Complete Sequence of One Copy of the \textit{psbA} Gene from the Thermophilic Cyanobacterium \textit{Synechococcus elongatus}*

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One copy of the \textit{psbA} gene which codes for the photosystem II reaction center D-1 protein from the thermophilic cyanobacterium \textit{Synechococcus elongatus} has been sequenced. It is feasible that a disulfide bridge between D-1 Cys\textsubscript{212} and D-2 Cys\textsubscript{212} is responsible for the thermostability of the photosystem II reaction center from \textit{Synechococcus elongatus}.

One of the three copies of the \textit{psbA} gene in \textit{Synechococcus elongatus} was sequenced completely and compared with the three copies of the \textit{psbA} gene in the cyanobacterium \textit{Anacystis nidulans} R2 (PCC 7942), formerly called \textit{Synechococcus} R2 [1]. Like in \textit{Anacystis nidulans} R2 there are also most probably three copies of the \textit{psbA} gene in \textit{Synechococcus elongatus} (unpublished results). An EcoRI-Apal restriction endonuclease fragment of 2.6 kb contains one complete copy of one \textit{psbA} gene and in addition 330 base pairs of a second \textit{psbA} gene. The third \textit{psbA} gene is not located on this fragment. The complete \textit{psbA} gene contains an open reading frame of 360 amino acids which is homologous to \textit{psbA} genes of other organisms and encodes the photosystem II reaction center D-1 protein (Fig. 1). The \textit{psbA} gene from \textit{Synechococcus elongatus} has an \textit{E. coli} like consensus promoter sequence at $-10$: TATATT but differs at the $-35$ sequence: TTTCGA.

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-81 TTAAGTTAATGCTTAAGGCCCTTGACGTTGTAGCTGTTCAGGTTTGGTAAATC

\textbf{TATATTGGAGCTCTTTACGACT}

1 ATG ACC ACA ACT CTC CAA CGT CGC G AA AGC GCG A AT TTG TGG GAG

M T T T L Q R R E S A N L W E

M T T A L Q R R E S A S L W Q

26 CGG TTT TGT TAC CGG AGG ATT GAT AAC CGC CTT TAT GTG

R F C N W V S T D N R L Y V

Q F C E W V T S T D N R L Y V

91 GGC TGG TTT GGG GTG ATC ATG ATC CCC ACC CTA TTA GCC GCA ACC

W F G V I M I P T L L I M A T

W F G V L M I P T L L T A T

136 ATC TGC TGT GTG ATT GCC TTC ATC GCT GCC CCC CTT GTG GAC ATC

I C F V I A F I A A P P V D I

I C F I V A F I A A P P V D I

181 GAT GGC ATC CGT GAG CCT GTT TCT GGC TCT TTG CTC TAT GCC AAC

D G I R E P V S G S L L Y G N

D G I R E P V A G S L M Y G N

* EMBL accession no. Z 16081.

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226 AAC ATC ATC ATC ACG GGT GCA GGT GTC GGC TCT AGC AAC GCC ATT GGC
76 N I I T G A V V P S S N A I G
N I I S G A V V P S S N A I G
* * * * * * * * * * * * * * *

271 TTG CAC TTC TAC CCC ATT TGG GAA GCT GCT TCC CTC GAT GAG TGG
91 L H F Y P I W E A A S L D E W
L H F Y P I W E A A S L D E W
* * * * * * * * * * * * * * *

316 CTC TAC AAC GGT GGG CCC TAC CAA CTG ATC ATC TTC CAC TTC CTG
106 L H F Y P I W E A A S L D E W
L H F Y P I W E A A S L D E W
* * * * * * * * * * * * * * *

361 TTG GGT GCC TTC TGC TAC ATG AGT GGG CTC CAG TGG GAA CTT CAC TAC
121 L G A S C Y M G R Q W E L T Y
I G V F C Y M G R E W E L S Y
* * * * * * * * * * * * * * *

406 CGC CTC GGT ATG CGG CCT TGG TTC ATC ATC TTG CCT GCT GCC TAC TCT GCC CCC
136 R L G M R P W I C V A Y S A P
R L G M R P W I C V A Y S A P
* * * * * * * * * * * * * * *

