Growth yields and light-capture in PhycoCyanin and PhycoErythrin-rich picocyanobacteria, across photic regimes and growth phases

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Supporting Information

Tab. S1. Linear regression, coefficient of determination (R square), Pearson correlation coefficients (R), and *p*-value used to calculate the pigment content (µg mL^{-1}) of two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) (Culture Collection of Baltic Algae) of *Synechococcus* sp. based on absorbance (A) measurements.

Pigment	Abs	Linear_regression	R_square	R	*p*_value
Chl *a*	665	Chl *a* µg/mL = (Abs_{665}*13.411029)+0.154793	0.865	0.930	0.000
Car	480	Car µg/mL = (Abs_{480}*5.469880)+0.089971	0.791	0.890	0.000
PE	565	PE µg/mL = (Abs_{565}*26.760737)-0.143872	0.698	0.840	0.000
PC	620	PC µg/mL = (Abs_{620}*29.979866)-0.182611	0.807	0.900	0.000
APC	650	APC µg/mL = (Abs_{650}*3.873803)+0.021964	0.087	0.300	0.000

Tab. S2. Three-way factorial ANOVA testing whether peak PAR, photoperiod, strain, and their interactions (Source_of_variation), significantly influence the chlorophyll specific exponential growth rate (µ; d^{-1}), estimated from logistic fits of chlorophyll proxy $OD_{680} - OD_{720}$ vs. cumulative diel PUR, for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) (Culture Collection of Baltic Algae) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Df – degrees of freedom; Sum Sq – sum of squares; Mean Sq – mean sum of squares; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Source_of_variation	Df	Sum Sq	Mean Sq	*F*_value	*p*_value
Par_ue	5	0.049	0.010	3.276e+30	0.000
Photoperiod	3	0.076	0.025	8.367e+30	0.000
Strain	3	0.003	0.001	3.151e+29	0.000
Par_ue:Photoperiod	13	0.040	0.003	1.025e+30	0.000
Par_ue:Strain	15	0.007	0.000	1.593e+29	0.000
Photoperiod:Strain	9	0.004	0.000	1.306e+29	0.000
Par_ue:Photoperiod:Strain	39	0.017	0.000	1.434e+29	0.000
Residuals	88	0.000	0.000	NA	N/A

Tab. S3. One-way ANOVA of a three parameter model (Harrison and Platt 1986) from pooled data (All) and data fit across different photoperiods (8, 12, 16, or 24) from chlorophyll specific exponential growth rate vs. cumulative diel PUR (Fit_model), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Strain	Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
PC-rich_056	8_All	41	8.063	1.807e+03	0.000
PC-rich_056	12_All	41	8.063	2.822e+01	0.001
PC-rich_056	16_All	41	8.063	8.566e+00	0.012
PC-rich_056	24_All	41	8.063	2.333e+01	0.001
PC-rich_077	8_All	41	3.015	6.193e+01	0.000
PC-rich_077	12_All	41	3.015	2.477e+01	0.001
PC-rich_077	16_All	41	3.015	1.855e+01	0.002
PC-rich_077	24_All	41	3.015	1.073e+01	0.007
PE-rich_048	8_All	41	6.731	1.443e+01	0.004
PE-rich_048	12_All	41	6.731	8.361e+01	0.000
PE-rich_048	16_All	41	6.731	8.403e+00	0.013
PE-rich_048	24_All	41	6.731	8.234e+01	0.000
PE-rich_127	8_All	41	13.016	1.453e+02	0.000
PE-rich_127	12_All	41	13.016	2.060e+03	0.000
PE-rich_127	16_All	41	13.016	6.908e+00	0.020
PE-rich_127	24_All	41	13.016	7.812e+01	0.000

Tab. S4. One-way ANOVA of a three parameter model (Harrison and Platt 1986) from pooled data (All) and data fit across different peak PAR (30, 90, 180, 300, 600 together with 900) from chlorophyll specific exponential growth rate vs. cumulative diel PUR (Fit_model), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Strain	Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
PC-rich_056	30_All	41	8.063	1.807e+03	0.000
PC-rich_056	90_All	41	8.063	2.822e+01	0.001
PC-rich_056	180_All	41	8.063	8.566e+00	0.012
PC-rich_056	300_All	41	8.063	2.333e+01	0.001
PC-rich_056	900_All	41	8.063	3.360e+00	0.030
PC-rich_077	30_All	41	3.015	6.193e+01	0.000
PC-rich_077	90_All	41	3.015	2.477e+01	0.001
PC-rich_077	180_All	41	3.015	1.855e+01	0.002
PC-rich_077	300_All	41	3.015	1.073e+01	0.007
PC-rich_077	900_All	41	3.015	6.508e-01	0.822
PE-rich_048	30_All	41	6.731	1.443e+01	0.004
PE-rich_048	90_All	41	6.731	8.361e+01	0.000
PE-rich_048	180_All	41	6.731	8.403e+00	0.013
PE-rich_048	300_All	41	6.731	8.234e+01	0.000
PE-rich_048	900_All	41	6.731	1.357e+00	0.328
PE-rich_127	30_All	41	13.016	1.453e+02	0.000
PE-rich_127	90_All	41	13.016	2.060e+03	0.000
PE-rich_127	180_All	41	13.016	6.908e+00	0.020
PE-rich_127	300_All	41	13.016	7.812e+01	0.000
PE-rich_127	900_All	41	13.016	3.523e+00	0.026

Tab. S5. One-way ANOVA of a three parameter model (Harrison and Platt 1986) from pooled data (All) and data fit across different photoperiods (8, 12, 16, or 24) from chlorophyll specific exponential growth rate vs. cumulative diel PAR (Fit_model), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Strain	Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
PC-rich_056	8_All	135	18.854	1.089e+03	0.000
PC-rich_056	12_All	135	18.854	1.412e+01	0.000
PC-rich_056	16_All	135	18.854	7.420e+00	0.000
PC-rich_056	24_All	135	18.854	1.279e+01	0.000
PC-rich_077	8_All	131	5.672	2.749e+01	0.000
PC-rich_077	12_All	131	5.672	8.972e+00	0.000
PC-rich_077	16_All	131	5.672	5.640e+00	0.000
PC-rich_077	24_All	131	5.672	4.027e+00	0.000
PE-rich_048	8_All	133	16.660	2.122e+01	0.000
PE-rich_048	12_All	133	16.660	1.997e+01	0.000
PE-rich_048	16_All	133	16.660	3.576e+00	0.000
PE-rich_048	24_All	133	16.660	8.068e+01	0.000
PE-rich_127	8_All	133	26.508	6.568e+01	0.000
PE-rich_127	12_All	133	26.508	6.758e+03	0.000
PE-rich_127	16_All	133	26.508	1.515e+01	0.000
PE-rich_127	24_All	133	26.508	5.207e+01	0.000

Tab. S6. One-way ANOVA of a three parameter model (Harrison and Platt 1986) from pooled data (All) and data fit across different peak PAR (30, 90, 180, 300, 600 together with 900) from chlorophyll specific exponential growth rate vs. cumulative diel PAR (Fit_model), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Strain	Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
PC-rich_056	30_All	135	18.854	1.089e+03	0.000
PC-rich_056	90_All	135	18.854	1.412e+01	0.000
PC-rich_056	180_All	135	18.854	7.420e+00	0.000
PC-rich_056	300_All	135	18.854	1.279e+01	0.000
PC-rich_056	900_All	135	18.854	2.573e+00	0.003
PC-rich_077	30_All	131	5.672	2.749e+01	0.000
PC-rich_077	90_All	131	5.672	8.972e+00	0.000
PC-rich_077	180_All	131	5.672	5.640e+00	0.000
PC-rich_077	300_All	131	5.672	4.027e+00	0.000
PC-rich_077	900_All	131	5.672	7.428e-01	0.844
PE-rich_048	30_All	133	16.660	2.122e+01	0.000
PE-rich_048	90_All	133	16.660	1.997e+01	0.000
PE-rich_048	180_All	133	16.660	3.576e+00	0.000
PE-rich_048	300_All	133	16.660	8.068e+01	0.000
PE-rich_048	900_All	133	16.660	1.893e+00	0.034
PE-rich_127	30_All	133	26.508	6.568e+01	0.000
PE-rich_127	90_All	133	26.508	6.758e+03	0.000
PE-rich_127	180_All	133	26.508	1.515e+01	0.000
PE-rich_127	300_All	133	26.508	5.207e+01	0.000
PE-rich_127	900_All	133	26.508	2.800e+00	0.002

