

# Bacterial Community is Associated with the Degree of Soil Organic Matter Decomposition in Moist Acidic Tundra Soil

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## BACKGROUND

The increasing temperature in Arctic tundra deepens the active layer, which is the upper layer of permafrost soil that experiences repeated thawing and freezing. The increasing of soil temperature and the deepening of active layer seem to affect soil microbial communities. Therefore, information on soil microbial communities at various soil depths is essential to understand their potential responses to climate change in the active layer soil.

## MATERIALS & METHODS

Sampling site: Council, Alaska (64° 50' N, 163° 42' W)

Soil physicochemical properties: soil pH, total carbon (TC), total nitrogen (TN)

Pyrosequencing of 16S rRNA gene: The V2-V3 region, Roche GS-FLX 454

Analysis of sequencing data: Qiime software package

Statistical analysis: R and PRIMER-E (ANOSIM, NMDS, CCA, MANTEL)

## MAIN QUESTIONS

1. How different the bacterial community structure between active layer and permafrost?
2. What is the main environmental factor associated with vertical distribution of bacteria?

## RESULTS & DISCUSSION

### Active Layer vs. Permafrost

Soil profile was classified by decomposition rate of soil organic matter. Active layer was O horizon and developed 30 cm depth, Transition layer was OA horizon and developed 30~70 cm depth, and Permafrost was A horizon and developed below 70 cm depth (O, a layer dominated by organic matter; OA, a transitional horizon which is more like the O horizon; A, a mineral horizon).

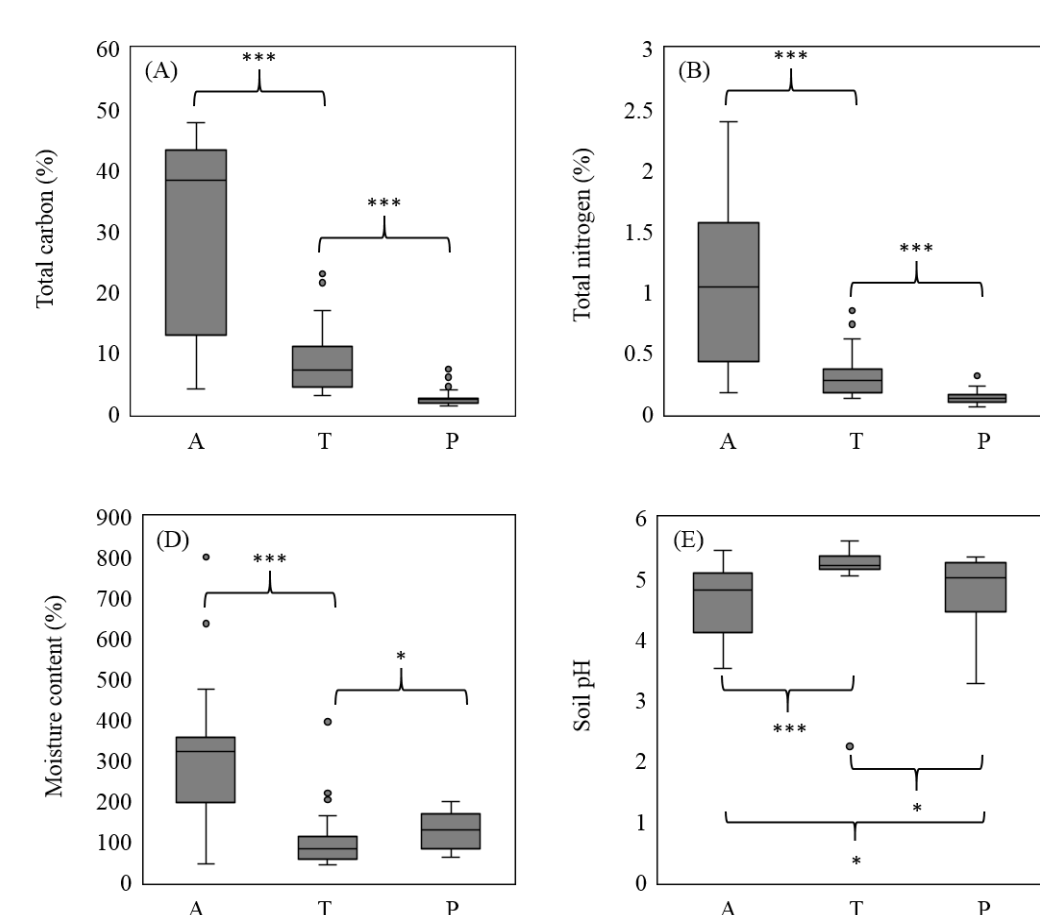


Fig. 1. Boxplots of soil parameters. X-axis scale is soil horizon of A, active layer; T, transition layer; P, permafrost. Whiskers indicate the highest and lowest values, and asterisks indicate significance (\*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ; \*\*\*,  $P < 0.001$ ).

