Vertical Distribution of Bacterial Communities in Active Layer soil of Moist Acidic Tundra, Alaska

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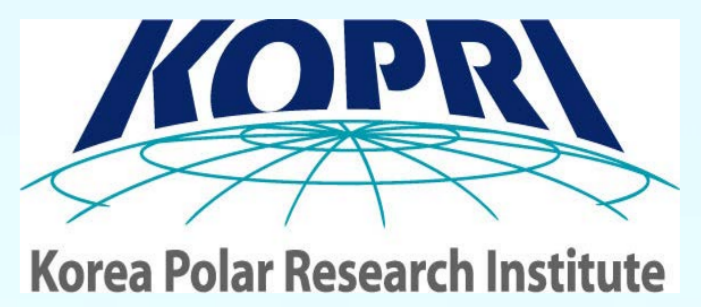
Introduction

Permafrost is defined as a subsurface layer which remains frozen for two or more years. The surface of permafrost is covered with an active layer that undergoes seasonally freezing and thawing. Increasing atmospheric temperature can influence the active layer depth, and lead to the degradation of permafrost (Johnstone et al., 2010; Nossov et al., 2013).

High latitude areas contain nearly half of the global soil carbon, and the warming effect in this area is predicted to be the greatest and most rapid than anywhere else (IPCC, 2007; Tarnocai et al., 2009).

A considerable amount of soil carbon in the Arctic area will be changed due to is vulnerability of the warming effects (Grosse et al., 2011). This process mainly occurs in the surface and active layer of the soil in the Arctic region.

Understanding of the soil microbial community structure is essential to elucidate microbial processes. However, enormous studies have mainly focused on the surface to handspan depth of soil where the biomass is highest. Microbial communities can be found in deeper soil, but it has been poorly understood.

Here, we observed the soil bacterial community structure along the soil depth in the active layer of Alaskan tundra soil, and we investigated the relationships between soil properties and bacterial community in soil.

Materials and Methods

Site description and soil core sampling
- Council, Alaska (N64°50′, W163°42′)
- 3 points (randomly selected)
- Soil cores obtained with 50 cm length using stainless steel core (5 cm diameter)

Physical and chemical properties of Soil
- Total nitrogen, total carbon, total phosphorus
- Soil pH, EC (electron conductivity)

*Amplification of 16S rRNA genes and pyrosequencing*
- The V1-V3 region of the 16S rRNA gene was amplified by PCR
- GS-FLX 454 pyrosequencer (Roche)

