Nucleotide sequence of the chloroplast large subunit rRNA gene from Chlamydomonas reinhardtii

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The chloroplast large subunit (LSU) rRNA gene from the green alga Chlamydomonas reinhardtii features a group I intron and codes for three distinct rRNA species designated 7S, 3S and 23S rRNAs (1-3). The regions encoding these rRNAs are not contiguous; they are separated by short sequences that are probably transcribed together with the remainder of the gene into a primary transcript and are removed subsequently by endonucleolytic cleavage. Only part of the *C. reinhardtii* chloroplast LSU rRNA gene sequence has been reported so far (1-3). We have recently undertaken a phylogenetic analysis of the chloroplast LSU rRNA gene in the genus Chlamydomonas and, in the course of this study, have completed the sequence of the C. reinhardtii gene and confirmed the positions of the 5' termini of the three mature RNAs encoded by this algal gene The sequence we determined covers a total of 2896 nucleotides, some of which overlap with the sequence published previously (positions 1-730 and 2213-2896). It includes the regions encoding the 7S, 3S and 23S rRNAs (framed nucleotides), but not that encoding the intron (its insertion position is denoted by the arrow). The underlined nucleotides differ from those found at the corresponding positions in the partial sequence that was previously available. Using primer extension experiments, we confirmed the positions of the 5'termini of the 7S and 3S rRNAs as determined by Rochaix and Darlix (2) by direct RNA sequencing. Using the same approach, we found that the 5' terminus of the 23S rRNA resides 56-59 bases upstream of the tentative positions identified by these authors.

