

# 中国，天山ウルムチ No.1 氷河における微生物相と硝化・脱窒遺伝子解析

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## Impact of microbial communities on nitrogen cycles on Urumqi Glacier No.1 in China

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Many kinds of microorganisms, including snow algae and bacteria, have been found on glaciers in various parts of the world. However, our knowledge of the nitrogen cycling microbial communities of the glacier ecosystems is still very limited. In order to clarify distributions of ammonia-oxidizing and denitrifying microorganisms on Urumqi Glacier No.1 in China, we analyzed DNA and RNA using molecular genetic tools, including pyrosequencing of 16S rRNA gene PCR amplicons.

Analysis of 16S rRNA genes revealed the presence of ~400 bacterial OTUs on the glacial surface. Based on the dominant phylotypes and UniFrac analysis, the bacterial community on the glacier could be divided into three types, corresponding to the snow-covered, snow- and ice-covered, and bare-ice areas of the glacier. The glacial samples contained nitrifying bacteria such as genera *Nitrosomonas*, *Nitrospira*, *Candidatus Nitrotoga* and a large number of unclassified genera in *Nitrosomonadaceae*. Quantitative digital PCR of nitrifying and nitrate reducing genes revealed that copy numbers of ammonia oxidizers and nitrate reducers showed altitudinal distribution on the glacier. This study yields an initial insight into the glacial ecosystem of bacteria carrying genes for the nitrifying and denitrification pathway in a glacial environment.