Bacterial diversity profiles associated with patterned ground features on Antarctic nunataks

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INTRODUCTION

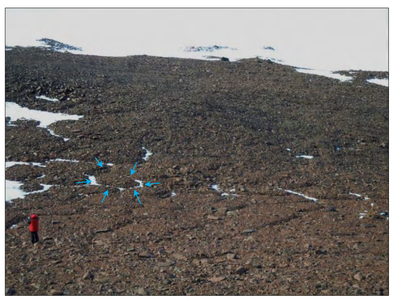

Figure 1. Photograph of patterned soil at Grunehogna. The edges of one of the polygons highlighted with arrows (note the snow-filled crack).

The Antarctic continent is almost exclusively covered by permanent ice with less than 0.32% of the land-mass representing ice-free terrestrial habitats. These ice-free frigid deserts experience extremely low precipitation and temperatures. Antarctic soils are frequently exposed to repeated cycles of freeze-thaw events and as a result of ice on the soil surface, water from the underlying soil is drawn up by capillary action and concomitant uplifting of soil particles occurs. As a result of this cryoturbation of the substrata, frost-sorted polygons, circles, steps or stripes (i.e. patterned ground) are formed (Figure 1). Antarctica is the coldest, driest and windiest continent on Earth consequently Antarctic terrestrial ecosystems exhibit low-complexity food web structures and are generally dominated by microorganisms that have a disproportionate importance in ecosystem functioning in these habitats. Abiotic factors greatly influence microbial populations and along with desiccation and cold temperatures, soils and their properties are also important elements. To date, research on Antarctic soils have focussed on the continental cold desert soils of the Dry Valleys in Victoria Land, on maritime terrestrial systems, and the Antarctic Peninsula. This study aims to characterise the terrestrial microbiota of nunataks in Dronning Maud Land and to determine if there are differences in the intra- and/or inter-polygonal physico-chemical and bacterial diversity profiles.

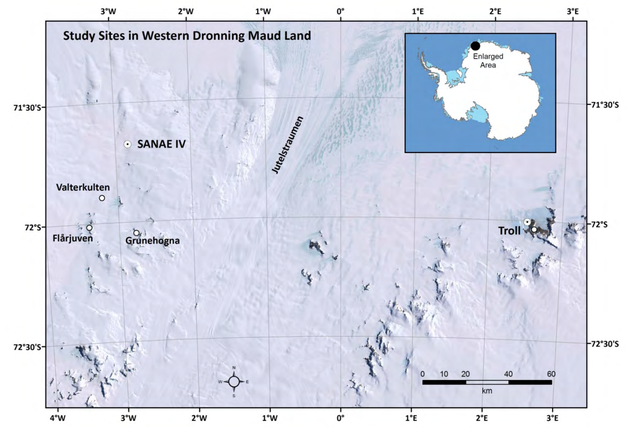

Figure 2. Map of Antarctica highlighting the location of the nunatak study sites.