1	GAATTAAGGCGTACGGTGGAGACCTAGGCACTCAGAGACGAAGAAGGGCGCAGATACCGGCGATACGCTTCGGGGAGCTGGCAACAAGCTTTGATCCGAAGATTCCCGAATAGGGCAACAC	75
121	TCATAGAACTACCTATATAATTCATAGTTAGGTAAGAGGCAA <u>CCCAGTGAACTGAAACATCTAAGTAGCTGGAGGAAAAGAAAG</u>	
241	GAACAGCCTAAACCTATGTCGCAAGATGTAGGGGTCGTGGGASGACAACATAAAAATCGCTATTTTAA <mark>TACGAAGCAGCTGAATCCTGCACCATAGATGGTGAAAGTCCAGTAGT</mark> AAAA	3S
361	AGAAAATTTAGATITTIGTCTAATCCCGAGTAGCATGGGGCACGTGAAATCCCGTGTGAATCAGCGAGGACCACCTCGTAAGGCTAAATACTCCTGAGTGACCGATAGCGAAATAGTACC	1
481	ACGAGGGAAAGGTGAAAAGAACCCCTGTTGGGGAGTGAAATAGAACATGAAACCGTATGCTGACAAGCAGTGGGAGCAAGAATGCTTGTGACCGGTGCCTGTTGAAAAATGAGCCGG CG	1
601	ACTTATAGGGAGTGGGTTGGGTTGGGTGAGGTAAAAATCCGGGAGCCCAAGCGAAAGCGAGTCTGGATAGGGCGCAAATGGTCACTTCTTATGGACCCGGACCCGGGTGATCTATTCATGGCC <u>A</u> G	
721	GATGAAGCTT96GTAACACCAAGTGGAGGTCCGAACCGACCGATGTTGAAAAATCGGCGGATGAGCTGTGAATAGGGGAGAAATTCCAATCGAACTCGGAGCTAGCT	
841	ATGCGTTGAGGCGCAGCGGTAACGATGAACTGTCTTGGGGTAAAGCTACTGTTTCGATGCGGGCTGCGAAAGCGGTACCAAGTCGTGGCAAACTCAGAATACAAGACATGTCTTCCGT AA	t i
961	ACCASTGAGACASTGGGGGATAASCTTCATTGTCAAGAGGGAAACAGCCCAGATCACCAGCTAAGGCCCCTAAATGGTCACTAAGTGGAAAAGGATGTGAGAATGCTGAAACAACCAS GA	
1081	OGTTTGCTTAGAAGCAGCCACCCTTCAAAGAGTGCGTAAAAGCTCACTGGTAAAAGCGTTCTTGCGCCGGAAAATGGCCGGGGACTAAGTGACCTGCCGAAGCTGTGATAATAATTTATTATAT	
1201	AAATTATAGGTAGGGGAGCGTTCCGCTCTCGGGTGAAGTTTTCACGTAAGTGGGGATGGACGAAGCGGAAGTGAGAATGTCGGCTTGAGAAACATTGGTGAGAATCCAATGC CC	
1321	CGAAAACCTAAGGGTTCCTCCACTAGGTTCGTCCATGGGGGGTTAATAACAGGCCTAAGACTAGGCCAAACGGCGTCGTCGATGGAAAACAGGTTAATATTCCTGTACGAGTTAAATATTCCTGTACGAGTTAAATATCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCTGTACGAGTTAATATTCCGGGGGGTTAATATTCCTGTACGAGTTAATATTCCGGGGGGGTTAATATTCCGGGGGGGG	
1441	ATCTGROGGACGAAGGAGGCTAAGCTAGAACTGTTTTTGGATTGCAGTGGAAGCGTTTAGACGTTGAGAGATAGAAAAAAAGCTATCTTGAGGAGACGTGATCCCTATTTGATGGTTC	
1561	GCCGTCGAGTAGCTAGTGATGTCATACTTCCAAGAAAAGCTCATACATCTTTATAATTTAATGACCTGTACCTGAAACCGACACAGGTAGGT	235
1681	AACTCTCTCTAAGGAACTCGGCAAACTGGCCCCGTAACTTCGGAAGAAGGGGCACCCATCCGTAACAAGGTGGGTCGCAGGCCCAGGCCCAGGCGACTGTTTACCAAAAACACAGGT CT	
1801	CCGCAAAGTCGTAAGACAATATATGGGGGCTGACGCCTGCCCAGTGCCGGAAGGTTAAGGAAGTTGGTTATTTCGTAAGAAAAAAGCTGACGACCGAAGCCCCGGTGAACGGCGGTCG TA	
1921	ACTATAACGATCCTAAGGTAGCGAAATTCATTGTCGAGTAAGTTTCGACCTGCACGAAAGGCGTAACGATCTGGGCGCTGTCTCGGAGAGAGGCTCGGTGAAATAGACTTGTCCCGTG AA	
2041	GATGCGGACTACCTACGACAGAAAGACCCTATGAAGCTTGACTGTATCTTGGAATTGGGTTTGGGCTTTCCTGCGCAGCCTAGGTGGGAGGCTATGAAGATTACCTTCCGGG GT	
2161	AATTAGAGCCGTCATTGAGAGACCACTCTGGAAGAGCTAGAATCCTAATGGGGATCCTTGAATCAGGACCCTTGACAGTTTCAGGTGGGCAGTTTATTTGGGGCGAATGCCTCCTAAAAG	
2281	GTAACGGAGGCGTGCAAAGGTTCCCTCAGTCTGGACGGAAATCAGACATTGAGTGTAAAGGCAAAAGGGAGCTTGACTGCAAGACCTACAAGTCGAGCAGGGGCGAAAGCC	
2401	GATCCGAC9GTGCC9CGTGGAAGGGCCGTCGCTCAAC9GATAAAAGTTACTC <u>TA</u> 9GGATAACAGGCTGATCTTCCCCAAGAGT <u>T</u> CACATCGAC9GGAA3GTTTGGCACCTCGATGTCG GC	1
2521	TCATCACATCCTC0GTCTGTAGTAGGTCCGAA000TT00GCTGTTC0CCCATTAAA3T03TACGTGAGTCAAAACGTCGTGAGACAGTTTGGTCCATATCCGGTGTAGGCGTTA	
2641	GAGCATTGAGAGTAGCCTTTCATAGTACGAGAGGAGCCTGAAAGGACATGCCAATTGTGTACCAGTTCTCATTCCAATGGGAAACGCTGGGTAGCTACGCATGGATAGATA	
2761	GCATCTANGTAGGAAGCTAAACTCAAGATGAGTGCTCTCTAAGGCCGCGGCGGCTAGACAAGCCGTTATATAGGTATCAGGTGTACAGTCAGCAATGGCTTTAGCCGAGATATACTAAAGG CC	
2881	GTTTGATTTTGACCTT	-

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