

Bacterial Community Shift in Depth Profiles of Permafrost Soil in Alaska

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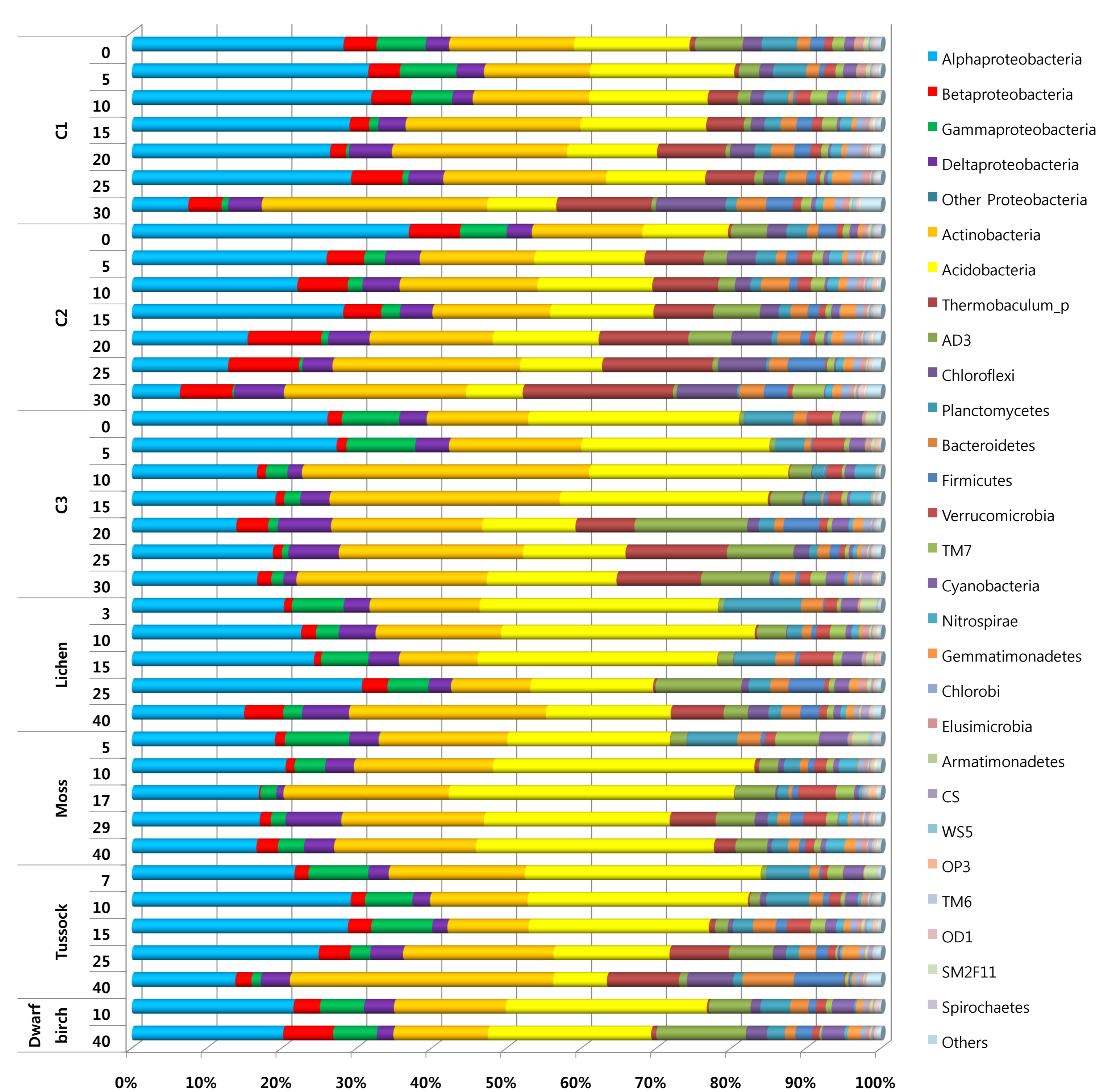


