

Supporting Information

Light-driven proton pumps as a potential regulator for carbon fixation in marine diatoms

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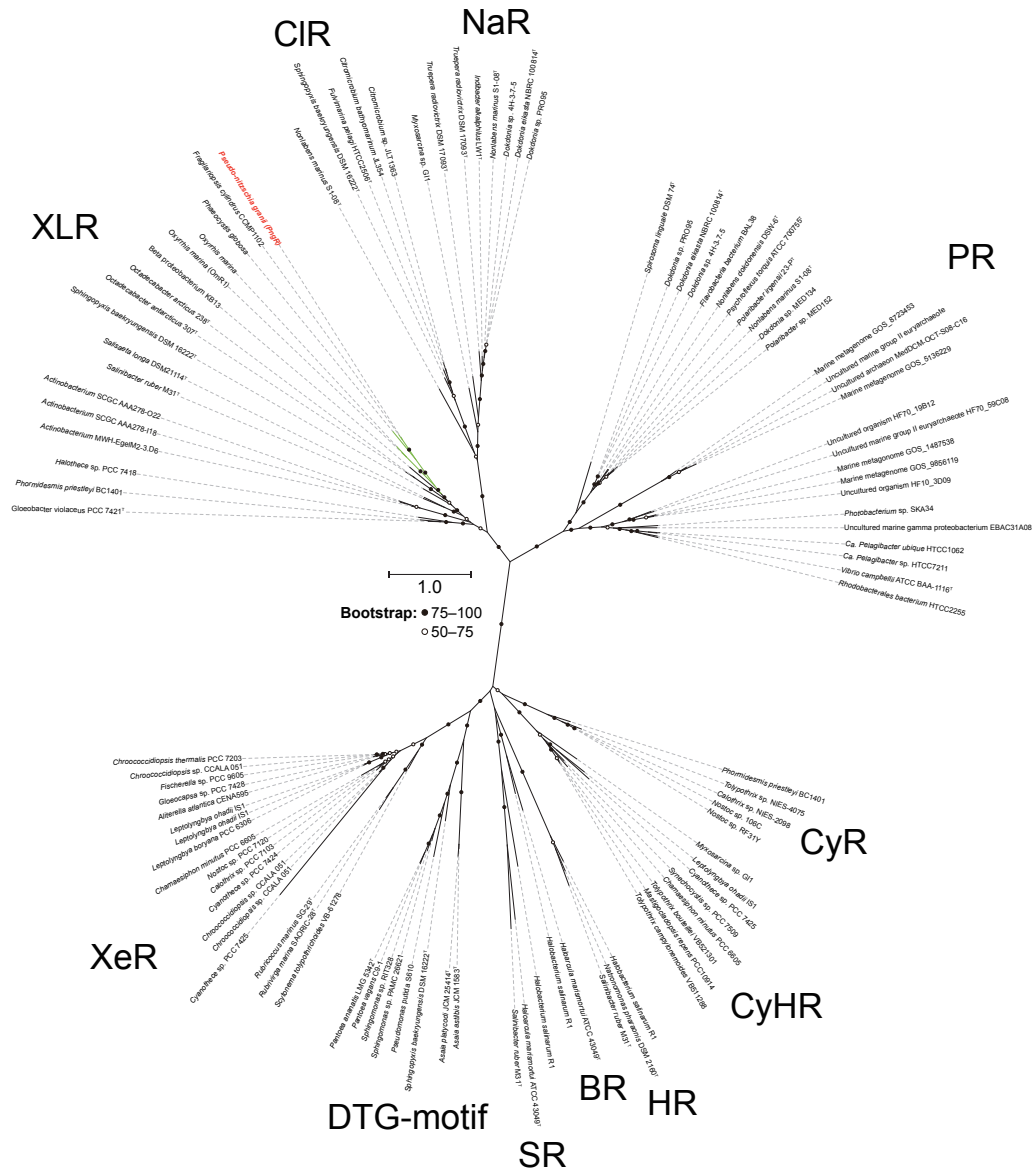
Supplementary Results and Discussion