RESULTS

MICROBIAL COMMUNITY ANALYSIS

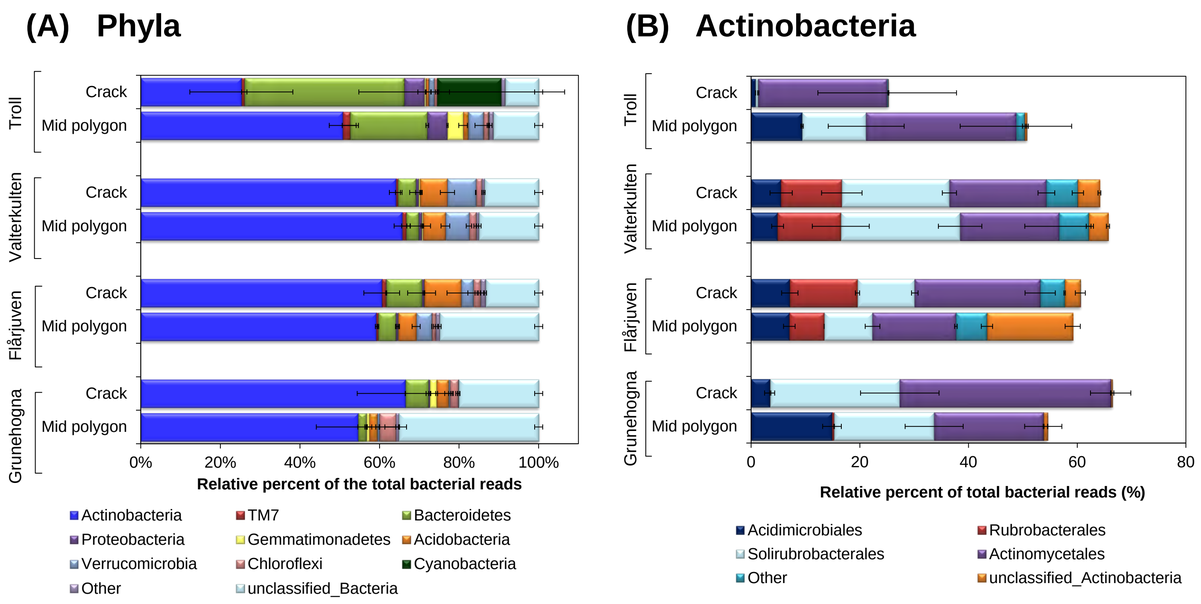

Figure 2. Relative abundances of the dominant phyla (A) and Actinobacterial orders (B) in soil from within the middle of the polygon and the crack around the edges of the polygon sampled in December 2012. DNA was isolated from the biomass using the PowerSoil DNA extraction kit (MoBio) followed by PCR amplification of the bacterial 16S rRNA hypervariable regions V4/V5. After curation of 454-pyrosequencing data (removal of chimeras, reads <200 bp and reads containing ambiguous nucleotide or a homopolymeric stretch >7), a total of 54 213 reads were classified using the Ribosomal Database Project. Other = reads assigned to minor phyla.

- **Similar overall bacterial phyla distribution between the soil samples except for those from Troll which differed significantly**
- **With Troll as the exception, similar bacterial community profiles were observed between the crack and the middle of the polygons**
- **High prevalence of Bacteroidetes at Troll, Actinobacteria dominate at all sites (high prevalence of Gamma-radiation resistant *Rubrobacter* species at Valterkulten and Flårjuven)**

OPERATIONAL TAXONOMIC UNITS

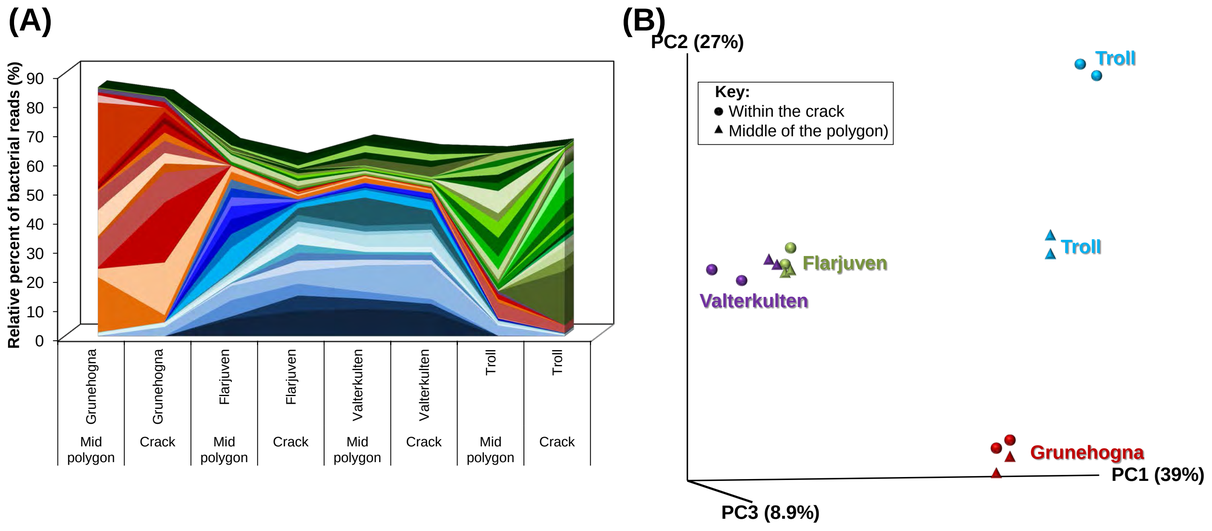

Figure 5. Comparative analysis of the numerically dominant OTUs **(A)**. OTUs were determined at a distance value of 0.03 using Mothur software. **(B)** Principal Component Analysis (PCoA) generated with a UniFrac distance matrix of the microbial populations within duplicate soil samples from Grunehogna, Valterkulten, Troll and Flårjuven. OTUs represented by a single read were removed from the dataset and the PCoA was done with normalised data sets. The percentage variation for each of the principle coordinates is indicated on the respective axes.

