Phycobilisome rod mutants in *Synechocystis* sp. strain PCC6803

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The phycobilisome is a large pigment-protein assembly that harvests light energy for photosynthesis. This supramolecular complex is composed of two main structures: a core substructure and peripheral rods. Linker polypeptides assemble phycobiliproteins within these structures and optimize light absorption and energy transfer. Mutations have been constructed in three rod-linker-coding genes located in the *cpc* operon of *Synechocystis* sp. strain PCC6803. The *cpcC1* gene encoding the 33 kDa linker is found to be epistatic to *cpcC2* encoding the 30 kDa linker, indicating a specific role for each of these two linkers in rod growth. Three allelic mutants affecting *cpcC2* revealed a polar effect of commonly used cassettes (*aphl, aadA*) on the operon steady-state transcripts and an effect of rod linker availability on the amount of phycocyanin incorporated in the phycobilisome. This led to the proposal that regulation of rod length could occur through processing of transcripts upstream of the *cpcC2* gene.

INTRODUCTION

Phycobilisomes are sizeable (5–10 MDa) biliprotein complexes that harvest light for photosynthesis in cyanobacteria and red algae (Sidler, 1994). Although a phycobilisome (PBS) is composed of hundreds of biliproteins and fewer linker polypeptides (de Marsac & Cohen-Bazire, 1977), light energy absorbed anywhere within the particle is efficiently transferred towards a specific biliprotein which functions as a terminal-energy emitter (Glazer, 1989). A phycobilisome consists of six rods radiating from a core associated with the thylakoid membrane. Phycocyanin (PC) is a biliprotein (phycobiliprotein) found in the rods, whereas the core is composed of allophycocyanin (AP). Some cyanobacteria and red algae contain different biliproteins (i.e. phycocerythrin) in their rods. PC and AP carry the same blue chromophore called phycocyanobilin, the properties of each phycocyanobilin being strongly influenced by its protein environment. Rods containing only PC are composed of two or three (depending on the strain) disc-shaped hexamers of PC, in which a monomer is an (αPC, βPC) heterodimer. Specific rod linkers (L<sub>R</sub>) assemble the PC hexamers into rods and tune their electronic properties in order to optimize directional energy transfer (Glazer, 1989).

As the PBSs in cyanobacteria constitute a substantial fraction of the total soluble proteins (50%), their degradation can supply amino acids for the synthesis of essential proteins under nutrient-limited conditions (Allen & Smith, 1969). Indeed, the PBS is degraded in a specific and orderly manner during nitrogen starvation of non-diazotrophic cyanobacteria (Yamanaka & Glazer, 1980). This process, known as bleaching or PBS trimming, requires the *nblA* gene, which is induced and necessary for PBS trimming under nitrogen starvation (Collier & Grossman, 1994; Luque et al., 2003). During PBS trimming, PC hexamers and associated linkers most distal to the core are degraded first (Richaud et al., 2001; Yamanaka & Glazer, 1980). Another type of PBS trimming occurs under high-light conditions and does not involve *nblA* (Collier & Grossman, 1994; Garnier et al., 1994; Lönnberg et al., 1985).

PBSs are not required for phototrophic growth (Ajlani & Vernotte, 1998; Bruce et al., 1989) so mutations affecting different linkers are of special interest because they provide the opportunity for observing PBS biogenesis in normal growth conditions. Understanding PBS assembly has been enhanced by mutational analysis of *Synechococcus* sp. strain PCC7002, but this strain contains only two PC hexamers and two linkers per rod. The phycobilisome of *Synechocystis* sp. strain PCC6803 consists of a three-cylindrical core from which six rods radiate, each rod being composed of three stacked PC hexamers and three rod linkers (Elmorjani et al., 1986). Most of the rod-subunit-encoding genes are clustered in the *cpc* operon. In *Synechocystis* sp. strain PCC6803, this operon contains five genes: *cpcB* and *cpcA* encode the βPC and zPC subunits, respectively, while *cpcC2*,
cpcC1 and cpcD encode the rod linkers L*R30, L*R33 and L*R10, respectively. Two independent genes (cpcG1 and cpcG2) encode the rod-core linker (LRC2) that attaches the proximal PC hexamer to the core (Cyanobase: http://www.kazusa.or.jp/cyano/Synechocystis/).

