

MICROBIAL DIVERSITY OF THE ACTIVE LAYER SOIL FROM THE CANADIAN HIGH ARCTIC



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I am open to all Possibilities!

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OBJECTIVE

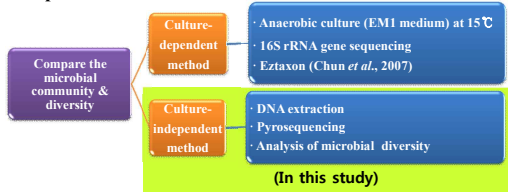
Microbial diversity in Arctic permafrost-affected soils remain poorly understood (Wagner, 2008). In this study, bacterial and archaeal diversity in an active layer from the Canadian high Arctic soil was analyzed by using a high resolution pyrosequencing method.

CONCLUSIONS

- The soil in Resolute of Canada is alkaline.
- Methane producing and consuming may occur in the active layer soil of Resolute, Canada.
- Our results may provide an base value for comparing the variation of microbial community and diversity with climate changes.

MATERIALS & METHODS

■ Pipe line

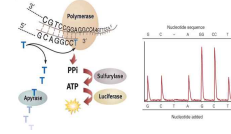


■ Sampling & DNA extraction



- Study area is located in Resolute, Canada (N, 74° 41' ; W, 94° 54')
- Genomic DNA was extracted using the UltraClean Soil DNA kit (MoBio)

■ Pyrosequencing



■ Primer sets

- Bacteria**
27F (GAG TTT GAT CMT GGC TCA G)
518R (WTT ACC GCG GCT GCT GG)
- Archaea**
21F (TCC GGT TGA TCC YGC CGG)
516R (GGT DTT ACC GCG GCK GCT G)

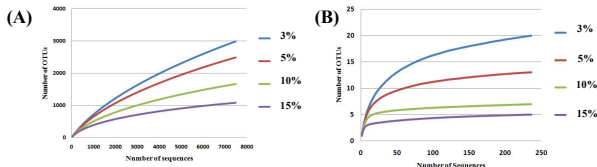
■ Bioinformatics analysis

- Microbial diversity: OTUs using the CD-HIT program
- Species richness/evenness: Chao1, ACE, Shannoneven and Simpson even using MOTHUR program

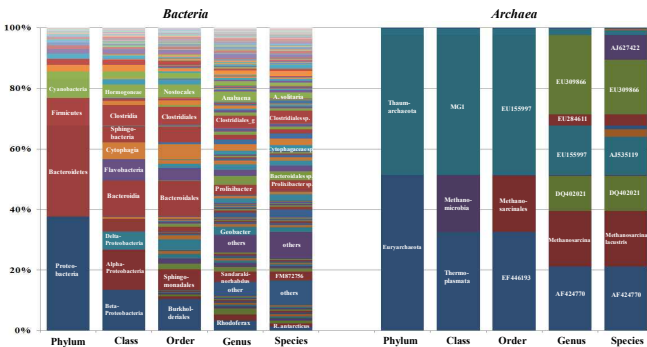
FIGURES & TABLES

▼ Table 1. Summary of bacterial and archaeal sequences including the number of total and target reads, estimated number of OTUs, richness by Chao1 and ACE and evenness by Shannon Simpson indices using MOTHUR program by <math>< 3\%</math> cutoff value.

	No. of total reads	No. of target reads	No. of OTUs	Chao1	ACE	Shannoneven	Simpson even
Bacteria	8,393	7,796	2,547	6,836	10,642	0.92	0.23
Archaea	1,111	245	14	25	23	0.79	0.40



▲ Fig. 1. Rarefaction curve for (A) *Bacteria*; (B) *Archaea*. Rarefaction is shown for OTUs that were clustered at cutoff 3% (species), 5% (genus), 10% (family) and 15% (order) using furthest neighbor method.



▲ Fig. 2. Relative abundances of *Bacteria* and *Archaea* were analyzed.

▼ Table 2. Highly abundant reads from the microbial diversity.

Domain	Division	The closest taxa	No. of reads	
Bacteria	Firmicutes	Clostridiales sp.	271	
	Bacteroidetes	Prolixibacter sp.	231	
	Bacteroidetes	Bacteroidales sp.	192	
	Alphaproteobacteria	FM1872756	189	
	Bacteroidetes	Cytophagaceae sp.	136	
	Cyanobacteria	Anabaena solitaria	133	
	Bacteroidetes	AB240270	130	
	Bacteroidetes	Flavobacteriaceae sp.	117	
	Bacteroidetes	Cytophages sp.	105	
	Bacteroidetes	Geobacter sp.	101	
	Bacteroidetes	Flavobacterium sp.	101	
	Bacteroidetes	Sphingobacteriales sp.	95	
	Betaproteobacteria	Rhodiferax antarcticus	87	
	Bacteroidetes	DQ833502	78	
	Betaproteobacteria	4P001105	72	
	Archaea	Euryarchaeota	AF424770	52
		Euryarchaeota	Methanosarcina lacustris	45
Thaumarchaeota		EU309866	44	
Thaumarchaeota		AJ535119	31	
Euryarchaeota		DQ402021	28	
Thaumarchaeota	AJ627422	20		

RESULTS & DISCUSSION

- Rarefaction curves were not saturated (Fig. 1). However, in the *Archaea*, the curves were gentle than *Bacteria* (Fig. 1). The diversity index indicated that the bacterial diversity is higher than that of *Archaea*.
- The abundance and diversity of *Bacteria* were much higher than those of *Archaea*. The low abundance and diversity of *Archaea* may reflect unsuitable for specific archaeal primer sequences.
- Major phyla of *Bacteria* were *Proteobacteria* (37.8%), *Bacteroidetes* (30.1%), *Firmicutes* (9.1%) and *Cyanobacteria* (6.4%).
- However, the phyla of *Acidobacteria* (1.6%) and *Actinobacteria* (2.1%), which were dominant group in soils were minor in this study. The pH of the soil in Resolute (Canada) was 7.5 (Anaka et al., 2008). So, the soil pH may impact on the *Acidobacteria*.
- Dominant species contained several cultivable bacterial cells: *Flavobacterium* sp. (*Bacteroidetes*), *Anabaena solitaria* (*Cyanobacteria*) and *Rhodiferax antarcticus* (β -*Proteobacteria*) (Table 2). Generally they were occurred in permafrost environments (Gilichinsky, 2008).
- Among the bacterial species, methane oxidizing *Proteobacteria* belong to *Methylococcaceae* (0.9%), *Methylocystaceae* (0.03%) and *Beijerinckiaceae* (0.01%) (Bowman 1999; Dedysh et al. 2002, 2004) were detected.
- Archaea* contained two major phyla: *Euryarchaeota* (51.4%) and *Thaumarchaeota* (46.1%) (Fig. 2). *Thaumarchaeota* which is a newly-proposed phylum have been supposed to play important roles in biogeochemical cycles (Muller et al., 2010).
- The most dominants of *Archaea* was uncultured (Table 2). Just one cultivable species, *M. laticus* which is a methanogen, was detected. Methane producing *Archaea*, such as *M. laticus* and *Methanosphaerula* sp., were detected in the active layer. It means that the active layer may be an anaerobic condition and they may be potentially sources of atmospheric methane (Cadillo-Quiroz et al., 2008).
- Methane producing and consuming may occur in the active layer soil of Resolute, Canada.

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