451 CTG GCT TCT GCC TTT GCA GTC TTC TTG ATC TAC CCC ATT GGT CAA
151 L A S A F A V F L I Y P I G Q
V A A A T A V F L I Y P I G Q
* * * * * * * * * * * * * * *

496 GGC AGC TTC TCT GAC CGG ATG CCC CTC GGT ATC TCT GGT GCC TAC TCC
166 G S F S D G M P L G I S G T F
G S F S D G M P L G I S G T F
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541 AAC TTT ATG ATT GTG TTT CAA GCG GAG CAC AAC ATT CTC ATG CAC
181 N F M I V F Q A E H N I L M H
N F M F V F Q A E H N I L M H
* * * * * * * * * * * * * * *

586 CCC TTC CAC CAA CTG GGT GTA GCC ATG CAC GGT TCT CTG GCC GCC GGT GTC TTT GGT GGG GCG CTG
196 P F H Q L V A G V F G C A L
P F H M L G V A G V F G G S L
* * * * * * * * * * * * * * *

631 TTC TGC GCC ATG CAC GGT TCT CTG GTG ACC TCC AGC TGG ATC CTC
211 F C A M H G S L V T S S L I R
F S A M H G S L V T S S L V R
* * * * * * * * * * * * * * *

676 GAA ACC ACC GAA ACC GAA TCC GCC AAC TAC GGT TAC AAA TTT GTT
226 E T T E T E T E T E S A N Y G Y K F G
E T T E T E S Q N Y G Y K F G
* * * * * * * * * * * * * * *

721 CAA GAG GAA GAA ACC TAC AAC ATC GTG GCT GCC CAC GGT TAC TTT
241 Q E E E T Y N I V A A H G Y F
Q E E E T Y N I V A A H G Y F
* * * * * * * * * * * * * * *

766 GCC CGG TTG ATC TTC CAA TAC GCC AGC TTC AAC AAC AGC CGC TCC
256 G R L I F Q Y A S F N N S R S
G R L I F Q Y A S F N N S R S
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The predicted amino acid sequence of the coded D-1 protein was compared to the two different polypeptides coded by the three \textit{psbA} genes from \textit{Anacystis nidulans} R2 (ANPSBA I and ANPSBA II/III). The amino acid sequence differs in 47 residues from the ANPSBA I D-1 protein and in 44 residues from the ANPSBA II/III D-1 protein. The homologies are 86.7\% and 87.8\%, respectively. The first 16 amino acids of \textit{Synechococcus elongatus} differ in 12 amino acids from either the gene product of ANPSBA I or ANPSBA II/III.

The purpose of this study was to determine whether there are some specific changes in the amino acid sequence of the D-1 protein that are responsible for the fact that \textit{Synechococcus elongatus} has optimal photosynthetic rates at a temperature of 57 °C [2]. At this temperature the photosystem II reaction center proteins D-1 and D-2 of other organisms are rapidly denatured. At 46 °C, the rate of electron transport in \textit{Synechococcus elongatus} is reduced by 50\% [3]. Most of the changes in the \textit{Synechococcus elongatus} D-1 protein are conservative as compared to other D-1 proteins. There is however, a prominent exchange of Ser\textsubscript{212} to Cys in transmembrane helix IV. Based on the model of the photosystem II reaction center [4] it is feasible that D-1 Cys\textsubscript{212} is connected via a disulfide bridge to D-2 Cys\textsubscript{212}, located in transmembrane helix IV (distance of the \textit{a-C} atoms of the two Cys is 7.2 Å). This might be one reason for the thermostability of the photosystem II reaction center in \textit{Synechococcus elongatus}.

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Fig. 1. Nucleotide sequence and deduced amino acid sequence of one of the \textit{psbA} genes from \textit{Synechococcus elongatus}. For comparison, the sequence of the gene product from ANPSBA II from \textit{Anacystis nidulans} R2 is given in the third row. Identical amino acids are marked by an asterisk.