Photocycle of PngR

To analyze the photocycle of PngR, we performed flash-photolysis experiment. Extended Data Fig. 5A shows the flash-induced difference spectra over the spectral range of 380–700 nm. The depletion and recovery of absorbance at ~ 510 nm correspond to the bleaching of the original state, while an increase and decrease of absorbance at ~ 410 and 570 nm were characteristically observed. Extended Data Fig. 5B shows the time courses of the difference absorbance changes at the three wavelengths of 410, 510 and 570 nm. Following the illumination, an absorption increase at ~ 570 nm was observed together with the depletion of the original state. An absorption increase at ~ 410 nm was then observed with a concomitant absorption decrease at ~ 570 nm within 0.5 ms. Considering the temporal and spectral ranges of the absorption changes, the absorbances at 570 and 410 nm were tentatively attributed to the K- and M-intermediates, respectively. The absorbance at ~ 410 nm decreased with the concomitant absorbance increase at ~ 570 nm, which was tentatively assigned as the O-intermediate, within 10 ms. Finally, the absorbance at ~ 570 nm was depleted with recovery of the original state within 300 ms. Thus, after the light absorption, PngR sequentially forms K-, M- and O-intermediates, and then returns to the original state. To estimate the decay time constants of the intermediates, the temporal absorption changes at 410, 510 and 570 nm were fitted with a triple-exponential function assuming the irreversible sequential model. The decay time constants of the K-, M- and O-intermediates were estimated as 0.061, 0.83 and 61 ms, respectively. Finally, we investigated how proton uptake and release happen during the photocycle since PngR exhibits a proton pumping function.

Proton uptake and release by PngR during the photocycle were detected as the time course of the absorbance changes at 450 nm by using pyranine, a pH-sensitive dye. Pyranine works as a pH indicator, and the absorbance of pyranine at 450 nm was decreased under acidic conditions. As a result, the absorbance of pyranine increased within 5 ms and then decreased within 100 ms (Extended Data Fig. 5B), which indicates that the substrate proton was first taken up from the bulk solution and then released from PngR during photocycle. These absorbance changes were observed coincident with those of O-intermediate, which suggests that proton uptake and release are coincident with the formation and decay of O-intermediate, respectively. Based on these results, we propose a photocycle model of PngR as shown schematically in Extended Data Fig. 5C.

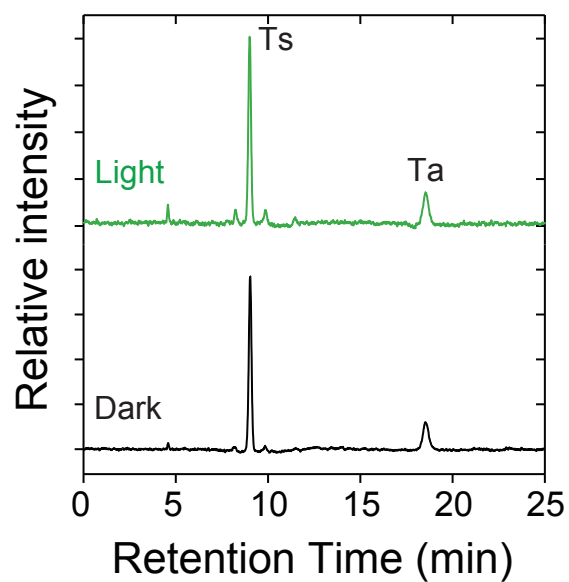
Extended Data Figs.