Using interposon mutagenesis, we have constructed and characterized deletion mutants in the three rod-linker genes located in the cpc operon of Synechocystis sp. strain PCC6803. Characterization of the PBS assembly process in the mutants yielded a scheme for PBS-rod biogenesis in Synechocystis sp. strain PCC6803 in which the insertion of L*R30 is excluded in the absence of L*R33. This result differs from studies with mutants of Synechococcus sp. strain PCC7942 lacking rod-linker genes, in which it has been proposed that L*R30 and L*R33 could occupy interchangeable positions within the rods (Bhalerao et al., 1991, 1993).

We demonstrated, by monitoring steady-state RNA levels in the mutants, that the cassette insertion affected gene expression in its vicinity, regardless of orientation. This polar effect provided us with strains containing different levels of the rod linkers, and whose absorption spectra showed that the PC level incorporated in the PBS varied proportionally. This result leads to the proposal that transcriptional regulation of the rod-linker genes adjusts the light-harvesting capacity of the photosynthetic apparatus by modulating the PBS rod length.

METHODS

Bacterial growth conditions. Wild-type and mutant strains of the cyanobacterium Synechocystis sp. strain PCC6803 were grown photoautotrophically in an illuminated orbital incubator at 32°C in a CO2-enriched atmosphere and under continuous light (40 μM m−2 s−1). Allen’s medium (Allen, 1968) was modified as follows: 30 μM ferric citrate, 3 μM disodium EDTA, 30 mM sodium nitrate, 250 μM potassium phosphate, 250 μM magnesium sulphate, 250 μM calcium chloride, 200 μM sodium carbonate, 10 mM sodium bicarbonate and microelements as in Allen’s medium. All chemicals were purchased from Sigma. For growth on plates, the above medium was supplemented with 1.5% (w/v) Difco Bacto agar and 2 mM sodium thiosulphate. Plates were incubated at 30°C under continuous light (30 μM m−2 s−1). Where appropriate, media were supplemented with 25–50 μg kanamycin ml−1, 25–50 μg spectinomycin ml−1 and 5–10 μg streptomycin ml−1. Escherichia coli strain DH5α was used as plasmid host for cloning. Strains and plasmids used in this work are listed in Table 1.

Nucleic acid purification and reactions. Genomic DNA was isolated from Synechocystis sp. strain PCC6803 essentially as described by Cai & Wolk (1990). Total RNA was extracted according to Aiba et al. (1981), with slight modifications. For Northern blotting, 10 μg total RNA was denatured with glyoxal/DMSO, loaded on 0.8% (w/v) agarose gels, and run in 10 mM sodium phosphate, pH 7 (Sambrook et al., 1989). Transfer to nylon membranes, hybridization, washing and stripping were performed according to the membrane manufacturer’s instructions (Millipore). Hybridization with the constitutively expressed rnpB gene (Vioque, 1992) was performed to estimate the loading of RNA samples. DNA probes were labelled by random priming using the Ready-To-Go kit (Amersham), using [α-32P]dCTP. Blots were imaged using a Molecular Dynamics phosphorimager. DNA probes were as follows: probe 1, 80 bp Hpal–SpeI (cpcA–cpcC2 intergenic region) plus 350 bp Nhel–Hpal (cpcC1–cpcD intergenic region plus 200 bp of cpcD); probe 2, 600 bp from NotI–Hpal (cpcC1 to cpcD); probe K, 1.2 kb PsI fragment from pUC4K; probe rnpB, 500 bp HindIII–EcoRI fragment containing rnpB from Synechocystis sp. strain PCC6803 (Vioque, 1992).