Analysis of pyrosequencing data
- Qiime software package

Statistical analysis using R (3.0.0) and PRIMER-E V6
- Analysis of similarity (ANOSIM), non-metric multidimensional scaling (NMDS), classification and regression tree (CART)
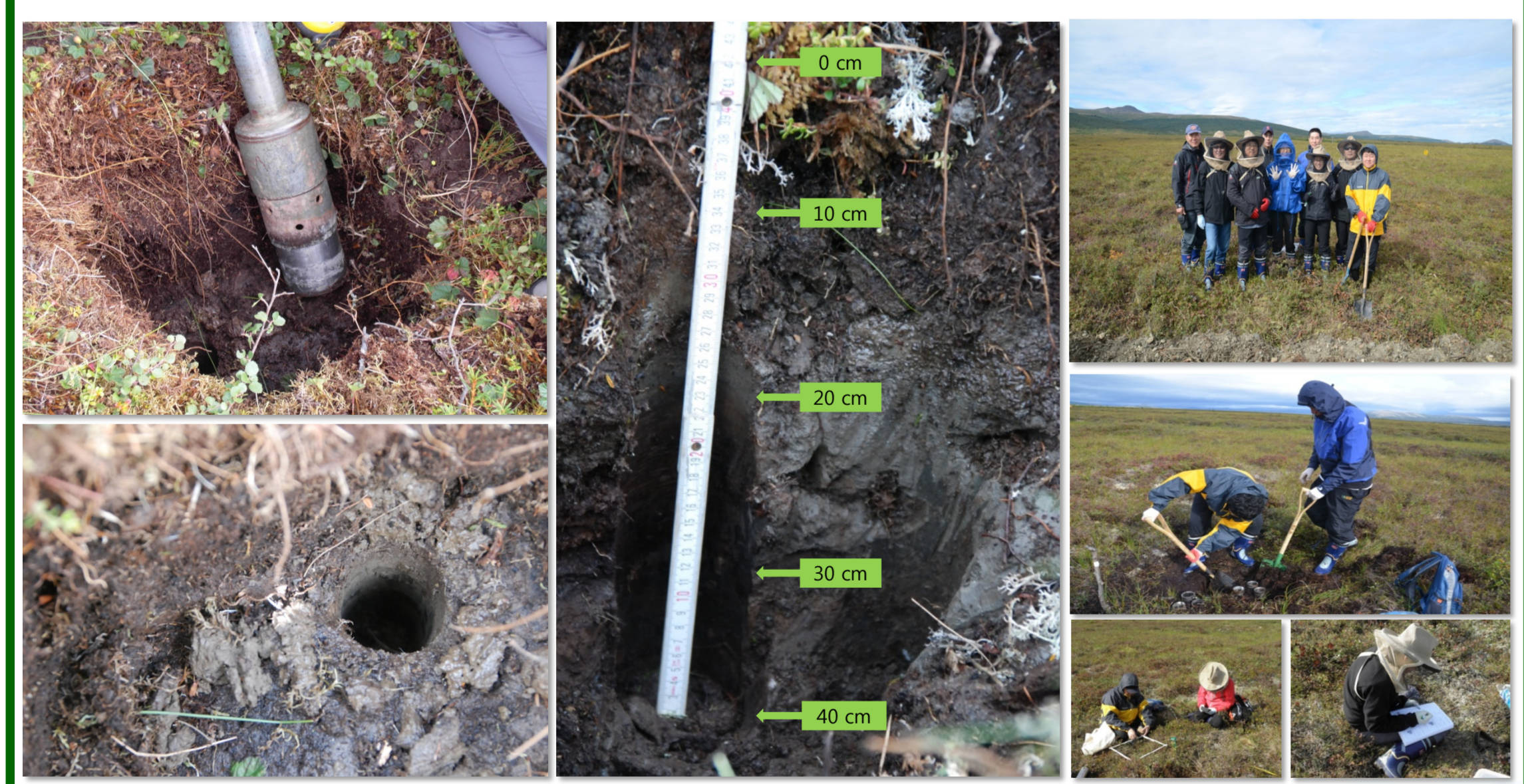
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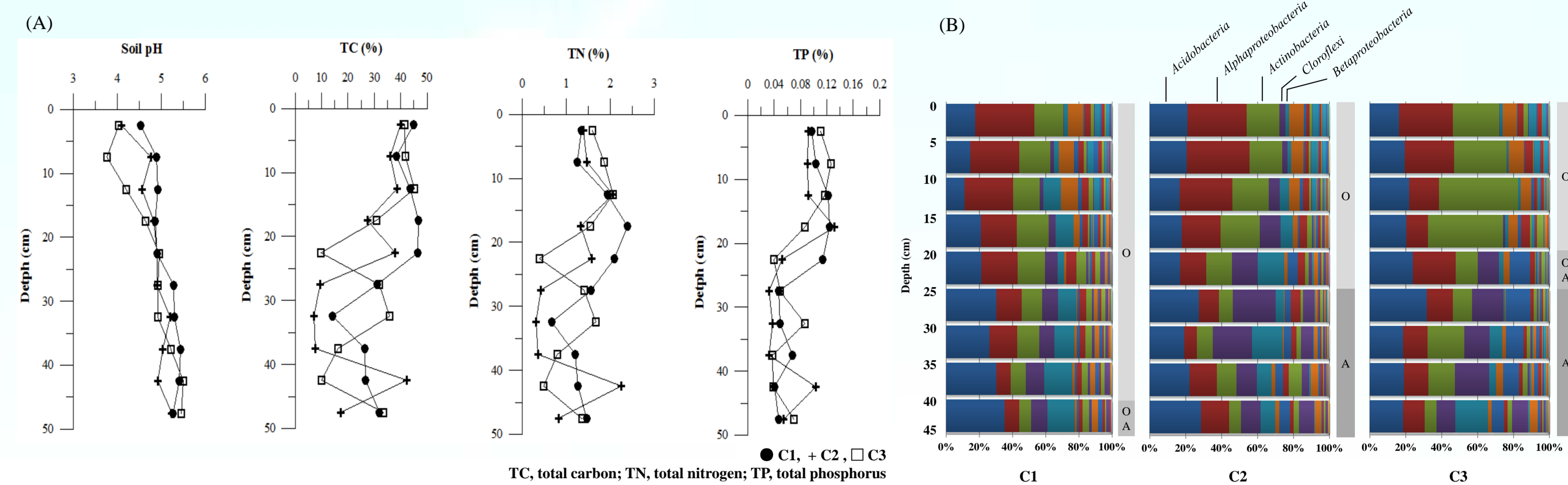
Tables and Figures

