COMPARATIVE ANALYSIS OF MICROBIAL COMMUNITIES INHABITING TWO DIFFERENT ROCK TYPES IN HIGH ARCTIC: MARTIAN ANALOGUE STUDIES

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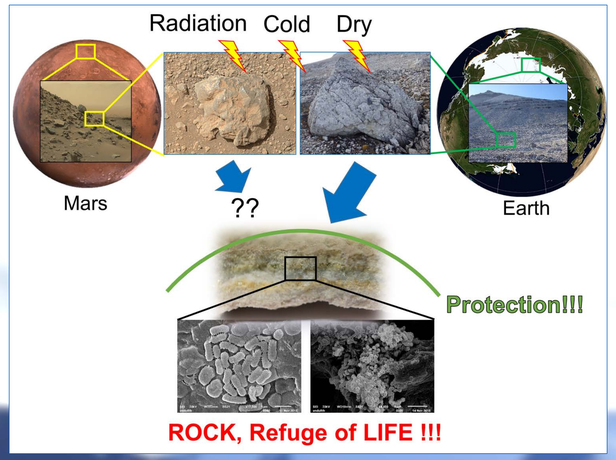
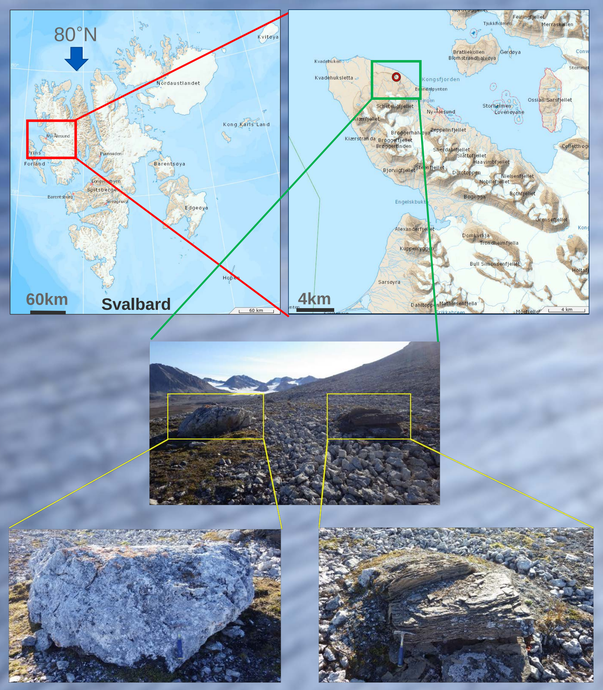
Introduction



Study area & Materials

< Svalbard >

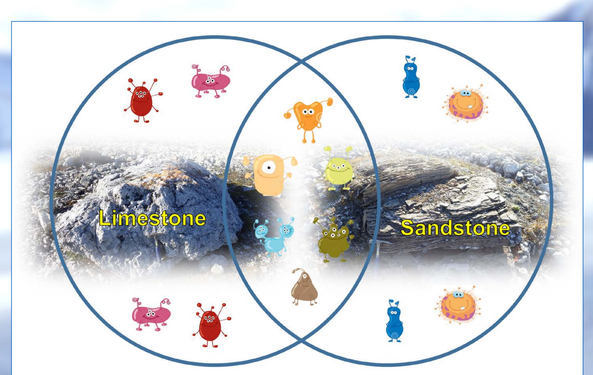
- Norwegian archipelago by the Arctic Ocean
- Location: 74° ~ 81° north latitude
  10° ~ 35° east longitude
- Average temperature: 4 ~ 6 °C (summer)
  −16 ~ −12 °C (winter)
- Martian analogue sites: AMASE program
- Materials: Limestone and Sandstone (triplicate)



Objectives

- ***To investigate the major members of microbial communities colonizing lithic environments of cold and dry region***
- ***To examine the effects of rock type on community structure in a single geographic location***

Conclusion



- ***Rock-inhabiting microbial communities living in high Arctic region revealed a high diversity of organisms.***
- ***Rock-inhabiting microbes seem to be influenced by ROCK TYPE at fine taxonomic level.***
- ***Some microorganisms show preference according to rock type.***

Further study

- ***Ongoing work examining site-specific factors such as substrate chemistry, microclimate, and host rock structure will help clarify how microbial populations and population diversity have evolved in this high Arctic cold desert habitat.***

Acknowledgements

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Results

1. Microbial Community Composition in Rocks

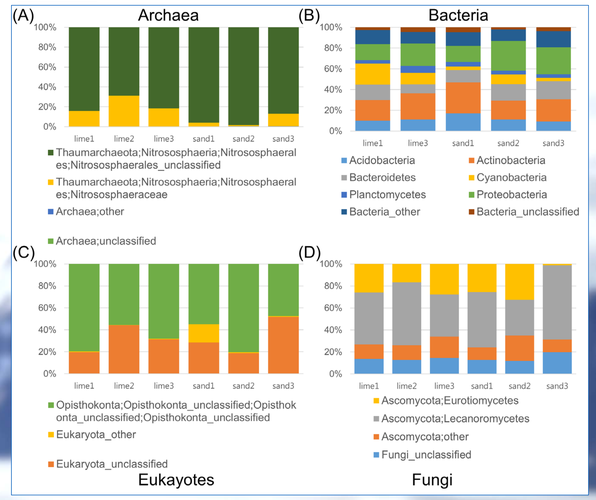

Fig. 1 Relative abundances of dominant microbial taxa in rock samples. (A) Archaeal community composition at family level (B) Bacterial community composition at phylum level (C) Eukaryotic community composition at family level (D) Fungal community composition at class level

At high level of taxonomic resolution, we did not detect any significant correlations between rock type and community composition (Fig. 1). In both limestone and sandstone, archaeal communities were dominated by *Thaumarchaeota.*

At the phylum level, the bacterial communities were dominated by five bacterial phyla, *Actinobacteria*, *Acidobacteria*, *Proteobacteria*, *bacteroidetes*, and *planctomycetes* in both rock types.

