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The scarce ice-free terrestrial areas of Antarctica are among the most extreme environments on Earth and are therefore dominated by microorganisms. The Belgian station, Princess Elisabeth, is located in an inland mountainous regions of the Sør Rondane Mountains (SRM). During the BelSPO project MICROBIAN (2016-2021), 96 samples were collected from a wide range of bedrock types (granite, marble, gneiss and moraine) and nunataks/ridges (Fig. 1). The soil and biological crusts' microbiomes were studied using amplicon sequencing of the SSU rRNA gene of pro- and eukaryotes. Preliminary results suggest that pH and bedrock type were the most important structuring factors for both Bacteria and Eukaryotes in these ice-free regions.

MATERIAL AND METHODS

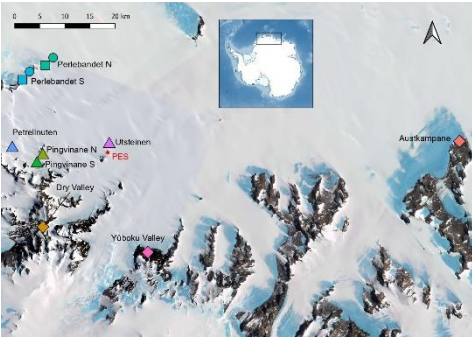


Fig. 1 Map of the sampling sites, in the Sør Rondane Mountains (SRM).

RESULTS

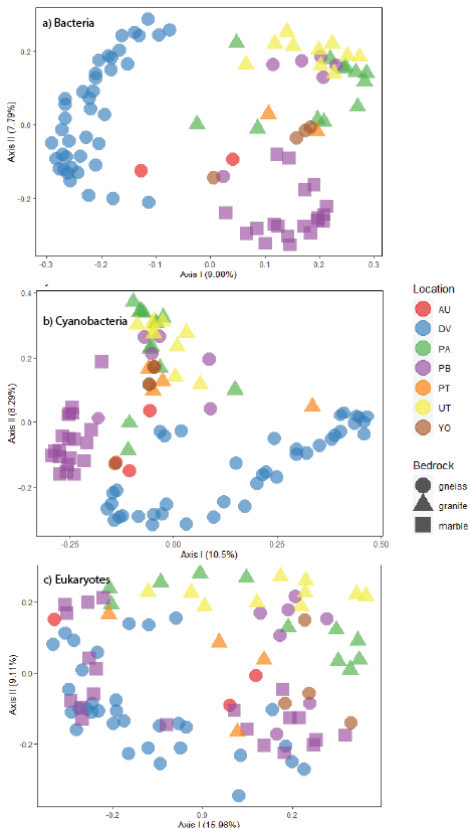


Fig. 2 PCoA plots describing bacterial (a), cyanobacterial (b) and eukaryotic (c) beta-diversity from each sampling location and bedrock type.

DNA extraction and Illumina sequencing (2x300 bp)

- 16S general bacterial primers (pA / BKL1)
- 16S cyanospecific primers (CYA359F / CYA781Ra)
- 18S general eukaryote primers (TAReuk454FWD1/ TAReukREV3)

Bioinformatic analysis

- USEARCH + UPARSE pipeline resulting in
- 21234 OTUs for bacteria (OTU clustering at 97.5 % sequence-similarity)
- 3681 OTUs for cyanobacteria (OTU clustering at 99 % sequence-similarity)
- 436 OTUs for eukaryotes (OTU clustering at 97 % sequence-similarity)

Statistical analysis

- Beta-diversity: PCoA with Hellinger-transformed OTU table and Bray-Curtis dissimilarity
- PERMANOVA (adonis package) and ANOVA (aov package) analysis between the Bray-Curtis dissimilarity matrix of the OTU table and the log or squared-root transformed environmental variables
- dbRDA with relative-abundance data using Bray-Curtis distances. Environmental and spatial explanatory variables were identified with a forward, stepwise selection, following Sokol et al. (2013).
- Variation partitioning to assess the relationship between beta diversity and environmental and spatial gradients

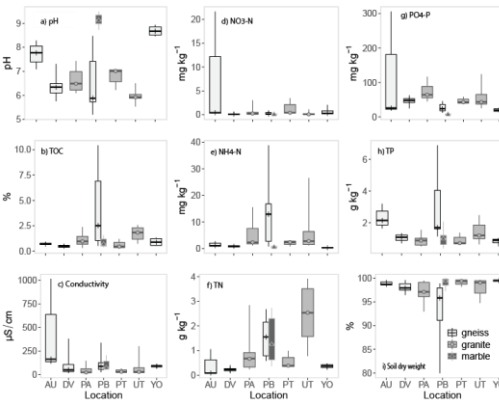


Fig.3. Geochemical data for each sampling location: a) pH, b) Total Organic Carbon (TOC), c) Conductivity, d) NO₃, e) NH₄, f) Total Nitrogen (TN), g) PO₄, h) Total Phosphorus (TP), i) Soil dry weight. Colours indicate the bedrock type (dark grey: marble, grey: granite, light grey: gneiss).

DISCUSSION AND CONCLUSION

Bedrock

Bedrock plays an important role in the community structures. As shown in the PCoA plots (Fig. 2), marble and granite seem to especially influence bacterial and cyanobacterial communities, which confirms and extends the results of Tytgat et al. (2016).

Geochemical soil properties

Of the 9 geochemical soil properties (Fig. 3), pH explained the highest variation (11% for bacterial, 8% for cyanobacterial and 3% for eukaryotes). In addition (data not shown), elevation appeared to be an important structuring factor (10 % for Bacteria, 5% for Cyanobacteria and 2 % for Eukaryotes).

In conclusion, soil microorganisms in the SRM are more influenced by **environmental parameters** than the spatial ones, with **pH and elevation** being the most important structuring factors. Marble and granitic soils host more specific communities of both Bacteria and Cyanobacteria, whereas this is not the case for Eukaryotes.