Supporting Information for

Upper Ocean Dynamics Select for *Synechococcus* Light Color Generalists

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Introduction

This supplement describes the model equations and parameters used in this study.

Text S1.

Model equations. Equations describing the model environment, taken from (Stomp et al., 2008) were modified for type IV chromatic acclimation as described below. Table S1 includes a list of model parameters and, where appropriate, their values.

The specific absorption spectrum of the chromatic acclimater strain ($k_{acclimator}$) was determined by the acclimation fraction, v, which varied between $0 - 1$, and the specific absorption spectrum of the acclimator strain measured in blue light ($k_{acclimater,blue}$) and green light ($k_{acclimater,green}$) as calculated in Eqn. S1 and displayed in Fig. S1

$$k_{acclimater}(\lambda) = v k_{acclimater,blue}(\lambda) + (1 - v) k_{acclimater,green}(\lambda) \tag{S1}$$

where λ is the wavelength of light.

Change in v over time (Eqn. S2) is a function of the time taken to acclimate, controlled by a CA4 parameter α_c which is dependent on light color (subscript c), and the photons absorbed by the acclimater strain, $\gamma_{acclimater}$ (see Eqn. S7 below)

$$\frac{dv}{dt} = \alpha_c \frac{\varphi_c}{z_m} \int_0^{z_m} \frac{\delta \gamma_{acclimater}(z,v)}{\delta v} dz \tag{S2}$$

where z is size of one depth layer, z_m is the maximum depth of the mixed layer, and φ_c is the photosynthetic efficiency at each light color (subscript c), which is constant among strains.

Light penetrating the ocean at each wavelength and depth is a function of the incoming light spectrum at the ocean surface, I_{in}; the specific absorption by each *Synechococcus* strain k_i, where i represents each strain; the cell abundance of each strain N_i; the absorption by water a_w; and the absorption by other plankton, a_{other}, where a_{other} was either 0, absorption by chlorophyll-a (a_{CHL}), or absorption by coccolithophores (a_{Coccos}) as described in Eqns. S3 – S5 below:

$$I(\lambda, z) = I_{in} \exp(-(\sum_{i=1}^n k_i(\lambda)N_i + a_w(\lambda) + a_{other}(\lambda))z) \tag{S3}$$

with

$$a_{CHL}(\lambda) = [\text{CHL}] \ (A_{CHL}(\lambda) \ ([\text{CHL}]^{-B_{CHL}})), \tag{S4}$$

$$a_{Coccos}(\lambda) = [\text{coccolithophores}] \ (k_{coccos}), \tag{S5}$$

with the quantities in square brackets representing concentrations.

Change in the abundance of the *Synechococcus* strains with time, $\frac{dN_i}{dt}$ (Eqn S6) is given by the difference between cell loss and growth, where growth was a function of the photosynthetic efficiencies φ_i, and the number of photons absorbed by each strain at each depth interval $\gamma_i(z)$ – a match between the strain's specific absorption spectrum k_i, and the available light (Eqn. S7). Equations S6 and S7 are unmodified from the original formulation of Stomp et al., (2008):

$$\frac{dN_i}{dt} = [\frac{1}{z_m} \int_0^{z_m} \frac{p_{max,c} \gamma_i(z)}{\frac{p_{max,c}}{\varphi_i} + \gamma_i(z)} dz]N_i - LN_i \tag{S6}$$

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$$\gamma_i(z) = \int_{400}^{700} I(\lambda, z) k_i(\lambda) d\lambda \tag{S7}$$

where $p_{max,c}$ is the maximum growth rate in each light color, which is a constant among strains, and L is the specific loss rate constant.