Despite the potential contribution of thawing permafrost soil to the global climate change, the research of the microbial diversity has been scarce. In this study, we investigate the bacterial community in active layer soil from the Alaskan high Arctic based on 16S rRNA genes. These bacterial habitats contained relatively low number of OTUs ranged from 397 to 1728 compared to the temperate habitats. Although the bacterial diversity was relatively low, 20 known divisions and 27 unknown divisions were detected. The phyla of Proteobacteria (35.2%), Actinobacteria (20.9%) and Acidobacteria (16.5%) were predominant. Community shift was observed significantly along the soil depth profiles, which certain increase or decrease of relative abundance was detected in some phyla. The comparison between communities based on PCoA indicated that the bacterial composition was separated at 15 cm depth. This suggests that certain environmental parameters drive the formation of bacterial composition in this habitat. This study provides new insight regarding the bacterial communities in the Alaskan high Arctic permafrost.

Conclusion

1. Although relatively low microbial diversity in this habitat was observed, unexpected diverse microbes and some indigenous bacterial division such as Thermobaculum were observed.
2. Bacterial community shift was recognized along the soil depth profiles in all sites based on the analysis of Bacterial communities and community clustering and different bacterial community patterns below 30 cm were notable for further study.
3. The study presented here may extend new perspective for the research regarding the correlation between bacterial communities and environmental factors in the high Arctic permafrost soil of Alaska.