Fig. 1. Depth distribution of physical and chemicals soil properties (A) and soil bacterial community structure (B).

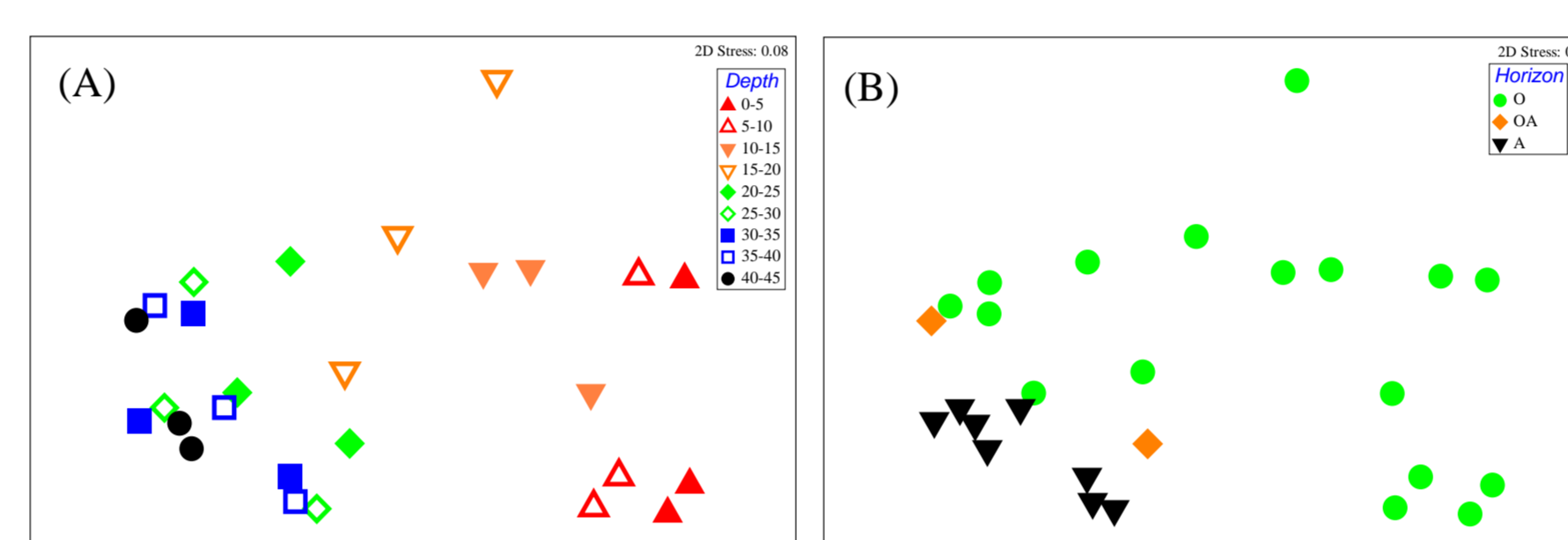TC, total carbon; TN, total nitrogen; TP, total phosphorus

Fig. 2. Nonmetric multidimensional scaling (NMDS) plots derived from Bray-Curtis similarity coefficients between soil samples, with symbols coded by depth (A) and soil profile (B).

Table 1. The physical and chemical factors of that significant correlated with bacterial communities. The Spearman's rank correlations (r) and significance (P) were determined by Mantel tests between the bacterial community structure and environmental variables.