Tab. S7. One-way ANOVA of a three parameter model (Harrison and Platt 1986) from pooled data (All) and data fit across different photoperiods (8, 12, 16, or 24) from chlorophyll specific exponential growth rate vs. PSII electron flux (JV_{PSII}; µmol e^- µmol Chl a^{-1} d^{-1}) (Fit_model), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Strain	Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
PC-rich_056	8_All	61	11.802	3.972e+00	0.016
PC-rich_056	12_All	61	11.802	7.712e-01	0.730
PC-rich_056	16_All	61	11.802	2.287e-01	1.000
PC-rich_056	24_All	61	11.802	3.332e+00	0.037
PC-rich_077	8_All	61	9.014	1.125e+00	0.459
PC-rich_077	12_All	61	9.014	1.377e+00	0.350
PC-rich_077	16_All	61	9.014	6.146e-01	0.861
PC-rich_077	24_All	61	9.014	1.562e+00	0.260
PE-rich_048	8_All	61	16.583	1.332e+00	0.339
PE-rich_048	12_All	61	16.583	1.977e+00	0.174
PE-rich_048	16_All	61	16.583	5.540e-01	0.903
PE-rich_048	24_All	61	16.583	6.716e-01	0.817
PE-rich_127	8_All	53	21.117	7.994e+00	0.004
PE-rich_127	12_All	53	21.117	4.159e+00	0.057
PE-rich_127	16_All	53	21.117	5.525e-01	0.882
PE-rich_127	24_All	53	21.117	1.100e+00	0.504

Tab. S8. One-way ANOVA of a three parameter model (Harrison and Platt 1986) from pooled data (All) and data fit across different peak PAR (30, 90, 180, 300, 600 together with 900) from chlorophyll specific exponential growth rate vs. PSII electron flux (JV_{PSII}; µmol e^- µmol Chl a^{-1} d^{-1}) (Fit_model), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Strain	Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
PC-rich_056	30_All	61	11.802	3.972e+00	0.016
PC-rich_056	90_All	61	11.802	7.712e-01	0.730
PC-rich_056	180_All	61	11.802	2.287e-01	1.000
PC-rich_056	300_All	61	11.802	3.332e+00	0.037
PC-rich_056	900_All	61	11.802	2.156e+00	0.044
PC-rich_077	30_All	61	9.014	1.125e+00	0.459
PC-rich_077	90_All	61	9.014	1.377e+00	0.350
PC-rich_077	180_All	61	9.014	6.146e-01	0.861
PC-rich_077	300_All	61	9.014	1.562e+00	0.260
PC-rich_077	900_All	61	9.014	1.295e+00	0.287
PE-rich_048	30_All	61	16.583	1.332e+00	0.339
PE-rich_048	90_All	61	16.583	1.977e+00	0.174
PE-rich_048	180_All	61	16.583	5.540e-01	0.903
PE-rich_048	300_All	61	16.583	6.716e-01	0.817
PE-rich_048	900_All	61	16.583	3.125e+00	0.007
PE-rich_127	30_All	53	21.117	7.994e+00	0.004
PE-rich_127	90_All	53	21.117	4.159e+00	0.057
PE-rich_127	180_All	53	21.117	5.525e-01	0.882
PE-rich_127	300_All	53	21.117	1.100e+00	0.504
PE-rich_127	900_All	53	21.117	3.784e+00	0.002

Tab. S9. One-way ANOVA of single phase exponential decay fit model (Fit_model) of pooled data across different strains for a given phase of growth (exponential; _Exp, pre-stationary; _St) and across different phase of growth for a given strain (_Exp_St) from PUR/PAR ratio in relation to the cumulative diel PAR (µmol photons $m^{-2}d^{-1}$), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
056_077_Exp	43	0.025	2.813e+01	0.000
048_127_Exp	51	0.217	NA	N/A
056_048_Exp	51	0.307	2.762e+01	0.000
077_048_Exp	51	0.307	5.976e+01	0.000
056_127_Exp	51	0.217	1.607e+01	0.000
077_127_Exp	51	0.217	4.064e+01	0.000
056_077_St	20	0.006	-1.491e-01	1.000
048_127_St	2	0.000	5.386e+00	0.168
056_048_St	17	0.009	9.648e-02	0.999
077_048_St	17	0.009	-2.066e+00	1.000
056_127_St	2	0.000	1.415e+01	0.067
077_127_St	2	0.000	2.812e+00	0.294
056_Exp_St	7	0.008	1.882e+00	0.195
077_Exp_St	20	0.006	3.039e+00	0.007
048_Exp_St	17	0.009	1.681e+01	0.000
127_Exp_St	2	0.000	4.128e+01	0.024

Tab. S10. One-way ANOVA of single phase exponential decay fit model (Fit_model) of pooled data across different strains for a given phase of growth (exponential; _Exp, pre-stationary; _St) and across different phase of growth for a given strain (_Exp_St) from Phycobiliprotein to Chl a ratio in relation to the cumulative diel PAR (µmol photons m−2d−1), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
056_077_Exp	49	38.089	1.531e+01	0.000
048_127_Exp	52	54.559	NA	N/A
056_048_Exp	52	39.302	4.333e+00	0.005
077_048_Exp	52	39.302	5.202e-01	0.670
056_127_Exp	52	54.559	1.067e+01	0.000
077_127_Exp	52	54.559	7.063e+00	0.000
056_077_St	24	3.580	-1.005e+01	1.000
048_127_St	19	3.343	NA	N/A
056_048_St	19	2.239	-2.229e-01	1.000
077_048_St	19	2.239	2.276e+00	0.088
056_127_St	19	3.343	-1.195e+00	1.000
077_127_St	19	3.343	2.686e-01	0.925
056_Exp_St	25	2.081	1.399e+01	0.000
077_Exp_St	24	3.580	9.255e+00	0.000
048_Exp_St	19	2.239	9.531e+00	0.000
127_Exp_St	19	3.343	8.820e+00	0.000

Tab. S11. One-way ANOVA of single phase exponential decay fit model (Fit_model) of pooled data across different strains for a given phase of growth (exponential; _Exp, pre-stationary; _St) and across different phase of growth for a given strain (_Exp_St) from effective absorption cross section of PSII (σ_{PSII}'; nm^2 $quanta^{-1}$) measured under diel peak PAR growth light under Ex590nm (orange) excitation in relation to the cumulative diel PAR (µmol photons $m^{-2}d^{-1}$), for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Res.Df - residual degrees of freedom for each model; Res.Sum Sq - residual sum of squares for each model; *F*_value – Fisher's *F*-test statistic; *p*_value - level of significance.

Fit_model	Res.Df	Res.Sum Sq	*F*_value	*p*_value
056_077_Exp	97	116.359	9.926e-01	0.469
048_127_Exp	72	106.728	-1.652e+00	1.000
056_048_Exp	97	116.359	3.764e+01	0.000
077_048_Exp	112	134.219	8.037e+00	0.000
056_127_Exp	72	106.728	2.599e-01	1.000
077_127_Exp	72	106.728	4.636e-01	0.995
056_077_St	41	3.366	1.522e+01	0.000
048_127_St	45	38.775	3.762e+00	0.001
056_048_St	34	17.489	1.158e+02	0.000
077_048_St	34	17.489	-3.922e+00	1.000
056_127_St	45	38.775	1.566e+02	0.000
077_127_St	45	38.775	1.078e+02	0.000
056_Exp_St	17	0.150	1.650e+02	0.000
077_Exp_St	41	3.366	2.245e+01	0.000
048_Exp_St	34	17.489	1.146e+00	0.339
127_Exp_St	45	38.775	2.921e+00	0.001

Tab. S12. *T*-test of linear fit model (Fit_model) of pooled data across different strains for a given phase of growth (exponential; _Exp, pre-stationary; _St) and across different phase of growth for a given strain (_Exp_St) from effective absorption cross section of PSII (σ_{PSII}'; nm^2 $quanta^{-1}$) measured under diel peak PAR growth light under Ex_{445nm} (blue) excitation in relation to the cumulative diel PAR (µmol photons $m^{-2}d^{-1}$, for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Estimate - estimation statistics; Std.Error - standard error of the estimate; *t*_value – *t*-test statistic; *p*_value - level of significance.