Construction of plasmids and mutants. Primers pcf and pcr (5′-GTAGGGCTGTGTTCTCCATAG-3′ and 5′-CAACTCCTCAACGGTTCCG-3′, respectively) were used for the PCR amplification of the cpc operon from Synechocystis sp. strain PCC6803 total DNA. Primers were designed according to the Cyanobase complete genome sequence. The 4-2 kb PCR product was digested with MfeI and PsI and cloned into EcoRI- and PsI-digested pUC9. The resulting plasmid, denoted pCPC, carried a 4 kb fragment which contained the five genes of the cpc operon plus 480 bp upstream of the cpcB start codon and 260 bp downstream from the stop codon of the last gene, cpcD. Part or all of cpcC2 and cpcC1 were substituted by the Km cassette in the inactivation plasmids pC30K+, pC30K−, pC33K+ and pCBK+ (Table 1). Mutants 30F, 30R, 33 and CB were created by transformation of the wild-type Synechocystis sp. strain PCC6803 with each of these plasmids, respectively, followed by screening for Km+ colonies. pC2Ω was constructed starting from an Eagl-digested pPC plasmid treated for 20 min with BAL31 nuclease, then SpeI digested, treated with the Klenow DNA polymerase and ligated; the resulting plasmid contained a 685 bp deletion in cpcC2. Subsequently, the Ω cartridge was inserted in the BseRI site. Transforming CB and the wild-type with plasmid pC2Ω and screening for Km+ colonies resulted in A303D and D3, respectively. Transformation of the wild-type with pUCDM and screening for Sp colonies gave the D4 mutant. For trans-complementations of cpcC1 and cpcD, pS1C1 and pS1D were respectively used to transform the appropriate strains (Table 1). pS1D was constructed to express cpcD from the psbAII promoter by inserting into pPSBA2 a 380 bp Ndel–BamHI fragment containing cpcD plus a BamHI fragment carrying the apH1 gene (Fig. 1). The cpcD-containing fragment was amplified using the following oligonucleotides: f1 (5′-GAATTCCATGTTAGTCATTCTTC-3′) and r1 (5′-GGATCCCTGACTCGATGGCATTTC-3′). Ndel and BamHI sites are underlined. pS1C1 was constructed to express cpcC1 from the psbAII promoter by inserting a 3.5 kb HinII fragment from 30 bp upstream of the cpcC1 start codon (containing the ribosome-binding site) to 35 bp downstream of the cpcC1 stop codon plus the Ω cassette in pPSBA2 (Fig. 1).

Plasmids constructed by the cloning of PBS products were sequenced to verify the fidelity of the PCR amplification. Complete segregation of the mutant alleles was confirmed by PCR, and in some cases the PBS products were subjected to restriction analysis to ascertain the identity of the amplified fragments (data not shown).

PBS isolation and analysis. Cells were broken by vortexing with glass beads. Phycobilisommes were prepared from Synechocystis sp. strain PCC6803 as described by Ajlani et al. (1995) and Glazer (1988). Absorption spectra were recorded on a Varian Cary-5E double-beam spectrophotometer, with a data interval of 0.5 nm. Proteins were analysed by SDS-PAGE on a 10–20% linear polyacrylamide gradient in a modified Tris/glycine buffer (Flig & Gregerson, 1986) or 4–12% Bis-Tris gels (NuPAGE, Novex) in MES-SDS buffer. OD at 620 nm was used to ensure approximately equal loading of different PBS samples; about 0.3 OD250 ml (100 μl from a sample at OD250 = 3) was loaded per well. PBS-containing samples were concentrated by precipitation with 10% (w/v) trichloroacetic acid prior to loading. Proteins were visualized using Coomassie Brilliant Blue stain.
RESULTS

Characterization of L30-deficient strains

Three different strategies were used to inactivate cpcC2, encoding the L30 linker, in order to estimate any polar effect on flanking genes. The 30f and 30r strains carried a deletion in cpcC2 that was replaced by opposite orientations of the Km cassette. The Δ30D3 strain contained a deletion in cpcC2 plus the Ω cartridge inserted between cpcC1 and cpcD. A control strain, designated D3, contained only the Ω insertion at the same location (Fig. 1 and Table 1).

The PBSs from each of the mutants were purified in order to determine their polypeptide composition. Sucrose gradients from all the PBS preparations contained a dark-blue band in the 1 M sucrose layer at positions near those expected for a complete PBS, indicating that PBSs were assembled. However, the assembled particles were at slightly higher positions on the sucrose gradient than those of the wild-type and the D3 strain, which indicated that the absence of L30 resulted in the assembly of a smaller PBS. The reduction of the PBS size is accompanied by the absence of L30, which was replaced by opposite orientations of the Km cassette. The Δ30D3 strain contained a deletion in cpcC2 plus the Ω cartridge inserted between cpcC1 and cpcD. A control strain, designated D3, contained only the Ω insertion at the same location (Fig. 1 and Table 1).

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Table 1. Bacterial strains and plasmids used in this study

