

Supporting Information

CpeF is the bilin lyase that ligates the doubly linked phycoerythrobilin on β -phycoerythrin in the cyanobacterium *Fremyella diplosiphon*

Christina M. Kronfel, Carla V. Hernandez, Jacob P. Frick, Leanora S. Hernandez, Andrian Gutu, Jonathan A. Karty, M. Nazim Boutaghou, David M. Kehoe, Richard B. Cole, and Wendy M. Schluchter

Fig. S1: Doubly bound PEB structure, the *peb* operon and modeled CpeF structure

Fig. S2: Phenotypes of *F. diplosiphon* strains grown in $\sim 15 \mu\text{mol m}^{-2} \text{s}^{-1}$ of green light

Fig. S3: Recombinant CpeF coexpressions with HT-CpeBA

Table S1: Spectral properties of PBS purified from WT and $\Delta cpeF$

Table S2: Observed MALDI-MS peaks of tryptic digested recombinant HT-CpeB peptides

Table S3: Oligonucleotide primers used in this study

Table S4: Plasmids used in this study

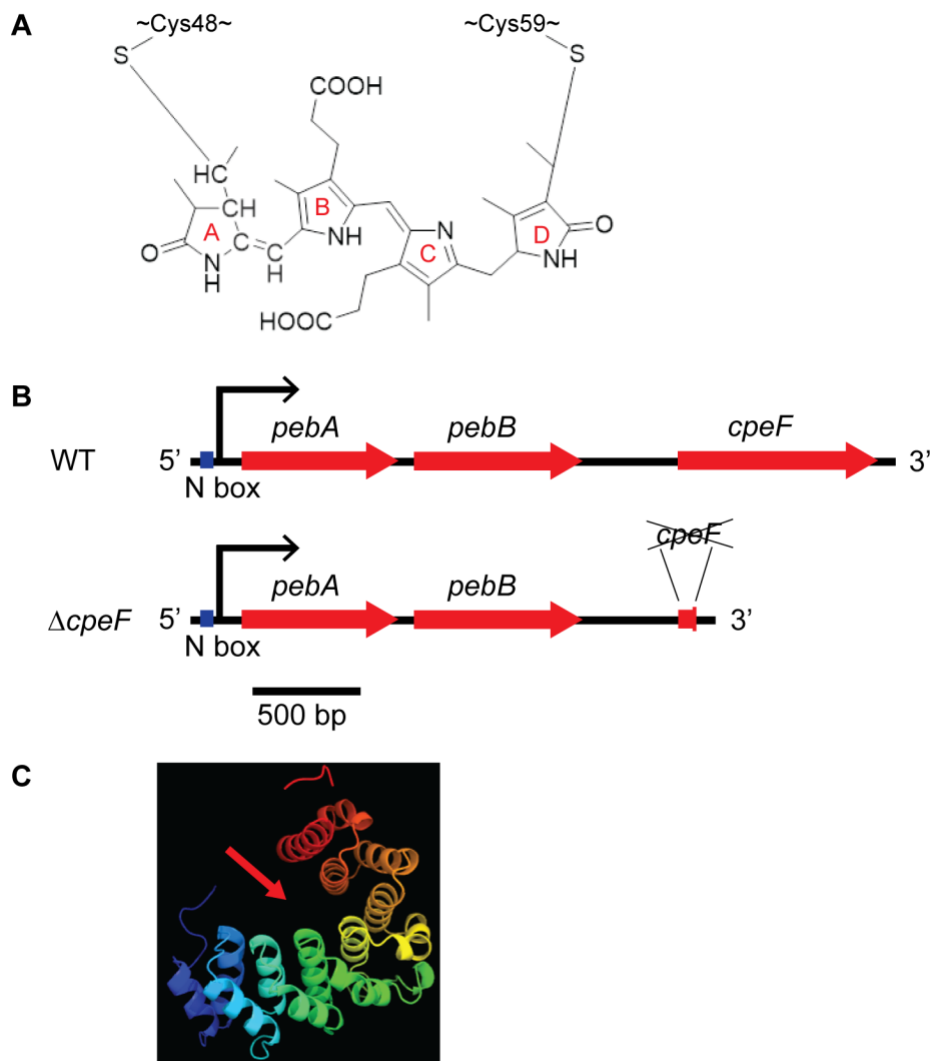


Fig. S1: Doubly bound PEB structure, the *peb* operon and modeled CpeF structure

(A) Structure of PEB doubly bound to specific Cys residues (Cys-48 and Cys-59 of CpeB from *F. diplosiphon*) of phycobiliproteins by thioether linkages to the A and D rings (1). (B) Diagrams of the *peb* operon containing the genes that encode the PEB synthesis proteins (PebA and PebB) and the bilin lyase CpeF from WT and $\Delta cpeF$ strains of *F. diplosiphon*. Possible transcription regulation site is labeled “N box” (2). (C) Predicted 3D structure of CpeF from *F. diplosiphon* using Phyre² prediction system (3,4). The red arrow indicates the possible PEB binding location in the groove of CpeF.

