

Microbiome diversity and function in the Sør Rondane Mountains, East Antarctica - MICROBIAN

Summary

Context

The scarce ice-free areas in Antarctica are among the most extreme terrestrial environments on Earth. Life in these places is dominated by microbes. As a consequence, food webs are strongly truncated, with few metazoans consuming organic matter and microbial biomass. Elucidating the factors that shape the biodiversity of these microbiomes and control their contribution to biogeochemical processes, provides the scientific basis for habitat mapping and classification, for developing conservation strategies, for guiding long-term monitoring efforts and for predicting their possible response to future environmental changes. In this respect, inland nunataks in East Antarctica, like the Sør Rondane Mountains (SRM), are far less well-studied than those in more coastal locations and in the McMurdo Dry Valleys. This is surprising given their long-term exposure and their potential role as ice-free refugia during Neogene and Pleistocene glacial maxima and that the environmental conditions in these inland nunataks are different from those in coastal regions. The Sør Rondane Mountains (SRM) represent a c. 900 km² large nunatak, encompassing a large range of terrestrial habitats differing in geology and soil characteristics, exposure time and microclimatic conditions.

Objectives

The objectives of the MICROBIAN project were to (i) use a combination of remote sensing and close-range field observation techniques to map physical habitat characteristics and the presence and extent of microbial mat and biological crust communities in a radius of 200 km around the Princess Elisabeth Station Antarctica (PEA), (ii) generate a comprehensive inventory of the taxonomic and functional diversity of microbial communities in these habitats, and cultivate and characterize bacterial and cyanobacterial indicator taxa and deposit them as reference material in the BCCM collections, (iii) measure key ecosystem functions, including photosynthesis, in microbial communities representative of the major habitats in the region, (iv) use mesocosm field experiments to mimic the possible effects of future climate change on the functional and taxonomic diversity of these microbial ecosystems, and (v) conduct field experiments to inform policy-makers in view of decision making regarding environmental protection and prevention measures to reduce the introduction and spread of non-native species and to avoid cross-contamination between sites. The project will provide a proof of concept to use high resolution satellite images for identifying regions of particular biological interest in East Antarctica and more broadly make a significant contribution to understanding Antarctic terrestrial microbial ecology.

Conclusions

The use of high resolution multi-look optical satellite imagery allowed for an accurate estimation of the elevation, slope and aspect of Antarctic nunataks. These factors relate to water retention and light availability, which are important in determining the presence, composition and functioning of microbial communities in these environments. Additional drone

acquisitions proved to be high performance, allowing for the estimation of centimetre scale slope and aspects of individual sampling sites. The drone data also revealed inaccuracies in the GPS locations of the individual sampling sites, but will hence allow for refining those coordinates based on field photographs. Ground truthing for future research will also require setting up a denser regular network of temperature loggers to better analyse the effect of temperature and improve results accuracy. The Digital Elevation Model and temperature (both in situ and satellite) data collected in MICROBIAN could be used for setting up and evaluating a diurnal solar irradiance and surface heating model. These models could then be used to determine light and liquid water availability at the different mountain sides. This is important given the effect of these factors on the microbial communities and since large differences in temperature and relative humidity were observed between sampling plots along the moisture gradient in the different regions. The installed snowfences, however, mitigated temperature fluctuations compared to exposed gravels in the control zones. Sampling locations within the same bedrock type tended to have similar soil chemical characteristics. It is worthwhile to note, however, that the 'Dry Valley' region appeared to be unique in terms of the soil characteristics measured in this study, and did not resemble moraine samples from other regions (Austkampane and Yûboku Valley), probably because of the very peculiar soil and microclimatic conditions.

Analysis of the amplicon sequencing data showed that pH and bedrock type were the main abiotic factors structuring microbial communities in the ice-free regions. Bacterial communities mainly consisted of Actinobacteria, Acidobacteria and Cyanobacteria. Bacteroidetes and Chloroflexi were also particularly abundant while the remaining abundant phyla consisted of Proteobacteria, Abditibacteriota, Deinococcus-Thermus and Patescibacteria. Actinobacteria and Cyanobacteria often seemed to be inversely correlated, with Cyanobacteria being less abundant in moraine samples, while Actinobacteria being the most abundant. In contrast, Cyanobacteria represented an important portion of the Yûboku Valley diversity, where the only known lake systems within the western SRM are situated. Acidobacteria were found to be well represented in all kind of soils. In the eukaryotes, Chlorophyta was the most important phylum followed by Metazoa, Cercozoa and Ciliophora. Metazoa seemed to be well represented in all kind of soils but less in moraine soils, with Cercozoa being more abundant there and in marble soils.

Using shotgun metagenomics, we were able to reconstruct 373 draft genomes from 14 phyla with an average completeness of 86.29%. Genes for aerobic organotrophic respiration were among the most abundant, while genes for anaerobic respiration and fermentation were low across all samples. Among the genes not involved in aerobic respiration, the two most abundant genes are those encoding RuBisCO (*rbcL*; 47.6%) and form I carbon monoxide dehydrogenase (*coxL*; 23.3%) respectively. Genes involved in phototrophy were relatively rare (*psaA*; 8.21%, *psbA*; 12.4%, RHO; 6.7%). Our results suggest that atmospheric trace gas oxidation and chemosynthesis might be an important process in the Sør Rondane Mountains, supporting primary production independently of photoautotrophy. The distribution of these genes was positively correlated to elevation, and inversely correlated to moisture and total organic carbon. The highest abundance of genes involved in these alternative processes was found in the more extreme oligotrophic samples from Austkampane and the 'Dry Valley' region.

Combined, our results show that geographical aspects of the nunataks influence the presence and composition of microbial communities, in addition to bedrock type and geochemical factors such as pH. In these ultraoligotrophic environments, alternative primary production pathways seem to be crucial for the functioning of the microbial communities.

Our data were also used in policy support activities as part of SCAR and CEP meetings, e.g. for the proposal of the creation of an ASPA in the Sør Rondane Mountains. They were also presented during various outreach and knowledge disseminating activities.