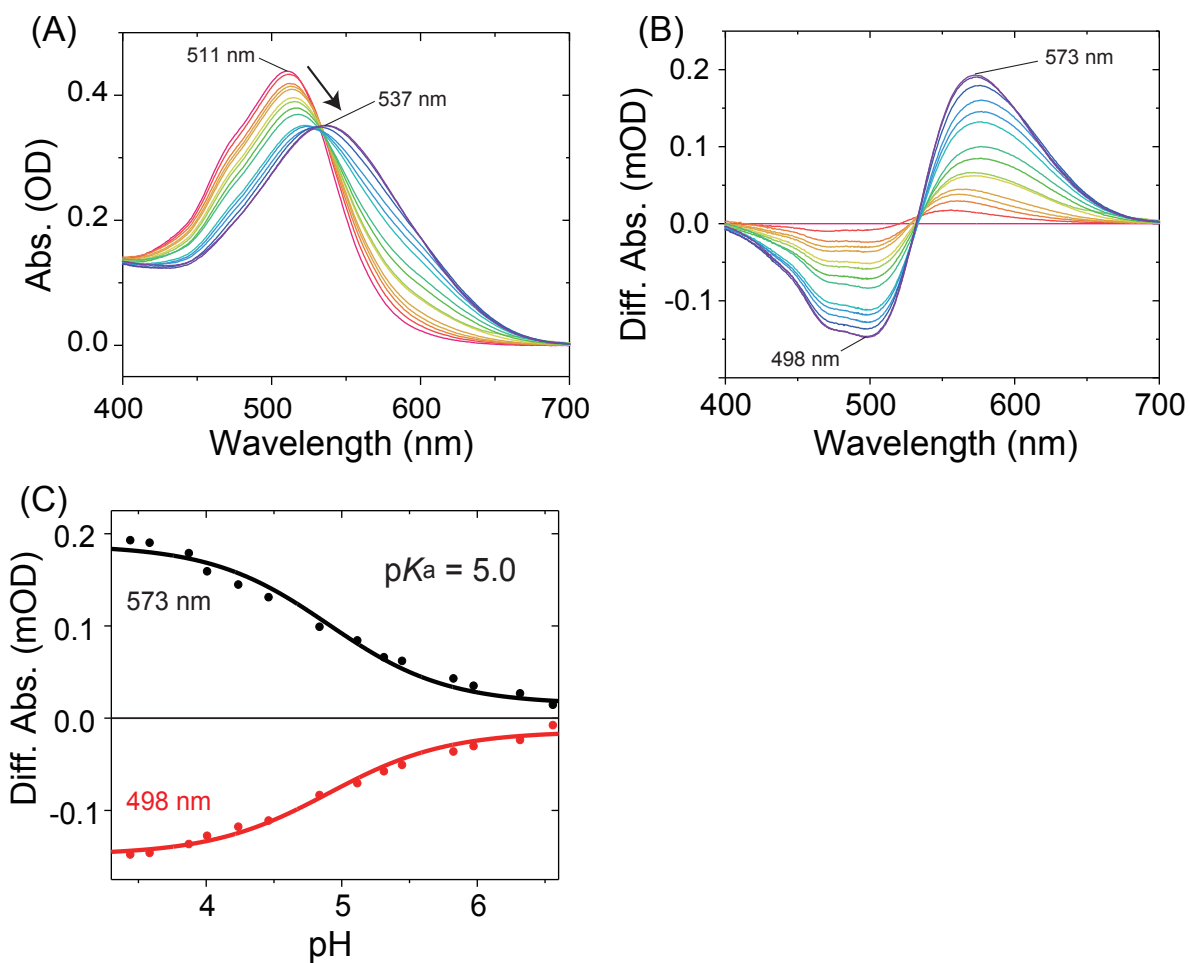
Extended Data Fig. 1. Phylogenetic position of diatom rhodopsin and the rhodopsin sequences used in this analysis. A maximum likelihood tree of amino acid sequences of microbial rhodopsins. Diatom rhodopsin (PngR) is indicated by red character and bootstrap probabilities ($\geq 50\%$) are indicated by black and white circles. Green branches indicate eukaryotic rhodopsins used in this analysis, and black branches indicate prokaryotic rhodopsins. Rhodopsin clades are as follows: XLR (Xanthorhodopsin-like rhodopsin), CIR (Cl⁻-pumping rhodopsin), NaR (Na⁺-pumping rhodopsin), PR (proteorhodopsin), XeR (xenorhodopsin), DTG-motif rhodopsin, SR (sensory rhodopsin-I and sensory rhodopsin-II), BR (bacteriorhodopsin), HR (halorhodopsin), CyHR (cyanobacterial halorhodopsin), and CyR (cyanorhodopsin).

