Update section

Sequence

Primary structure of the \textit{psbN-psbH-petC-petA} gene cluster of the cyanobacterium \textit{Synechocystis} PCC 6803

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The cloning and nucleotide sequence of the \textit{Synechocystis} PCC 6803 \textit{psbH} gene has previously been reported [1, 2]. This gene encodes the so-called '9 kDa phosphoprotein' of photosystem II (PS II). In \textit{Synechocystis} PCC 6803 the \textit{psbH} gene is located within a 4.2 kb \textit{Hind} III restriction fragment [1]. Further sequencing of 3657 bp of this fragment (Fig. 1) has revealed that the genes for two components of the cytochrome \textit{b}_{6-f} complex, \textit{petC} encoding the Rieske Fe-S protein and \textit{petA} encoding apocytochrome \textit{f} are located downstream of \textit{psbH}. Both \textit{petC} and \textit{petA} have been identified by their considerable overall similarity to other published sequences and by the conserved motifs involved in binding the high potential Fe-S centre (\textit{petC}) and haem (\textit{petA}) which are underlined in Fig. 1.

Additionally, \textit{psbN}, encoding another low molecular mass component of PS II [3], commences 86 bp upstream of the \textit{psbH} start codon on the opposite DNA strand. Like all \textit{psbN} sequences currently available it consists of 43 codons. Although only 5 of 19 residues are definitely identical to the \textit{Synechococcus vulcanus} amino-terminal sequence [3], the carboxy terminus of the \textit{psbN} protein is highly conserved across species. Overall the deduced \textit{Synechocystis} protein has 55.8\% identity to liverwort [4] and 48.8\% identity to all available higher plant \textit{psbN} protein sequences. With retention of the amino-terminal Met, as happens in \textit{S. vulcanus}, the predicted MW of the \textit{Synechocystis} \textit{psbN} protein is 4512 Da which closely agrees with the observed value of 4.7 kDa for the \textit{S. vulcanus} protein on SDS-PAGE [3]. The DNA sequence encoding the majority of \textit{psbN} was reported in [2], but the gene was not identified.

The \textit{petC-petA} gene organisation has been characterised in one other cyanobacterium, the filamentous \textit{Nostoc} PCC 7906, where the genes were found to be cotranscribed [5]. However \textit{psbH} was not located within 356 bp upstream of \textit{petC} in this organism.

There are two possible Met translation start codons for the \textit{Synechocystis petC} gene which are shown in capitals in Fig. 1. Neither is preceded by strong Shine-Dalgarno-like consensus sequences. Only the downstream Met codon (commencing

\footnotesize{The nucleotide sequence data reported will appear in the EMBL, GenBank and DDBJ Nucleotide Sequence Databases under the accession number X58532.}