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WP1, D1.1, D3 A CATALOGUE OF THE ACTIVE MICROBIAL DIVERSITY ON GLACIER SURFACES

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Introduction

Glaciers and ice sheets are uniquely characterized by their harsh environmental extremes, where microorganisms are the main drivers of biogeochemical processes (Anesio & Laybourn-Parry, 2012). On their icy surfaces, a variety of microbial habitats can be found, including snow, ice, dirt cones, glacial streams and lakes, and cryoconite holes –- microbial oases of biodiversity formed by dark particulates of aggregated biological and inorganic material that lower the local surface albedo. Vegetation on glacier surfaces is non-existent or limited to glacier mice (i.e. moss) at the margins of glaciers (e.g. Hotaling et al., 2020; Porter et al., 2008; Uetake et al., 2014). As such, microbial primary producers serve as keystone species in these environments, playing an active role as the sole providers of carbon sources to sustain and shape a broader microbial community. On ice and snow, algae thrive and darken the surface through seasonal blooms, while cyanobacteria play a pivotal role in the formation of cryoconite granules (Langford et al., 2010; Takeuchi et al., 2010; Wejnerowski et al., 2023). In addition to these primary producers, the glacier surface may host a range of other microorganisms, including archaea, bacteria (mainly Alpha- and Beta-Proteobacteria, Bacteroidetes, and Actinobacteria), metazoa, and protists, as well as viruses. For a thorough overview of the microbiome of glaciers and ice sheets, we refer to Anesio et al. (2017) and the references within.

The surface microbiome of glaciers and ice sheets has been extensively studied worldwide through DNA-based approaches, such as amplicon sequencing of taxonomic marker genes and metagenomics. A vast amount of sequencing data is available, yet it currently appears unorganized in publicly accessible databases. Recently, an open-access repository was established by Y. Liu et al. (2023) for supraglacial bacteria and archaea found in Arctic, Tibetan, and Antarctic glaciers. This comprehensive database covers ice, snow, and cryoconite holes and includes 815 amplicon sequencing datasets, 1005 genomes of bacterial isolates, 208 metagenomic datasets, and 3375 metagenome-assembled genomes from 248 studies and 23 publications (accessible at: https://nmdc.cn/4gdb/). Despite this noteworthy contribution, the repository still captures only a fraction of the publicly available data, emphasizing the need for continued eforts to systematically catalog the glacier surface microbiome.

Our aim is to establish a comprehensive catalogue of the total microbial diversity on glacier surfaces worldwide using data from DNA and RNA-based approaches, providing information on both the organisms present and those that are truly active. Included in the catalogue will be a variety of organisms spanning all domains of life, extending beyond just bacteria and archaea. At present, metatranscriptomic data from glacier surfaces is still scarce; however, there is an emerging trend in studies applying metatranscriptomics to investigate the active microbial population in glacier habitats. As of fall 2024, several studies featuring vast amounts of metatranscriptomic data of glacier samples are being drafted at institutes affiliated with the ICEBIO consortium but are yet to be published. The present catalogue summarizes the status quo of data collected from glacial surfaces worldwide.

Catalogue insights

The current version of the catalogue includes only amplicon sequencing data that is publicly available from the Sequence Read Archive, a database curated by the National Center for Biotechnology Information (NCBI). A thorough search was conducted across multiple queries in the NCBI BioProject database to identify data linked to published articles. Any data not associated with a publication was excluded from the catalogue to ensure a high standard of quality. This approach allows users to easily reference the original studies for deeper insights into the data and facilitates comparative analyses by providing clear context regarding the data's origin and collection methods. Additionally, where possible, metadata was corrected and expanded with relevant information sourced from the publication or supplementary materials, including primer sequences, collection dates, geographical coordinates and locations, and various subcategories that provide additional insights into the samples (e.g. green/red snow, ice core/scrapings). This metadata, along with the data used to create this catalogue, will be readily accessible to users, removing the necessity for complex data transformations and streamlining their research processes.