### The vertical distribution of microbial community structure changed along soil horizons.

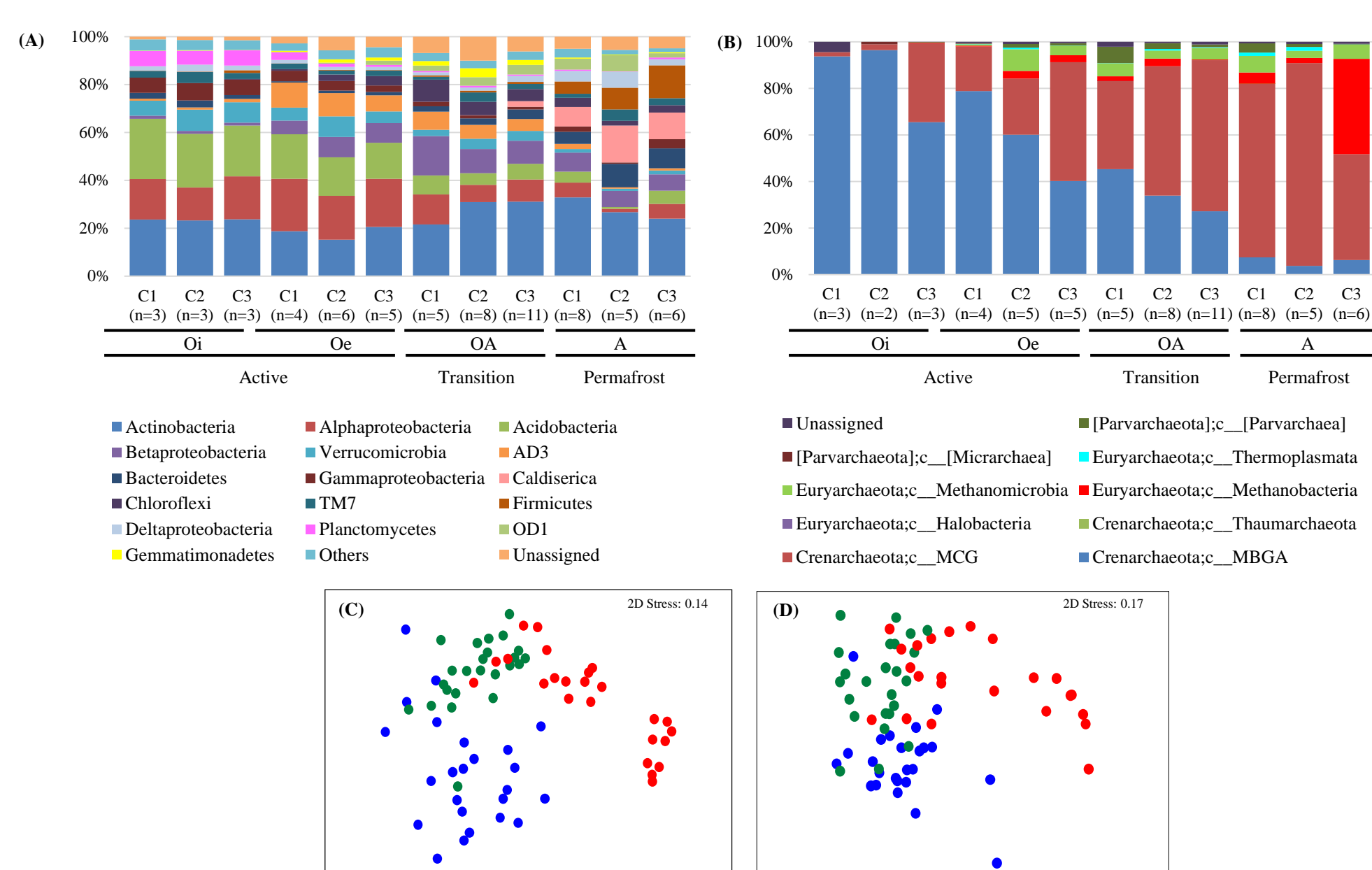


Fig. 2. Relative abundances of bacterial taxa at phylum level (A) & archaeal taxa at class level (B). Bacterial (C) & archaeal (D) community compositional structure between soil horizons as indicated by NMDS plot based on the Bray-Curtis dissimilarity. ● active layer; ● transition layer; ● permafrost.

