



**TITLE: Molecular insights into factors controlling marine picocyanobacterial diversity and abundance**

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Marine picocyanobacteria of the genera *Synechococcus* and *Prochlorococcus* are numerically dominant in vast tracts of the ocean. Using a combination of radiotracer and flow cytometric sorting studies we have evaluated the importance of each genera in marine CO<sub>2</sub> fixation [1]. Although a minor component numerically, photosynthetic picoeukaryotes (PPEs) are also important marine primary producers. However, these PPEs can also act as bacterivores in oligotrophic gyre ecosystems, actively consuming picocyanobacteria [2, 3]. Such biotic control of natural picocyanobacterial populations likely also includes viral lysis. Indeed, cyanophages actively shut down host CO<sub>2</sub> fixation whilst maintaining photosynthetic electron transport during infection [4].

As well as biotic control of cell abundance, natural picocyanobacterial populations are also structured genetically by abiotic factors such as temperature, nutrient availability and light intensity [5]. Specifically for *Synechococcus*, we have developed a high resolution phylogenetic framework to fine tune the geographical partitioning of this genus *in situ*, which is particularly well typified along Atlantic Meridional Transects [6]. In concert with in-depth genomic and metagenomic studies, we aim to uncover the specific adaptation mechanisms of the numerous *Synechococcus* phylotypes observed, that will help explain the successful colonization of this genus throughout the marine environment.

[1] Jardillier et al., (2010) ISME J 4: 1180-1192; [2] Hartmann et al., (2012) PNAS 109: 5756-5760; [3] Hartmann et al., (2013) Env. Micro Rep. 5: 835-840 [4] Puxty et al., (2016) Curr. Biol. 26: 1585-1589 [5] Scanlan et al., (2009) MMBR 73: 249-299; [6] Farrant et al., (2016) PNAS E3365-E3374.