The catalogue below includes data from approximately 50 published articles covering diverse regions, including the Antarctic, Arctic, Andes, Himalayas, Urals, Alps, and more. These articles were selected based on the following searches conducted in the NCBI BioProject database, where results were individually verified for their inclusion in published articles. The searches included:

1. _cryoconit AND "bioprojectsra"[Filter]*_
   (52 results)
2. _(glaci AND snow) AND "bioproject sra"[Filter]*_
   (36 results)
3. _(glaci AND ice) AND "bioproject sra"[Filter]*_
   (181 results)
4. _(glaci) NOT cryoconite_ NOT (glaci* AND snow) NOT (glaci* AND ice) AND "bioproject sra"[Filter]**
   (421 results)
5. _((arctic OR antarctic_) AND (snow OR ice)) AND "bioproject sra"[Filter] NOT ((glaci*) NOT cryoconite* NOT (glaci* AND snow) NOT (glaci* AND ice) AND "bioproject sra"[Filter])**
   (282 results)

In total, 871 BioProjects were explored within the NCBI BioProject database, and 68 relevant projects were identified (see Table 1), of which a few were sourced from other locations. The data has been filtered to include only data generated by Illumina MiSeq and HiSeq sequencing platforms to first streamline the updating process of the catalog with new data from these commonly used instruments. Of the 68 projects, approximately 50 contain Illumina MiSeq and HiSeq sequencing data and are currently being processed to create the first version of the live catalogue of the microbial diversity on glacier surfaces. The catalogue serves as an invaluable resource for researchers investigating microbial diversity and activity in glacier ecosystems by providing a centralized data repository that enhances access to relevant information and supports more thorough analyses.

Table 1. Overview of studies investigating microbial communities in glacier habitats, including snow, ice, and cryoconite holes with publicly available amplicon sequencing data. The table highlights sampling sources and the targeted taxonomic marker genes.

Reference	Habitat						Taxonomic marker gene			DOI
	Snow	Ice	Cryoconite hole	Dust/air	Biofilm	Glacial runoff	16S	18S	ITS	
(Malard et al., 2019)	+						+			https://doi.org/10.3389/fmicb.2019.00461
(Vonnahme et al., 2016)			+				+			https://doi.org/10.5194/bg-13-659-2016
(Garcia-Lopez et al., 2021)		+					+	+		https://doi.org/10.3389/fmicb.2021.714537
(Lutz et al., 2019)	+		+				+	+		https://doi.org/10.3390/microorganisms7060160
(Christner et al., 2018)		+					+	+		https://doi.org/10.5194/tc-12-3653-2018
(Weisleitner et al., 2019)			+				+			https://doi.org/10.3389/fmicb.2019.01019
(Sommers et al., 2019)			+				+	+		https://doi.org/10.3389/fmicb.2019.00065
(Miller et al., 2021)	+	+				+	+			https://doi.org/10.1088/1748-9326/abf06b
(Millar et al., 2021)			+				+	+		https://doi.org/10.3389/fmicb.2021.738451
(Cameron et al., 2016)		+	+				+			https://doi.org/10.1093/femsec/fiv164
(Franzetti et al., 2017)			+				+			https://doi.org/10.1111/1758-2229.12499
(Havig & Hamilton, 2019)	+					+	+	+		https://doi.org/10.1016/j.gca.2018.12.024
(Chen et al., 2022a)			+				+			https://doi.org/10.3389/fmicb.2021.784273
(Rathore et al., 2022)			+				+		+	https://doi.org/10.1111/1758-2229.13017
(Winkel et al., 2022)	+	+					+	+	+	https://doi.org/10.3389/fmicb.2022.876848
(Hodson et al., 2021)	+	+					+			https://doi.org/10.1029/2020JG005706
(Bradley et al., 2023)	+	+					+	+		https://doi.org/10.1111/gbi.12535
(Sanchez-Cid et al., 2023)	+						+			https://doi.org/10.1093/femsec/fiad042
(Keuschnig et al., 2023)	+						+			https://doi.org/10.1186/s40168-023-01473-6
(Rassner et al., 2024)	+			+			+			https://doi.org/10.1111/1462-2920.16617
(Jaarsma et al., 2023)		+	+		+		+	+		https://doi.org/10.1093/femsec/fiad119
(K. Liu et al., 2021)	+					+	+			https://doi.org/10.1111/1462-2920.15788
(Chen et al., 2022a)			+				+			https://doi.org/10.5194/tc-16-1265-2022
(Cameron et al., 2020)			+				+			https://doi.org/10.1111/1462-2920.15059
(Uetake et al., 2016)	+						+			https://doi.org/10.1093/femsec/fiw127
(Ferrario et al., 2017)			+				+			https://doi.org/10.1016/j.envpol.2017.07.039
(Hell et al., 2013)			+				+			https://doi.org/10.1038/ismej.2013.51
(Buda et al., 2024)			+				+			https://doi.org/10.1016/j.chemosphere.2023.140738
(Gladkov et al., 2024)			+				+			https://doi.org/10.1038/s41598-024-64452-3
(Antony et al., 2024)			+				+	+	+	https://doi.org/10.1016/j.scitotenv.2024.173187
(Pittino et al., 2023b)			+				+			https://doi.org/10.1128/spectrum.01004-22
(Pittino et al., 2023a)			+				+			https://doi.org/10.1038/s41598-022-24373-5
(Sommers et al., 2018)			+				+	+		https://doi.org/10.1093/femsec/fix167
(Webster-Brown et al., 2015)			+				+			https://doi.org/10.1093/femsec/fiv144
(Sommers et al., 2020)			+				+	+		https://doi.org/10.3390/microorganisms8111747
(Segawa et al., 2020)			+				+			https://doi.org/10.1093/femsec/fiaa199
(Li et al., 2023)						+	+			https://doi.org/10.1007/s11356-023-28250-0