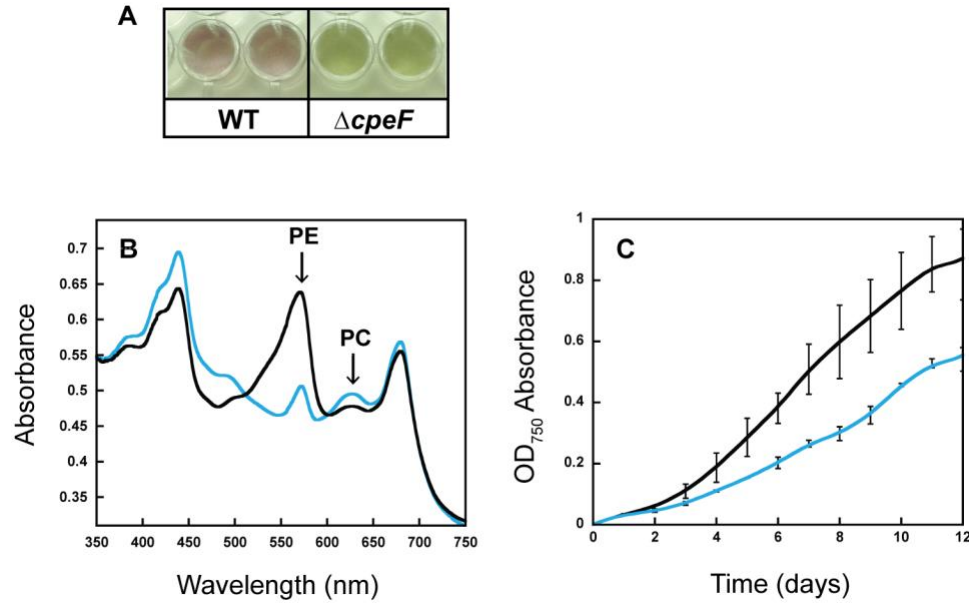


Fig. S2: Phenotypes of *F. diplosiphon* strains grown in $\sim 15 \mu\text{mol m}^{-2} \text{s}^{-1}$ of green light

(A) Liquid cell cultures of WT and $\Delta cpeF$ *F. diplosiphon* grown in approximately $\sim 15 \mu\text{mol m}^{-2} \text{s}^{-1}$ of green light. (B) Whole cell absorbance spectra of WT (black line) and $\Delta cpeF$ (cyan line) cells. PE and PC peaks are indicated with arrows. (C) Average growth curves of two independent replicates each for WT (black line) and $\Delta cpeF$ (cyan line) cells with OD readings taken at 750 nm every 24 hours for 12 days. Error bars represent the ranges.