Bacterial communities

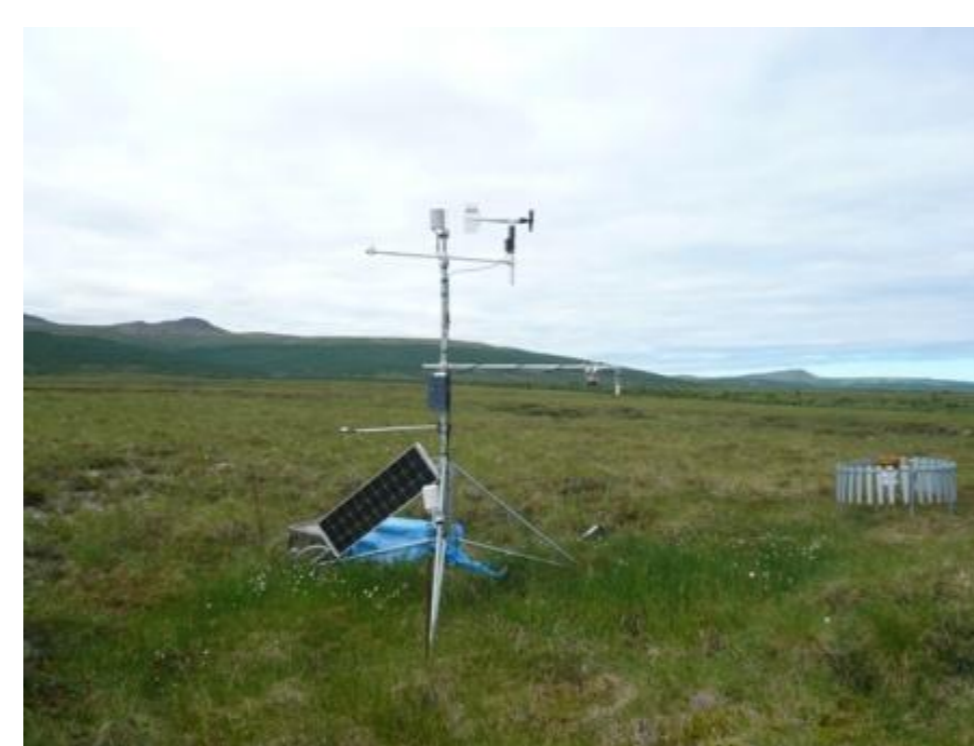
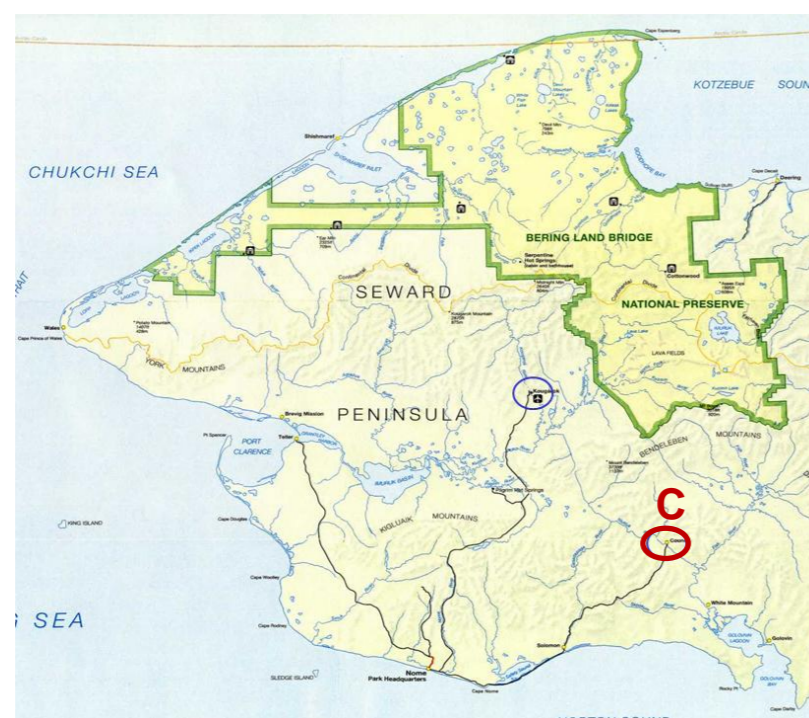
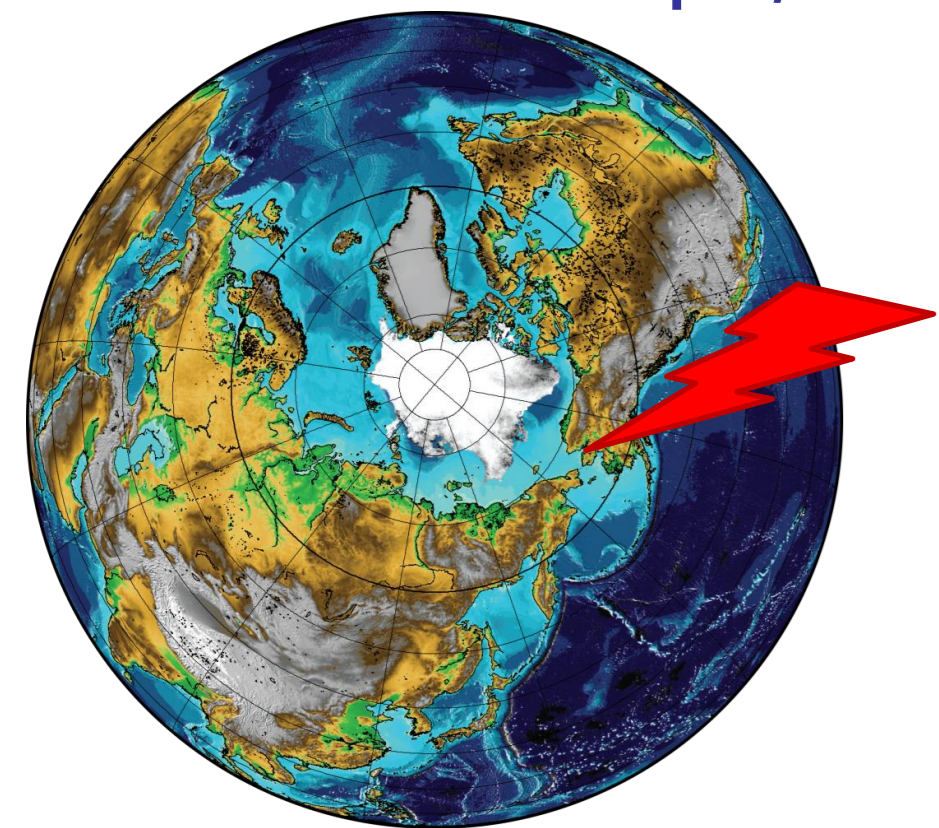


Total 47 divisions were recovered including 20 well-known phyla and 27 candidate phyla, which only have been reported from diverse environments. Well-known phyla were dominated through the soil depth profiles, while candidate phyla were more comprised in deeper layers. Community shifts were observed significantly along the soil depth profiles in all study sites. The relative abundance of certain divisions was changed. Alphaproteobacteria and Acidobacteria were decreased from surface to deeper layer, whereas Thermobaculum were increased or appeared in deeper layer. Except these significant change of number, decreased divisions along depth profiles were Planctomycetes, Verrucomicrobia, Cyanobacteria, Armatimonadetes and TM6, whereas increased divisions were TM7, Nitrospirae, Gemmatimonadetes, Chlorobi, CS, OD1 and SM2F11.