PngR	-----	-----	-----	--MVTANQFT	IVYD--VLSF	SLATMMATTI	FLWMRVPSVH
XR	--MLQEL---	-----	-----	-PTLTPGQYS	LVFN--MFSF	TVATMTASFV	FFVLRANNVA
GR	M-LMTVFSSA	PELALLGSTF	AQVDPSNLSV	SDSLTYGQFN	LVYN--AFSF	AIAAMFASAL	FFFSQAQLVG
BR	--MLELLPTA	V-----	-----	-EGVSQAQIT	GRPEWIWLAL	GTALMGLGTL	YFLVKGMGVS
PR	MKLLLLILGSV	IALPTFAAGG	-----	-GDLDASDYT	GV----SFWL	VTAALLASTV	FFFVERDRVS
NaR	--MTQELGNA	NFENFIGAT-	-----	-EGFSEIAYQ	FTSH--ILTL	GYAVMLAGLL	YFILTICKVD
							85 89 (91) (95)
PngR	-EKYKSALII	SGLVTFIAAY	HYLRIFNSWT	EAYEWTAE-G	E--LSATASP	FNDAY--RYM	DWLLT VP ⁸⁵ LLL
XR	-PKYRISMMV	SALVVFIAGY	HYFRITSSWE	AAYA-LQN-G	M--YQPTGEL	FNDAY--RYV	DWLLT VP ⁸⁹ LLT
GR	-QRYRLALLV	SAIVVSIAGY	HYFRIFNSWD	AAYV-LEN-G	V--YSLTSEK	FNDAY--RYV	DWLLT VP ⁸⁵ LLL
BR	DPDAKKFYAI	TTLVPAIAFT	MYLSMLLGYG	LT-----	---MVPFGGE	QNPIYWARYA	DWLF TTP ⁸⁵ LLL
PR	-AKWKTSLTV	SGLVTGIAFW	HYMYMRGVWI	ET-----	-----GD	SPTVF--RYI	DWLLT VP ⁸⁵ LLI
NaR	-KKFQMSNIL	SAVVMVSAFL	LLYAQAQNT	SSFTFNEEVG	RYFLDPSGDL	FNNGY--RYL	NWLI DVP ⁸⁵ MLL
							96 (102)
PngR	I EIILVMKLP	ADESRSKATT	LGIASAAMIA	IGYPGELAMS	DDSLGTRWVY	WIGAMLPFLY	IVQ ⁹⁶ TLLVGLN
XR	V ELVLVMGLP	KNERGPLAAK	LGFLAALMIV	LGYPGEVSEN	AALFGTRGLW	GFLSTIPFVW	ILYILFTQLG
GR	V ETVAVLTLP	AKEARPLLIK	LTVASVLMIA	TGYPGEISDD	IT---TRIIW	GTVSTIPFAY	ILYVLWVELS
BR	L DLALLV---	-DADQGTILA	LVGADGIMIG	TGLV ⁹⁶ GALTKV	YS---YRFVW	WAISTAAMLY	ILYVLF ⁹⁶ FGFT
PR	C EYLLILAAA	TNVAGSLFKK	LLVGSLVMLV	FGYMGEAGIM	AA-----WPA	FIIGCLAWVY	MIYELWAGEG
NaR	F QILFVVSLT	TSKFSSVRNQ	FWFSGAMMII	TGYIGQFYEV	SNLT-AFLVW	GAISSAFFFH	ILWWMKKVIN
							212 216 (227) (231)
PngR	DATQSEADPA	IRDLIKGVQW	WTVISWCTYP	VVYVFPMM-G	ITG-----TN	AIVGIIQ---L	GYSVSD I IISK
XR	DTIQRQS-SR	VSTLLGNARL	LLLATWGFYP	IAYMIPMA-F	PEAFPSNTPG	TIVALQ---V	GYTIAD V LAK
GR	RSLVRQP-AA	VQTLVRNMRW	LLLLSWGVPY	IAYLLPML-G	VSG-----TS	AAVG ²¹² VQ---V	GYTIAD V LAK
BR	SKAESMR-PE	VASTFKVLRN	VTVVLWSAYP	VVWLIGS---	-EG-----A	GIVPLNIETL	LFMVL D VSAK
PR	KSACNTASPA	VQSAYNTMMY	IIIFGWAIYP	VGYFTGYL-M	GDG-----G	SALNLN---L	IYNLAD F VNK
NaR	EGKEGIS-PA	GQKILSNIWI	LFLISWTLYP	GAYLMPYL ²¹² TG	VDGFLYS-ED	GVMARQ---L	VYTIAD V SSK
PngR	CGVGLMIYQI	TIAKSYAL--	--KKGNEETP	LYG-----	-----		
XR	AGYGVLIYNI	AKAKSEEEGF	NVSEMVEPAT	ASA-----	-----		
GR	PVFGLLVF ⁹⁶ AI	ALVKT ⁹⁶ KAD--	--QESSEPHA	AIGAAANKSG	GSLIS		
BR	VGFGLLILL--	---RSRAI-F	GEAEAPEPSA	GDGAAATSD-	-----		
PR	ILFGLIIWNV	AVKESSNA--	-----	-----	-----		
NaR	VIYGVLLGNL	AITLSKNKEL	--VEANS---	-----	-----		