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Properties</th>
<th>Source or reference</th>
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<tr>
<td><strong>Strains</strong></td>
<td></td>
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<tr>
<td>WT</td>
<td>Wild-type strain of <em>Synechocystis</em> sp. strain PCC6803</td>
<td>Pasteur Culture Collection</td>
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<tr>
<td>30f</td>
<td>ΔcpcC2::aphl – deletion of 68% of cpcC2 (codon 21–208), aphl insertion (Km°)</td>
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<td>30r</td>
<td>ΔcpcC2::aphl – as above but aphl in the opposite orientation (Km°)</td>
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<td>Δ30D3</td>
<td>ΔcpcC2, cpcD−::Ω – deletion of 83% of cpcC2 (codon 2–230) and termination of the cpc operon transcription before cpcD (Sp°, Sm°)</td>
<td>This work</td>
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<tr>
<td>D3</td>
<td>cpcD−::Ω – Ω insertion between cpcC1 and cpcD, transcription termination before cpcD (Sp°, Sm°)</td>
<td>This work</td>
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<tr>
<td>33</td>
<td>ΔcpcCl::aphl – deletion of 50% of cpcC1 (codon 77–220), aphl insertion (Km°)</td>
<td>This work</td>
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<td>CB</td>
<td>ΔcpcC2Cl::aphl – total deletion of cpcC2 and cpcC1 (codon 2 of cpcC2 to the last codon of cpcC1), aphl insertion (Km°)</td>
<td>This work</td>
</tr>
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<td>33c</td>
<td>33 transcomplemented with cpcC1 in the psbAII locus (Km°, Sp°, Sm°)</td>
<td>This work</td>
</tr>
<tr>
<td>CBc</td>
<td>CB transcomplemented with cpcC1 in the psbAII locus (Km°, Sp°, Sm°)</td>
<td>This work</td>
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<td>D4</td>
<td>cpcD−::Ω – Ω insertion in HinclII of cpcD, transcription termination within cpcD (Sp°, Sm°)</td>
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<td>WD</td>
<td>WT plus cpcD in the psbAII locus (Km°)</td>
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<td>D3D</td>
<td>D3 plus cpcD in the psbAII locus (Km°, Sp°, Sm°)</td>
<td>This work</td>
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<tr>
<td>D4D</td>
<td>D4 plus cpcD in the psbAII locus (Km°, Sp°, Sm°)</td>
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<td><strong>Plasmids</strong></td>
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<td>pCPC</td>
<td>4 kb MfeI–PstI genomic fragment carrying the cpc operon (Ap°)</td>
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<td>pC30K+</td>
<td>Derivative of PCPC with Km cassette inserted between XhoI–Eagl (Km°, Ap°)</td>
<td>This work</td>
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<tr>
<td>pC30K−</td>
<td>As above with aphl gene in an opposite orientation (Km°, Ap°)</td>
<td>This work</td>
</tr>
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<td>pAC2Ω</td>
<td>2.7 kb AgeI–PstI fragment carrying part of the operon minus 685 nt deletion from cpcC2. Ω was inserted 35 bp downstream of cpcC1 (Ap°, Sm°/Sp°)</td>
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<td>pC33K+</td>
<td>Derivative of PCPC with Km cartridge inserted between MscI–Nael (Km°, Ap°)</td>
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<td>pCBK+</td>
<td>Derivative of PCPC with Km cartridge inserted between SpeI–Nhel (Km°, Ap°)</td>
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<tr>
<td>pUCD9</td>
<td>Nhel–PstI fragment carrying cpcD with Ω inserted at HinclII site (Ap°)</td>
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<td>pPSBA2</td>
<td>500 bp upstream and 500 bp downstream of the psbAII ORF separated by a multiple cloning site cloned in pSL1180 (Ap°)</td>
<td>Lagarde et al. (2000)</td>
</tr>
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<td>pS1D</td>
<td>cpcD and the Km cartridge inserted in the multiple cloning site of pPSBA2 (Ap°, Km°)</td>
<td>This work</td>
</tr>
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<td>pS1C1</td>
<td>cpcC1 and the Ω cartridge inserted in the multiple cloning site of pPSBA2 (Ap°, Sm°/Sp°)</td>
<td>This work</td>
</tr>
<tr>
<td>pUC4K</td>
<td>Origin of the Km° cassette containing the aphl gene (Amp°, Km°)</td>
<td>Oka et al. (1981)</td>
</tr>
<tr>
<td>pDW9</td>
<td>Origin of the Ω fragment containing the adaA gene plus strong translation-transcription terminators on both sides (Amp°, Sm°/Sp°)</td>
<td>Golden &amp; Wiest (1988); Prentki &amp; Krisch (1984)</td>
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</table>
The polypeptide composition of purified PBSs from the mutants was analysed by Coomassie-stained SDS-PAGE. In addition to the phycobiliproteins (PC and AP) in the 20 kDa range, wild-type PBSs contain seven polypeptides (Fig. 2a, lane WT). Four of these polypeptides, not encoded by the \(cpc\) operon, were invariably present in all strains: L_C, core linker; L_{RC}, rod-core linker; FNR, Ferredoxin NADP\(^+\) Reductase and L_{CM}, core-membrane linker. As expected, the L_{30}R polypeptide was absent from the three \(cpcC2\)-deleted strains, \(D_{30D3}, 30f\) and \(30r\). At the same time, these strains exhibited decreasing amounts of the L_{33}R polypeptide (traces, if any, in \(30r\)) (Fig. 2a). The L_{10}R polypeptide was detected only in the \(30f\) PBS, albeit in lesser amount than in the wild-type PBS.

