Cloning and sequence analysis of the phycocyanin genes of the marine cyanobacterium *Synechococcus* sp. WH7803

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In 1979 unicellular phycoerythrin-containing cyanobacteria assigned to the genus *Synechococcus* were discovered to be abundant in the surface waters of temperate and tropical oceans [6, 11], and this group of picoplankters is now recognized to make a large contribution to the primary productivity of the oceans [see 12]. Two distinct populations of marine *Synechococcus* strains may be distinguished on the basis of the predominant chromophore associated with phycoerythrin [9]; the phycourobilin-rich strains are characteristic of the open ocean whereas those with a lower phycourobilin content are found in shelf waters. In addition to phycoerythrin, the major light-harvesting phycobiliprotein, marine *Synechococcus* species contain phycocyanin, allophycocyanin and occasionally phycoerythrocyanin [10]. In this report we describe the cloning and sequencing of the genes encoding the α and β subunits of phycocyanin of *Synechococcus* sp. WH7803, a low-urobilin strain characteristic of shelf isolates [9].

Chromosomal DNA, partially digested with *Sau3A*, from *Synechococcus* sp. WH7803 was used to construct a library in lambda charon 35. One clone from this library was isolated which hybridized strongly with plasmid pAQPR1 [4]: pAQPR1 carries the α-(cpcA) and β-phycocyanin (cpcB) genes of the freshwater cyanobacterium *Synechococcus* sp. PCC7002. A 1.6 kb *Bam HI* fragment from this clone was sub-cloned into pBR322 to yield plasmid pJN12.1. We determined the nucleotide sequence (Fig. 1) of this 1.6 kb *Bam HI* fragment by the dideoxy chain-termination method following a combination of random and directed subcloning into M13 mp18 and mp10. Analysis of the nucleotide sequence reveals two open reading frames, at positions 257–775 and 820–1308, which on the basis of homologies detected with previously sequenced phycocyanin genes were identified as the cpcB (β-subunit) and cpcA (α-subunit) genes. The cpcB and cpcA genes are, respectively, 84.8% and 83.1% homologous to the equivalent genes in the freshwater species *Anacystis nidulans* R2 (*Synechococcus* sp. PCC7942) [7, 8] and are organized in the same fashion as that seen in the other cyanobacteria with the cpcB upstream from the cpcA gene [see 3]. The two genes are separated by an intergenic region of 44 bp and there is a possible

The nucleotide sequence data reported will appear in the EMBL, GenBank and DDBJ Nucleotide Sequence Databases under the accession number X59809.
Shine-Dalgarno sequence (GGAG) 7 bp upstream from cpcB though none can be recognized for the cpcA gene. No recognizable promoter sequences can be detected upstream from cpcB; however, in Anabaena sp. PCC7120 transcription was found to be initiated from a point ca. 260 bp