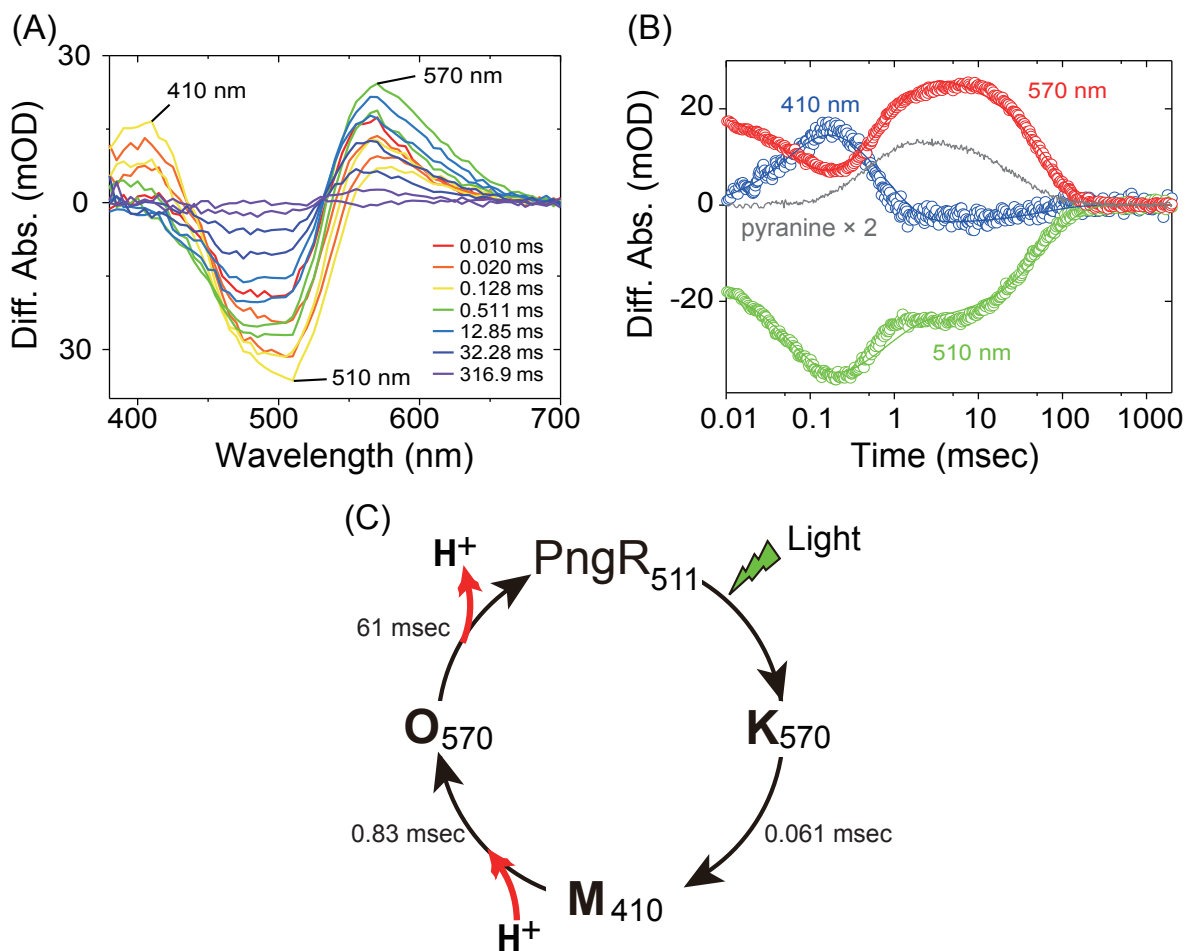
Extended Data Fig. 2. Sequence alignment of rhodopsins. The accessions and rhodopsin families are as follows: PngR (AJA37445.1, XLR), XR (WP_011404249.1, XLR), GR (BAC88139.1, XLR), BR (CAP14056.1, BR), PR (AAG10475.1, PR), and NaR (BAN14808.1, NaR). All rhodopsins except NaR function as proton pump. Columns of functionally important residues are shown in bold. The numbers above the columns indicate amino acid numbers in BR, and PngR in parentheses. Known functions are as follows: primary proton acceptor (Asp85 in BR), proton donor (Glu96), counterion (Asp212), Schiff base (Lys216). Two carboxylates, Asp (D) and Glu (E), are shown in blue, and Schiff base Lys (K) is shown in red.