The purified PBSs from the mutants were further characterized by comparing their absorption spectra to that of the wild-type PBS. In wild-type PBS, PC (\(\lambda_{\text{max}} = 620\) nm) is the major phycobiliprotein (\(\sim 75\%\)). PBSs from the \(cpcC2\)-deleted strains all exhibit lower amounts of incorporated PC. Consequently, the contribution of AP (\(\lambda_{\text{max}} = 650\) nm) to the PBS absorption spectrum becomes evident. PBSs from 30r had a spectrum corresponding to the lowest relative amount of PC and 30f had an intermediate amount, while \(D_{30D3}\) PBS contained the largest amount of PC (Fig. 2b). The increasing amounts of PC incorporated into the PBSs of the three allelic mutants, \(30r, 30f\) and \(D_{30D3}\), were proportional to the amount of the L_{33}R polypeptide detected in their PBSs (Fig. 2a). Since L_{33}R is the product of \(cpcC1\) located downstream of the inactivated \(cpcC2\) gene, the different amounts of L_{33}R might be due to different polar effects of the \(cpcC2\) mutations on \(cpcC1\) expression.

The steady-state level of \(cpc\) transcripts was monitored in the mutants by Northern blot. The wild-type operon specifies three differently sized mRNAs which start upstream of the translation initiation codon of \(cpcB\) and terminate at three different sites (Fig. 3a). The smaller and most abundant transcript (\(\sim 6\) kb), containing \(cpcB\) and \(cpcA\), does not seem to be affected in any of the mutants (Fig. 3b, panel 1). Two larger and less-abundant transcripts, which contain the linker-encoding genes \(cpcC2, cpcC1\) and \(cpcD\), are detected at \(3\sim 4\) and \(3\sim 8\) kb in the wild-type (Fig. 3b, panels 1 and 2, lane WT). The size and relative abundance of these transcripts are changed in the mutants. In the 30r and 30f
strains, they would be about 0.6 kb larger due to the deletion in cpcC2 and the Km cassette insertion; their sizes should be 4.0 and 4.4 kb, respectively. They were undetectable in the 30r strain and present in a drastically reduced amount in strain 30f (Fig. 3b, panel 2). In D3, the 3.8 kb transcript is absent due to the strong transcription terminators present in Ω, while the 3.4 kb transcript seems less abundant than in the wild-type. This might be due to a stem–loop disturbed by the Ω insertion (see Discussion). In Δ30D3, a shorter form of this transcript (2.7 kb due to the deletion in cpcC2) is detected and seems fairly abundant.

The blot was hybridized with a Km probe and overexposed to detect mRNAs containing the Km cassette (Fig. 3b, panel K). In 30f, two major transcripts are detected at 4.0 and 2.9 kb, while in strain 30r, the 4.0 kb one was barely detectable and the 2.0 kb transcript that also hybridized to probe 1 was obvious. Larger bands (around 2.5 kb) could be the products of abortive transcription and degradation of the full operon transcript. The 4.0 kb transcripts correspond to the transcription of the whole operon through the Km cassette. Their low amounts demonstrate that the insertion of the Km cassette destabilizes those transcripts. The 2.9 and 2.0 kb transcripts, in 30f and 30r, respectively, are the products of readthrough transcription from the aphI promoter. The 2.9 kb transcript detected in 30f terminates at the end of the cpc operon: it should then contribute to the translation of cpcC1 and cpcD. The size of the 2 kb transcript in 30r implies that it terminates within cpcB. Part of this transcript is an antisense RNA to the 1.6 kb mRNA containing cpcB and cpcA.

Characterization of the L_{33}^{3R}-deficient strain

cpcC1, encoding the L_{33}^{3R} linker, was inactivated by replacing an internal fragment with the Km cassette; the resulting mutant was denoted 33. A strain in which both cpcC2 and cpcC1 genes were totally deleted and replaced by the Km cassette was also constructed and denoted CB (Fig. 1 and Table 1).

