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Soil Microbial Composition and Diversity in the Low Arctic Tundra of Salluit

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Abstract: The microbial community in the Arctic region is still poorly understood. In this study, we used high throughput sequencing to investigate the composition, structure, and diversity of the soil bacterial community in the Canadian low Arctic tundra in relation to different vegetation coverage.

1. Background & Summary

Soil microbiology in the polar regions is relatively understudied compared to other biomes. Intensifying climate changes and human disturbances in recent years have brought upon drastic changes to the polar landscapes. One of such disruptions is related to the rapid vegetation changes such as coverage and density[1]. Such persistent changes will bring upon disruption to the microbial productivity, functions, and composition that are dependent on the supply of plant materials[2]. Here, we investigated the structure and composition of soil microbes along three different vegetation gradients in the low Arctic tundra of Salluit.

In order to do so, DNA extracted from soil samples collected from the Canadian low Arctic tundra were subjected to 16S rRNA gene amplicon sequencing. Approximately 473–1130 amplicon sequence variants (ASVs, Average: 850 ASVs) were detected from the samples, of which 59%

sequences from all the pooled samples were classified as uncultured bacteria at the genus level. Proteobacteria, Acidobacteria, Verrucomicrobia, Chloroflexi, and Actinobacteria were the main bacterial phyla in the soil samples collected from this area (Figure 2). Soil bacteria community at phylum level also showed differences according to the environmental gradients (Figure 3).

2. Location

Sampling was carried out during the summer season in 2017 at Salluit (62.1°N 75.4°W), located at the low Arctic in Canada as a part of the Arctic Challenge for Sustainability (ArCS) project to map the biodiversity in the Arctic and to assess the changes in the region due to climate change (https://www.nipr.ac.jp/arcs/e/project/). The annual mean air temperature in Salluit is approximately –8.5 °C with a mean annual precipitation of 300 mm[3]. The site is made up of permafrost with hilly and rocky elevations. Three study sites (S1, S2, and S3) were chosen for this study (Figure 1). At each site, three transects (A, B, and C), each situated 50 m apart, were set up at three different environmental conditions with low (A: top of a hill), intermediate (B: mid-slopes), and high (C: lower slopes) vegetation coverages, respectively.

3. Methods

3.1. Soil Sampling

Twenty-five topsoil samples were collected using a sterile scoop from each transect at 6 m intervals. The samples were placed into a 5 mL sampling tube containing RNA later Stabilization Solution (Ambion, Austin, Texas) and frozen at −20°C immediately after sampling. All samples were shipped to Japan in their frozen state for further analysis. DNA was extracted from each soil sample using Fast DNA Spin Kit for Soil (MP Biomedical, Santa Ana, CA) according to the manufacturer's instruction.

3.2. 16S Amplicon Sequencing and Analysis of Amplicon Sequences

The bacterial and archaeal 16S rRNA genes were sequenced in the Illumina MiSeq sequencing platform. The V3-V4 region of the 16S rRNA gene was amplified using the primer set 341F/806R according to the Illumina 16S metagenomic sequencing library protocol and subjected to paired-end sequencing with MiSeq Reagent Kit v3 (600 – cycle) (Illumina), according to the manufacturer's directions. The resulting sequences were analyzed using QIIME2 (Ver. 2019.10) pipeline[4]. Read pairs were demultiplexed based on the unique barcode sequence and then merged. Demultiplexed sequences were quality filtered and denoised using DADA2[5]. Taxonomy was assigned to the resulting ASVs using the SILVA 132 database.

4. Data Records

All MiSeq platform 16S rRNA gene raw reads for each sample, in fastq format, were deposited to NCBI Sequence Read Archive (SRA, http://www.ncbi.nlm.nih.gov/sra/) under the accession number PRJNA541059, BioSample accession numbers SAMN12916231–SAMN12916455), run accession numbers SRR10288457–SRR10288681 and experiment accession numbers SRX7001445–SRX7001669. The deposited raw reads can be used directly for downstream bioinformatics analysis using tools such as QIIME and Mothur.

