Project Number:	**101072761**
Project name:	**Center for Glacial Biome Doctoral Network**
Project Acronym:	**ICEBIO**
Call:	**HORIZON-MSCA-2021-DN-01**
Topic:	**HORIZON-MSCA-2021-DN-01-01**
Type of Action:	**HORIZON-TMA-MSCA-DN**
Project Start Date:	**1 October 2022**
Project Duration:	**48 months**
Deliverable Title:	**Core microbiome across various glacier-fed streams in the Pamir area**
Deliverable Number:	**D2.8, D21**
Type:	**Document, report**
Due date (month):	**40**
Lead Beneficiary:	**EPFL**
Dissemination Level:	**PU – Public**
Work Package No:	**WP2**
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Funded by the European Union

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WP2, D2.8, D21 Core microbiome across various glacier-fed streams in the Pamir area

Global warming has profound impacts on glacier ecosystems. As global temperatures continue to rise, glaciers are retreating at an unprecedented rate, posing significant ecological and environmental challenges. Particularly, glacier retreat significantly reshapes glacier-fed. Evidence suggests that retreating glaciers often result in an increase in "generalist" taxa (those common in all ecosystems), while reducing the abundance of cold-adapted "specialist" taxa. This shift reflects a weakening of environmental selection pressures as conditions become less extreme. Furthermore, GFSs are inherently limited in carbon and phosphorus, but glacier retreat and associated "greening" are altering nutrient inputs and stoichiometric balance. These changes may significantly affect microbial metabolic potential, yet the specific pathways through which nutrient regimes shape community composition and function remain poorly understood. Understanding the microbial mechanisms by which climate change influences glacial ecosystems is vital for predicting future impacts on biodiversity, biogeochemical cycling, and ecosystem services in mountain environments.

From summer 2023 to summer 2025, systematic sampling was conducted across 19 glaciers in the Alps and Kyrgyz Mountains. At each glacier, glacier ice cores, glacier-fed stream sediments were sampled to capture downstream microbial community changes. A total of 34,691 ASVs were identified through 16S rRNA gene sequencing. Glacier ice exhibited lowest γ-diversity (7415 ASVs) and lowest α-diversity, highlighting the strong constraints imposed by extreme environmental conditions and limited microbial dispersal. 28,063 ASVs were identified in the sediments, which exhibited highest γ-diversity. However, streamwater showed the highest average α-diversity, whereas sediments were slightly lower. This discrepancy may be attributed to the high spatial heterogeneity and the abundance of biofilm-associated microhabitats in sediments. Phylogenetic analyses revealed habitat-specific enrichment for multiple ASVs. Notably, several abundant ASVs exclusively detected in specific environments were located on long phylogenetic branches, indicating divergence and potentially reflecting distinct ecological adaptations and strong environmental specificity.