

30. FROM PICOCYANOBACTERIA TO COLONIAL CHROOCOCCOID CYANOBACTERIA: ECOLOGICAL AND PHYLOGENETIC ASPECTS

30-O Genetic diversity and niche adaptation in marine picocyanobacteria: a genomic and metagenomic perspective. Laurence Garczarek¹ - Hugo Doré¹ - Gregory K. Farrant¹ - Francisco M. Cornejo-Castillo² - Florian Humily¹ - Morgane Ratin¹ - Antoine Bisch³ - Frances D. Pitt⁴ - Martin Ostrowski⁵ - David J. Scanlan⁴ - Silvia G. Acinas² - Frédéric Partensky¹

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Prochlorococcus and *Synechococcus* are the two most abundant and widespread oxyphototrophs of the ocean. Although these two genera generally co-occur, *Prochlorococcus* dominates in warm, oligotrophic areas from 40°S to 45°N, while it is often outcompeted by *Synechococcus* in coastal and mesotrophic waters. In order to better understand the factors controlling their respective phylogeography, we sequenced 32 strains belonging to the marine *Synechococcus/Cyanobium* radiation, an effort that more than doubled the number of currently available genomes in public databases and nicely complemented the existing dataset in terms of genetic and pigment diversity. Extensive comparisons of 53 *Synechococcus* and 28 *Prochlorococcus* genomes allowed us to considerably refine the core and pan-genomes at various taxonomical levels. Heatmaps of pairwise ANI between all 81 genomes demonstrated that according to the 94% ANI identity criteria, most sub-clades IIIa members would belong to the same species, (and this also holds true for members of clade V and subclade VIIa), while every single other *Synechococcus* strain would constitute a distinct species, even within a given subclade.

In complement to these comparative genomic analyses, we also analyzed 109 metagenomes from the *Tara* Oceans expedition by recruiting reads targeting the high resolution taxonomic marker *petB*, encoding cytochrome *b₆*, using a *miTag* approach. These analyses unveiled a previously unsuspected genetic diversity within both *Prochlorococcus* and *Synechococcus* genera. By delineating Ecologically Significant Taxonomic Units (ESTUs), i.e. genetically related organisms occupying a given oceanic niche, based on the distribution patterns of picocyanobacterial communities, we identified three major *Prochlorococcus* assemblages along the cruise transect and eight for *Synechococcus*. Analyses of the biogeography of these ESTUs also revealed that there was a remarkable correlation between these assemblages and specific environmental cues and that picocyanobacterial communities of the Pacific Ocean were drastically different from those of other oceanic regions. Sharp community shifts were also observed over short geographic distances, e.g. around the Marquesas Islands or between southern Indian and Atlantic Oceans, pointing to a tight correlation between ESTU assemblages and specific physico-chemical parameters. Altogether, our study demonstrates that *petB*-ESTUs provide a much finer prediction of picocyanobacterial 'ecotypes' than do phylogenetic clades, bringing novel insights into the ecology, diversity and biology of the two most abundant phototrophs on Earth.

30-O Comparative genomics and phylogenetic analyses of non-marine picocyanobacteria. Patricia Sánchez-Baracaldo¹ - Nathan A. M. Christmas¹ - Andrea Di Cesare² - Cristiana Callieri²

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Picoplanktonic cyanobacteria contribute up to 80% of the total primary production in lakes, depending on the season, water chemistry and hydrography. While picocyanobacteria play a key in role as primary producers in lake systems worldwide, little is known about their genomic structure or phylogenetic relationships. Large-scale multi-gene (135 proteins and two ribosomal RNAs, SSU and LSU) phylogenetic analyses have confirmed that freshwater picocyanobacteria, including *Cyanobium* and *Synechococcus*, are sister to marine *Synechococcus* and *Prochlorococcus*; both clades diverged from a freshwater single cell cyanobacteria ancestor. We sequenced the genomes of eight strains of non-marine picocyanobacteria including localities from Europe, South and Central America. Comparative genomics show, for the first time, that picocyanobacteria could possess the genetic machinery necessary to perform nitrogen

fixation as revealed by two strains such as LL (L. Albano) and 3B3 (L. Candia). Highly reduced genomes (genome streamlining) seem to be characteristic of strains from ultraoligotrophic lakes such as 1G10 (L. Nahuel Huapi); a similar trend has been observed in marine *Prochlorococcus*. Five strains (8F6 L. Alchichicha, 6H9 L. Atexcac, LL L. Albano, 3B3 L. Candia and 1G10 L. Nahuel Huapi) contain the red pigment phycoerythrin and include the first examples of complete genomes containing Type IIB phycoerythrin clusters previously identified in cyanobacteria from the Baltic Sea. Phylogenetic evidence supports the idea that these genes pigment may have been acquired via lateral gene transfer from marine lineages.