Oscillation between incoming light colors (e.g. blue and green) with time, t, in the model was controlled by a switch, F (S8), with F > 0 resulting in one color (e.g. blue) and F < 0 resulting in the other color (e.g. green) using an IF WHEN statement. The oscillation period was determined by A, where A values of 5, 1, 0.5, 0.3 and 0.1 resulted in corresponding oscillation periods of 0.6, 3, 6, 11, and 31 days, respectively.
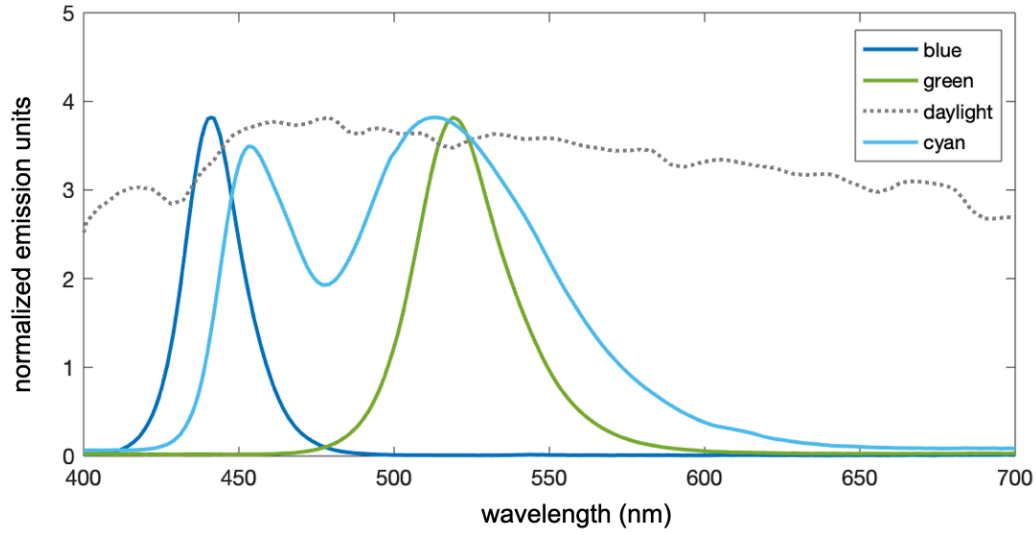
$$F = \sin(At) \tag{S8}$$

Figure S1. Peak normalized emission spectra of blue (PARsource), green (Illuminati) and cyan (Cyril McCormick, University of California, Irvine) LED lights measured using an LI-180 spectrometer (LI-COR) and the above-water spectrum of daylight measured in sunny conditions in the Mediterranean and adjusted to a surface PAR-integrated intensity of 1000 μmol photons m^{-2} s^{-1}.
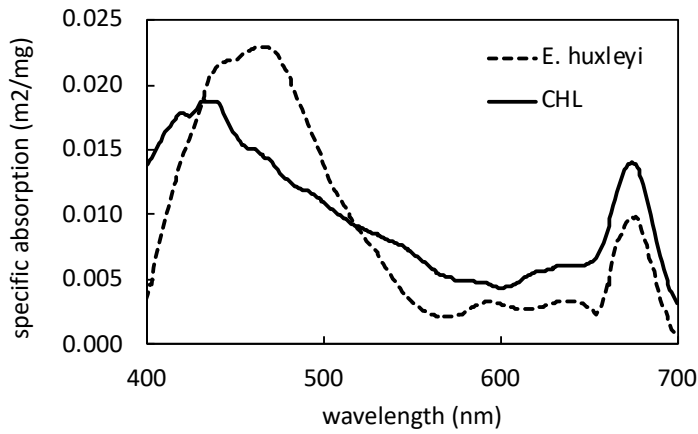