Sucrose gradients of PBS preparations from 33 and CB contained a dark-blue band at a position significantly higher on the gradient than those of the wild-type PBS, indicating that assembled PBSs were much smaller in size. Again, free PC bands at the top of the gradients indicate the presence of unincorporated PC in the cells. The SDS-PAGE of purified PBSs showed no trace of either L_{33}^{3R} or L_{30}^{3R} in CB. More surprisingly, both linkers were also absent in strain 33. The relative amounts of L_{30}^{3R} were also significantly reduced in both mutants (Fig. 4a, lanes 33 and CB). PBSs from 33 and CB have identical absorption spectra, similar to the spectrum of 30r (Fig. 4b). The absence of L_{30}^{3R} in the PBS from strain 33 suggests that L_{30}^{3R} was not incorporated into the PBS in the absence of L_{33}^{3R}. In order to corroborate this hypothesis and to exclude any polar effect of the cpcC1 mutation, both CB and 33 were complemented with a transcriptional fusion in which cpcC1 was

![Fig. 2.](http://mic.sgmjournals.org/4151)

(a) Polypeptide composition of purified PBS from wild-type, WT, and from rod-linker-deficient strains 30r, 30f, Δ30D3 and D3 analysed by SDS-PAGE (10–20% linear acrylamide gradient in Tris/HCl). The identities of polypeptides are labelled on the left. Masses of the molecular markers are indicated in kDa on the right. (b) Absorption spectra of purified PBSs from wild-type and rod-linker-deficient strains. Wild-type and D3 PBSs have similar absorption spectra (λ_{max} 620 nm), the lower amounts of PC incorporated in the Δ30D3, 30f and 30r PBSs revealed the contribution of AP (λ_{max} 650 nm) to their absorption spectra. The decreasing height of the 620 nm peaks reflects the decreasing amount of PC in the PBS. The spectra were normalized to the 655 nm absorption.

http://mic.sgmjournals.org
placed under the control of the strong psbAII promoter in the psbAII locus (Fig. 1, pS1C1). The resulting strains were denoted CBc and 33c, respectively. This insertion is neutral to Synechocystis sp. strain PCC6803, since it has been shown that psbAIII can support photoautotrophic growth in the absence of psbAII (Mohamed & Jansson, 1989). The SDS-PAGE showed that CBc PBSs recovered L33R, demonstrating that the ectopic cpcC1 gene was expressed and capable of complementing the deleted gene. PBSs from 33c recovered both L33R and L30R, confirming that the absence of both linkers in 33 was due only to the deletion of cpcC1 (Fig. 4a). Absorption spectra showed increased amounts of PC in CBc and 33c PBSs compared to their parent mutants CB and 33, respectively. The extent of this increase was more spectacular in 33c, since it recovered two rod linkers and their associated PC (Fig. 4b). These results prove that cpcC2 was functional in strain 33; the absence of its product, L30R, in the PBS was due to an epistatic effect of cpcC1 on cpcC2. It is noteworthy that the relative amounts of L10R also increased in the PBSs of 33c compared to CB, Cbc and 33 (Fig. 4a).

**Characterization of L10R-deficient and trans-complemented strains**

The D3 strain (described in the L10R section) was indistinguishable from the wild-type with respect to growth rate and fluorescence emission characteristics. The polypeptide profile of D3 PBS confirmed the absence of the L10R linker and revealed a small decrease in the L33R to L30R ratio (Fig. 2a). Close examination of the D3 PBS absorption spectrum revealed a higher contribution from AP (shoulder at 650 nm), which means that the D3 PBS contained less PC (Fig. 5b). In this mutant, the Ω cassette was inserted upstream of cpcD, destroying a stem–loop structure that might stabilize the 3–4 kb mRNA where cpcC1 is at the 3’ end. In order to verify this possibility, a mutant was created by inserting the Ω cassette in the cpcD ORF. PBS from this mutant, denoted D4, lacked L10R but contained a normal L33R to L30R ratio, and the absorption spectra were identical to that of the wild-type (Fig. 5a). Therefore, the decrease in L33R and the modified absorption spectra observed in D3 were due to the absence of the stem–loop in the 3–4 kb mRNA (see Discussion). Similar results were obtained in Synechococcus sp. strain PCC7002 mutants in which the stem–loop between cpcC and cpcD was deleted (de Lorimier et al., 1990a).