- **Distinct microbial populations within soils at Troll and Grunehogna**
- **A marked similarity in microbial diversity profiles between Valterkulten and Flårjuven soils**
- **Little differentiation between microbial populations within the polygons and cracks between polygons with Troll as the exception**

ABIOTIC ASPECTS

Distance (km)	Grunehogna	Valterkulten	Flårjuven	Troll
Grunehogna	0	23	21	193
Valterkulten	23	0	14	210
Flårjuven	21	14	0	214
Troll	193	210	214	0

Table 1. Distance matrix for the sample sites

Site	Rock composition
Grunehogna	Doleritic & dioritic sill/dykes with some quartzites, arkoses & siliceous siltstone
Valterkulten	Doleritic & dioritic sill/dykes
Flårjuven	
Troll	Granite & gneiss

Table 2. Substrate composition of the sample sites

- **All four sites experienced very few thaw cycles. Valterkulten exhibited a more sustained thaw profile compared to the remaining three nunataks**
- **Grunehogna and Flårjuven closely mirroring each other in temperature and soil particle size profiles**
- **Large distance between Troll and rest of sites (separated by Jutelstraumen)**
- **Valterkulten and Flårjuven composed of the same rock type, Grunehogna is similar whilst Troll differs**
- **Soil substrate is stony with low proportions of silt and clay but high proportions of sand. Mostly coarse sand due to granitic source material at Troll. Flårjuven dominated by large particles**

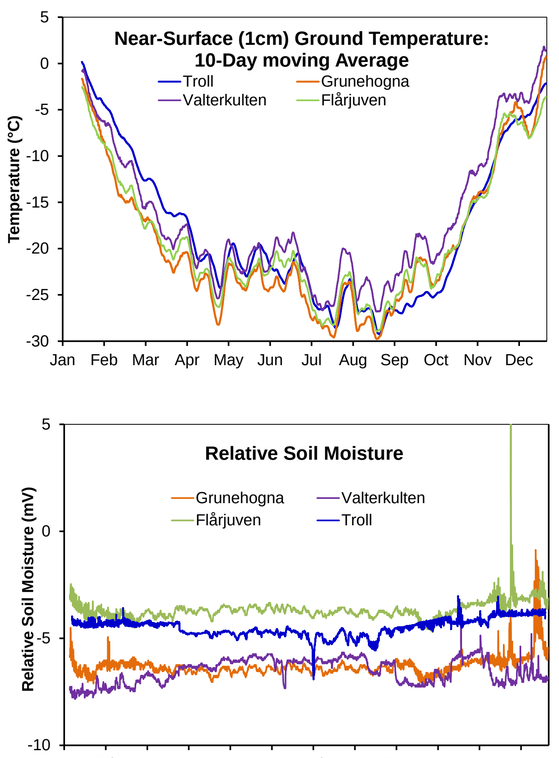

Figure 3. Substrate, environmental and physical properties for four nunataks in Western Dronning Maud Land during the austral year 2013. Temperature ad soil moisture were monitored by XYZ datalogger. Soil particle size was ascertained by sieving of sample sediment through respective sieve sizes.

CONCLUSIONS

- **With the exception of Troll, the potential increase in water availability in the polygon cracks (due to meltwater) did not affect the microbial population profiles**
- **The variation between the crack and middle of the polygon at Troll may be as a result of increased coarse sand which may facilitate water retention in the cracks**
- **Flårjuven and Valterkulten exhibited very similar bacterial population profiles whilst little overlap was observed for Troll and Grunehogna. This may be attributed to the rock composition at these sites or to the relative distance between the sites.**

ACKNOWLEDGEMENTS

FUNDING
South African National Antarctic Programme
LOGISTICAL SUPPORT
South African Department of Environmental Affairs

COLLECTION OF ABIOTIC DATA
Rosie Dwight
Dave Scott