Figure S2. Representative graphs of the specific absorption spectra (m^2 mg^{-1}) of chlorophyll-*a* (the result of $(A_{CHL}(\lambda)$ $([CHL]^{-B_{CHL}}))$ in Eqn. S4 with [CHL] = 10 mg m^{-3}) and for the coccolithophore *E. huxleyi* (k_{coccos}, Eqn. S5) used to calculate phytoplankton absorption in the model.
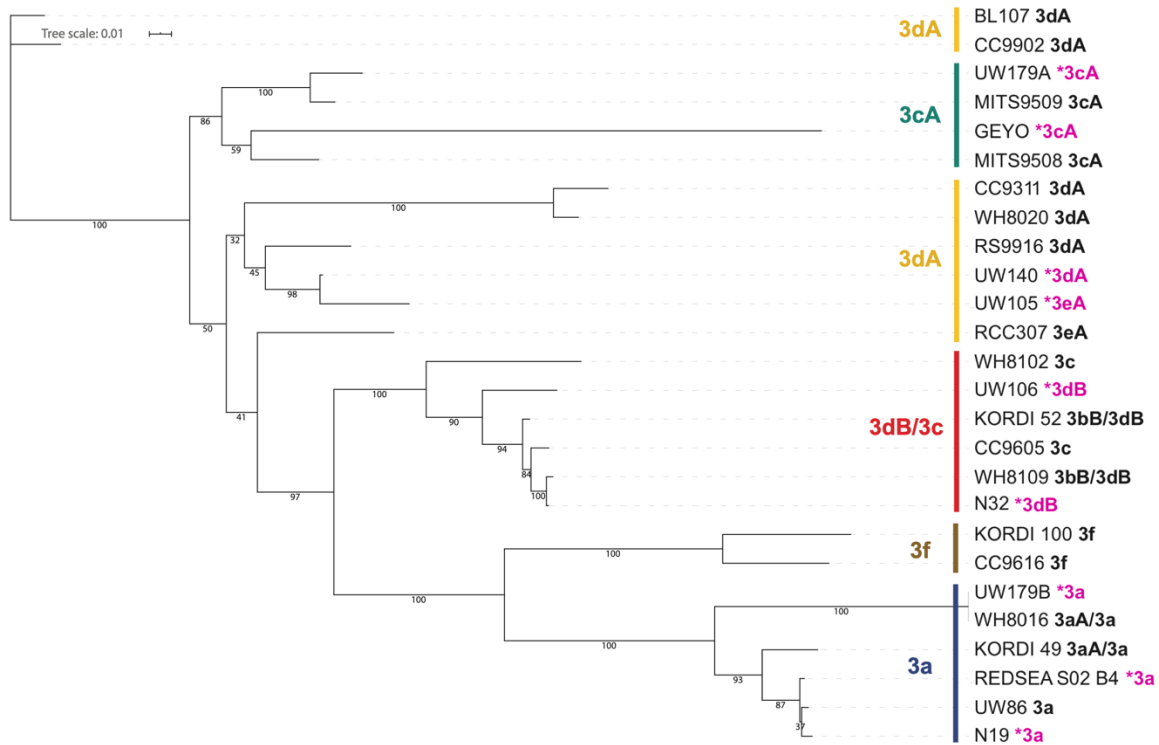
Figure S3. Phylogenetic tree rooted in *mpeAB* and showing the partition of *Synechococcus* pigment types into specialists (3a, 3c, 3cA, 3f) and generalists (3dA and 3dB). 3c strains were separated from 3dB strains by subtraction using the gene *mpeW* which is only present in 3dB strains. Previously unknown or unconfirmed pigment types that were assigned in this study are indicated with * and highlighted in pink.
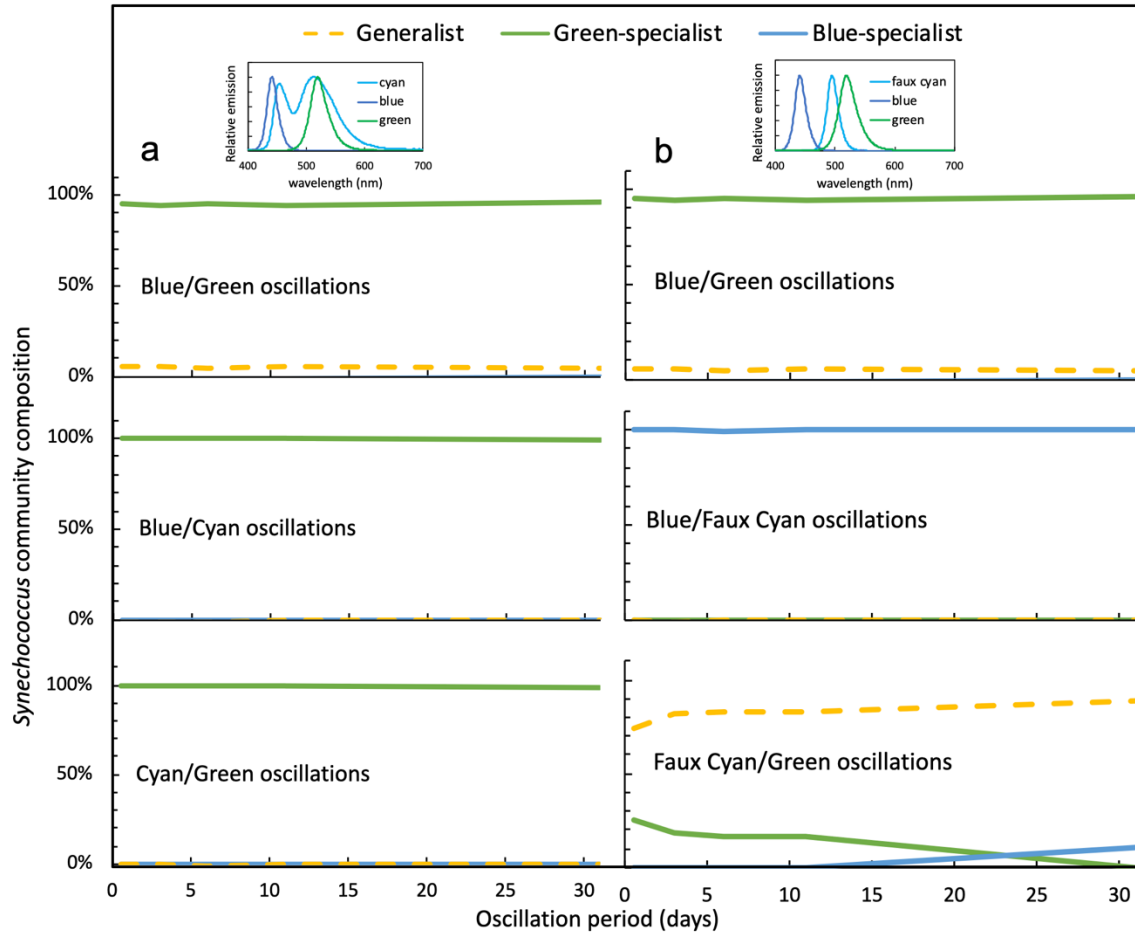
Figure S4. Comparison of model results across oscillation periods between LED light colors that include cyan light with a wide (a) and narrow (b) spectral emissions at 1 m