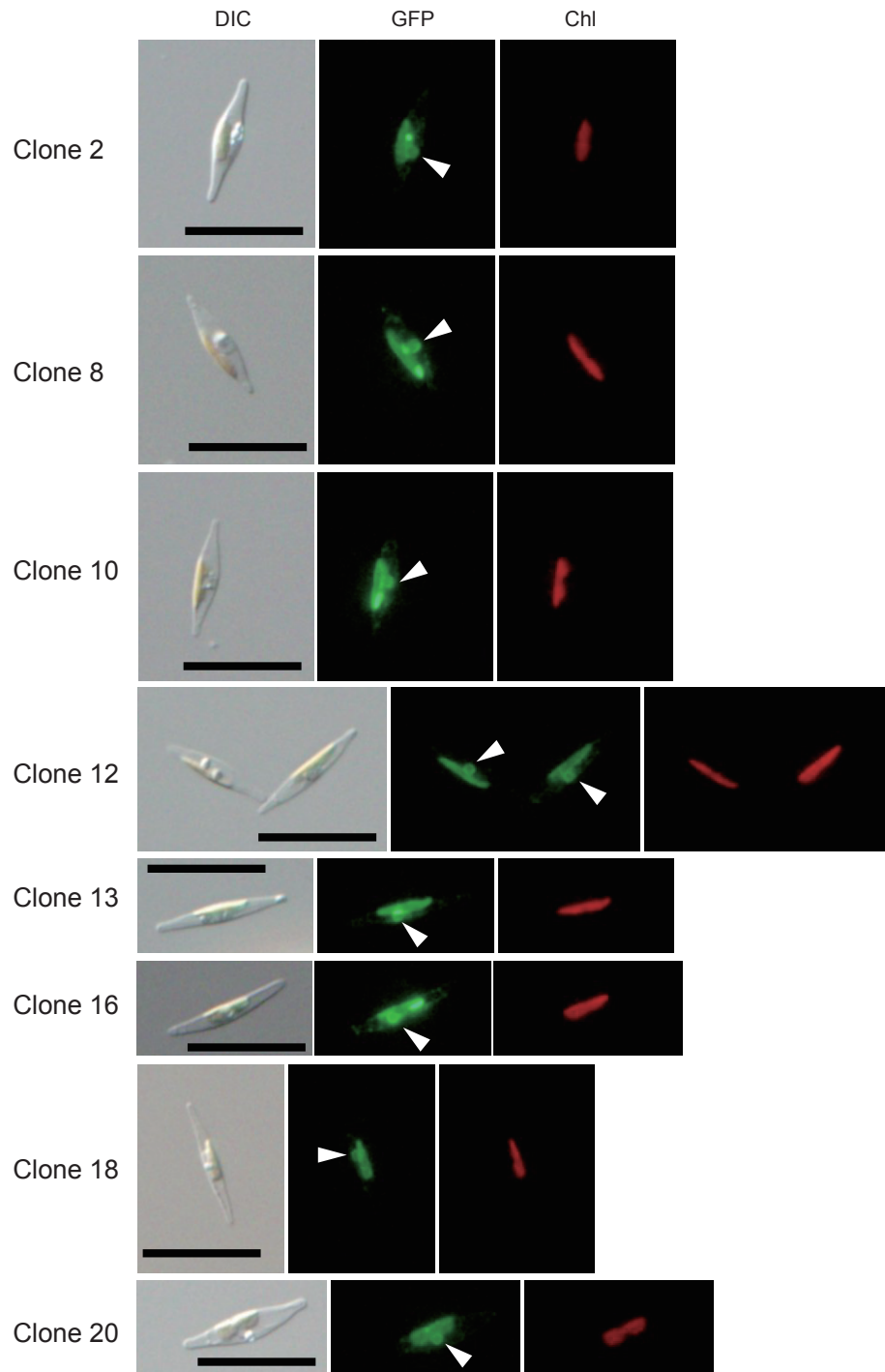
Extended Data Fig. 3. Retinal configuration of PngR. HPLC patterns of retinal isomers of PngR with (green line) and without (black line). Ts and Ta represent all-*trans*-15-*syn* and all-*trans*-15-*anti* retinal oximes, respectively.