Fit_model	Estimate	Std.Error	*t*_value	*p*_value
056_077_Exp	-1.451e-09	1.058e-09	-1.372	0.171
056_048_Exp	-2.188e-09	1.313e-09	-1.666	0.097
056_127_Exp	-8.236e-10	1.412e-09	-0.583	0.560
048_127_Exp	1.365e-09	1.603e-09	0.851	0.395
077_048_Exp	-7.373e-10	1.233e-09	-0.598	0.550
077_127_Exp	6.274e-10	1.336e-09	0.470	0.639
056_077_St	2.453e-09	1.349e-09	1.818	0.071
056_048_St	5.254e-09	2.098e-09	2.505	0.014
056_127_St	1.745e-09	1.862e-09	0.937	0.350
048_127_St	-3.509e-09	1.658e-09	-2.116	0.036
077_048_St	2.801e-09	1.263e-09	2.217	0.028
077_127_St	-7.077e-10	1.209e-09	-0.586	0.559
056_Exp_St	2.487e-09	1.643e-09	1.514	0.132
077_Exp_St	6.391e-09	9.166e-10	6.973	0.000
048_Exp_St	9.930e-09	1.695e-09	5.860	0.000
127_Exp_St	5.056e-09	1.621e-09	3.120	0.002

Tab. S13. *T*-test of linear fit model (Fit_model) of pooled data across different strains for a given phase of growth (exponential; _Exp, pre-stationary; _St) and across different phase of growth for a given strain (_Exp_St) from effective absorption cross section of PSII (σ_{PSII}'; nm^2 $quanta^{-1}$) measured under diel peak PAR growth light under Ex_{445nm} (blue) excitation in relation to Phycobiliprotein to Chl *a* ratio, for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Estimate - estimation statistics; Std.Error - standard error of the estimate; *t*_value – *t*-test statistic; *p*_value - level of significance.

Fit_model	Estimate	Std.Error	*t*_value	*p*_value
056_077_Exp	0.003	0.008	0.424	0.672
056_048_Exp	0.078	0.009	9.082	0.000
056_127_Exp	0.039	0.009	4.382	0.000
048_127_Exp	-0.039	0.009	-4.416	0.000
077_048_Exp	0.075	0.008	8.954	0.000
077_127_Exp	0.036	0.009	4.117	0.000
056_077_St	-0.023	0.007	-3.495	0.000
056_048_St	-0.062	0.016	-3.788	0.000
056_127_St	-0.037	0.014	-2.606	0.009
048_127_St	0.026	0.023	1.143	0.253
077_048_St	-0.039	0.014	-2.823	0.005
077_127_St	-0.013	0.012	-1.117	0.264
056_Exp_St	0.083	0.013	6.327	0.000
077_Exp_St	0.057	0.009	6.590	0.000
048_Exp_St	-0.057	0.018	-3.217	0.001
127_Exp_St	0.008	0.020	0.389	0.698

Tab. S14. *T*-test of linear fit model (Fit_model) of pooled data across different strains for a given phase of growth (exponential; _Exp, pre-stationary; _St) and across different phase of growth for a given strain (_Exp_St) from effective absorption cross section of PSII (σ_{PSII}'; nm^2 $quanta^{-1}$) measured under Ex_{590nm} (orange) excitation in relation to the Phycobiliprotein to Chl *a* ratio, for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Estimate - estimation statistics; Std.Error - standard error of the estimate; *t*_value – *t*-test statistic; *p*_value - level of significance.

Fit_model	Estimate	Std.Error	*t*_value	*p*_value
056_077_Exp	-0.369	0.092	-4.000	0.000
056_048_Exp	0.149	0.082	1.812	0.070
056_127_Exp	0.606	0.099	6.122	0.000
048_127_Exp	0.457	0.090	5.084	0.000
077_048_Exp	0.518	0.083	6.267	0.000
077_127_Exp	0.976	0.097	10.089	0.000
056_077_St	0.077	0.029	2.669	0.008
056_048_St	-0.610	0.079	-7.751	0.000
056_127_St	-0.299	0.071	-4.191	0.000
048_127_St	0.311	0.177	1.759	0.080
077_048_St	-0.688	0.076	-9.099	0.000
077_127_St	-0.377	0.070	-5.371	0.000
056_Exp_St	0.440	0.117	3.761	0.000
077_Exp_St	0.887	0.091	9.780	0.000
048_Exp_St	-0.319	0.148	-2.164	0.031
127_Exp_St	-0.465	0.247	-1.882	0.060

Tab. S15. *T*-test of linear fit model (Fit_model) of pooled data across different strains for a given phase of growth (exponential; _Exp, pre-stationary; _St) and across different phase of growth for a given strain (_Exp_St) from effective absorption cross section of PSII (σ_{PSII}; nm^2 $quanta^{-1}$) measured under Ex590nm (orange) excitation in relation to the Phycobiliprotein to Chl *a* ratio, for two PhycoCyanin(PC)-rich cultures (056, 077) and two PhycoErythrin(PE)-rich cultures (048, 127) of *Synechococcus* sp., grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. Estimate - estimation statistics; Std.Error - standard error of the estimate; *t*_value – *t*-test statistic; *p*_value - level of significance.

Fit_model	Estimate	Std.Error	*t*_value	*p*_value
056_077_Exp	-0.118	0.060	-1.962	0.050
056_048_Exp	0.216	0.058	3.693	0.000
056_127_Exp	0.841	0.076	11.067	0.000
048_127_Exp	0.625	0.076	8.187	0.000
077_048_Exp	0.334	0.060	5.526	0.000
077_127_Exp	0.959	0.075	12.806	0.000
056_077_St	0.397	0.027	14.566	0.000
056_048_St	-0.120	0.064	-1.873	0.062
056_127_St	0.086	0.061	1.411	0.159
048_127_St	0.206	0.114	1.801	0.073
077_048_St	-0.516	0.048	-10.776	0.000
077_127_St	-0.310	0.044	-7.121	0.000
056_Exp_St	0.317	0.075	4.234	0.000
077_Exp_St	0.831	0.061	13.656	0.000
048_Exp_St	-0.019	0.122	-0.155	0.877
127_Exp_St	-0.438	0.209	-2.099	0.036

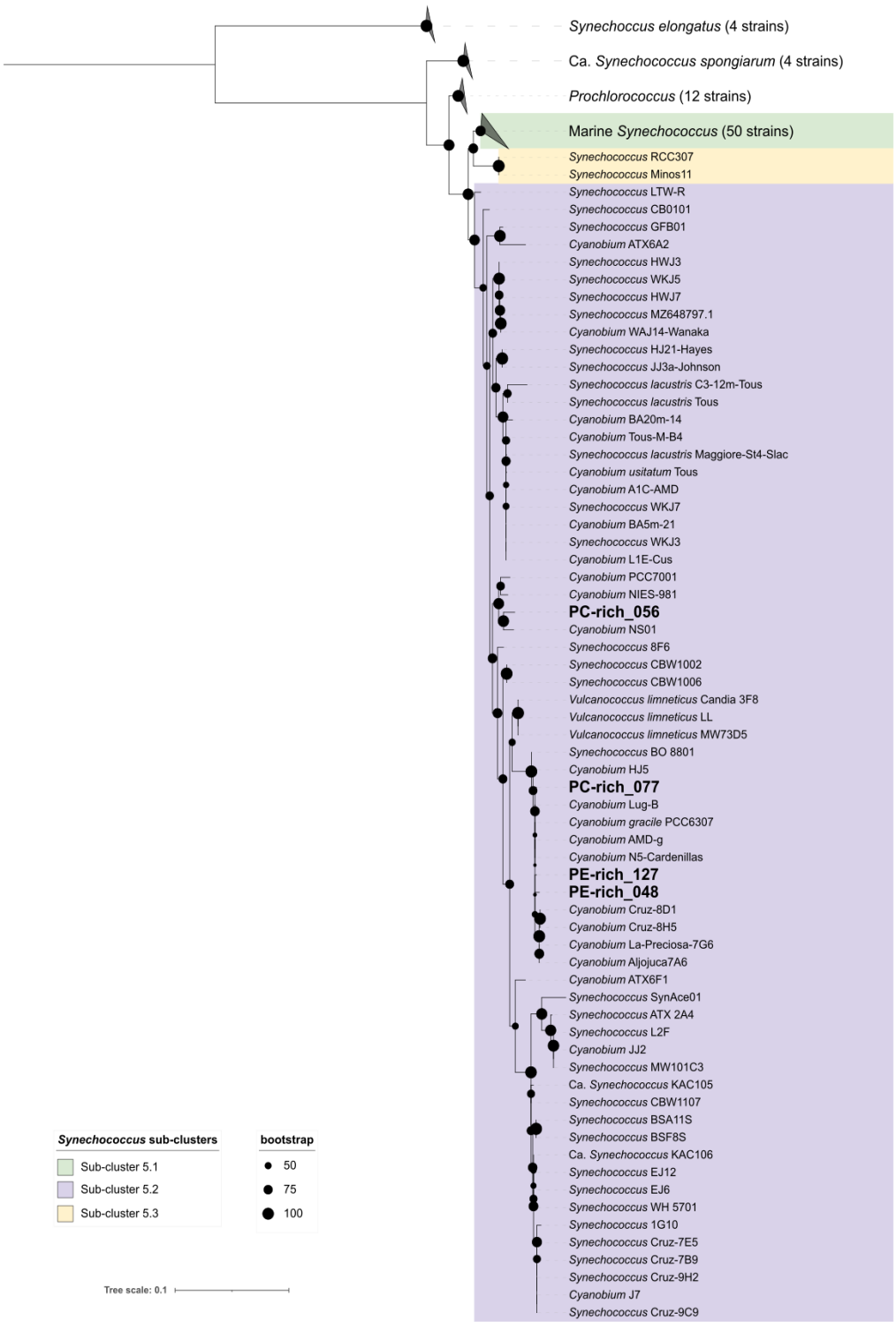


Fig. S1. Phylogenetic tree derived from partial 16S rRNA gene sequences using topology given by Maximum Likelihood (1000 bootstraps). Support values are indicated by the size of internal nodes. Strains used in this study are shown in bold.