In eukaryotes, *opisthokonta* was the most abundant group across the entire rock samples. For fungi, *Ascomycota* was the most abundant phylum across the entire sample set. At the class level, the rock fungal communities were dominated by two fungal classes: *Eurotiomycetes*, *Lecanoromycetes*.

2. Distinct Microbial Communities between Limestone and Sandstone

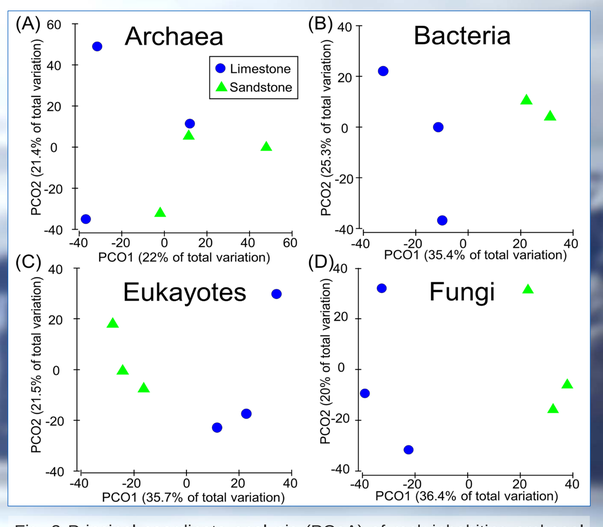

Fig. 2 Principal coordinate analysis (PCoA) of rock-inhabiting archaeal communities (A), bacterial communities (B), eukaryotic communities (C), and fungal communities (D). The analysis was based on the Bray-Curtis similarity matrix constructed using the square-root-transformed OTU. Points that are closer together on the ordination have communities that are more similar.

The lithological characteristics that control lithic community composition are more complicated than expected for microbial communities. We found that limestone and sandstone clustered apart when analyzed based on Bray-Curtis similarity matrix constructed using the square-root-transformed OTU (Fig. 2). The first two components of the PCoA explained over 40-60% of the variability between rock samples in archaea, bacteria, eukaryotes, and fungi.

3. Distinctly Abundant OTUs between Limestone and Sandstone

Given the distinct clustering pattern in community composition by rock types, we further investigated in more detail what microbial taxa determine more strongly the distinct community composition in different rock type (Table 1). Various genera were preferentially abundant in each rock type. For example, *Nitrososphaera*, *Hymenobacter*, *Aureobasidiaceae*, and *Herpotrichiellaceae* were more abundant in limestone, whereas CP012850_g, *Angustibacter*, and OTU00193 were found more abundantly in sandstone. These results suggest that substrate preferences are found when one looks at fine taxonomic resolution.

Table 1. Differentially abundant microbial family or genera in rock. Differences in relative abundance of microbial family or genera between Limestone and Sandstone are represented with Metastats *P* values. Significantly different (P<0.01) and relatively abundant genera or family (OTUs of the top five most significant per domain) were displayed

Domain	OTUs	Phylum	Family or Genus	Limestone	Sandstone	*p*-value
Archaea	OTU00045	*Thaumarchaeota*	*Nitrososphaera*	**1.03**	0	0.002
	OTU00193	*Thaumarchaeota*	*Nitrososphaera*	**0.49**	0	0.007
	OTU00326	*Thaumarchaeota*	EU284611_g	**0.31**	0	0.010
	OTU00701	*Thaumarchaeota*	CP012850_g (FJ790592_s)	**0.13**	0	0.009
	OTU00708	*Thaumarchaeota*	CP012850_g (CP012850_s)	0	**0.06**	0.008
Bacteria	OTU00099	*Bacteroidetes*	*Segetibacter*	**0.07**	0	0.008
	OTU00225	*Cyanobacteria*	EU753646_g	**0.26**	0	0.007
	OTU00248	*Actinobacteria*	EU289467_g	**0.09**	0.02	0.008
	OTU00413	*Bacteroidetes*	*Hymenobacter*	**0.10**	0.01	0.008
	OTU00658	*Actinobacteria*	*Angustibacter*	0	**0.04**	0.008
Eukaryotes	OTU00018	*Ascomycota*	*Aureobasidiaceae*	**1.77**	0.18	0.002
	OTU00130	*Ascomycota*	*Xanthopyreniaceae*	**0.03**	0	0.005
	OTU00205	*Ascomycota*	*Gyalectaceae*	**0.03**	0	0.003
	OTU00211	*Viridiplantae*	*Microthamniales*	**0.03**	0	0.005
	OTU00218	*Ascomycota*	*Dothideomycetes*	**0.03**	0	<0.001
Fungi	OTU00046	uncultured fungus	uncultured fungus	**1.63**	0	<0.001
	OTU00193	uncultured fungus	uncultured fungus	0	**0.06**	<0.001
	OTU00202	*Ascomycota*	*Herpotrichiellaceae*	**0.15**	0	<0.001
	OTU00384	*Ascomycota*	*Lecanoraceae*	**0.04**	0	<0.001
	OTU00829	*Ascomycota*	*Verrucariaceae*	**0.01**	0	<0.001