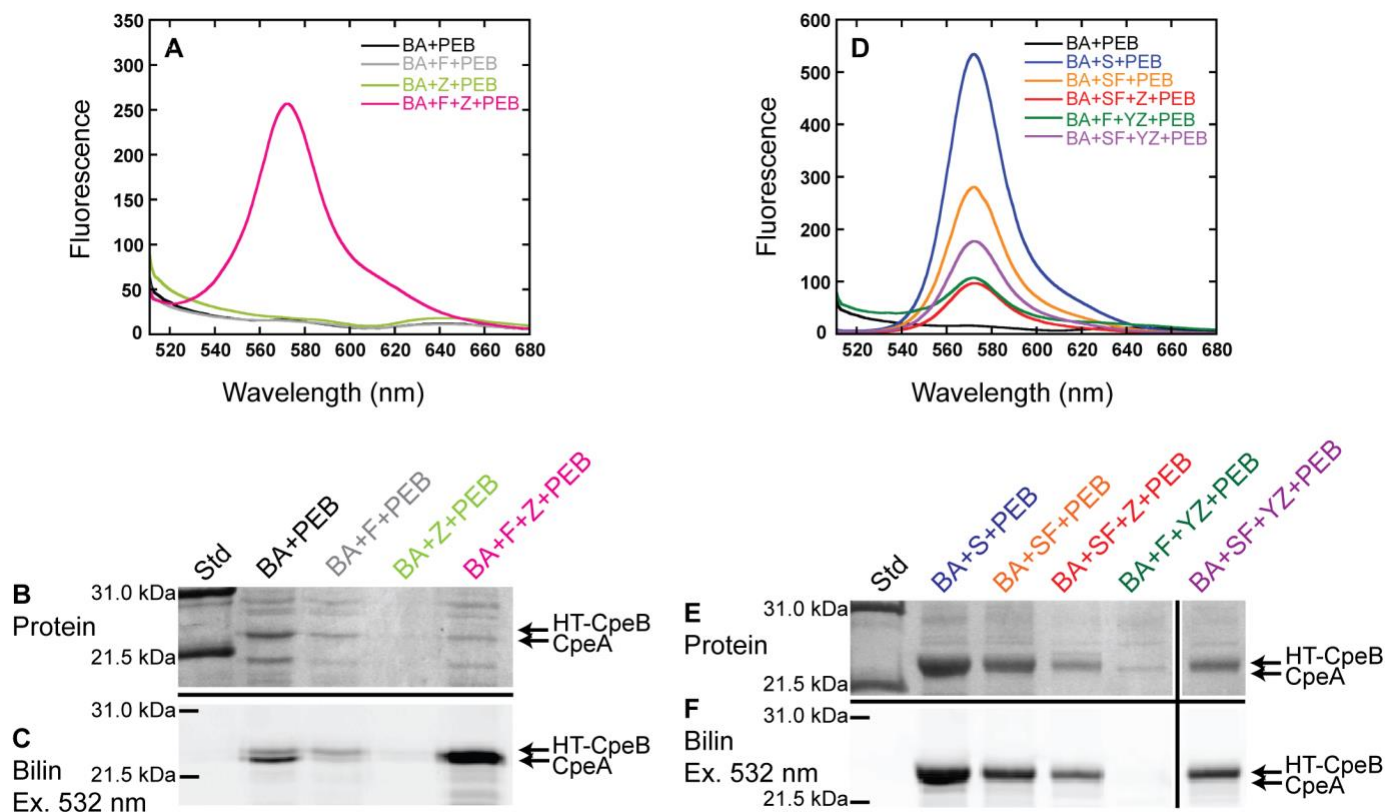


Fig. S3: Recombinant CpeF coexpressions with HT-CpeBA

(A) Fluorescence emission (excitation set at 490 nm) spectra of purified HT-CpeBA obtained from *E. coli* cells expressing pCpeBA and pNT-PebS (BA+PEB; black) in addition to pCpeF2 (BA+F+PEB; grey); pNT-CpeZ3 (BA+Z+PEB; lime green); or pCpeF2 and pNT-CpeZ3 (BA+F+Z+PEB; magenta). All spectra were obtained using undiluted samples. (B) The Coomassie-stained SDS-polyacrylamide gel for purified HT-CpeBA samples from panel A. Lane “Std” indicates the molecular weight standard. (C) The Zn-enhanced fluorescence of the gel in panel B excited at 532 nm. (D) Fluorescence emission (excitation set at 490 nm) spectra of purified HT-CpeBA obtained from *E. coli* cells expressing pCpeBA and pNT-PebS (BA+PEB; black) in addition to pCpeS (BA+S+PEB; blue); pCpeSF2 (BA+SF+PEB; orange); pCpeSF2 and pNT-CpeZ3 (BA+SF+Z+PEB; red); pCpeF2 and pNT-CpeYZ (BA+F+YZ+PEB; green); or pCpeSF2 and pNT-CpeYZ (BA+SF+YZ+PEB; purple). All spectra were obtained by diluting the samples 151-fold except for the two samples BA+PEB and BA+F+YZ+PEB which were undiluted. (E) The Coomassie-stained SDS-polyacrylamide gel for purified HT-CpeBA samples from panel D. Lane “Std” indicates the molecular weight standard. (F) The Zn-enhanced fluorescence of the gel in panel E excited at 532 nm. These results are representative of three independent replicates.

Table S1: Spectral properties of PBS purified from WT and Δ cpeF

Strain and fraction	PE Abs λ_{\max} (nm)	PC Abs λ_{\max} (nm)	AP Abs λ_{\max} (nm)	Fluorescence emission λ_{\max} (nm) excited at 490 nm
WT bottom	568	615	649	582 (sh), 669
Δ cpeF middle	577	617	649	576 (sh), 673
Δ cpeF bottom	577	617	649	576 (sh), 673

“Abs” is an abbreviation for absorbance.