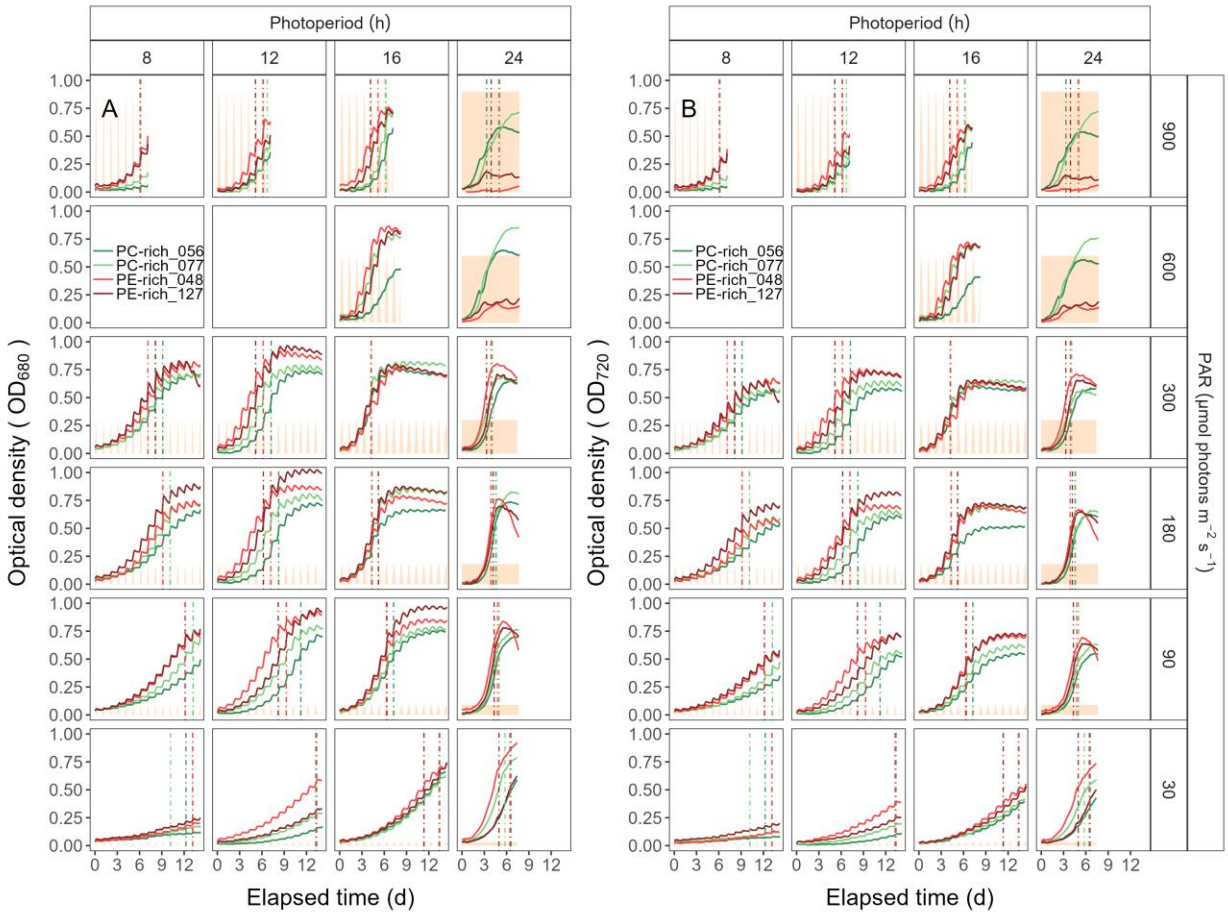


Fig. S2. Growth curves, tracked as OD_{680} (**A**) and OD_{720} (**B**) vs. elapsed time (d). Growth curves were estimated over 5-min intervals for two PC-rich cultures (056; dark green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. The vertical lines represent the time when the cultures reached the maximum of the 1st derivative of OD_{680}, or maximum absolute hourly growth (tMaxAHG), taken as an index of transition from exponential to pre-stationary growth phases. The orange area represents the photoperiods, with peak PAR x 1/1000 to scale to the Y axis.