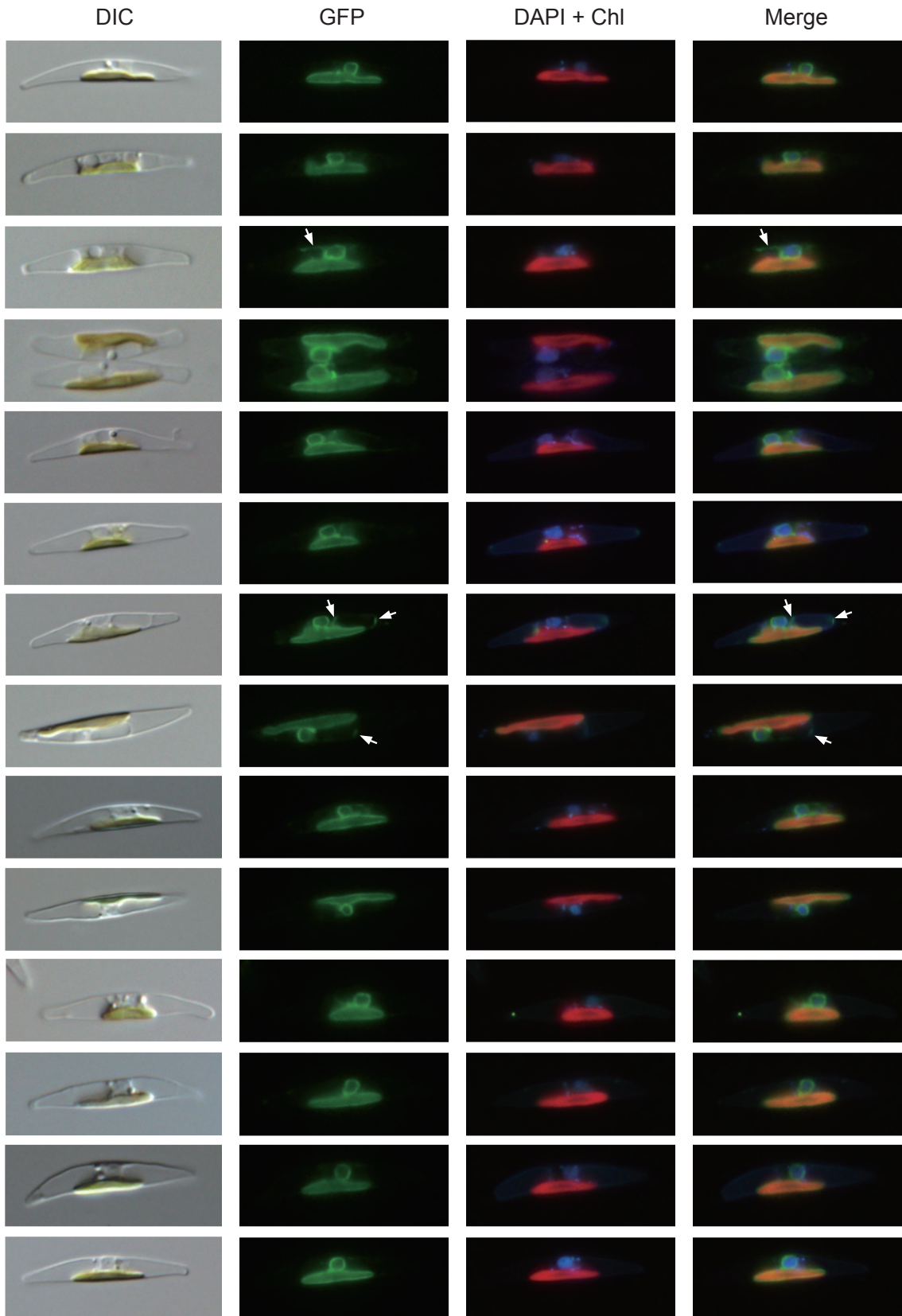
Extended Data Fig. 4. pH-induced spectral changes of PngR. (A) Absorption spectra of PngR at acidic pH from 7.0 to 3.4 in Buffer A containing 50 mM Tris-HCl, 1 M NaCl and 0.05% (w/v) DDM. (B) Difference absorption spectra; each spectrum was obtained by subtracting the spectrum at pH 7.0. (C) Plots of the difference absorbance at 498 and 573 nm against the pH values. The titration curve was analyzed using the Henderson-Hasselbalch equation assuming single pK_a value (solid lines).



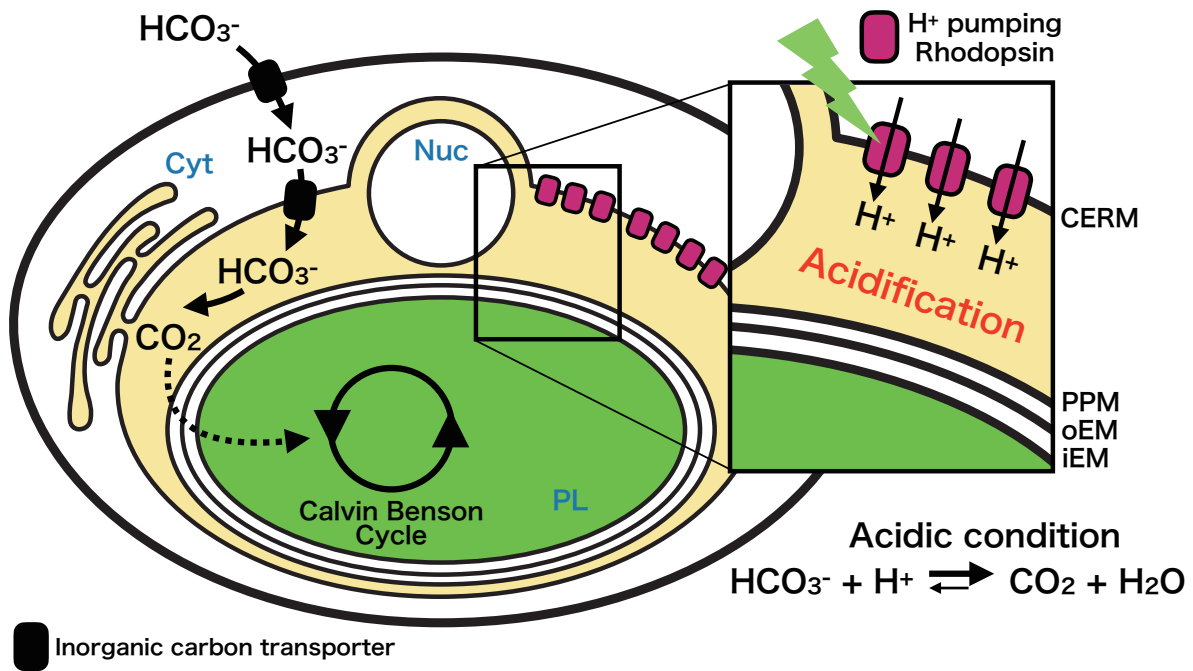
Extended Data Fig. 5. Photoreaction kinetics of PngR with timing of proton release and uptake. (A) Flash-induced difference absorption spectra over the spectral range of 380 to 700 nm in Buffer A containing 50 mM Tris-HCl (pH 7.0), 1 M NaCl and 0.05% (w/v) DDM. (B) Time courses of absorbance changes at 410, 510, and 570 nm. The black solid lines indicate the fitting curves. The absorption changes of pyranine monitored at 450 nm were enlarged 2 times and are shown as a gray solid line. (C) Proposed photo cycle model of PngR with the timing of the proton release and uptake.