(McCutcheon et al., 2021)	+	+	+		+	+	+	+	+	https://doi.org/10.1038/s41467-020-20627-w
(Perini et al., 2019)	+	+	+			+	+		+	https://doi.org/10.3389/fmicb.2019.00557
(Ambrosini et al., 2017)			+				+			https://doi.org/10.1007/s00248-016-0914-6
(Cameron et al., 2017)			+				+			https://doi.org/10.1111/1758-2229.12510
(Y. Liu et al., 2017)			+				+			https://doi.org/10.1093/femsec/fix072
(Smith et al., 2018)	+	+	+			+	+			https://doi.org/10.1093/femsec/fiy090
(Gokul et al., 2019)	+	+	+				+			https://doi.org/10.1093/femsec/fiz177
(Franzetti et al., 2016)			+				+			https://doi.org/10.1038/ismej.2016.72
(Gokul et al., 2016)			+				+			https://doi.org/10.1111/mec.13715
(Edwards et al., 2014)			+				+			https://doi.org/10.1111/1574-6941.12283
(Stibal et al., 2015)			+				+			https://doi.org/10.1111/1758-2229.12246
(Zarsky et al., 2013)		+	+	+			+			https://doi.org/10.1088/1748-9326/8/3/035044
(Remias et al., 2023)	+	+						+	+	https://doi.org/10.1093/femsec/fiad134
(Garcia-Lopez et al., 2022)		+					+	+		https://doi.org/10.3389/fmicb.2022.825632
(Díaz et al., 2023)	+	+					+			https://doi.org/10.3389/fmicb.2023.1154815
(Varliero et al., 2021)		+					+			https://doi.org/10.1017/jog.2021.30
(Alcamán-Arias et al., 2021)		+					+			https://doi.org/10.3390/microorganisms9010088
(Zeng et al., 2020)		+					+			https://doi.org/10.1128/mbio.02641-20
(Bomberg et al., 2019)		+				+	+		+	https://doi.org/10.3389/fmicb.2019.01583
(Ali et al., 2021)										https://doi.org/10.1007/s10123-020-00153-x
(Thomas et al., 2020)	+	+				+	+			https://doi.org/10.1016/j.scitotenv.2019.135264
(Q. Liu et al., 2015)		+					+			https://doi.org/10.1016/j.syapm.2015.09.005
(Jia et al., 2024)	+	+				+	+			https://doi.org/10.1016/j.envint.2024.108788
(Qi et al., 2022)				+			+			https://doi.org/10.1016/j.scitotenv.2022.154980
(Hotaling et al., 2022)	+						+	+	+	https://doi.org/10.1128/msphere.00503-22
(Šantl-Temkiv et al., 2018)				+			+			https://doi.org/10.1093/femsec/fiy031
(Azzoni et al., 2018)	+						+			https://doi.org/10.1017/aog.2018.18
(Stoppiello et al., 2023)	+	+					+		+	https://doi.org/10.3390/biology12091193
(Ji et al., 2022)	+						+	+	+	https://doi.org/10.1111/nph.17764
(Smirnova et al., 2021)	+						+			https://doi.org/10.1002/mbo3.1152
(Rosa et al., 2020)	+			+					+	https://doi.org/10.1038/s41598-020-78630-6

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