5. Technical Validation

The Illumina Sequence Viewer (SAV) was used to validate and check the quality of sequences resulting from the MiSeq run. Sequence reads from run with low cluster density, low error rate generated from the alignment with 10 % PhiX control spike, and a phred Q-score (Q30) greater than 70 % were retained for further analysis.

6. Usage Notes

Requests for permission to reuse the content (raw data) from this paper can be submitted in writing to the following email address: uchida@nipr.ac.jp.

7. Figures

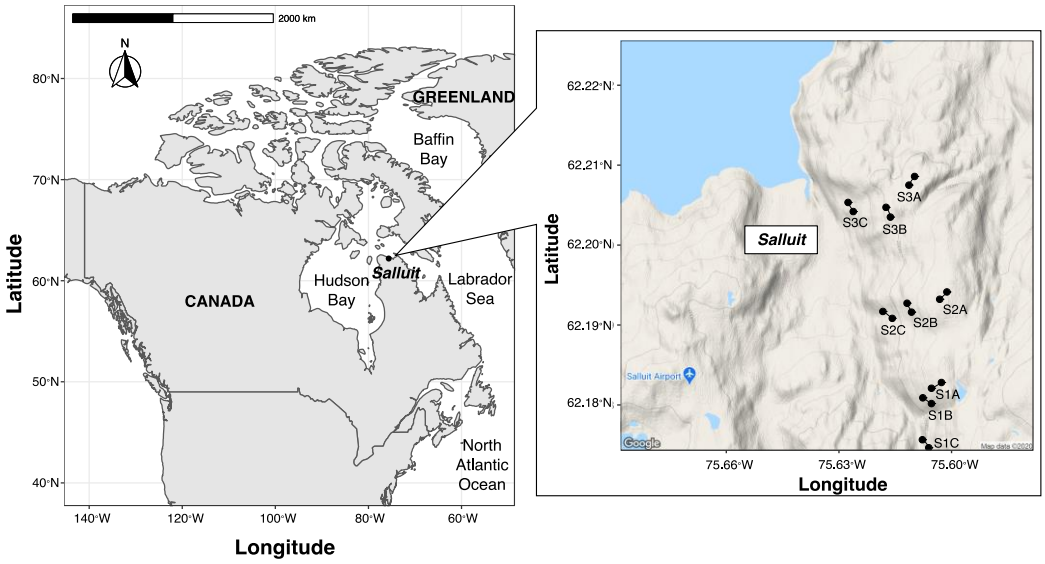

Fig. 1. Sampling sites at Salluit.