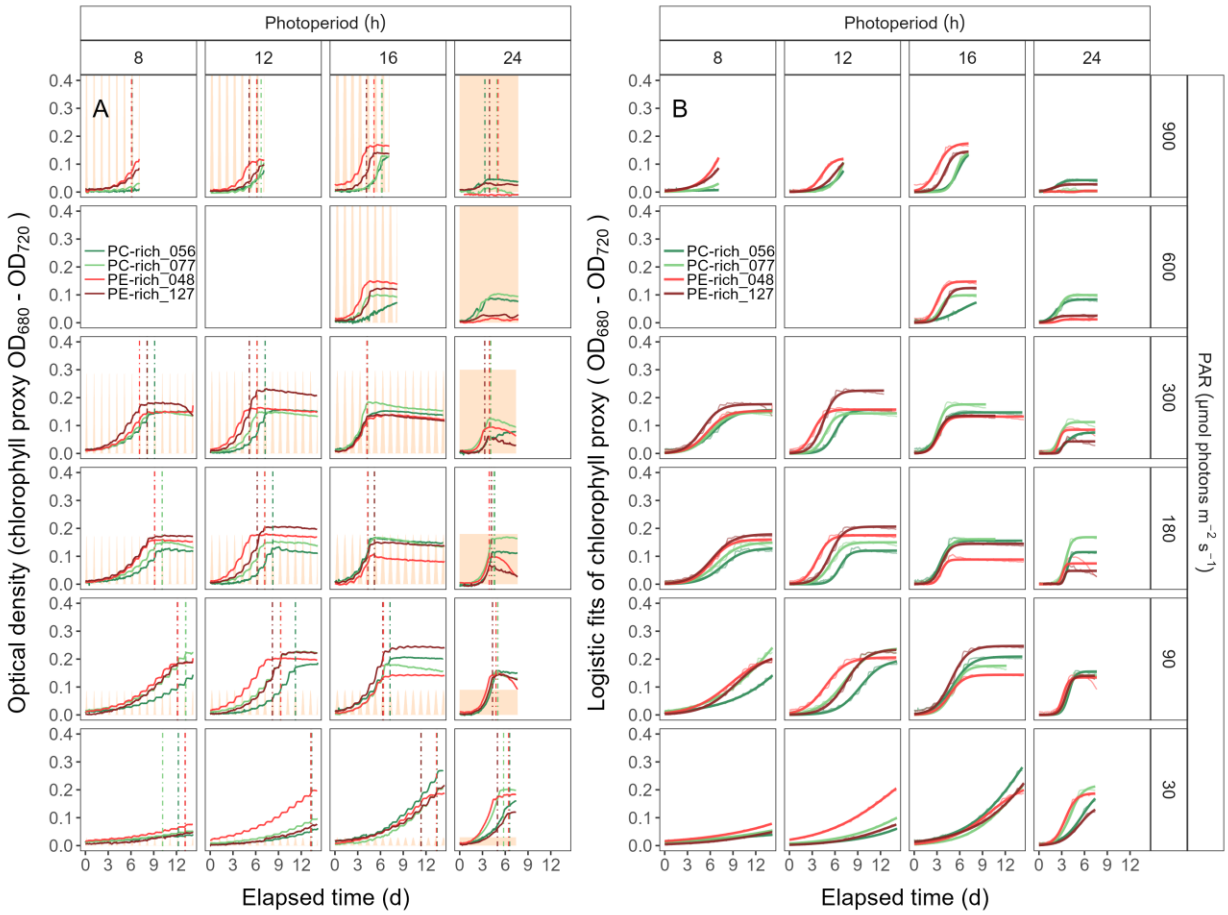
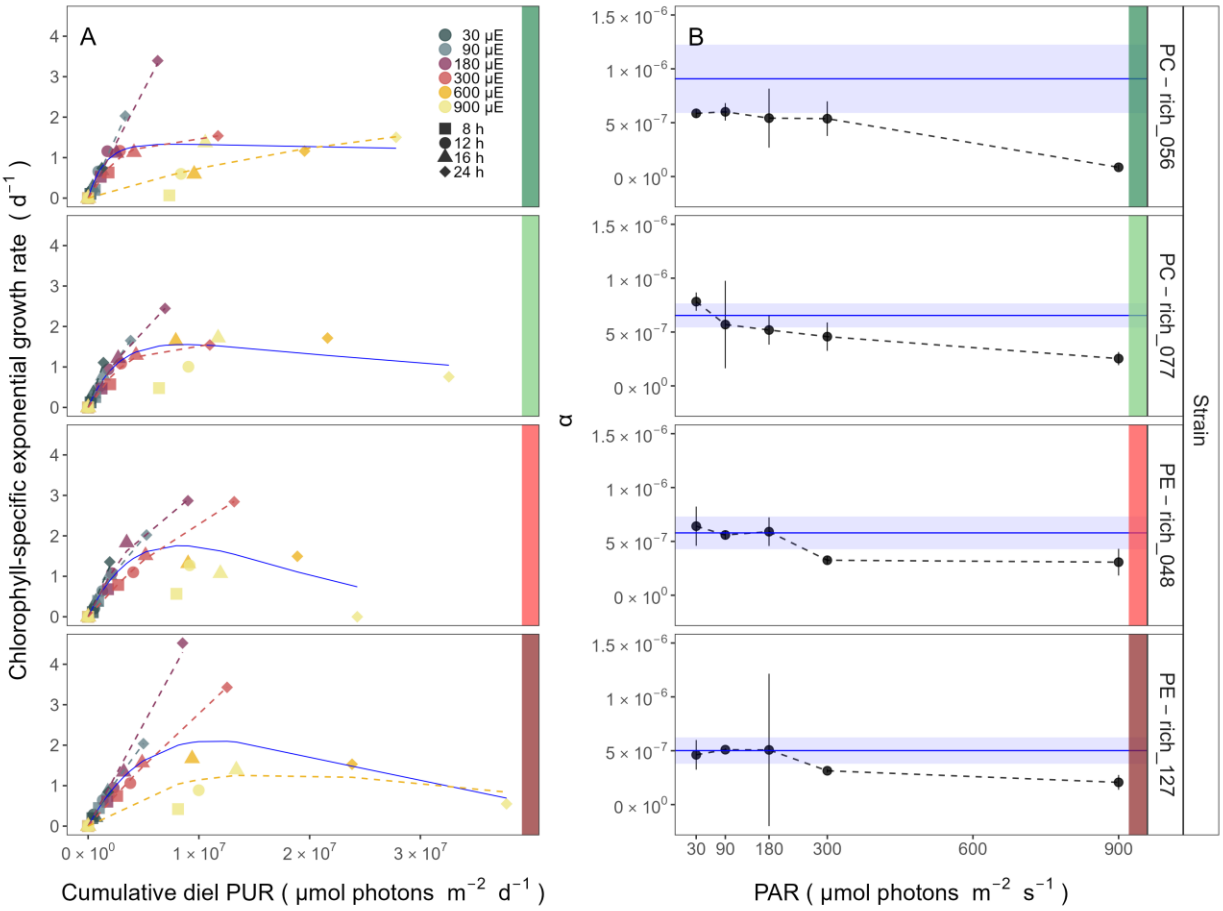


Fig. S3. (**A**) Growth curves (tracked as chlorophyll proxy OD_{680}-OD_{720}; Δ OD) vs. elapsed time (d). Growth curves were estimated over 5-min intervals for two PC-rich cultures (056; dark green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30, 90, 180, 300, 600, or 900 peak PAR µmol photons $m^{-2}s^{-1}$; and photoperiods of 8, 12, 16, or 24 h. The vertical lines represent the time when the cultures reached the maximum of the 1st derivative of OD_{680}, or maximum absolute hourly growth (tMaxAHG), taken as an index of transition from exponential to pre-stationary growth phases. The orange area represents the photoperiods, with peak PAR x 1/2000 to scale to the Y axis. (**B**) Logistic fits (thick lines) of chlorophyll proxy OD_{680}-OD_{720} (Δ OD) vs. elapsed time (d). Growth curves (thin line) measured over 5-min intervals for each strain were also presented.



212

213 **Fig. S4.** (**A**) Chlorophyll-specific exponential growth rates (d^{-1}) vs. cumulative diel Photosynthetically Usable
214 Radiation (PUR, µmol photons $m^{-2}d^{-1}$). Growth rates (± SE falling within symbols) were estimated from logistic fits
215 of chlorophyll proxy $OD_{680} - OD_{720}$ (ΔOD) vs. elapsed time (Fig. 1, Fig. S3B), for two PC-rich cultures (056; dark
216 green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30
217 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 (orange), or 900 (yellow) peak PAR µmol photons $m^{-2}s^{-1}$
218 (µE); and photoperiods of 8 (square), 12 (circle), 16 (triangle), or 24 (diamond) h. Solid blue line shows a fit of the
219 pooled growth rates through peak PAR for each strain, with a three parameter model (Harrison and Platt, 1986). We
220 also fit the same model separately for 30 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 together with 900
221 (orange) peak PAR µmol photons $m^{-2}s^{-1}$, only when they were each significantly different (ANOVA, $p < 0.05$) from
222 the fit of pooled data. (**B**) Alpha parameters of the initial rise of growth rate (α) vs. cumulative diel
223 Photosynthetically Usable Radiation (PUR), estimated from data pooled for each peak PAR (points (± SE)
224 connected by dashed lines), and estimated for all data across all peak PAR, for each strain (solid blue horizontal line
225 ± SE).