Since the loss of L10R produced no detectable phenotype, we attempted the overexpression of cpcD to shed light on its function. A fragment starting at the cpcD initiation codon and ending downstream of its transcription terminator was used to produce a construct placing cpcD under the
control of the psbAII transcriptional and translational signals in plasmid pS1D (Fig. 1). Transformation of the wild-type with this construct resulted in strain WD. This strain produced a high level of a 0.4 kb mRNA containing cpcD, indicating that the ectopic cpcD was transcribed at the level expected from the psbAII promoter (Northern

Fig. 4. (a) Polypeptide composition of purified PBS from wild-type, WT, rod-linker-deficient and complemented strains CB, CBc, 33, 33c analysed by SDS-PAGE (NuPage 4–12% acrylamide gradient in Bis-Tris/HCl). The identities of polypeptides are labelled on the left. Masses of the molecular marker are indicated in kDa on the right. (b) Absorption spectra of purified PBSs from wild-type, rod-linker-deficient and complemented strains; the absorption spectra of CB and 33 contained the lowest amounts of PC (λmax 620 nm). The increasing height of the 620 nm peaks reflects the increasing amount of PC in the PBSs of the complemented strains CBc and 33c. The spectra were normalized to the 655 nm absorption.

Fig. 5. (a) Polypeptide composition of purified PBSs from cpcD mutant strains analysed by SDS-PAGE (NuPage 4–12% acrylamide gradient in Bis-Tris/HCl). The identities of polypeptides are labelled on the left. Masses of the molecular marker are indicated in kDa on the left. (b) Absorption spectra of purified PBSs. The contribution of AP (arrow at 650 nm) was more obvious in the D3 and D3D spectra. The spectra were shifted for better viewing.
DISCUSSION

In this study, we have constructed and characterized ten mutants with different modifications in three PBS rod-linker genes, located in the cpc operon of Synechocystis sp. strain PCC6803. This operon contains five genes and produces three transcripts from one transcription initiation site. The site was mapped 251 bp upstream from the translation start for cpcB in Synechocystis sp. strain PCC6714 (Imashimizu et al., 2003), a strain that is closely related to Synechocystis sp. strain PCC6803. Sequence analysis identified a stable stem–loop structure downstream from cpcA which might act as a transcriptional terminator (not followed by a polyT stretch) or as a 3′ stabilizer to an abundant 1-6 kb transcript containing cpcB and cpcA. This structure was intact in all mutants, which explains the constant amount of this transcript in the different strains.

Less-abundant 3′ and 3-8 kb transcripts containing cpcC2, cpcC1 and cpcD, in addition to cpcB and cpcA, appear to be generated by a readthrough of the above RNA structure and two rho-independent terminations downstream of cpcC1 and cpcD, where significant stem–loops and polyT stretches are detected. The large transcript containing cpcD was absent in both D3 and Δ30D3 due to transcription termination at the Ω cassette edge. The fact that the 3′-4 kb transcript was less abundant in D3 suggests that the Ω terminator does not provide a 3′ stabilizer effect. The reduced levels of the larger transcripts in strains 30f and 30r explain the decrease of L^R_33 and L^R_{10} in their PBSs (Fig. 3b, panel 2). The detected readthrough transcripts from the Km cassette (aphl gene) in strain 30f (Fig. 3b, panel K) should contribute to the translation of genes downstream of the inserts cpcC1 and cpcD. The lower amount of L^R_33 and L^R_{10} in 30f PBS (Fig. 2a) suggests that the transcripts initiating from the aphl promoter are less abundant or are unstable. In the 30r strain, the Km cassette severely disturbed the full operon transcript (larger transcripts are barely detectable) and produced an antisense RNA to the 1-6 kb transcript, which explains the lower PC content in this strain. Note that this aphl transcript terminates in cpcB (where a significant stem–loop structure and a polyT stretch are detected), and not at the stem–loop structure downstream of cpcA. This observation suggests that the latter structure is an RNA-processing site, rather than a terminator. This possibility was evoked for the cpc operon of Anabaena PCC7120 (Belknap & Haselkorn, 1987).

The three allelic cpcC2 mutants, 30r, 30f and Δ30D3, contained trace, reduced and almost-normal amounts of L^R_{33}, respectively (Fig. 2a). We showed that this was due to different expression levels of cpcC1. This gene undergoes a polar effect from the Km cassette inserted upstream in 30f and 30r and from the downstream Ω cassette insertion in Δ30D3. These polar effects resulted in a decreased amount of the cpcC1 product, L^R_{33}; consequently the amount of PC incorporated in the PBS decreased. This result suggests that transcriptional regulation of the rod-linker genes could adjust the light-harvesting capacity of the PBS by modulating the amounts of PC incorporated into the rods. Decrease of the level of a larger transcript relative to a smaller one in response to high light levels has been shown to occur in the cpc operon of Anabaena PCC7120 (Belknap & Haselkorn, 1987). The relative level of the transcripts could be modulated through transcription termination at the stem–loop downstream of cpcA by RNA processing at this site followed by degradation of the linker-encoding mRNA. In Synechocystis sp. strain PCC6803 and Synechococcus sp. strain PCC6301 PBSs, the L^R_{33} to L^R_{10} ratio was repeatedly <1, decreasing under high-light conditions (our unpublished observations; Löneborg et al., 1985). In view of the cpcC2 and cpcC1 co-transcription, one must imagine a form of regulation in which cpcC2 is down-regulated first. Endoribonuclease processing downstream of cpcA followed by 5′→3′ progressing degradation (Rauhut & Klug, 1999) of the linker-encoding RNA could accomplish this, since cpcC2 would be down-regulated first and cpcC1 would be protected by the 3′ stem–loop structures. Further experiments are needed to test this hypothesis.