“sh” is an abbreviation for shoulder in the spectrum.

Table S2: Observed MALDI-MS peaks of tryptic digested recombinant HT-CpeB peptides

Sample *	CpeB Cys-80 (m/z)	CpeB Cys-165 (m/z)	CpeB Cys-48/Cys-59 (m/z)
B+F+PEB	ND	ND	ND
B+S+PEB	1250.7	ND	ND
B+S+F+PEB	1250.7	ND	ND
BZ+F+PEB	ND	ND	ND
BZ+S+PEB	1250.7	ND	ND
BZ+S+F+PEB	1250.7	ND	4627.4

CpeB peptides contain a PEB chromophore (587 m/z) at the specified Cys residues when indicated by an m/z value which are represented with a +1 charge state.

“ND” represents PEB modified peptides that were not detected in MS results.

* See Fig. 4 for sample descriptions.

Table S3: Oligonucleotide primers used in this study

Primer name ^a	Sequence (5' to 3') ^b	Plasmid(s) created
cpeF-f2	CCAACAGAGGAAGATCCCCGCGCAAATTGA ACGTCAATCCGAAGAAGATGATTGGTAAC	<i>cpeF</i> deletion construct
cpeF-r	CGGATTGACGTTCAATTTGCGCGGGATCTT CCTCTGTTGGAGCTTCTG	<i>cpeF</i> deletion construct
Nco-cpeF-r2	TC <u>ACCATGG</u> ATTACATCAACGTGCAGGTAG C	<i>cpeF</i> deletion construct
Nco-cpeF-f	TC <u>ACCATGG</u> CCATTCCCCAGGACTAGACT ATCAGGTGAGCGATCGCGG	<i>cpeF</i> deletion construct
FdcpeA.R.EcoRI	AAGAATTCCTAGGAGAGAGAGTTAATAGC GTA	pCpeBA
HTcpeB.F.BamHI	A <u>AGGATCC</u> GATGCTTGATGCTTTTTCTAGA GC	pCpeB2; pCpeBA; pCpeBZ
HTcpeB.R.EcoRI	CCGAATTCCTTAGCTCAAAGCAGAGATTACG CG	pCpeB2; pCpeBA; pCpeBZ
FdCpeB(C48S)	[phos]CAACGCTAGCTCCATGGTTTCTG	pCpeB(C48S)CpeA
FdCpeB(C59S)	[phos]CTGGAATGATCTCCGAAAACCAA GG	pCpeB(C59S)CpeA
pETDuet(XhoI del)	[phos]ACGTCGGTACCCTCCAGTCTGGTA AAGAAACCGCTG	pCpeB(C48S)CpeA; pCpeB(C59S)CpeA
HTcpeF2.F.XhoI	GCTCGAGAAGTCAATCACTCAACTCAG	pHT-CpeF2
HTcpeF2.R.HindIII	CCAAGCTTCCAATCATCTTCTTCGG	pHT-CpeF2
FdcpeF.F.NdeI	AATTTGTGCATATGAGTCAATCACTCAACT CAGAA	pCpeF2; pCpeSF2
FdcpeF.R.XhoI	AACTCGAGTTACCAATCATCTTCTTCGGAT TG	pCpeF2; pCpeSF2
FdcpeS.F.NcoI	AACCATGGAAACCAAAGTGTGATGAATAT TACA	pCpeSF2
FdcpeS.R.PstI	AACTGCAGCTAGGCACCAGTGTTTATGAAA AAATG	pCpeSF2
FdcpeY.F.BglIII	GATCAGATCTATGGATAAGCGCTTTTTTAA TTTC	pNT-CpeYZ
FdcpeZ.R.XhoI	GATCCTCGAGTTATTTTCTCCCCGCTG	pNT-CpeYZ
cpeZ.F.EcoRV	TGGATATCGATGCCGACAACAGAAG	pCpeBZ; pNT-CpeZ3
cpeZ.R.XhoI	CACTCGAGTTTATTTTCTCCCCGCT	pCpeBZ; pNT-CpeZ3

^a“F” and “R” are the forward and reverse primers, respectively.

^b Engineered restriction enzyme sites are underlined.