226

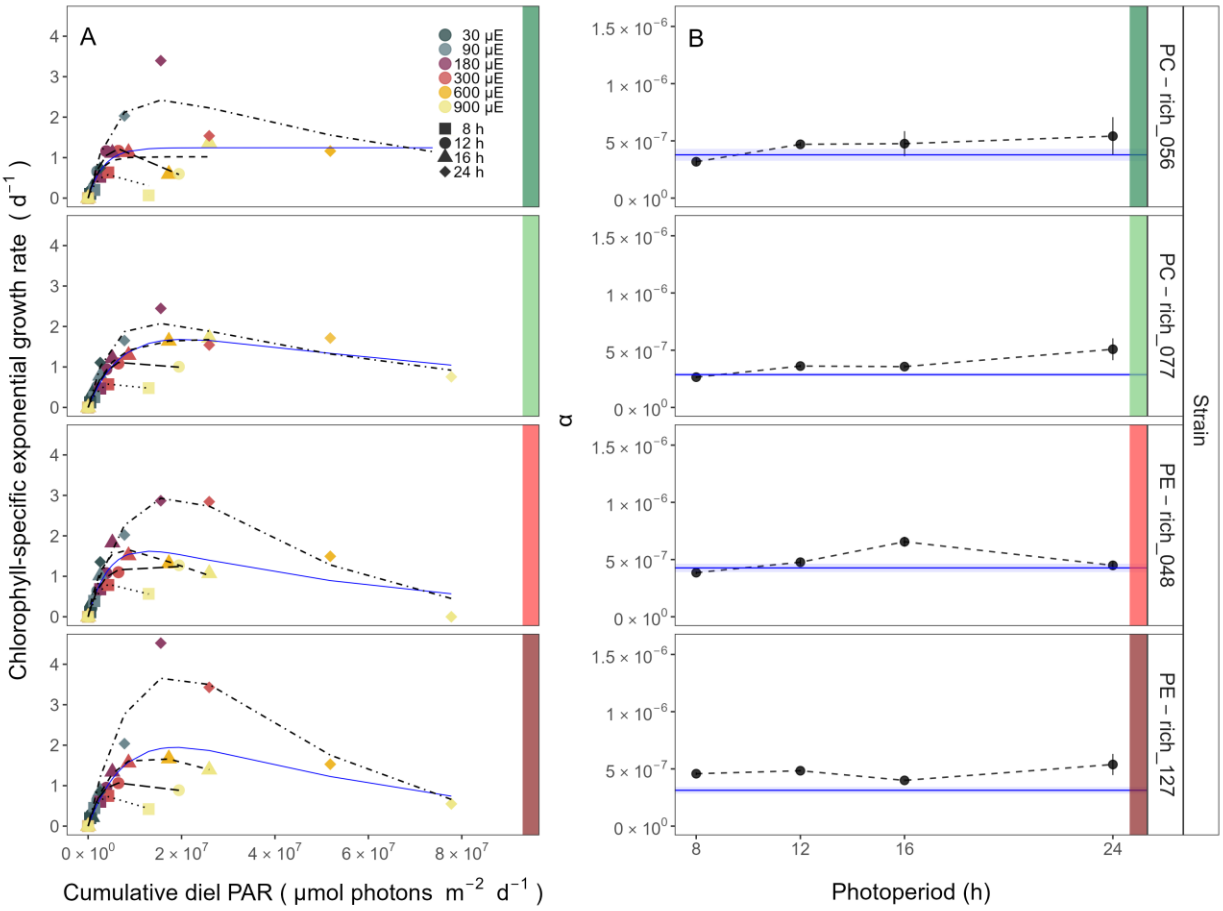


Fig. S5. (**A**) Chlorophyll-specific exponential growth rates (d^{-1}) vs. cumulative diel PAR (µmol photons $m^{-2}d^{-1}$). Growth rates (± SE falling within symbols) were estimated from logistic fits of chlorophyll proxy $OD_{680} - OD_{720}$ (ΔOD) vs. elapsed time (Fig. 1, Fig. S3B), for two PC-rich cultures (056; dark green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 (orange), or 900 (yellow) peak PAR µmol photons $m^{-2}s^{-1}$ (µE); and photoperiods of 8 (square), 12 (circle), 16 (triangle), or 24 (diamond) h. Solid blue line shows a fit of the pooled growth rates through photoperiod (h) for each strain, with a three parameter model (Harrison and Platt 1986). We also fit the same model separately for 8 (dotted line), 12 (long dash line), 16 (dashed line), or 24 (two dash line) h photoperiods, since for all strains they were each significantly different (ANOVA, $p < 0.05$) from the fit of pooled data. (**B**) Alpha parameters of the initial rise of growth rate (α) vs. cumulative diel PAR, estimated from data pooled for each photoperiod (points (± SE) connected by dashed lines), and estimated for all data across photoperiods (solid blue horizontal line ± SE), for each strain.

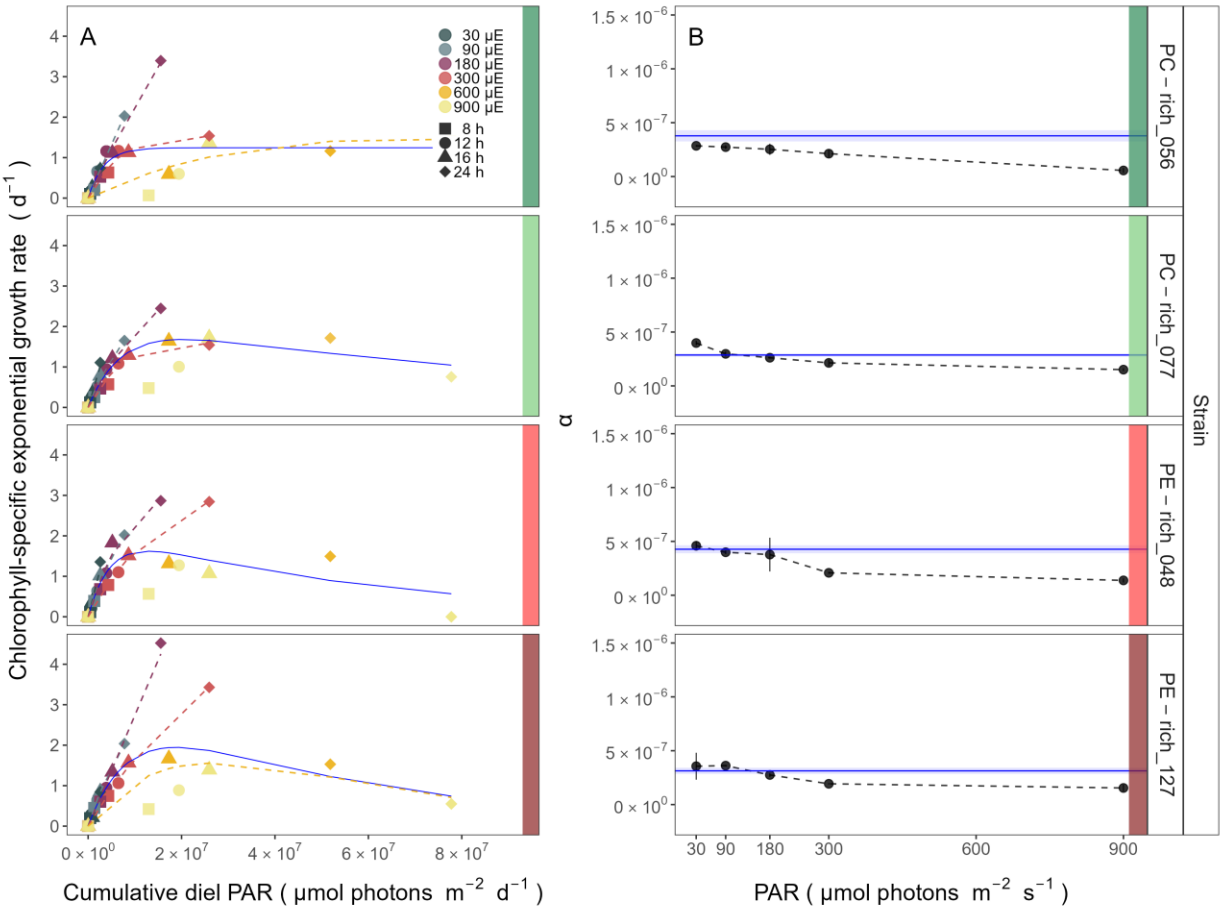


Fig. S6. (**A**) Chlorophyll-specific exponential growth rates (d^{-1}) vs. cumulative diel PAR (µmol photons $m^{-2}d^{-1}$). Growth rates (± SE falling within symbols) were estimated from logistic fits of chlorophyll proxy $OD_{680} - OD_{720}$ (ΔOD) vs. elapsed time (Fig. 1, Fig. S3B), for two PC-rich cultures (056; dark green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 (orange), or 900 (yellow) peak PAR µmol photons $m^{-2}s^{-1}$ (µE); and photoperiods of 8 (square), 12 (circle), 16 (triangle), or 24 (diamond) h. Solid blue line shows a fit of the pooled growth rates through peak PAR for each strain, with a three parameter model (Harrison and Platt, 1986). We also fit the same model separately for 30 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 together with 900 (orange) peak PAR µmol photons $m^{-2}s^{-1}$, only when they were each significantly different (ANOVA, $p < 0.05$) from the fit of pooled data. (**B**) Alpha parameters of the initial rise of growth rate (α) vs. cumulative diel PAR, estimated from data pooled for each peak PAR (points (± SE) connected by dashed lines), and estimated for all data across all peak PAR, for each strain (solid blue horizontal line ± SE).

