

Complete Sequence of One Copy of the *psbA* Gene from the Thermophilic Cyanobacterium *Synechococcus elongatus**

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One copy of the *psbA* gene which codes for the photosystem II reaction center D-1 protein from the thermophilic cyanobacterium *Synechococcus elongatus* has been sequenced. It is feasible that a disulfide bridge between D-1 Cys₂₁₂ and D-2 Cys₂₁₂ is responsible for the thermostability of the photosystem II reaction center from *Synechococcus elongatus*.

One of the three copies of the *psbA* gene in *Synechococcus elongatus* was sequenced completely and compared with the three copies of the *psbA* gene in the cyanobacterium *Anacystis nidulans* R2 (PCC 7942), formerly called *Synechococcus* R2 [1]. Like in *Anacystis nidulans* R2 there are also most probably three copies of the *psbA* gene in *Synechococcus elongatus* (unpublished results). An EcoRI-ApaI restriction endonuclease fragment of 2.6 kb contains one complete copy of one *psbA* gene and

in addition 330 base pairs of a second *psbA* gene. The third *psbA* gene is not located on this fragment. The complete *psbA* gene contains an open reading frame of 360 amino acids which is homologous to *psbA* genes of other organisms and encodes the photosystem II reaction center D-1 protein (Fig. 1). The *psbA* gene from *Synechococcus elongatus* has an *E. coli* like consensus promotor sequence at –10: TATATT but differs at the –35 sequence: TTTCAA.

-81		TTAAGTTAATGCTTAAGCCCTTGCACTTGATGACTGTTTTCAGGGTTTGTAATCAAA																	
		TATATTGGACTTATCAGACT																	
1	ATG	ACC	ACA	ACT	CTC	CAA	CGT	CGC	GAA	AGC	GCG	AAT	TTG	TGG	GAG				
1	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				
	*	*	*		*	*	*	*	*	*	*		*	*					
46	CGG	TTT	TGT	AAC	TGG	GTG	ACG	AGC	ACC	GAT	AAC	CGC	CTT	TAT	GTG				
16	R	F	C	N	W	V	T	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				
31	G	W	F	G	V	I	M	I	P	T	L	L	A	A	T				
	G	W	F	G	V	L	M	I	P	T	L	L	T	A	T				
	*	*	*	*	*		*	*	*	*	*	*		*	*				
136	ATC	TGC	TTT	GTG	ATT	GCC	TTC	ATC	GCT	GCT	CCC	CCT	GTG	GAC	ATC				
46	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	GGC	AAC				
61	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. Z16081.
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811	CTG	CAC	TTC	TTC	TTG	GCC	GCT	TGG	CCG	GTG	GTG	GGT	GTG	TGG	TTT
271	L	H	F	F	L	A	A	W	P	V	V	G	V	W	F
	L	H	F	F	L	A	A	W	P	V	V	G	I	W	F
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
856	ACC	GCC	TTG	GGG	ATC	AGC	ACC	ATG	GCC	TTT	AAC	CTG	AAT	GGC	TTT
286	T	A	L	G	I	S	T	M	A	F	N	L	N	G	F
	T	S	L	G	I	S	T	M	A	F	N	L	N	G	F
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
901	AAC	TTC	AAC	CAC	TCG	GTC	ATT	GAT	GCC	AAG	GGC	AAC	GTG	ATC	AAC
301	N	F	N	H	S	V	I	D	A	K	G	N	V	I	N
	N	F	N	Q	S	V	L	D	S	Q	G	R	V	I	N
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
946	ACC	TGG	GCG	GAC	ATC	ATC	AAC	CGT	GCC	AAC	TTG	GGT	ATG	GAA	GTG
316	T	W	A	D	I	I	N	R	A	N	L	G	M	E	V
	T	W	A	D	V	L	N	R	A	N	L	G	M	E	V
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
991	ATG	CAC	GAG	CGC	AAT	GCT	CAC	AAC	TTC	CCC	CTC	GAC	TTG	GCC	AGC
331	M	H	E	R	N	A	H	N	F	P	L	D	L	A	S
	M	H	E	R	N	A	H	N	F	P	L	D	L	A	A
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
1036	GCT	GAG	TCT	GCT	CCT	GTG	GCC	ATG	ATT	GCT	CCC	AGC	ATC	AAC	GGC
346	A	E	S	A	P	V	A	M	I	A	P	S	I	N	G
	G	E	A	T	P	V	A	L	T	A	P	A	I	N	G
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
1081	TAAGCAACGTTATCTACTGAACCTTTTACACAGCCGCTCCTAAACCTAGGGGCGGTTTTT														
1040	TATTGCGTTA CGGCCACGG GGAGTTTAAG GG														

Fig. 1. Nucleotide sequence and deduced amino acid sequence of one of the *psbA* genes from *Synechococcus elongatus*. For comparison, the sequence of the gene product from ANPSBA II from *Anacystis nidulans* R 2 is given in the third row. Identical amino acids are marked by an asterisk.

The predicted amino acid sequence of the coded D-1 protein was compared to the two different polypeptides coded by the three *psbA* genes from *Anacystis nidulans* R 2 (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 *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 *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 *Synechococcus elongatus*

is reduced by 50% [3]. Most of the changes in the *Synechococcus elongatus* D-1 protein are conservative as compared to other D-1 proteins. There is however, a prominent exchange of Ser₂₁₂ to Cys in transmembrane helix IV. Based on the model of the photosystem II reaction center [4] it is feasible that D-1 Cys₂₁₂ is connected *via* a disulfide bridge to D-2 Cys₂₁₂, located in transmembrane helix IV (distance of the α -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 *Synechococcus elongatus*.

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