depth. Inserts at the top of panels a and b indicate the emission spectra of LED lights used to generate the results for each panel with the wide cyan spectrum spanning 430 – 620 nm with two emission peaks around 446 and 515 nm, and the narrow spectrum having one emission peak at 495 nm with shoulders ±30 nm.
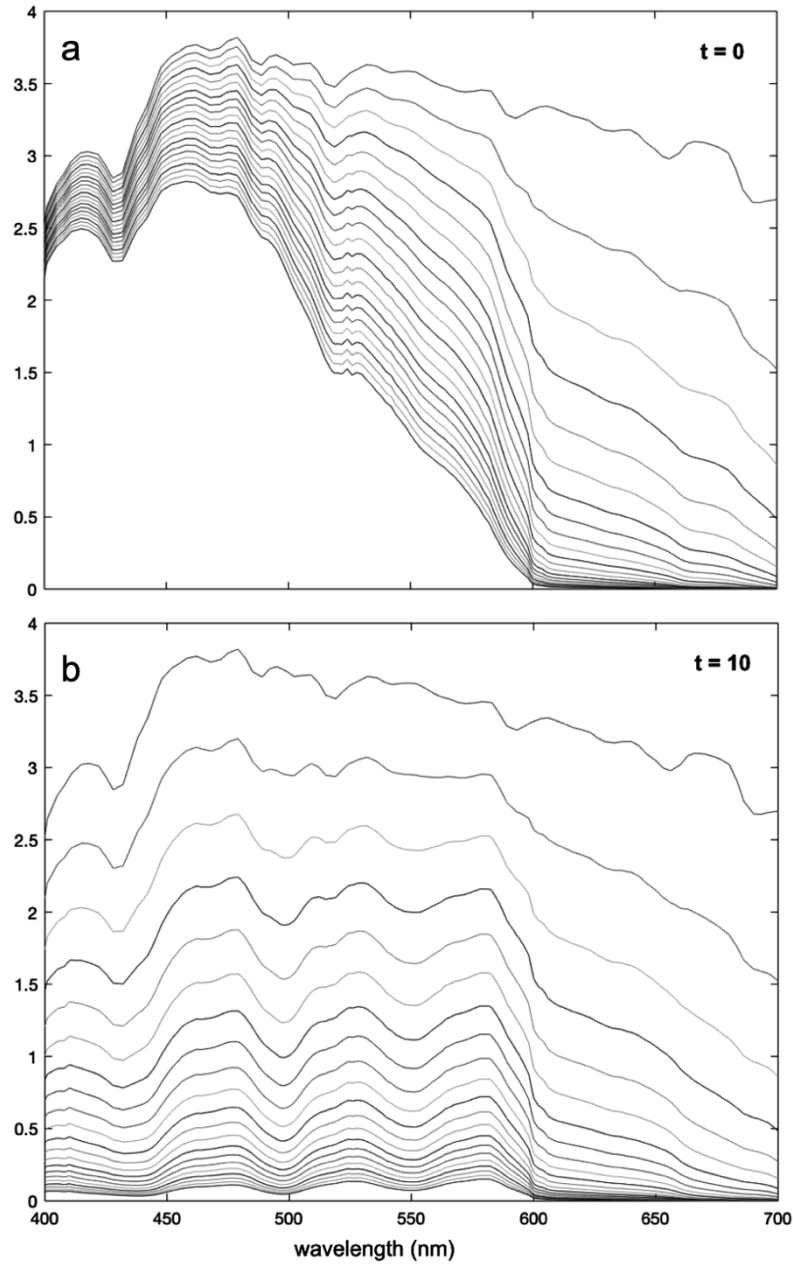
Figure S5. Penetration of the daylight spectrum through the model calculated at discrete depth layers, with each depth layer represented by a spectral line. No additional absorption by chlorophyll-dominated plankton was included. a) Light penetration at the beginning of the simulation (time, t = 0 days) with low abundance of *Synechococcus* strains and high background absorption by water. b) Light penetration during the simulation (t = 10 days) when the concentration of all three *Synechococcus* strains has increased and their absorption has decreased the relative availability of light from 440 − 500 nm compared to 500 − 550 nm at depth.

