

Microbial diversity of active layer soil from the Canadian high Arctic

Yoo Kyung Lee¹, Ok-Sun Kim¹, Hyemin Kim^{1,2}, Soon Gyu Hong¹, Jongsik Chun², and Bang Yong Lee³, ¹Division of Life Sciences, Korea Polar Research Institute (yklee@kopri.re.kr), ²School of Biological Sciences, Seoul National University, ³ Division of Polar Climate Research, Korea Polar Research Institute

Active layer is the surface layer of permafrost, which is an extraterrestrial analogue. The repeats of thawing and freezing make active layer an extreme environment for microorganisms. The bacterial and archaeal diversity in an active layer soil from the Canadian high Arctic was analyzed by using a high resolution pyrosequencing analysis. Since last few years, DNA sequencing-based microbial community studies have been widely propagated by the invention of pyrosequencing which produce millions of sequences in a single run (Ronaghi, 2001). This can exclude the time-consuming step such as constructing clone libraries and generates millions of sequencing in a single run. Therefore, tremendous sequence information in a sample can make be visualized the deep insights of microbial population.

Total 7,796 bacterial reads for 40 phyla and 245 archaeal reads for 4 phyla were collected, reflecting the high diversity of bacteria. Much higher diversity in bacteria than in archaea was confirmed from the statistical analysis. Among these 40 phyla, 22 phyla were assigned as well-known phyla such as *Proteobacteria* and *Bacteroidetes*, whereas 18 phyla assigned as candidate phyla such as TM7, OD1. *Proteobacteria* (most were from the class *Alphaproteobacteria* and *Betaproteobacteria*) and *Bacteroidetes* encompassed the majority of sequences with 67.8%. This is shown a good agreement of soil microbial communities in four different types of soils from Brazil, Florida, Illinois and Canada (Roesch et al., 2007), despite of targeting different region of 16S rRNA gene with this study. A good agreement was found that phylum *Proteobacteria* was the most dominant with 27.6 – 58.2% in all environments. *Bacteroidetes* was detected with 30.0% in case of Canadian permafrost, however, around 10% in other environments. The majority of the sequences from rhizosphere soil on Antarctica were affiliated to the *Actinobacteria* (28.7%) that were typically dominated in soil environment. In case of Archaea, relatively simple community composition was recognized. *Euryarchaeota* (51.4%) and *Thaumarchaeota* (46.1%) were major constituents of the archaeal community.

The relatives of major species in this study were also isolated from various environments, mainly from freshwater lakes and also from alpine or polar habitats. Taken together, our results indicated that analysis of 16S rRNA gene derived from bar-coded pyrosequencing reads provide the necessary resolution and discrimination to be useful as a next generation platform for microbial diversity study in the Arctic active layer soil.

References

- Ronaghi, M. (2001) Pyrosequencing sheds light on DNA sequencing. *Genome Res* 11: 3-11.
- Roesch, L.F.W., Fulthorpe, R.R., Riva, A., Casella, G., Hadwin, A.K.M., Kent, A.D. et al. (2007) Pyrosequencing enumerates and contrasts soil microbial diversity. *The ISME Journal* 1: 283-290.