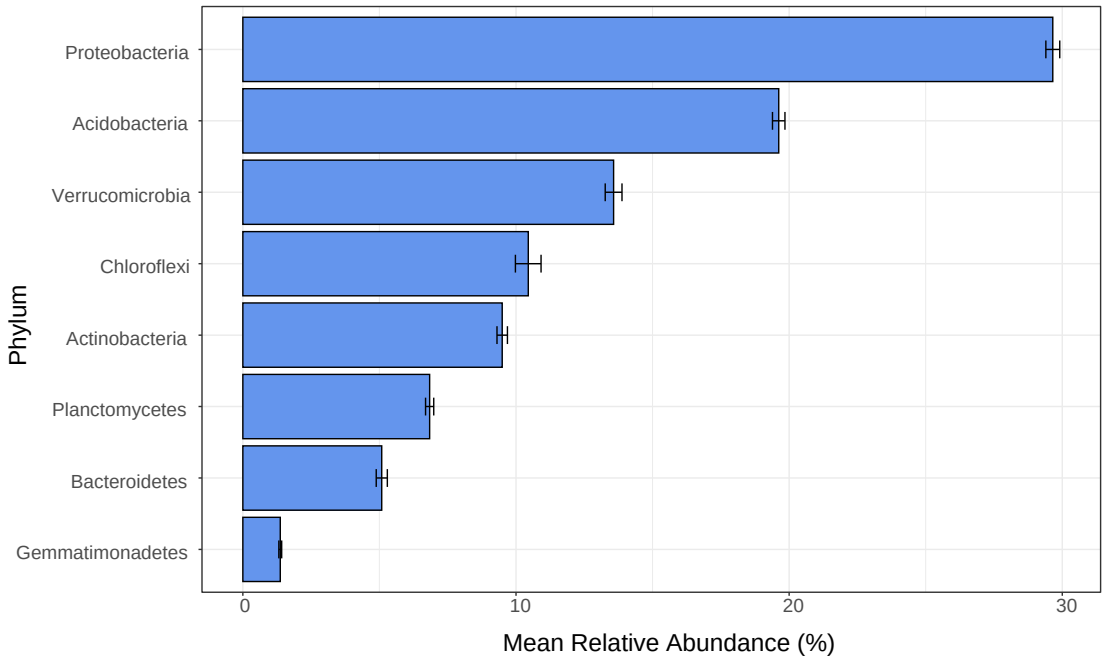

Fig. 2. The mean relative abundance of different microbial phyla from all samples collected in this study. Only phyla with relative abundance greater than 1.0 % are shown.

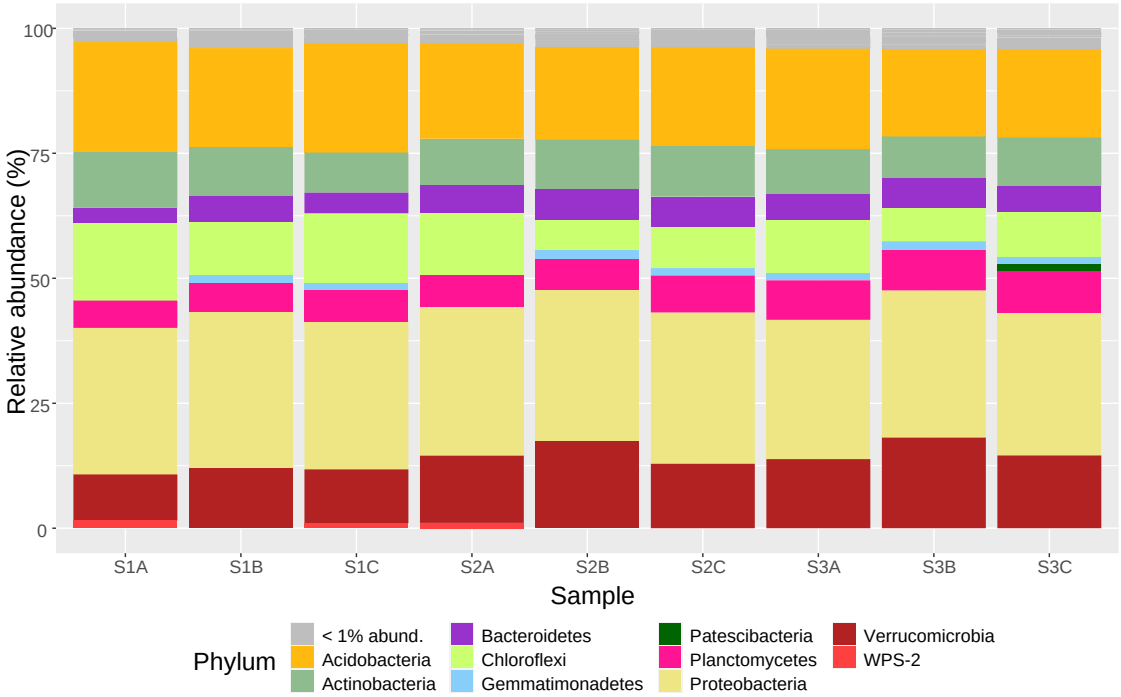

Fig. 3. Taxonomic composition of soil microbial communities, based on 16S rRNA gene sequencing, collected from three transects (S1, S2, S3) with different vegetation coverages (A: Low, B: Intermediate, C: High) at Salluit. Relative abundance was calculated based on the mean abundance of 25 samples collected from each site. Phyla with a relative abundance of less than 1.0 % are grouped as '< 1 % abund.'.

Author contributions

M. Uchida and A.S. Mori conceived and designed the study. R. Kaneko, S. Masumoto, and R. Kitagawa collected and processed samples. S-K Wong performed bioinformatics processing and drafted the manuscript. All authors were involved in the critical review and final drafting of the manuscript. All authors read and approved the final manuscript.

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Data Citation

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