

A next-generation approach to assess the cyanobacterial diversity and biogeography in the High Arctic (Svalbard)

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Polar ecosystems are extremely sensitive to global climate changes and human activities. Cyanobacteria are key photosynthetic organisms in these latitudes, due to their roles in soil aggregation, nitrogen fixation, carbon cycles, and secondary metabolite production among others. Previous works indicate that different cyanobacterial taxa/communities have different impacts on the environment, in both biogeochemical cycles and bioactive compound productions. Furthermore, the presence of biogeographical patterns in microorganisms, as found in macroorganisms, is an ongoing debate. In this study, during the 2013 MicroFun expedition, we sampled 72 locations around Svalbard including diverse biotopes such as glacial forefields, tundra soils, hot springs, soil crusts, microbial mats, wet walls, cryoconites, plankton and periphyton, in order to (1) assess the biodiversity of cyanobacteria around Svalbard, (2) verify the existence of biogeographical trends around the archipelago, and (3) compare these data with other polar (cold) areas, especially Antarctica. We used a pyrosequencing approach targeting cyanobacteria-specific 16S rRNA gene sequences to deeply study the cyanobacterial communities. Hundreds of cyanobacterial OTUs at 97.5% similarity were found, indicating a previously uncharacterized enormous diversity of these microorganisms around the archipelago. OTUs matching species of *Arthronema*, *Coleofasciculus*, *Leptolynbya*, *Lyngbya*, *Microcoleus*, *Nostoc*, *Oscillatoria*, and *Phormidium* were most abundant in the different locations. Preliminary assessment indicates that there are largely distributed 'cold-adapted' OTUs as well as unique ones only found in Svalbard. When considering the ecological range, some taxa appear unique to a particular biotope, but others can be observed in different environments.