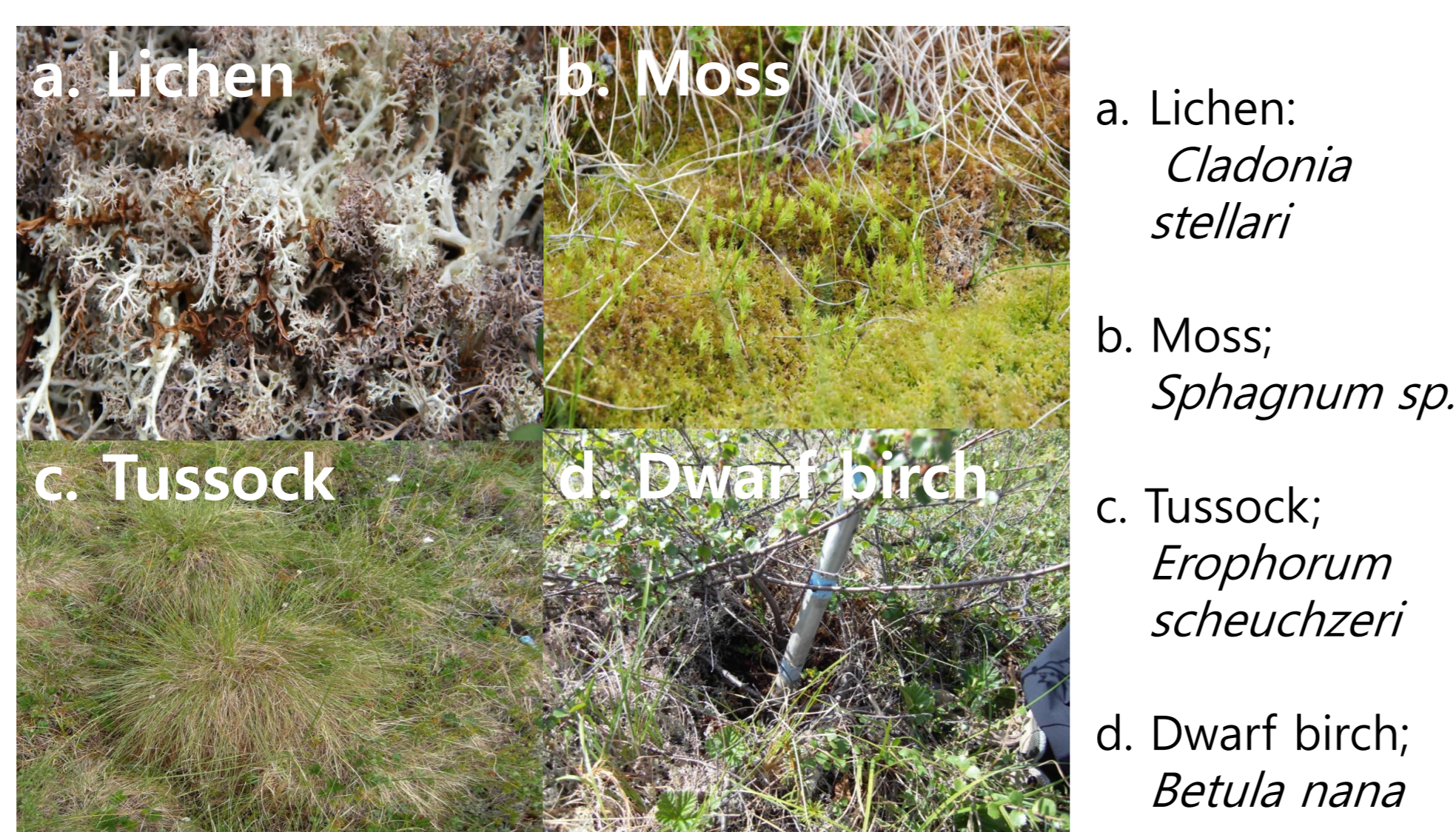
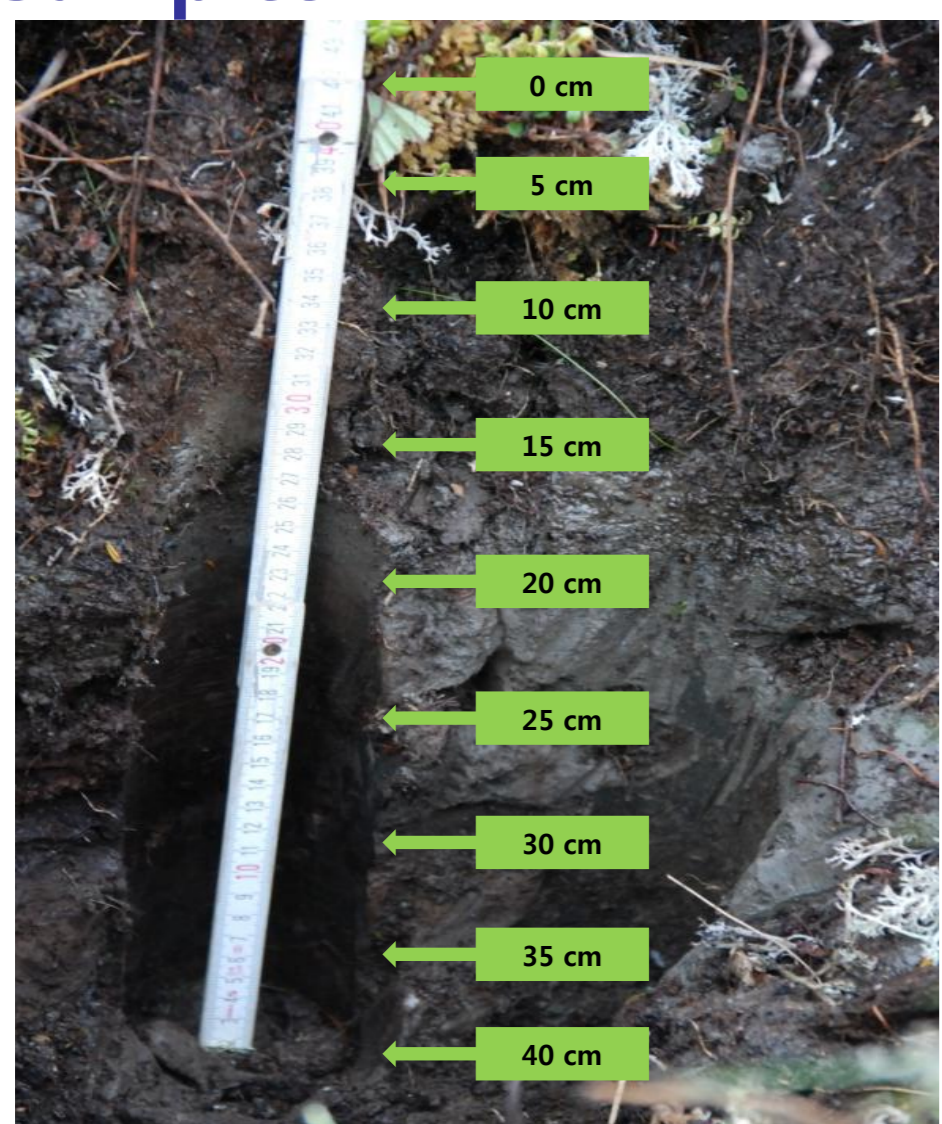
Field Description & Samples

