

# Archiving the Genomic and Genetic Resources of Glaciers

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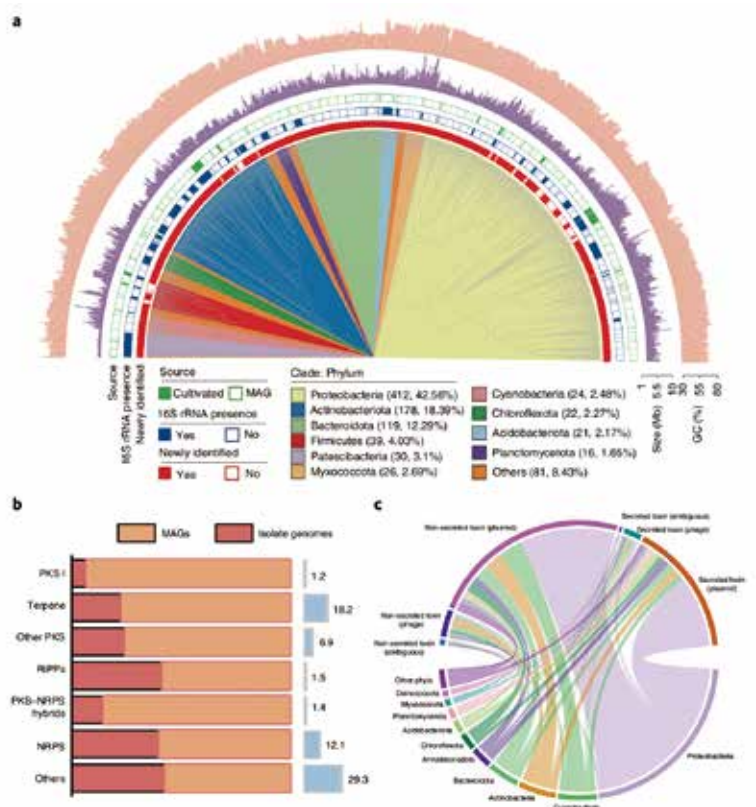
A new *Nature Biotechnology* study reported on June 27 has generated a genome and gene catalog of the Tibetan glacier microbiome. Notably, it reveals many unique organisms that have been found nowhere else.

LIU Yongqin at Lanzhou University in China, LUO Yingfeng at the Institute of Microbiology of the Chinese Academy of Sciences, and their colleagues gathered bacteria and the microscopic life forms called archaea from 21 glaciers on the Qinghai-Tibet plateau. Genetic sequencing of the samples yielded evidence of 968 microbial species and over 25 million genes.

The catalog provides a comprehensive overview of the microbial diversity and functions in glacier ecosystems, which could be useful for the bioprospecting of bioactive compounds and global comparison of glacier microbiomes.

Glaciers and ice sheets cover around 10% of Earth's surface and are the largest reservoir of fresh water. The Qinghai-Tibet Plateau glaciers are particularly vulnerable to global warming, which directly affects glaciers' mass balance and ice volume. This can have negative effects on biodiversity at regional and global scales.

The study performed a metagenomic assembly on 85 Tibetan glacier metagenomes and obtained 2,358 metagenome-assembled genomes. These were combined with the genomes of 883 cultivated bacterial isolates to



Genome and gene catalog of the Tibetan glacier microbiome. (Image by LIU *et al.*)

generate the genome component of the Tibetan Glacier Genome and Gene (TG2G) catalog. The catalog offers a platform for archiving, analysis, and comparison of glacier microbiomes at the genome and gene levels.

The study predicted the open reading frames of the metagenomes and genomes and predicted the functions of the encoded proteins by comparing them against several databases. They also predicted biosynthetic gene clusters (BGCs) encoding secondary metabolites and virulence factors, providing a comprehensive overview of the functions of the glacier microbiome.

The catalog contained over 25 million potential gene clusters encoding non-redundant proteins. The study also identified 15,954 putative secondary metabolite BGCs, which could be valuable for the bioprospecting of compounds with antibiotic and anticancer properties. The TG2G catalog could be useful in evaluating the effects of glacier retreat on public health and safety.

The study provides an overview of the microbial and functional potentials of glacier microbiomes, but further research is needed to investigate the source of these microorganisms and their activities in glacier

surface snow, ice, and cryoconite. In addition, how these microorganisms will respond to global warming and interact with microorganisms in glacier-fed streams and lakes during glacier melting needs to be carefully investigated.

Overall, the TG2G catalog offers a platform for data mining and comparison against glacier microbiomes globally. The study envisions the catalog forming the basis of a comprehensive global repository for glacier microbiome data, filling a major knowledge gap in the understanding of microbial diversity and functions in glacier ecosystems.

#### Reference

Liu, Y., Ji, M., Yu, T., et al. (2022). A genome and gene catalog of glacier microbiomes. *Nature Biotechnology*, 40(9), 1341-1348. doi:10.1038/s41587-022-01367-2