Table 1. The correlations between soil property and microbial community along soil layers. The Pearson correlation ( $r$ ) and significance ( $p$ ) determined by Mantel tests

Domain	Soil properties	Active layer		Transition layer		Permafrost	
		$r$	$p$	$r$	$p$	$r$	$p$
Bacteria	pH	0.781	0.001	0.145	0.127	0.139	0.166
	TC	0.402	0.001	-0.0002	0.473	-0.079	0.663
	TN	0.147	0.034	0.004	0.451	-0.163	0.919
	C/N ratio	0.548	0.001	0.003	0.448	0.187	0.099
	MC	0.382	0.001	0.307	0.027	-0.027	0.624
Archaea	pH	0.490	0.001	-0.083	0.707	0.494	0.002
	TC	0.052	0.239	0.222	0.055	0.180	0.123
	TN	-0.054	0.706	0.142	0.127	0.095	0.232
	C/N ratio	0.560	0.001	-0.074	0.762	0.261	0.085
	MC	0.097	0.199	0.040	0.283	-0.060	0.717

### Within Active Layer

The bacterial community changed along soil depth in active layer.

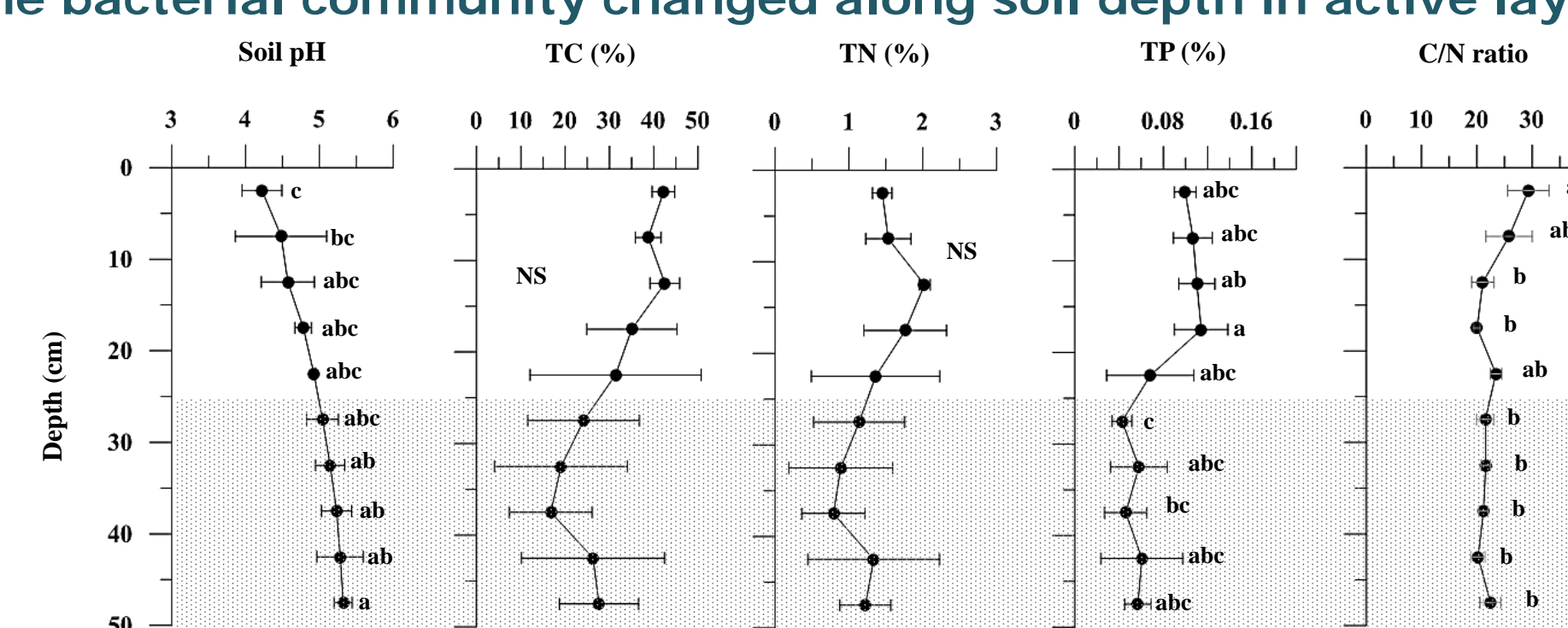


Fig. 3. Soil physical and chemical properties along soil depth. Soil horizon was separated by Oi (fibric) and Oa (sapric, shadow indicated). \* means in the same column followed by the same letters are not significantly different among depths at the  $\alpha=0.05$  level by Tukey's Honest Significant Difference. TC, total carbon content; TN, total nitrogen content; TP, total phosphorus content; C/N, a ratio of carbon and nitrogen content; NS, no significant differences among soil depths.

### The vertical distribution of microbial community structure changed along soil depth.

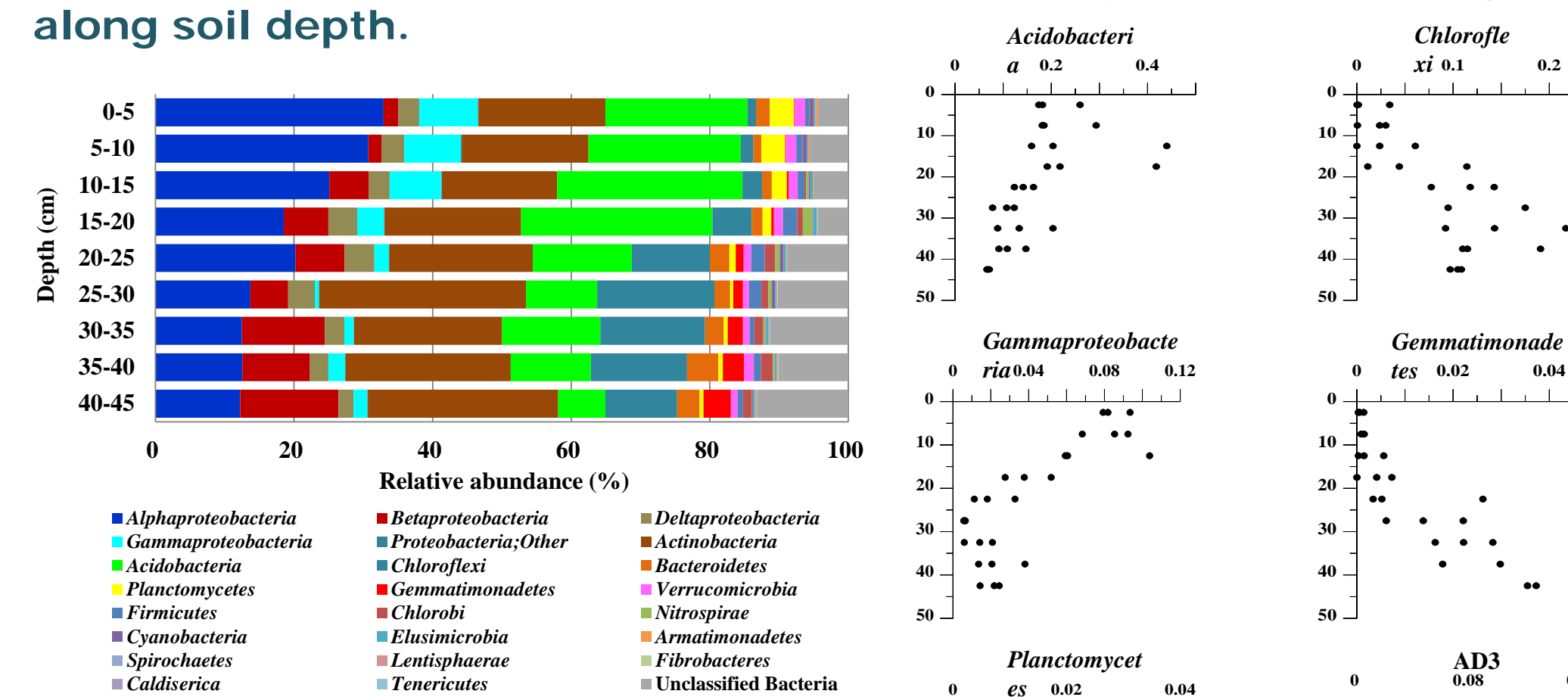


Fig. 4. Vertical distribution of bacterial community composition. Plots show depth profile of representative bacterial groups.

