# Supplementary material

## Supplementary Data 1: Parameterisation of photosystem II photoinactivation

Previous studies have analyzed photoinactivation in terms of rate constants, quantum yields (Fig. S1) or biological weighting functions [23-25,29,30,41,43-46]. We, however, used target theory [28] to parameterize the PSII photoinactivation rate as:

$$\text{PSII photoinactivation rate} = E \bullet |\sigma_i|$$

where E is the scalar irradiance (photons $nm^{-2}$ $s^{-1}$) and $|\sigma_i|$ ($nm^2$) is the magnitude of the effective target cross section for PSII photoinactivation (functional PSII lost $s^{-1}$). In this formulation $\sigma_i$ can be interpreted as the product of the absorbance cross section ($nm^2$) for the target which absorbs the inactivating photon, and a quantum yield (dimensionless) for the photoinactivation event per absorbed photon (see also Supplementary Data 2). Thus, $\sigma_i$ carries units of $nm^2$ but its nominal size does not reflect a physical size of the absorbing target. We estimated $\sigma_i$ for blue light as the exponential decay of PSII function plotted versus cumulative photon dose $nm^{-2}$ (Fig. 2), and found comparable values of $\sigma_i$ for across the five picocyanobacteria species in spite of their diverse antenna structures and ecophysiological properties .The ratio $\sigma_{PSII} : |\sigma_i|$ then estimates the relative probability of photosystem II photochemistry versus photoinactivation, for a given spectral quality of light.

Using an alternate model for photoinactivation we attempted to fit the PSII photoinactivation rate as a function of the photon dose per PSII, estimated as:

$$\text{PSII photoinactivation rate} = E \bullet \sigma_{PSII} \bullet \Phi_i$$

where E is again the scalar irradiance (photons $nm^{-2}$ $s^{-1}$), $\sigma_{PSII}$ is the effective absorbance cross section serving PSII photochemistry ($nm^2$ $PSII^{-1}$) and $\Phi_i$ is a quantum yield for photoinactivation relative to the photons delivered to PSII through the photosynthetic antenna [23]. For this parameterization we estimated $\Phi_i$ as the exponential decay of PSII function plotted versus cumulative photon dose $PSII^{-1}$ (Fig. S1), with $\sigma_{PSII}$ determined for each time point using flash fluorescence induction profiles. For blue light treatments of picocyanobacteria, this parameterization generated a 2.3 fold range of estimated $\Phi_i$ quantum yields across the five species (Fig. S1), contrasting with the tightly clustered values for $\sigma_i$ among the strains (compare with Fig. 2). Furthermore, the $\Phi_i$ model predicts increasing rates of photoinactivation with increasing $\sigma_{PSII}$, but the measured rates of photoinactivation across the cyanobacterial strains showed only a weak correlation with their $\sigma_{PSII}$ effective absorbance cross sections serving PSII photochemistry (Table 1). Therefore, photoinactivation by typical PAR in marine picocyanobacteria is more coherently and directly explicable through the simpler model of photoinactivation resulting from an initial event separate from the photosynthetic antenna [27,30]), which we parameterize herein as $\sigma_i$.

The target size parameterization we use allows ready estimation of the rate of primary photoinactivation as E • $\sigma_i$. Furthermore, $R_{PSII}$ can now be readily estimated, without inhibitor incubations, through a comparison of the underlying primary photoinactivation, E • $\sigma_i$, to the net change in photosystem II function over time, monitored using the widely available PSII fluorescence quantum yield ($F_V/F_M$).

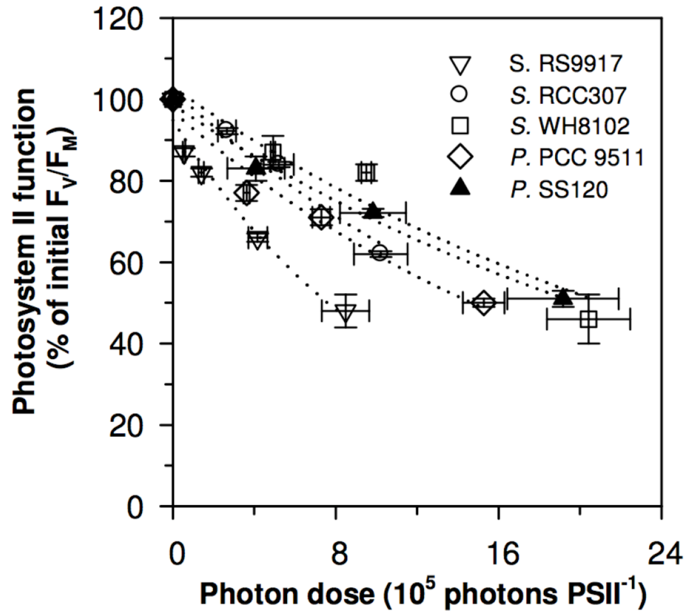


**Figure S1**: Exponential decays of PSII capacity in lincomycin treated cultures of the five picocyanobacteria. In contrast to Figure 2, the photoinhibitory photon dose was calculated as coming through the photosynthetic antenna, by multiplying E x time x $\sigma_{PSII}$ for the X-axis. Note the greater scatter among species in this plot compared to Figure 2.

**Supplementary Data 2 : D1 protein dynamics across marine cyanobacteria**

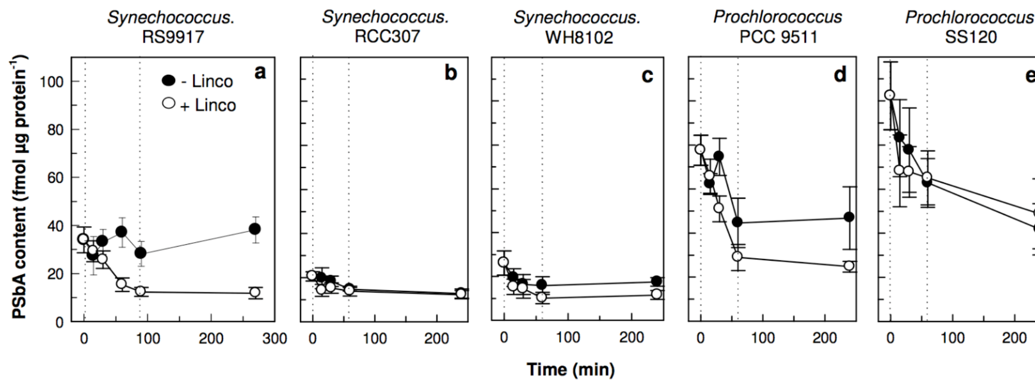


**Figure S2** : The initial level and subsequent variations in the core subunit D1 of Photosystem II among the five marine cyanobacteria during exposure to a high light episode and recovery. D1 protein was determined by quantitative immunoblotting in cultures treated (closed) or not (open) with the protein synthesis inhibitor lincomycin to block photosystem II repair (n=4, ± 1 s.e.). The high irradiance episode is delineated by dotted lines. Note that in the absence of repair, *Synechococcus* RSS9917 was able to degrade and clear D1 proteins from photoinactivated photosystems II (A) as seen by the rapid 70% decrease in D1 content in cultures treated with lincomycin. In contrast, *Prochlorococcus* SS120 appeared to have limited 30% clearance of D1 protein during the high light episode (E), in spite of suffering significant photoinactivation of PSII (Figure 1E).