Table S4: Plasmids used in this study

Plasmid name ^a	Recombinant proteins produced ^b	Parent vector	Antibiotic ^c	Reference
pPebS	Myovirus HO1 and HT-PebS	pACYCDuet-1	Cm	(5)
pNT-PebS	Myovirus HO1 and PebS	pACYCDuet-1	Cm	(6)
pCpeB2	<i>F. diplosiphon</i> HT-CpeB	pCDFDuet-1	Sp	This study
pCpeBA	<i>F. diplosiphon</i> HT-CpeB and CpeA co-expressed on 1 mRNA	pETDuet-1	Ap	This study
pCpeB(C48S)CpeA	<i>F. diplosiphon</i> HT-CpeB(C48S) and CpeA	pCpeBA	Ap	This study
pCpeB(C59S)CpeA	<i>F. diplosiphon</i> HT-CpeB(C59S) and CpeA	pCpeBA	Ap	This study
pCpeBZ	<i>F. diplosiphon</i> HT-CpeB and CpeZ	pCpeB2	Sp	This study
pCpeF2	<i>F. diplosiphon</i> CpeF	pCDFDuet-1	Sp	This study
pHT-CpeF2	<i>F. diplosiphon</i> HT-CpeF	pBAD- <i>Myc</i> -His A	Ap	This study
pCpeS	<i>F. diplosiphon</i> CpeS	pCOLADuet-1	Km	(7)
pCpeSF2	<i>F. diplosiphon</i> CpeS and CpeF	pCDFDuet-1	Sp	This study
pNT-CpeYZ	<i>F. diplosiphon</i> CpeY and CpeZ	pCOLADuet-1	Km	This study
pNT-CpeZ3	<i>F. diplosiphon</i> CpeZ	pCOLADuet-1	Km	This study

^a “NT-” is an abbreviation for “Non-Tagged” referring specifically to hexahistidine-tags.

^b Proteins produced as hexahistidine-tagged fusions are indicated as “HT-”.

^c Antibiotic resistance used to select for presence of the plasmid (Ap: ampicillin; Cm: chloramphenicol; Km: kanamycin; Sp: spectinomycin).

References

1. Ficner, R., Lobeck, K., Schmidt, G., and Huber, R. (1992) Isolation, crystallization, crystal structure analysis and refinement of B-phycoerythrin from the red alga *Porphyridium sordidum* at 2.2 Å resolution. *J. Mol. Biol.* **228**, 935-950
2. Alvey, R. M., Karty, J. A., Roos, E., Reilly, J. P., and Kehoe, D. M. (2003) Lesions in phycoerythrin chromophore biosynthesis in *Fremyella diplosiphon* reveal coordinated light regulation of apoprotein and pigment biosynthetic enzyme gene expression. *Plant Cell* **15**, 2448-2463
3. Kelley, L. A., Mezulis, S., Yates, C. M., Wass, M. N., and Sternberg, M. J. E. (2015) The Phyre2 web portal for protein modeling, prediction and analysis. *Nat. Protocols* **10**, 845-858
4. Zhao, C., Höppner, A., Xu, Q.-Z., Gärtner, W., Scheer, H., Zhou, M., and Zhao, K.-H. (2017) Structures and enzymatic mechanisms of phycobiliprotein lyases CpcE/F and PccE/F. *Proc. Natl. Acad. Sci.* **114**, 13170-13175
5. Dammeyer, T., Bagby, S. C., Sullivan, M. B., Chisholm, S. W., and Frankenberg-Dinkel, N. (2008) Efficient phage-mediated pigment biosynthesis in oceanic cyanobacteria. *Curr. Biol.* **18**, 442-448
6. Kronfel, C. M., Biswas, A., Frick, J. P., Gutu, A., Blensdorf, T., Karty, J. A., Kehoe, D. M., and Schluchter, W. M. (2018) Biogenesis of phycoerythrin. I. Defining the roles of the chaperone-like protein CpeZ and the phycoerythrobilin lyase CpeY in *Fremyella diplosiphon*. *Biochimica et Biophysica Acta (BBA) - Bioenergetics*, Under Review
7. Biswas, A., Boutaghou, M. N., Alvey, R. M., Kronfel, C. M., Cole, R. B., Bryant, D. A., and Schluchter, W. M. (2011) Characterization of the Activities of the CpeY, CpeZ, and CpeS Bilin Lyases in Phycoerythrin Biosynthesis in *Fremyella diplosiphon* Strain UTEX 481. *J. Biol. Chem.* **286**, 35509-35521