Council, Alaska

64° 50' 60" N, 163° 42' 32" W, 50 m asl
North wind or Northwest, 2-6 ms⁻¹ (max. 12 ms⁻¹)
Air temp, -30 - 20°C; soil temp, -15 - 10 °C
Maximum snow depth; 70 cm in May and November

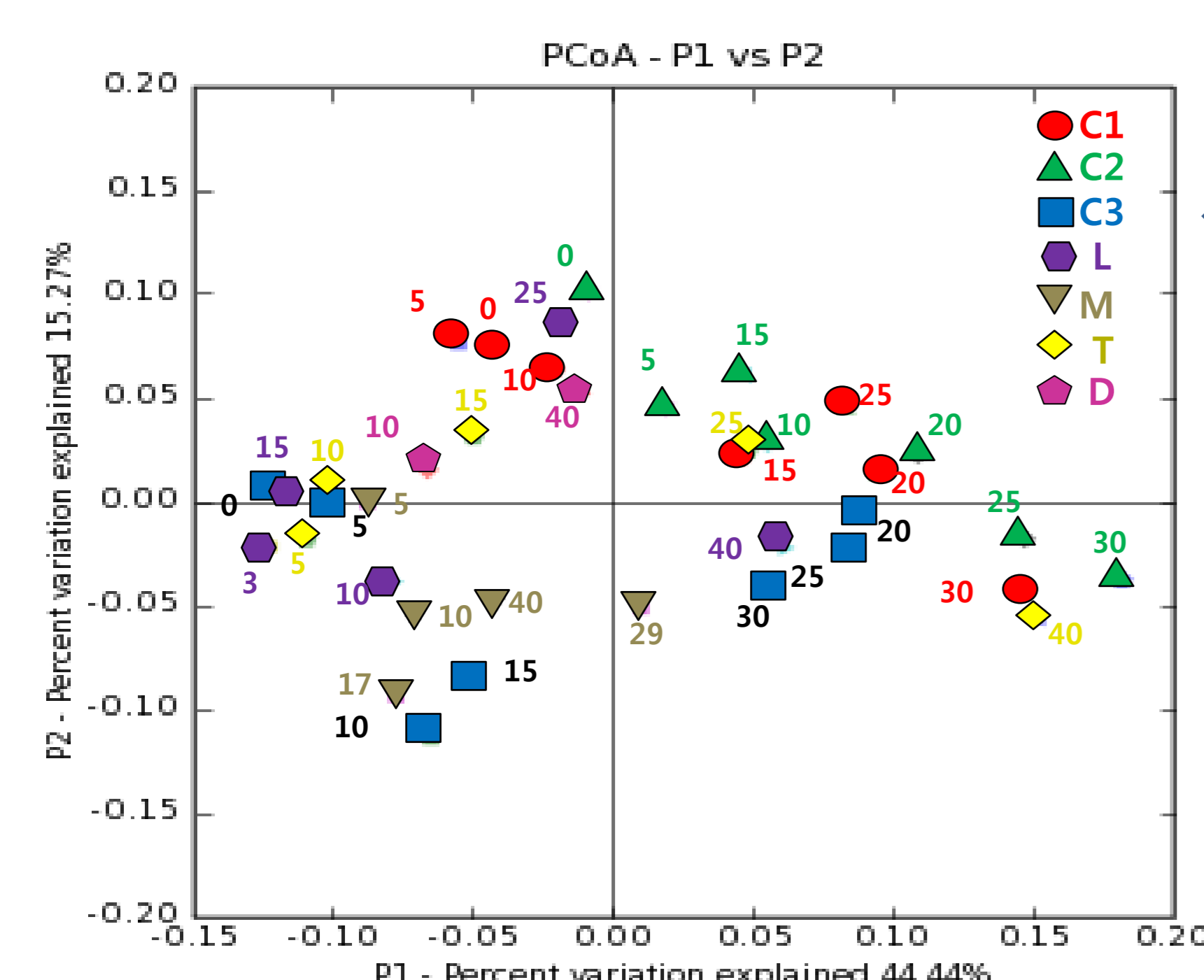


Samples



Soil depth (cm)	Soil profiles		C1	C2	C3	Lichen	Moss	Tussock	Dwarf birch
	Photo	Character color							
Surface			C1-0	C2-0	C3-0				
5 cm		undecomposed litter layer, yellow brown	C1-5	C2-5	C3-5	L-3	M-5	T-7	
10 cm			C1-10	C2-10	C3-10	L-10	M-10	T-10	D-10
15 cm		decomposed layer, reddish brown	C1-15	C2-15	C3-15	L-15	M-17	T-15	
20 cm			C1-20	C2-20	C3-20				
25 cm			C1-25	C2-25	C3-25	L-25	M-29	T-25	
30 cm		soil with ice, grey color	C1-30	C2-30	C3-30				
40 cm						L-40	M-40	T-40	D-40