### The dominant microbial OTUs were different between soil layers

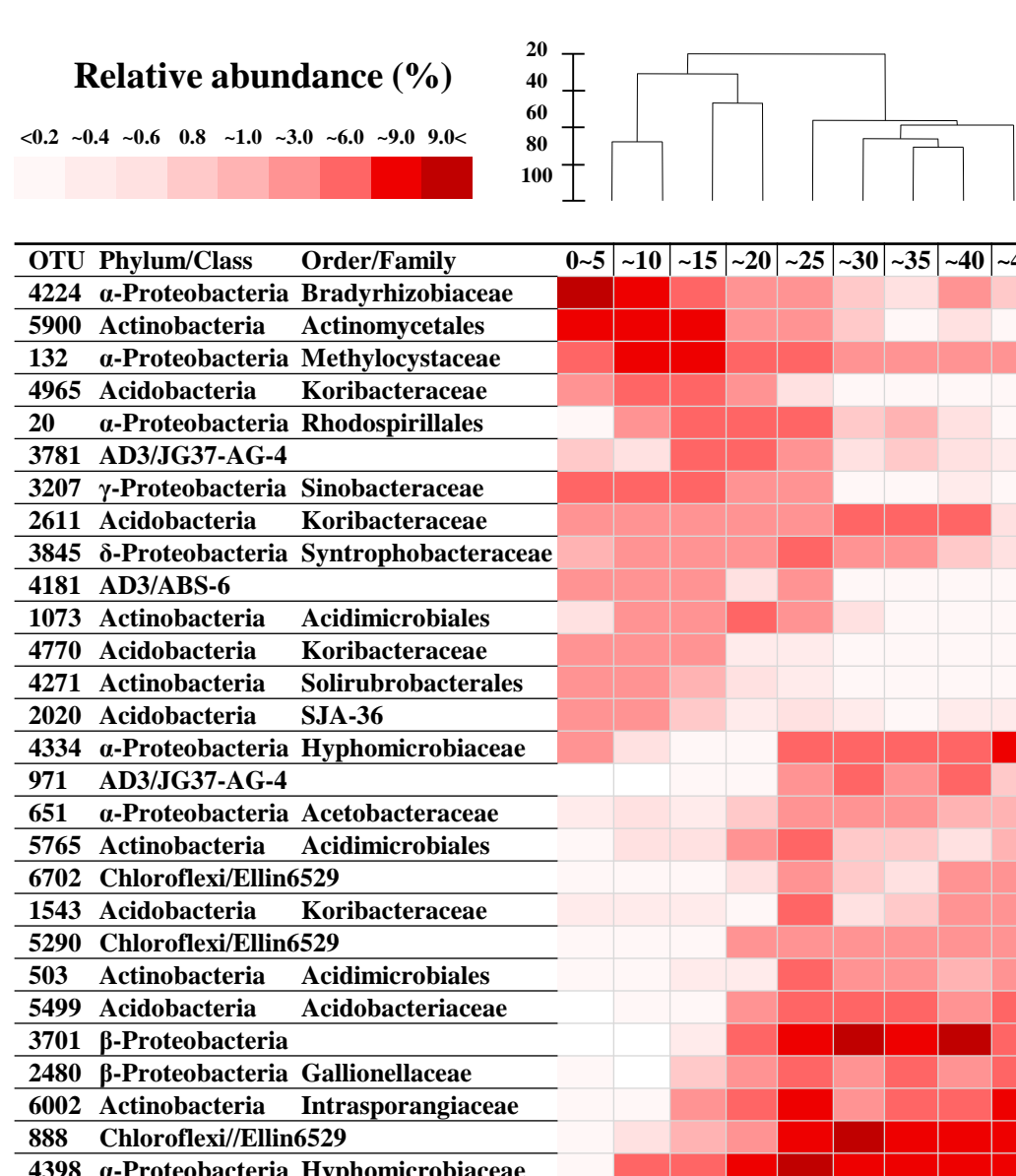


Fig. 5. Relative abundance of dominant bacterial OTUs which represented over 0.5% from total sequences. Upper dendrogram indicates the bacterial community similarity between soil depths.

Table 2. The correlation between soil property and bacterial community within soil horizon. The Pearson correlation ( $r$ ) and significance ( $p$ ) determined by Mantel tests. Significant correlation between a soil property and bacterial community structure is shown in bold (\*  $p < 0.05$ ; \*\*  $p < 0.001$ ). P values corrected using 'fdrtool' function in R.