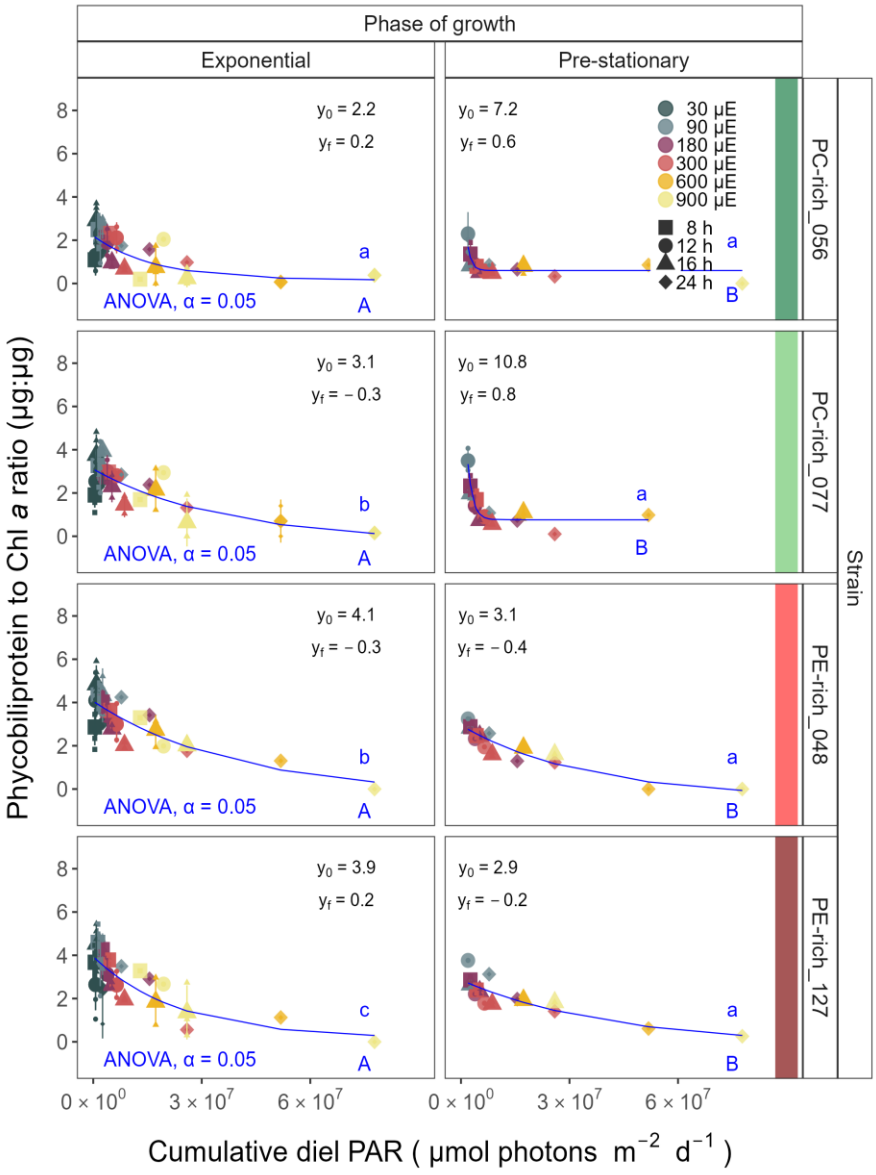


Fig. S7. Changes of Phycobiliprotein to Chl *a* ratio (µg:µg) vs. cumulative diel PAR (µmol photons $m^{-2}d^{-1}$). Phycobiliprotein to Chl *a* ratio was estimated for two PC-rich cultures (056; dark green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 (orange), or 900 (yellow) peak PAR µmol photons $m^{-2}s^{-1}$ (µE); and photoperiods of 8 (square), 12 (circle), 16 (triangle), or 24 (diamond) h. Figure presents data (smaller symbols) and means (bigger symbols) from exponential or pre-stationary phase of growth. Blue solid line shows single phase exponential decay fit for data from each strain and growth phase, fit parameters are presented. Different lowercase letters indicate statistically significant differences between the fit models for different strains within a given phase of growth. Different uppercase letters indicate statistically significant differences between the fit models for different phases of growth within a given strain (ANOVA; $p < 0.05$).

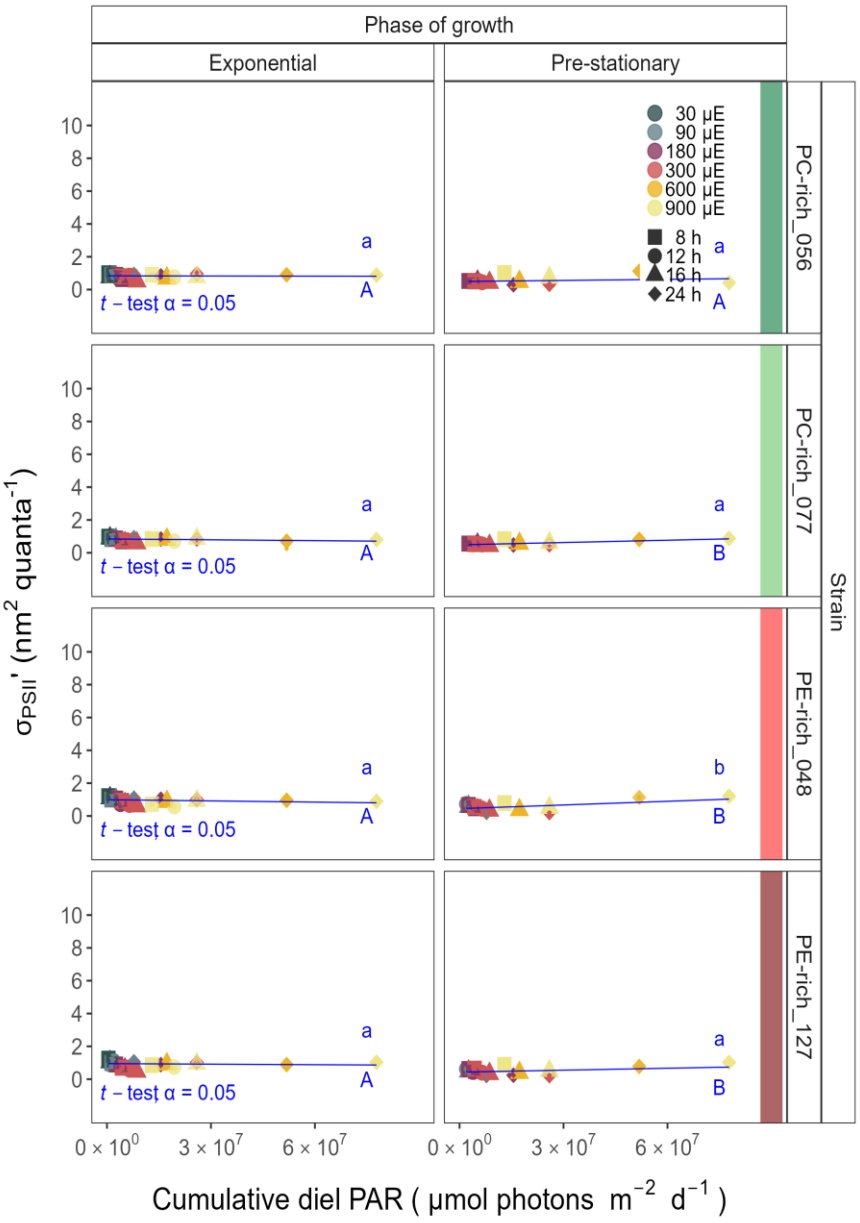


Fig. S8. Effective absorption cross section of PSII (σ_{PSII}'; nm^2 quanta^{-1}) measured under diel peak PAR growth light under blue (Ex_{445nm}) excitation vs. cumulative diel PAR (µmol photons m^{-2}d^{-1}). σ_{PSII}' was estimated for two PC-rich cultures (056; dark green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 (orange), or 900 (yellow) peak PAR µmol photons m^{-2}s^{-1} (µE); and photoperiods of 8 (square), 12 (circle), 16 (triangle), or 24 (diamond) h. Figure presents data (smaller symbols) and means (bigger symbols) from exponential or pre-stationary phase of growth. Blue solid line shows linear model fit for data from each strain and growth phase. Different lowercase letters indicate statistically significant differences between the fit models for different strains within a given phase of growth. Different uppercase letters indicate statistically significant differences between the fit models for different phases of growth within a given strain (*t*-test; $p < 0.05$).

