

Nucleotide sequence of the chloroplast *petD* gene of *Chlamydomonas eugametos*

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In land plant chloroplast DNAs, the gene coding for subunit IV of the cytochrome *b6/f* complex (*petD*) is interrupted by a group II intron and is part of a well-known operon containing also the *psbB*, *psbH* and *petB* genes (1). We have located the chloroplast *petD* gene of *Chlamydomonas eugametos* on the 1.4 kbp *Hind*III subfragment of *Eco*RI fragment 4 (2) and determined its sequence. In contrast to land plants, this green algal gene is continuous and unlinked to *psbB* and *petB* (3). Like its land plant homologues, it encodes a protein of 160 amino acid residues with three potential membrane-spanning regions (underlined) (4). The amino acid sequence derived from the *C. eugametos* *petD* gene is 82%, 82% and 83% identical with the corresponding sequences from *Marchantia polymorpha* (1), tobacco (5) and spinach (6), respectively. No putative -10 and -35 promoter elements were identified upstream of the region corresponding to the 5' terminus of the *C. eugametos* *petD* transcript (1.2 kb) as determined by S1 nuclease protection (see the region delimited by the bracket) and primer extension (5' termini are indicated by triangles, with their size reflecting RNA abundance) analyses. Sequences capable of forming stem-loop structures with at least 10 nucleotides in the stem (arrows) were found upstream and downstream of the coding region.

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1  AAGCTTTGCGCAACTAAACAAATCAGACTTTTAATCTTCTAGTTTATAGAGTCAGATAATCGATTAAACATAAAAACCTGTGTTCTAAAGTTAAACTGTCCACTAAAGC
121 TACAGTCACTCGAACCTTAAATAAAGGCATCGTCAAAAGCGCGCAGSCCTTGACTAAACCTTAAACCTGTTGGGAGGCCACAGCTCAAGGCCCTGTTTATCTCCGAAACGCCCTCCAC
241 TCAAAACACGCAATCTTAAATTCGACCTACCGCTATATTCTTCTAGGCGTAAGGCCACGCTGTTTAAAGAAAAACAAAGCCCTACCTGCAACGCGAACAGGGTGAAGCC
361 AAAACAAAGCAAGAAAAATAATAAACTTAAATAAAAGCGATTCTGTTATATATAATCTGTTAAAGGTTAAATCTGTTAAAGGCGCACAAAGGGCCCTGTTACGTTGGTGCAGCGCAA
51
481 OCCAGTACTACCTTAATCTCGCGGGGCGATCCCCCGGAGGTTAAAGGTTAAACAGGTTGGTACACGCTTACAGCTTACAGCTTATCTGTTACGTTGGTGAAGGCGAT
601 TGTTTTATTTGCGTCAAGAAGATAGAACGACTACGCTCTTTTAAAGGTTGCTAGTGTCTAGTTTGCTTCCAGTAAATTAGACCTCCGCTTATTTGCGCAAGCCAAAATAGGC
721 ACGTCACAGACTTCTTAACTCTAAATTCTGAAAAAAATAGTTGCTATTGCTTAAAGGCTACTGCTGCGGGGCAAAACCCGGGCAAGAATTGTTTCAAAAACAGCTG
841 AAAAACACTACAAATGCTGTTGACTAAACCTGACTTAAATGATCTGTTACGCTGAAACACTAGCAAAAGGTTGGTCAATAACACTTATGGAGAACGCTGGCCAAATGATC
1   M S V T K P D L N D P V N H Y R F A C C I G L A V L D P A A M G E F P A N P F A T P L R I
961 TTTTATATATTTCCCAAGTTGTAATCTTGGTACGTTCTGTTGTTATTTGGTCTGTTAGCTGGCTGCTATGGGAGGCCAGAAACCCATTGCGAACACCACTTGGAAATT
36 L L Y I F P V V I F G T F A C C I G L A V L D P A A M G E F P A N P F A T P L R I
1081 TACCTGAGTGTATTCTTACCCCTGTTTCCAATTTTAACTGACTCTGGCTAACAAACTACTAGAGGTGGCTGGCATGGCTGCAAGCTGCTTGGCTTCTCTAACAGCTGGCCATTGAA
76 L P E W Y F P V F Q I L R T V P N K L L G V L A M A A V F V G O L L T V P F F I E
1201 GTTTAACAAAGTCCAAAACCGTATGTCCTCTATTTCTACTATTTTATCTCTAGTGGTACTCTTAGTGGTACTCTGGCTGGTATAGGTTGGTGTACTTTCTCCAAATGATTTCTAA
116 S I N K F Q N P Y R F I A T I L F L V G T L V A V W L G I G A T F F P I D I S L
1321 CACTGGTGTATTTAAATAATTTGATTTCTTAAAGAACCTTTTGTGAACTAGTGTACTTTATACACAGTAACTGGTAACTAGTCAAACCTTGGACAACAACTTAAATTAATAG
156 T L G L F .cc
1441 TTATAACACTTACTTTGAAATC

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