The CB mutant is similar to the An112 mutant of Synechococcus sp. strain PCC6301 (Yamanaka et al., 1980) and the PR6009 mutant of Synechococcus sp. strain PCC7002 (de Lorimier et al., 1990b). All these mutants show that the L^R_{33} is involved in association of the core-proximal PC hexamers, at the base of every rod, with the core. Two modes of assembly are then possible for the remaining PC hexamers: (i) L^R_{33} and L^R_{10} are interchangeable – either can be present in both the intermediary and distal PC hexamers; (ii) the intermediary PC hexamers contain only one linker type, with the other specifically present in the distal PC hexamers. Careful characterization of mutants deficient in each of these linkers should favour one of these modes. Such
mutants constructed in Synechococcus sp. strain PCC7942 suggested that L30 could replace L33 in its absence (Bhalerao et al., 1991, 1993), favouring the first mode but in contradiction with the results presented here. Indeed, the first mode was excluded by two of our observations: (i) the absence of L30 prevented L30 attachment in the cpcC1-deficient strain 33, and (ii) transcomplementation of strain 33 with cpcC1 restored attachment of both L33 and L30. We therefore favour the second mode, with LR attaching the intermediary PC hexamer and L30 attaching the distal one. This mode is also in agreement with results obtained upon nitrogen starvation, where sequential loss of PC and associated linkers occurs. L30 disappears first from the PBS of Synechocystis sp. strain PCC6803 and Synechococcus sp. strain PCC6301 during the initial steps of nitrogen starvation, suggesting that this linker is associated with the peripheral PC hexamer (Richaud et al., 2001; Yamanaka & Glazer, 1980). In terms of genetics, cpcC2 and cpcC1 might have been created by gene duplication in an ancestral strain that contained only one cpcC, such as Synechococcus sp. strain PCC7002. The resulting genes then acquired different functions, and cpcC1 became epistatic to cpcC2. The domain that determines the specificity of L30 and L33 may lie within the C-terminal third of their sequences, since it is less conserved than the remaining two-thirds (28% and 55% identity for each, respectively). Specific interactions between these rod linkers seem to exclude their random insertion in Synechocystis sp. strain PCC6803 but not in mutants of Synechococcus sp. strain PCC7942. Amino acid sequence comparison of L33 and L30 from Synechocystis sp. strain PCC6803 and Synechococcus sp. strain PCC7942 did not provide an explanation for the differing results obtained in the two strains.

L10 was present, albeit in smaller amounts, in PBSs lacking the core-distal (30f) or both the intermediary and the core-distal PC hexamers (33 and CB). Its reduced level was first attributed to the polar effect of the Km cassette on cpcD expression in these strains, but the increased amounts of L10 in the 33c PBS compared to CB (Fig. 4a) suggests that, although the polar effect exists, L10 might have a higher affinity for a PC hexamer containing L30. Indeed L10 was proposed to be associated with the distal end of the rods (de Lorimier et al., 1990a). Its absence does not seem to affect PBS assembly or function in Synechocystis sp. strain PCC6803.

In cyanobacteria, the FNR contains an N-terminal domain that shares similarity to PBS linker polypeptides (Schluchter & Bryant, 1992). The highest similarity was found to the L10 linker (about 32% identity and 75% similarity over 80 amino acids), while lower similarities were found to the C-terminal domains of L33 and L30, and even to the core-associated linker LC. It has been proposed that the FNR shares the same binding site as L10 in the PBS rod of Synechococcus sp. strain PCC7002 (Gomez-Llojero et al., 2003). If they shared the same binding site, one would expect the relative amounts of FNR to increase in the absence of L10, which was not observed in any of the mutants constructed here. The binding site of the FNR has also been suggested to be the core-proximal PC hexamer in Synechocystis sp. strain PCC6803 (van Thor et al., 1999), but more direct evidence is needed in order to localize the linkers and the FNR in the PBS.

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