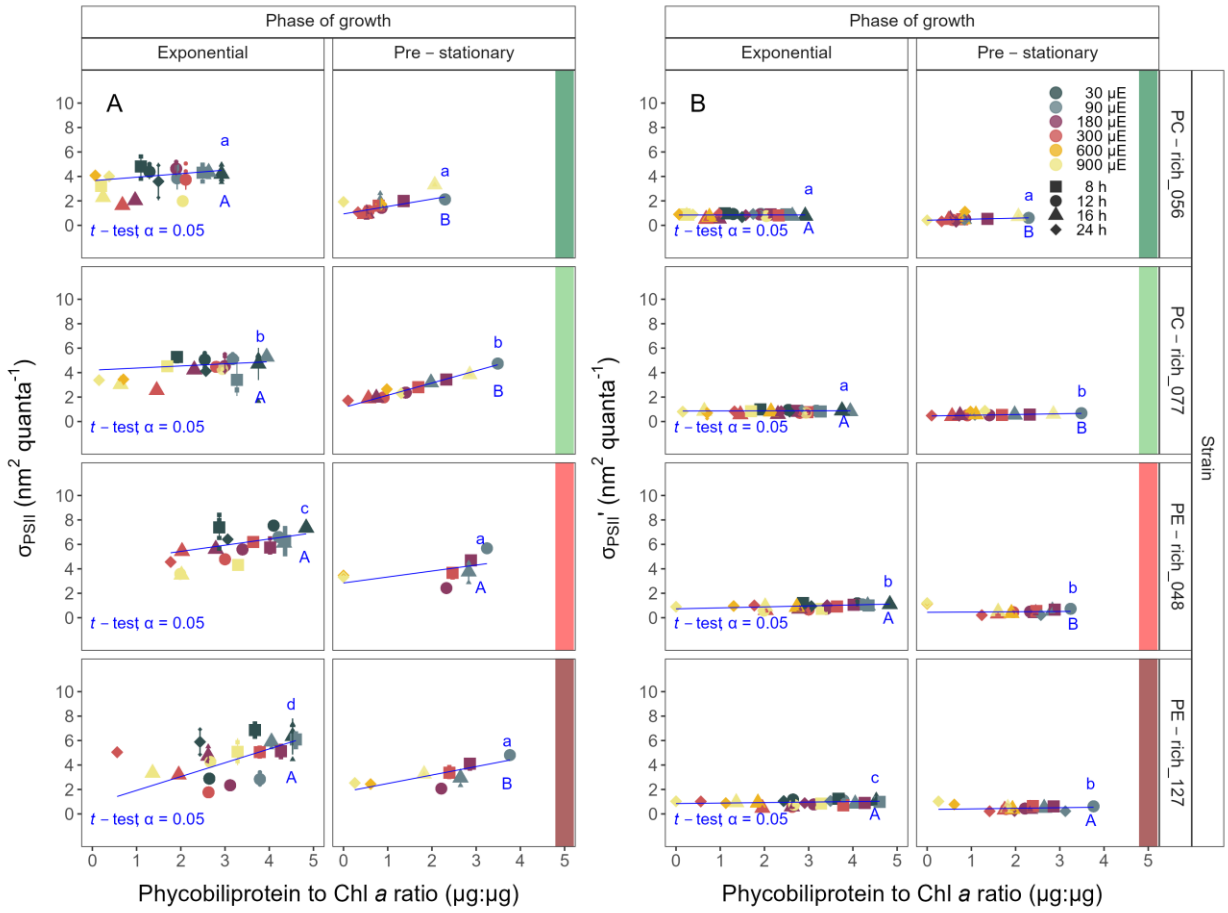


Fig. S9. (**A**) Changes of effective absorption cross section of PSII (σ_{PSII}; nm^2 quanta^{-1}) measured at the dark period under orange (Ex_{590nm}) excitation vs. the ratio of sum of µg phycobilins (PE, PC, APC protein, Phycobiliprotein) to µg Chl *a*. (**B**) Changes of effective absorption cross section of PSII (σ_{PSII}'; nm^2 quanta^{-1}) measured under diel peak PAR growth light under blue (Ex_{445nm}) excitation vs. the ratio of sum of µg phycobilins (PE, PC, APC protein, Phycobiliprotein) to µg Chl *a*. σ_{PSII}' was estimated for two PC-rich cultures (056; dark green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 (orange), or 900 (yellow) peak PAR µmol photons m^{-2}s^{-1} (µE); and photoperiods of 8 (square), 12 (circle), 16 (triangle), or 24 (diamond) h. Figure presents data (smaller symbols) and means (bigger symbols) from exponential or pre-stationary phase of growth. Blue solid line shows linear model fit for data from each strain and growth phase. Different lowercase letters indicate statistically significant differences between the fit models for different strains within a given phase of growth. Different uppercase letters indicate statistically significant differences between the fit models for different phases of growth within a given strain (*t*-test; $p < 0.05$).

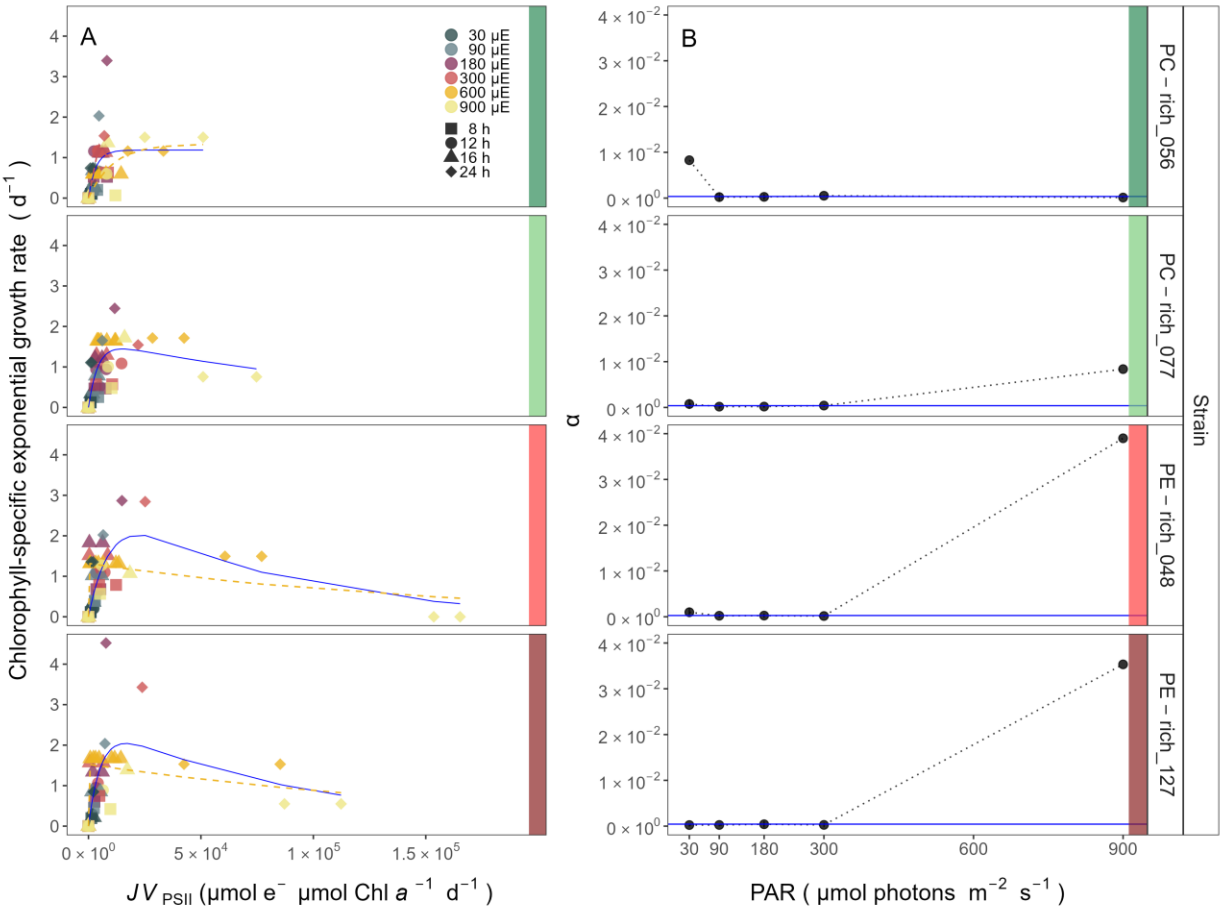


Fig. S10. (**A**) Chlorophyll specific exponential growth rates (d^{-1}) vs. cumulative diel PSII electron flux (JV_{PSII}; µmol e^- µmol Chl a^{-1} d^{-1}) measured under diel peak PAR growth light. Growth rates (± SE falling within symbols) were estimated from logistic fits of chlorophyll proxy $OD_{680} - OD_{720}$ (ΔOD) vs. elapsed time (Fig. S3). PSII flux was estimated using FRRf induction curves with excitation of chlorophyll (Ex_{445nm}, blue), for two PC-rich cultures (056; dark green, 077; light green) and two PE-rich cultures (048; light red, 127; dark red) of *Synechococcus* sp. grown at 30 (dark gray), 90 (light gray), 180 (purple), 300 (red), 600 (orange), or 900 (yellow) peak PAR µmol photons $m^{-2}s^{-1}$ (µE); and photoperiods of 8 (square), 12 (circle), 16 (triangle), or 24 (diamond) h. Solid blue line shows a fit of the pooled growth rates for each strain, with a three parameter model (Harrison and Platt 1986). We also fit the same model separately for 600 together with 900 (orange) peak PAR µmol photons $m^{-2}s^{-1}$, when they were significantly different (ANOVA, $p < 0.05$) from the fit of pooled data. (**B**) Alpha parameters of the initial rise of growth rate (α) vs. cumulative diel JV_{PSII}, estimated from data pooled for each peak PAR (points (± SE) connected by dashed lines), and estimated for all data across all peak PAR, for each strain (solid blue horizontal line ± SE).

References

Harrison, W. G., and T. Platt. 1986. Photosynthesis-irradiance relationships in polar and temperate phytoplankton populations. Polar biology **5**: 153–164.