Soil factors	All soil samples (n=27)		C1 (n=9)		C2 (n=9)		C3 (n=9)	
	r	p	r	p	r	p	r	p
Depth	0.427	0.001	0.437	0.034	0.337	0.06	0.364	0.04
C/N	0.207	0.013	0.301	0.077	0.491	0.015	-0.001	0.522
EC	0.119	0.041	0.006	0.38	0.184	0.155	0.166	0.136
pH	0.364	0.001	0.204	0.12	0.253	0.139	0.427	0.023
TC	0.089	0.095	-0.073	0.592	0.265	0.049	0.084	0.283
TN	-0.008	0.505	-0.076	0.598	0.092	0.228	0.010	0.447
TP	0.119	0.04	0.006	0.346	0.184	0.134	0.166	0.15

C/N, ratio of carbon and nitrogen; MC, moisture content; TC, total carbon; TN, total nitrogen; TP, total phosphorus; EC, electron conductivity. Underscore means $p<0.05$.
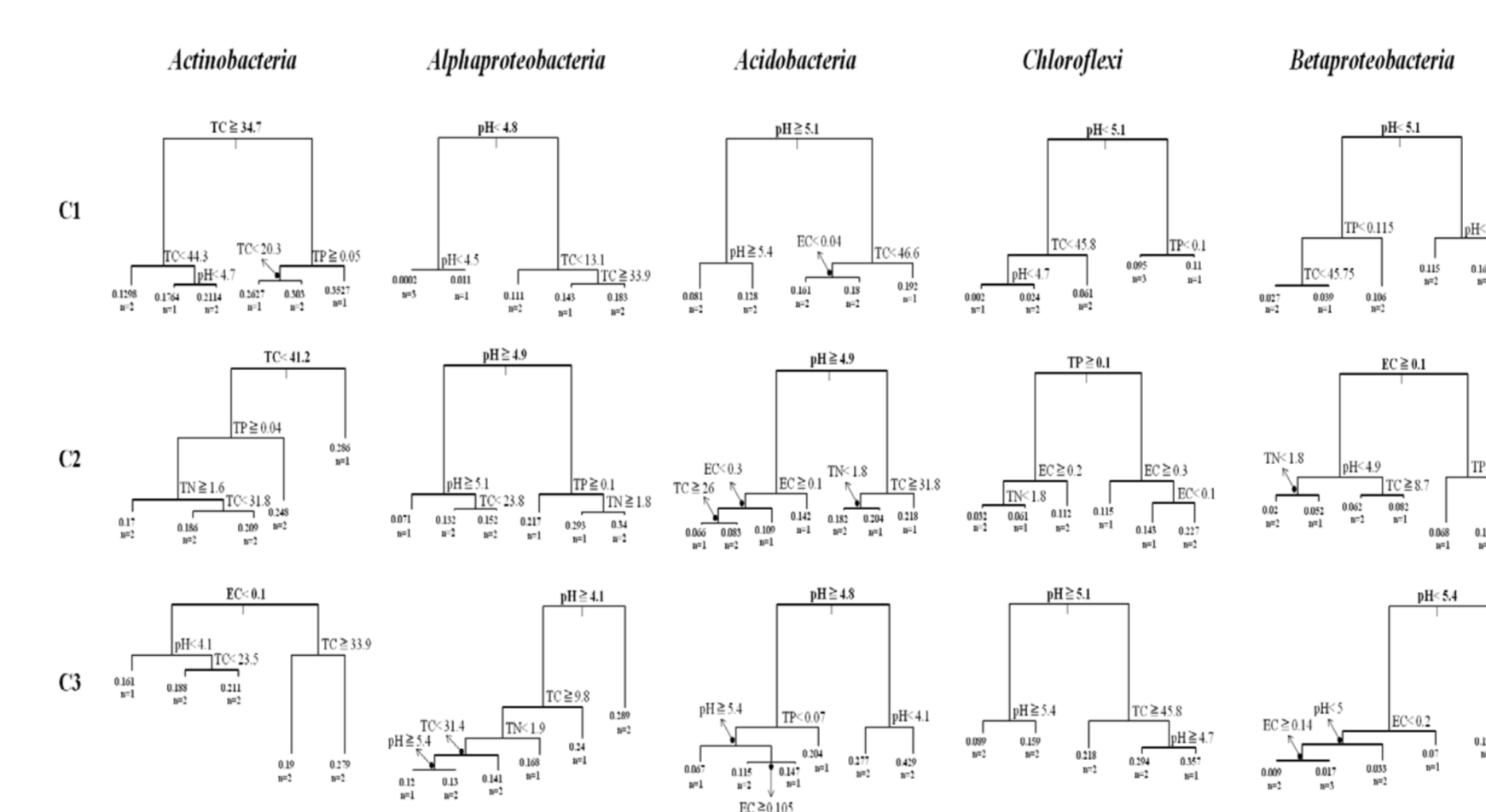