Extended Data Fig. 6. Subcellular localization of the exogenously introduced PngR and plastid in diatom cells. Transformed diatom cells were observed with DIC (Differential Interface Contrast) (Left). Green fluorescence from the recombinant protein (GFP) and the chlorophyll autofluorescence (Chl) are shown in center and right, respectively. The triangles show the location of nucleus, and GFP surrounds the nucleus. Scale bar indicates 20 μm .



Extended Data Fig. 7. Subcellular localization of the exogenously introduced PngR, nucleus and plastid in diatom cells. Transformed diatom cells were observed with DIC (Differential Interface Contrast) (Left). Green fluorescence from the recombinant protein (GFP) (Left center). The nuclear DNA stained with DAPI and the chlorophyll autofluorescence (DAPI + Chl) and merged image (Merge) are shown in right center and right, respectively. Arrows indicate GFP fluorescence outside the chloroplast; most of the GFP fluorescence is localized to the CERM, but it may also be observed in other organelles (e.g., vacuoles and periplasmic membranes).



Extended Data Fig. 8. A proposed model that proton transport by rhodopsin is involved in CCM. The proton transport of rhodopsin acidifies the region (the middle space) surrounded by the membrane of CERM and PPM. Abbreviation are as follows: Cyt (Cytosol), Nuc (Nucleus), PL (Plastid), CERM (Chloroplast endoplasmic reticulum membrane), PPM (Periplastidial membrane), oEM (Outer plastid envelope membrane) and iEM (Internal plastid envelope membrane).

Supplementary Tables

Table S1 Parameters, units and definitions. Parameters are listed roughly in the order of appearance.

Parameter	Unit	Definition
$[CO_2]_p$	$\mu\text{mol L}^{-1}$	CO ₂ concentration in the plastid
t	d	time
D	d^{-1}	diffusion coefficient
$[CO_2]_m$	$\mu\text{mol L}^{-1}$	CO ₂ concentration in the middle space
V_{max}	$\mu\text{mol L}^{-1} \text{d}^{-1}$	maximum C fixation rate
K	$\mu\text{mol L}^{-1}$	Half-saturation constant for C fixation
V_{Cfix}	$\mu\text{mol L}^{-1} \text{d}^{-1}$	C fixation rate
$[DIC]_m$	$\mu\text{mol L}^{-1}$	DIC concentration in the middle space
$[H^+]_m$	mol kg^{-1}	H ⁺ concentration in the middle space
K_1	mol kg^{-1}	temperature and salinity dependent constant 1
K_2	mol kg^{-1}	temperature and salinity dependent constant 2
T	K	temperature
S	‰	salinity

Table S2 Parameter values

Parameter	Value	Unit
K	44 ^{*1}	$\mu\text{mol L}^{-1}$
$[DIC]_m$	993 ^{*2}	$\mu\text{mol L}^{-1}$
T	298.15 ^{*3}	K
S	35 ^{*4}	‰

*1 Based on the middle value from (Young *et al.*, 2016, Jensen *et al.*, 2020)

*2 Observed value of DIC in a diatom *Phaeodactylum tricornutum* (Burns and Beardall, 1987). This is the only mean value we found for diatoms.

*3 Typical room temperature.

*4 Typical values of seawater (note that K_1 and K_2 values are relatively insensitive to S values).

Supplementary References

- Burns, B.D., and Beardall, J. (1987) Utilization of Inorganic Carbon by Marine Microalgae. *J Exp Mar Bio Ecol* **107**: 75-86.
- Young, J.N., Heures, A.M.C., Sharwood, R.E., Rickaby, R.E.M., Morel, F.M.M., and Whitney, S.M. (2016) Large variation in the Rubisco kinetics of diatoms reveals diversity among their carbon-concentrating mechanisms. *J Exp Bot* **67**: 3445-3456.
- Jensen, E.L., Maberly, S.C., and Gontero, B. (2020) Insights on the functions and ecophysiological relevance of the diverse carbonic anhydrases in microalgae. *Int J Mol Sci* **21**: 2922.