Soil <sup>†</sup>	Soil horizon	Acidobacteria	Actinobacteria	$\alpha$ -proteobacteria	Bacteroidetes	$\beta$ -proteobacteria	Chloroflexi	$\gamma$ -Proteobacteria	AD3
Whole		<b>0.426**</b>	0.093	<b>0.595**</b>	0.061	<b>0.303**</b>	<b>0.377*</b>	<b>0.496*</b>	<b>0.166*</b>
	Depth	<b>0.224*</b>	<b>0.224*</b>	<b>0.558**</b>	-0.156	0.061	<b>0.329*</b>	<b>0.728**</b>	<b>0.219*</b>
pH	Oi	0.429	-0.016	-0.111	-0.158	-0.224	0.077	-0.061	-0.158
	Oa	<b>0.412**</b>	-0.034	<b>0.273*</b>	<b>0.265*</b>	<b>0.447**</b>	<b>0.500*</b>	<b>0.255*</b>	0.142
TC	Oi	<b>0.258*</b>	0.258	-0.023	0.018	<b>0.211*</b>	<b>0.453*</b>	0.109	0.099
	Oa	0.089	-0.067	0.035	0.015	<b>0.354*</b>	-0.162	-0.183	0.111
TN	Whole	<b>0.210*</b>	-0.054	<b>0.226**</b>	0.072	-0.001	0.056	<b>0.181*</b>	0.104
	Oi	<b>0.300*</b>	<b>0.301*</b>	0.181	0.052	<b>0.211*</b>	-0.001	<b>0.225*</b>	0.153
TP	Oa	0.034	0.058	-0.105	-0.027	-0.112	-0.157	-0.109	-0.091
	Whole	<b>0.187*</b>	-0.113	0.047	<b>0.102*</b>	-0.054	-0.057	0.028	0.051
C/N	Oi	0.192	0.192	-0.002	0.010	-0.080	-0.092	0.043	0.089
	Oa	0.025	0.036	-0.100	-0.068	-0.118	-0.178	-0.102	-0.130
EC	Whole	<b>0.391**</b>	0.093	<b>0.263**</b>	<b>0.098*</b>	<b>0.098*</b>	<b>0.217*</b>	<b>0.303*</b>	<b>0.156*</b>
	Oi	0.192	0.192	-0.002	0.005	0.061	0.110	<b>0.448*</b>	0.089
AD3	Oa	0.075	-0.093	-0.189	0.047	-0.054	-0.247	-0.255	-0.148
	Whole	-0.132	-0.009	<b>0.243*</b>	-0.149	0.057	<b>0.305*</b>	0.141	-0.008
C/N	Oi	-0.233	-0.233	0.132	-0.235	-0.085	0.100	-0.056	-0.127
	Oa	-0.094	-0.162	0.181	-0.274	0.033	0.050	0.328	-0.239
EC	Whole	-0.150	-0.117	0.050	0.110	0.026	-0.095	-0.033	-0.114
	Oi	-0.216	-0.216	0.012	-0.084	-0.041	-0.197	-0.123	-0.205
AD3	Oa	0.043	-0.111	-0.144	<b>0.722*</b>	0.067	-0.162	-0.214	-0.030

<sup>†</sup> TC, total carbon content; TN, total nitrogen content; TP, total phosphorus content; C/N, a ratio of carbon and nitrogen content; EC, electron conductivity.

## CONCLUSION

- The bacterial community structures were significantly different along soil layers. Generally, bacterial communities were closely related with various soil properties in active layer. However, there were no relations with observed soil properties in permafrost.
- Unlike bacteria, archaeal communities showed correlations with a few soil properties. Perhaps, archaeal groups related with other soil properties which are not directly measured in this study such as O<sub>2</sub> concentration.
- The contribution to nutrient cycling of microbial communities was observed differently between active layer and permafrost. Microbes in active layer are participating in carbon and nitrogen cycling. However, microbes in permafrost are remarkably participating in carbon cycling which contribute to positive feedback in global warming.
- Different microbial communities have the different metabolic functions between active layer and permafrost. This study may help describing future microbial community structure related with further thawing permafrost.
- The bacterial communities of the upper Oi horizon were distinct from those in the lower Oa in active layer.
- A significant correlation was found between bacterial communities and soil pH as well as TP content.
- A more detailed consideration of a diverse set of soil environmental parameters is required in order to better understand the relationship between microbial community and soil properties in future studies.

## ACKNOWLEDGEMENTS

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