Fig. 3. Classification and regression tree (CART) analysis to describe the main properties for the dominant phyla *Actinobacteria*, *Alphaproteobacteria*, *Acidobacteria*, *Chloroflexi*, and *Betaproteobacteria* in the three core soil samples.
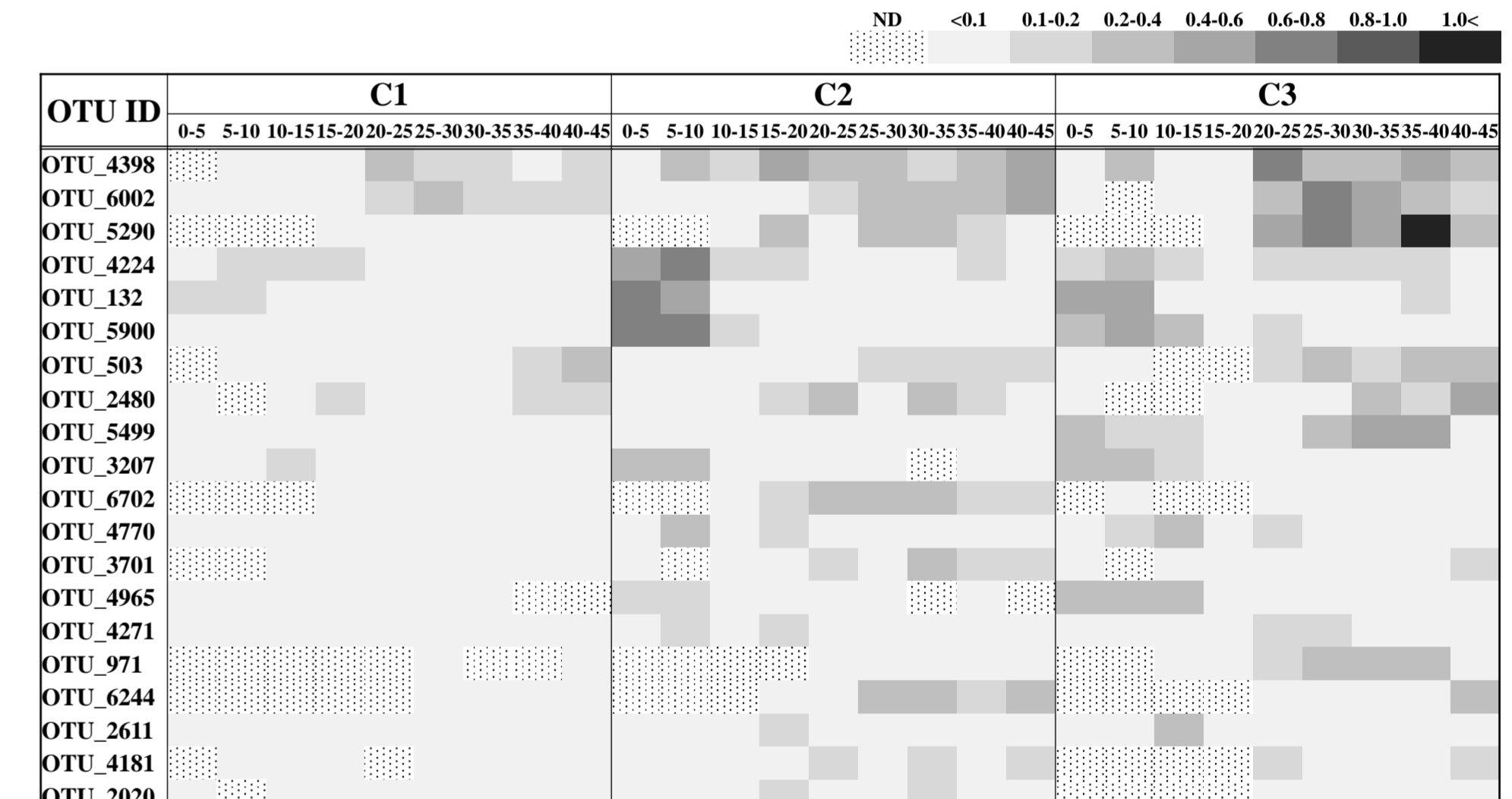

