A novel allophycocyanin gene (apcD) from *Cyanophora paradoxa* cyanelles

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Cyanelles from *Cyanophora paradoxa* contain genes that encode a cyanobacterial-type light harvesting system (1), although these organelles are functionally equivalent to plastids and are found as organelles in a eukaryotic cell. Previously two genes (apeA, apcB) encoding allophycocyanin subunits and two genes encoding phycocyanin subunit proteins have been identified (1, 2). We report that at least one more allophycocyanin gene (apcD), which according to its similarity with other genes is a member of the 2A gene family, is located on cyanelle DNA. This gene was found on DNA fragment BglII-18 (3), close to the large ribosomal protein gene operon (S10/spc) (4). The sequence of 783 nucleotides encodes an open reading frame of 162 codons specifying a protein with 66.1% identity and 96.3% homology to allophycocyanin 2A from *Calothrix* sp. (5). Included in the figure are putative transcription control signals, a sequence with similarity to *E. coli* promoters and a large inverted repeat which may form an extended (26 nucleotides with one mismatch) stem/loop structure.

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REFERENCES


**Figure 1.** Nucleotide sequence and deduced amino acid sequence of the allophycocyanin gene 2A from *Cyanophora paradoxa* cyanelles. The start and stop codons and a putative ribosome binding site are given in italics. Underlined are sequences at the 5'-end which may function as a promoter, and at the 3'-end an extended inverted repeat which may function as a transcription termination signal.