

# Drivers of the terrestrial cyanobacterial community composition in the Sør Rondane Mountains, East Antarctica

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The sparse ice-free regions of Antarctica harbor diverse microbial communities that can vary significantly between regions and micro-climatic conditions. The factors responsible for the diversity and community structure in inland nunataks of East Antarctica are still poorly understood. During the BELSPO MICROBIAN project, three sampling campaigns took place in the Sør Rondane Mountains during the austral summers of 2018, 2019 and 2020, resulting in more than 100 samples ranging from different types of barren bedrock to substrates covered by biofilms and well-developed biological soil crusts including lichens, mosses, microalgae and/or cyanobacteria. Cyanobacterial diversity was assessed by amplicon sequencing targeting the V3-V4 variable region of the 16S rRNA gene with cyanobacteria-specific primers using the Illumina MiSeq platform (2x300 bp). The recently developed CyanoSeq database was used for the taxonomic affiliation of the OTUs (99% similarity threshold). Whilst favorable habitats, such as sheltered spots in rocky areas, enhance the development of different kinds of cyanobacterial crusts, cyanobacteria were present even in the most extreme ones. Granitic soils were dominated by very diverse cyanobacterial crusts, mostly composed by filamentous cyanobacteria of the Leptolyngbyaceae, Oculatellaceae and Microcoleaceae families, and by Nostocaceae. Most abundant OTUs on gneiss bedrock were from the Cyanothecaceae and Microcoleaceae. In contrast, marble soils were dominated almost exclusively by the Chroococcidiopsaceae family. Moraine samples from very dry areas were mainly characterized by members of the Gomontiellaceae family whereas moraine samples taken close to a lake were rich in filamentous taxa as well, mostly belonging to the Leptolyngbyaceae, Oculatellaceae and Gomontiellaceae families. Next to bedrock type, other abiotic variables such as pH, NO<sub>3</sub> and TOC were especially important drivers of the community composition in each sampled site.