Fig. 4. Heat maps indicating differences in relative abundance of dominant OTUs.

Results and Discussion

Shift of bacterial community structure along soil depth.
- Bacterial community structure and composition changed with soil depth. Among the major groups, relative abundance of *Actinobacteria*, *Chloroflexi*, and *Betaproteobacteria* increased, whereas *Alphaproteobacteria* and *Acidobacteria* decreased along the soil depth in this study (Fig. 1). This result corresponded with many studies that observed changes in the microbial communities with soil depth.
- *Alphaproteobacteria* prefer high organic matter environments. And *Acidobacteria* dominated acidic environments. Thus, these groups may be well adapted and propagated in upper soils.
- *Actinobacteria* are known for degradation of recalcitrant organic soil matter such as high molecular weight substrates. *Chloroflexi* group were found to be are active at subzero temperature with anaerobic condition, and they can utilize geochemical substrates such as sulfide. *Betaproteobacteria* has demonstrated to be the most efficient mineral-weathering bacteria and can mineralize carbon substrates. Thus, these groups may adapt relatively well at deeper soils.
- The similarity of bacterial community was distinct between soil horizons (Fig. 2). Bacterial abundance and diversity in horizon O were relatively higher than that of horizon A in this study (p < 0.05). Generally, horizon O has a relatively higher biomass than other horizons. Among the soil cores, C1 showed a relatively high diversity compared to other core samples (data not shown). C1 might be deeper in horizon O(up to 40 cm) than other cores.

The relationships between bacterial community and soil properties.
- The three cores showed a different relationship between bacterial community and soil properties. Soil pH significantly correlated with soil bacterial communities. It might be that other soil properties such as TC, TN, TP were relatively uneven within soil depth than soil pH (Fig. 1A). Our results also showed that most of the major groups significantly correlated with soil pH (Fig. 3) compared to other soil properties. Currently, some studies showed a clear relationship between bacterial community and soil pH.

Evaluation of potential functional ecological roles of bacterial taxa
- Among the dominant OTUs, The genus *Afipia* (OTU_4224) are known to be pathogenic to humans. *Roseiarcus* (OTU_132) has the ability to grow in sugars and organic acids under micro anaerobic conditions. *Pseudolabrys* (OTU_4398) can utilize several organic acids under aerobic condition. *Aciditerrimonas* (OTU_503) were identified as an iron-reducing acidophilic bacterium. *Oryzihumus* (OTU_6002) can assimilate to various substrates. *Gallionella* (OTU_2480) is characterized by its oxidation of Fe (II). *Telmatobacter* (OTU_5499) is facultatively anaerobic and chemo-organotrophic. *Koribacter* (OTU_4770, 4965, and 2611) was shown to have candidate cellulases from glycoside hydrolase family 9.
- From the information of taxa affiliation, most of taxa revealed that they could grow above 30 °C, that is, these dominant OTUs may actively proliferate more and more, which is associated with warming effect in soil.

In conclusion, this study revealed that the relative abundance of soil bacterial community composition changes with increasing soil depth. Among the soil cores, we observed the different significant correlations between physicochemical soil properties with each core. Generally, the shift of bacterial community correlated with the soil horizon and pH with active layer depth in Arctic tundra soil.

Thank you for your attention. Any questions?