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## Soil substrate shapes edaphic cyanobacterial communities in the Sør Rondane

## Mountains, East Antarctica

Botany, Třeboň, Czech Republic

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## Abstract

Cyanobacteria are regarded as ecosystem engineers (Chrismas et al. 2018) in Antarctic ice-free areas because of their important role as primary producers. Yet, cyanobacterial communities and their drivers within edaphic ecosystems of inland Antarctica are often overlooked. A previous study (Savaglia et al. 2024) describing microbial communities from around 100 soil samples of the western Sør Rondane Mountains (East Antarctica) showed that substrate types were major structuring factors and several cyanobacterial phylotypes were recognized as putative keystone taxa. Here, cyanobacterial diversity was further investigated. Amplicon sequencing was applied using cyanobacterial specific primer targeting the V3-V4 region of the 16S rRNA gene via the Illumina MiSeq platform and taxonomy was assigned using the recent CyanoSeq database to the same samples set. Our results confirmed that substrate types shape cyanobacterial communities, providing a higher taxonomic resolution. Granite harboured the greatest cyanobacterial diversity with a high abundance of filamentous cyanobacteria (i.e. Leptolyngbyaceae, Gomontiellaceae, Microcoleaceae, Oculatellaceae, Nostocaceae), but also unicellular taxa (Cyanothecaceae). By contrast, cyanobacterial diversity was lower in the other substrate types, often dominated by only one taxon. Particularly, marble was dominated by Alitarella, gneiss by Cyanothece, and moraines from the dry and oligotrophic Austkampane and Widerøefjellet sites by Microcoleaceae and Gomontiellaceae, respectively. An indicator taxa analysis showed many unknown taxa uniquely encountered in the moraines of Yûboku-dani Valley, suggesting a high degree of endemicity where the only known lakes in the region occur. Overall, our data highlight the importance of using specific primers and up-todate taxonomy to accurately draw conclusions about microbial ecology.

Chrismas N.A. et al. 2018. FEMS Microbiology Ecology. doi:10.1093/femsec/fiy032

Savaglia V. et al. 2024. Frontiers in Microbiology. doi:10.3389/fmicb.2024.1316633