30-O The revision of phylogenetic relationships of some freshwater picocyanobacteria. *Iwona Jasser*¹, *Jan Kwiatowski*²

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Picocyanobacteria are the smallest primary producers in aquatic ecosystems. They are ubiquitous in marine and freshwater ecosystems, where together with heterotrophic bacteria serve as a base for microbial food webs. The occurrences, abundance, productivity of picocyanobacteria and their phylogenetic relationships have been studied intensively in various environments. While picocyanobacteria contribute substantially to the primary production (PP) in the marine ecosystems, their share in PP in freshwaters, especially in eutrophic environments is much smaller. Nevertheless, the variety of environments in which picocyanobacteria have been found in freshwaters is astounding, suggesting high diversity of these microorganisms. In freshwaters single-celled picocyanobacteria are mainly represented by two genera: *Synechococcus* and *Cyanobium*, of which *Synechococcus* has been considered polyphyletic. The phylogenetic analyses have shown that besides the positions of the *Synechococcus* and *Cyanobium* clades, many *Synechococcus* strains are intermixed with various picocyanobacteria. We have conducted phylogenetic analysis of over 200 sequences of rRNA operon, including sequences of 16S rRNA, tRNA-Ala, tRNA-Ile, 23S rRNA genes and internal transcribed spacer (ITS1) retrieved from GenBank. In this way we reviewed the phylogenetic positions of particular strains, which were previously claimed to belong to the endemic group M from Mazurian lakes. We also verified relationships between cosmopolitan groups, such as Group A (a *Cyanobium gracile* cluster), Group B (subalpine cluster I with *Synechococcus rubescens*), Group E (with Lake Biwa strains) and Group C/Cz (with strains firstly isolated from Czech lakes). Our analysis suggests that the Groups M and B are distantly related. The analysis confirmed also the position of two strains KS0807 and SM0807, isolated from two low-pH lakes in Poland, as belonging to Group B and Group A, respectively.

30-O Control factors and ecological role of autotrophic picocyanobacteria in a meromictic karstic lake. *Antonio Camacho*, *Antonio Picazo*, *Carlos Rochera*, *Maria Rosa Miracle*, *Eduardo Vicente*

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The factors that control the abundance and relative dominance of cyanobacteria in aquatic ecosystems have been extensively studied in both saltwater and freshwater ecosystems. Freshwater ecosystems show significant trophic gradients and diversity of environments and the relative relevance of cyanobacteria shifts from unicellular species in oligotrophic waters to filamentous or colonial species at higher trophic levels. In this work we studied different mechanisms that explain the dominance of autotrophic picocyanobacteria (Pcy), as well as the factors controlling their abundance and the ecological consequences of this dominance, in the model Lake La Cruz. This is a small, deep, meromictic lake, which additionally shows a strong seasonal thermal stratification, presenting a permanent carbonate oversaturation with the occurrence of annual whiting events. A sharp thermocline seasonally develops from April to October with the development of a highly productive deep chlorophyll maximum (DCM). The main photosynthetic microorganisms in the lake are autotrophic picocyanobacteria (Pcy), larger eukaryotic phytoplankton, and photosynthetic sulfur bacteria. Despite the diversity of photosynthetic microorganisms found in Lake La Cruz, Pcy dominate over the limnological cycle both in biomass and in the relative contribution to inorganic carbon assimilation. Maximum Pcy abundance of up to 14×10^6 cells ml⁻¹ was found, although the rest of photosynthetic microorganisms can also be seasonally significant in terms of biomass. Oxygenic photosynthesis is the most important process of inorganic carbon assimilation accounting for 89.7% ($164 \text{ g C m}^{-2} \text{ yr}^{-1}$) of total inorganic carbon assimilation, where Pcy are responsible of 80% of this assimilation. Anoxygenic photosynthesis accounts for 2.7% and chemolithoautotrophy for 7.6% of the total inorganic carbon assimilation. Different bioassays and experiments showed the relevance of