A COMPARATIVE STUDY OF ENDOLITHIC MICROBIAL COMMUNITES BETWEEN DIFFERENT TYPES OF ROCKS IN THE NORWEGIAN HIGH ARCTIC. Y. H. Choe[1], Y. K. Lee[1], M. Kim[1], J. S. Woo[1], M. J. Lee[1], [1]Korea Polar Research Institute (26 Songdomirae-ro, Yeonsu-gu, Incheon 406-840, Korea and yhchoe@kopri.re.kr).

Introduction: In extreme environments, such as the Arctic, endolithic communities are most of the extant life. The endolithic environment is thought to buffer microbial communities from intense solar radiation, temperature fluctuations, wind, and desiccation in environments where such environmental factors inhibit epilithic growth. Therefore, the endolithic environment is a critical habitat to explore in exobiological research.

The abundance of endolithic life in the high Arctic, combined with the potential for biosignature preservation, suggests that rocks associated with endolithic ecosystems may be the best hope for finding fossil evidence of past life on the Martian surface.

The goal of this study is to assess the activity and community composition of the endolithic community inhabiting rocks in the Norwegian high Arctic. To achieve this goal, we combined techniques of DNA sequencing, microscopy and spectroscopy. This work provides an overview of the polar microbial community and a new recognition of how environmental stresses such as prevailing polar desert conditions may affect the biogeochemical dynamics of high Arctic endolithic microorganisms.

Materials and methods: Endolithic samples were collected in August 2014 at various sites in Spitsbergen on Svalbard, Norway. Samples were collected with hardened steel chisels that were flame sterilized in the field with 100% ethanol and a butane torch. Duplicate rock samples at each site were collected into sterile, plastic tubes and bags, and transported to the laboratory in icebox keeping under ~4℃.

For scanning electron microscopy (SEM), rock pieces were sputter-coated with gold and examined with scanning electron microscope at 20 kV.

Homogenized rock samples were separated into subsamples and DNA was extracted as duplicates. DNA extractions were carried out on 3 g using a Fast DNA® SPIN Kit (MP Biomedicals).

Sequences generated from pyrosequencing of bacterial 16S rRNA gene amplicons were processed using the mothur pipeline. Statistical analyses were performed using the vegan R package.

Results: SEM images allow one to describe morphotypes and to estimate roughly the dimensions of the structures, but it is not possible to obtain information on the spatial organization of the organisms within the endolithic band. The images obtained illustrated bacterial colonization in the rocks.

They showed a wide distribution of single coccoid cells of about 5 μm in diameter attached to surfaces, Small globules forming aggregates covered grains of rock, and fine filamentous structures of 0.3 to 0.5 mm in width, lead to a network in the crevices of the rock.

Traces of interactions between living organisms and inorganic surfaces, such as biocorrosion or calcite formation, were not observed.

Discussion and Implication: Phylogenetic and statistical comparison of endolithic communities from this study with those from previous studies in similar environments support the hypothesis that patterns of microbial diversity are governed by similar principles observed in macro-ecological systems. The majority of the endolithic bacterial sequences were most closely matched to those of isolates or clones derived from cold/dry deserts (i.e., Antarctica, Atacama, and cold alpine environments). This indicates that endolithic bacteria in this region have little site variations and are under similar degrees of environmental constraints of the cold and dry Arctic. Results also provide insight into geobiolo-gical processes that shape the biosphere and help us understand in the cold and dry envionments possibly elsewhere in the Solar System.

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