown below the nucleotide sequences. Key features are marked: -221, -168, -120, -1, 120, 246, 368, 488, 608, 728, 848, 968, 1088, 1208, 1328, 1448, 1568, 1688, 1808, 1928, 2048, 2168, 2288, 2408, 2528, 2648, 2768, 2888, 3008, 3128, 3248, 3368, 3488, 3608, 3728, 3848, 3968, 4088, 4208, 4328, 4448, 4568, 4688, 4808, 4928, 5048, 5168, 5288, 5408, 5528, 5648, 5768, 5888, 6008, 6128, 6248, 6368, 6488, 6608, 6728, 6848, 6968, 7088, 7208, 7328, 7448, 7568, 7688, 7808, 7928, 8048, 8168, 8288, 8408, 8528, 8648, 8768, 8888, 9008, 9128, 9248, 9368, 9488, 9608, 9728, 9848, 9968, 10088, 10208, 10328, 10448, 10568, 10688, 10808, 10928, 11048, 11168, 11288, 11408, 11528, 11648, 11768, 11888, 12008, 12128, 12248, 12368, 12488, 12608, 12728, 12848, 12968, 13088, 13208, 13328, 13448, 13568, 13688, 13808, 13928, 14048, 14168, 14288, 14408, 14528, 14648, 14768, 14888, 15008, 15128, 15248, 15368, 15488, 15608, 15728, 15848, 15968, 16088, 16208, 16328, 16448, 16568, 16688, 16808, 16928, 17048, 1715. Arrows indicate possible termination stem-loop structures. A legend at the bottom explains the symbols used in the sequence.

Legend: The petunia *rbcL* gene is located within a 2.5kb *BamH I* fragment of petunia chloroplast DNA (4). An *EcoR I* site at -33 and the *BamH I* site at 1679 are common to petunia and tobacco and serve as internal reference points. Nucleotide and amino acid substitutions in tobacco are indicated above the petunia sequence with only amino acid substitutions shown in the coding region. A 21 bp insert in tobacco relative to petunia in the 3' region is indicated in brackets. Sequence data for *P. hybrida* cv. Roter Vogel R27 were reported (4) beginning with position 1309 through 1684. Sequence differences in this cultivar from cv. Mitchell are indicated in parentheses. The (t) below the codon GCA at position 1411 resulted in substitution of a valine (V) for an alanine in the Roter Vogel R27 cultivar. Prokaryotic - like -10 and -35 promoter sequences and ribosome binding site are underlined; probable transcription initiation by homology to tobacco (1) is shown as * at -182; arrows represent possible termination stem-loop structures.

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