

Characterization of bacteria associated with lichens found in cold environment

Faluaburu M Sailonga¹, Katsuhiko Kashihara¹, Satoshi Imura², Takeshi Naganuma¹

¹ *Graduate School of Biosphere Science, Hiroshima University (Hiroshima U)*

² *National Institute of Polar Research (NIPR)*

There are about one-fifth of all known fungal species which form symbiotic associations with green algae, cyanobacteria or with both photobionts. The photobionts get protection and moisture from the fungi, and in return the photobionts provide the fungi photosynthetic carbohydrates for its nutrition. These symbiotic life forms known as lichenized fungi or the ‘lichens’ are globally distributed, extending from the tropics to the Polar Regions. Recent studies suggest that non-photosynthetic bacteria may be an additional “third symbiont” component to the lichen symbiosis. Although there are few studies on species composition of bacteria-associated with lichens, bacterial-species composition of particular lichen species found in cold environments are still poorly understood.

To understand the lichen-association of fungi, algae or cyanobacteria and the non-photosynthetic bacteria, 18S/16S rRNA gene sequences were compared among rock-dwelling lichens which were earlier morpho-typed as genus *Umbilicaria*. The lichen specimens were collected from ice-free areas near Syowa Station, East Antarctica, at 5109 m Rwenzori Mountains, Uganda and at Spitsbergen, Arctic. Bacterial 16S rRNA sequences showing >98.65% similarities were grouped into “phylo-type” and carried BLASTN search to get closest similar microorganism on respective phylotypes. The eukaryotic 18S rRNA gene sequences by BLASTN search revealed fungal and algal component were affiliated with fungus *Umbilicaria yunnana* (rock tripe) and green alga *Trebouxia asymmetrica* respectively. The lichen associated bacterial 16S rRNA gene sequences’ phylotypes were found to be highly diverse and variable. Bacterial sequence assembly was dominated by phylotypes affiliated with Bacteroidetes (28%) and Proteobacteria (27%) phyla, particularly alphaproteobacteria followed closely by Sphingobacteriia and Cytophagia. At genus taxonomy, phylotypes affiliated to *Hymenobacter* dominates the sequences assembly. Antarctica’s and Arctic’s lichen associated bacterial composition are generally diverse and variable compared to the temperate lichen-bacterial composition found at Rwenzori Mountains, Uganda’s.