

Analysis of bacterial microbiota associated with *Umbilicaria* spp. lichens in polar regions

Zichen He¹, Martin W. Hahn², Takeshi Naganuma¹

¹ Graduate School of Integrated Sciences for Life, Hiroshima University, 739-8528 Japan

² Research Department for Limnology, University of Innsbruck, Mondsee, Austria

Lichens are very common and widely distributed organisms. Recently, the scholars are interesting in the symbiont and bacteria have also attracted attention as the third component. This study aimed to analyze the bacterial diversity and these physiological or ecological roles in the lichen-symbionts by culture-independent phylogenetic analysis, id est, phylotype analysis.

Total 27 lichen samples were collected from polar regions. 18 samples from Antarctica (Syowa station), 9 samples from Arctica. In Arctica samples, 2 from Nunavut (Canada), 2 from Gamvik (Norway), and 5 from Enotekio & Kittila (Finland). All the lichen-forming fungi of samples were affiliated with the few common genera of the ascomycete *Umbilicaria* spp. by Sanger sequencing method.

This study used Illumina MiSeq sequencing method and targeted V3-V4 region of bacterial 16S rRNA genes. Total 1,283,349 reads of MiSeq were analyzed. The phylotypes (OTUs) were determined with over 97% minimal similarity. About the results, 877,097 reads form Antarctica and 406,252 reads from Arctica. In Antarctica samples, average reads were 48,728 and average OTUs were 405; in Arctica samples, average reads were 45,139 and average OTUs were 203. The compositions of two different polar regions showed significant difference on phylum rank. Total 18 Antarctica samples, the average percentage of Bacteroidetes were 67.18%, and Proteobacteria were only 15.25%; total 9 Arctica samples, the average percentage of Bacteroidetes were only 3.97%, and Proteobacteria were 57.58%. On the other hand, the Arctica samples showed lower level at community richness, and the Antarctica samples showed lower level at community diversity.

In addition, 7 cosmopolitans of species rank were found in total 27 samples as follows, AM697086_s, EU861940_s, EU861966_s, FM874383_s, HQ327266_s, PAC000328_g_uc and *Sphingomonas pruni* group, which had close relationship with *Acidibrevibacterium* spp., *Gluconacetobacter* spp., *Mucilaginibacter* spp., *Gluconacetobacter* spp., *Acidisphaera* spp., *Acidiphilium* spp. and *Sphingomonas* spp, respectively. The reasons and functions were unknown, but the could be searched and analyzed by culturing and controlling experiments.

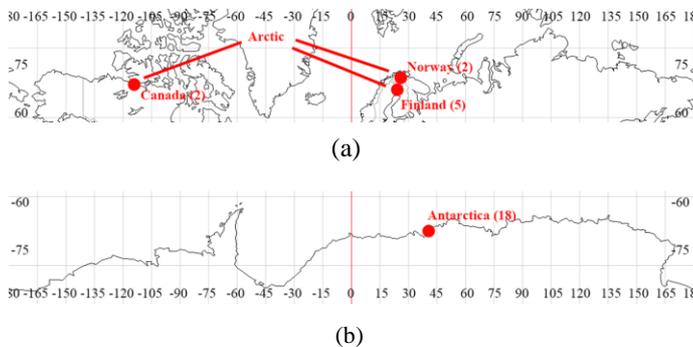


Figure 1. The sampling location of lichen samples with amounts. (a) Sample sites of Arctic. Nunavut (Canada), Gamvik (Norway), Enotekio & Kittila (Finland) are grouped in the Arctic because the latitudes of them are higher than 66° 34'N. (b) Sample sites of Antarctica.

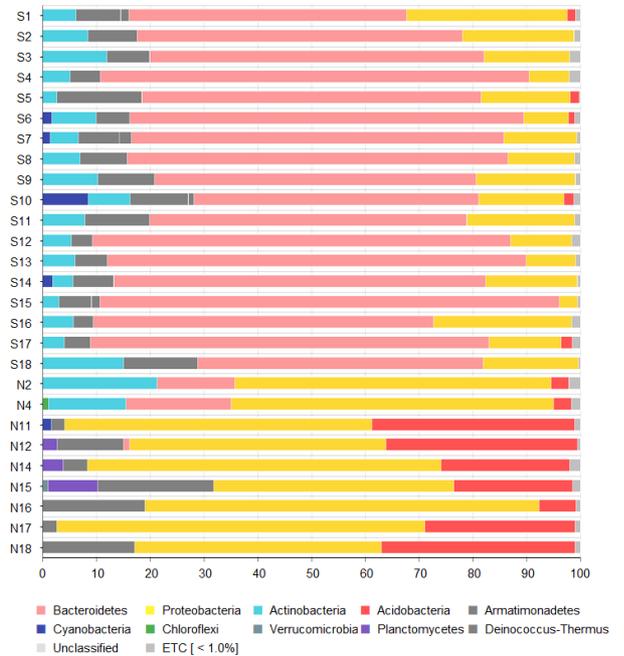


Figure 2. The 100% stacked column chart of compositions contained in phylum rank in each sample. The proportions less than 1.0% were grouped into ETC taxa. The predominant of phylum rank in Antarctica is Bacteroidetes, the predominant of Arctica is Proteobacteria.