PARAMETERS	SYMBOL	UNIT	VALUE	REFERENCE
Incident Light Spectrum	I_{in}	mol photons m^{-2} s^{-1} nm^{-1}	Fig S1	measured
PAR-integrated incident light intensity, daylight		mol photons m^{-2} s^{-1}	1000	measured
Specific absorption of Synechococcus strains	k_i	m^{-1} cell^{-1} nm^{-1}	Fig. 1, Eqn S1	measured
Background seawater absorption	a_w	m^{-1} nm^{-1}		(Buiteveld et al., 1994)
Chlorophyll absorption	a_{CHL}	m^{-1} nm^{-1}	Fig. S2, Eqn S4	(Bricaud et al., 1995)
Coccolithophore absorption	a_{Coccos}	m^{-1} nm^{-1}	Fig. 2S, Eqn S5	(Sadeghi et al., 2012)
Specific loss rate	L	hr^{-1}	0.005	
Max specific growth rate, green, white	$p_{max,green}$	day^{-1}	0.7	measured
Max specific growth rate, blue	$p_{max,blue}$	day^{-1}	0.5	measured
Photosynthetic efficiency, green, white	φ_{green}	cells (mol photons)$^{-1}$	2.4 x 10^6	measured
Photosynthetic efficiency, blue	φ_{blue}	cells (mol photons)$^{-1}$	1.2 x 10^6	measured
CA4 parameter, green	α_{green}	dimensionless	0.70	Tuned in the model
CA parameter, blue	α_{blue}	dimensionless	0.95	Tuned in the model

Table S1. Parameters for the light color competition model between *Synechococcus* blue and green-light specialist strains and type IV chromatic acclimater (CA4 generalist).

Classification	Phenotypic description	Pigment Type	CA4 genetic island	Marker genes
Target marine *Synechococcus* group	Contains both phycoerythrin I and phycoerythrin II which bind chromophores PUB and PEB	3	n/a	*mpeAB*
Specialists	low PUB	3a	n/a	*mpeAB*
	mid PUB	3b	n/a	*mpeAB*
	high PUB	3c	n/a	*mpeAB - mpeW*
	high PUB with slightly different gene composition from 3c	3f	n/a	*mpeAB*
Generalists	variable PUB	3dA	CA4-A	*mpeAB*
		3dB	CA4-B	*mpeAB + mpeW*
	variable PUB but smaller degree of variation	3eA / 3eB	CA4-A / B	*mpeAB*

Table S2. Description of genetic markers used to differentiate *Synechococcus* specialists and generalists in cruise metagenomic data taken from (Humily et al., 2014).