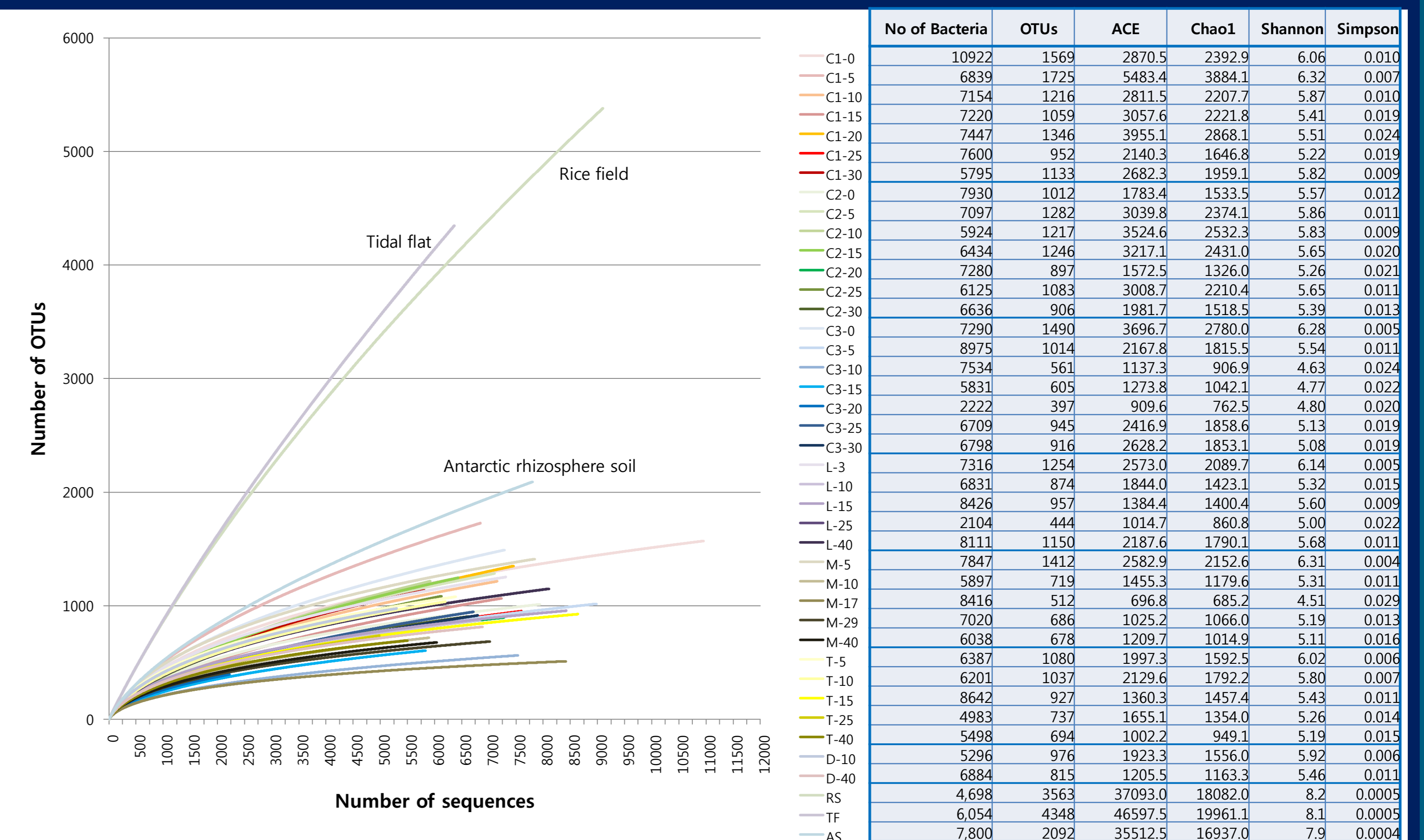
Community-Community clustering



Using Fast UniFrac analysis, community shifts were shown along the depth profiles in each site, which were coincided results with the bacterial community profiles. Upper layers and lower layers were divided by P1 except some samples, while C1, C2, and Dwarf birch were clustered together by PC2.

Based on 3% cutoff values, relatively lower diversity has been detected with less than 2000 OTUs comparing with other habitats such as rice field soil, tidal flat and Antarctic rhizosphere soil. Number of OTUs ranged from 397 to 1728. C1-5 has the highest diversity, whereas M-17 the lowest diversity.

Diversity comparison



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