Data in Brief 66 (2026) 112758

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

16S rRNA amplicon metabarcoding dataset from a retreating glacier forefield in the high tropical andes

Kelsey E. Reider[a,*], Clayton Fannin[a], Kiersten A. Hannah[a], Anthony R. Gelona III[a], Carly Anderson[a], Karen Barnard-Kubow[a,b], Ray A. Enke[a,b]

[a] James Madison University Department of Biology, 951 Carrier Drive MSC 7801, Harrisonburg, VA 22807, USA
[b] James Madison University Center for Genome and Metagenome Studies, 951 Carrier Drive MSC 7801, Harrisonburg, VA 22807, USA

ARTICLE INFO

Article history:
Received 25 July 2025
Revised 2 April 2026
Accepted 3 April 2026
Available online 16 April 2026

Dataset link: 16S Soil Metagenome Dataset from a Retreating Glaciers Area in the High Tropical Andes Mountains (Original data)

Keywords:
Biodiversity
Microbiome
Primary succession
Nutrient transfer
Glacier forefield
Climate change

ABSTRACT

Glaciers are retreating rapidly worldwide, particularly at high elevations, changing the environments and habitats of microorganisms, plants, and animals drastically and leaving behind nutrient-poor sediment. We sought to explore seasonal, elevational, and soil age differences in microbial community diversity found in moraine deposits exposed by recent deglaciation and previously exposed during the Little Ice Age in the Cordillera Vilcanota of southeastern Peru. In the wet and dry seasons of 2023, JMU students and other researchers collected soil samples from 35 sites across a 2.5 square kilometer range in the Andes mountains. Each sample was assigned to the season collected, elevation of collection, and age of exposure. Total DNA was extracted from samples and the 16S rRNA gene was amplified and sequenced on an Illumina MiSeq platform. The data were then processed and analyzed using the QIIME2 bioinformatics pipeline. This dataset

* Corresponding author.
E-mail address: reiderke@jmu.edu (K.E. Reider).

https://doi.org/10.1016/j.dib.2026.112758

will be useful to the field for studying ecological community and ecosystem formation in glacier forefields emerging from climate change.

Specifications Table

Subject	Biodiversity
Specific subject area	Characterization of soil microbial metagenomes from a retreating glacier forefield in the tropical Andes
Type of data	Table, Image, Chart, Graph, Figure
Data collection	Data were collected by sequencing 16S amplicons produced from sediment samples obtained in the Cordillera Vilcanota Mountain range of southeastern Peru.
Data source location	Cordillera Vilcanota, Cusco, Peru
Data accessibility	Repository name: NCBI SRA Data identification number: PRJNA1237301 Direct URL to data: https://www.ncbi.nlm.nih.gov/sra/PRJNA1237301 [1] Instructions for accessing these data: download raw and/or processed files
Related research article	N/A

1. Value of the Data

- This study provides a metabarcoding profile of the microbial diversity of glacial moraines in the southern Peruvian Andes.
- Understanding glacier forefield microbial diversity in relation to season, elevation, and substrate age can improve models of primary succession, including predictions for carbon dynamics and the rate at which recently deglaciated moraines may be colonized by plants and animals.
- Documenting community and ecosystem changes are important as microbes, plants, and animal communities are established following glacier loss.
- The data can be used in future comparative studies of variation in microbial community diversity and ecosystem development.

2. Background

Glaciers are rapidly retreating worldwide [2], threatening water supplies to downstream ecosystems and communities [3,4] and drastically altering the landscape, leaving behind nutrient-poor glacial till sediment deposits which limit ecosystem development for decades or even centuries [5]. It is imperative to understand the patterns of ecological function and community development during primary succession in high mountain landscapes [6,7], which requires an understanding of microbial diversity and community composition in glacier forefields. Microbes are the initial colonizers of recently exposed post-glacial sediment and play an important role in early soil formation [8]. Relatively little is known about differences in microbial communities across elevation and hydrological cycles in tropical Andean glacier forefields, where new land is rapidly being created by glacier loss [9].

The use of 16S rRNA gene amplicon sequencing to quantify microbial composition and diversity is supported by previous assessments of microbial diversity in the high Andes of Peru [10,11], and other recently deglaciated, high elevation, arid environments such as the Tibetan Plateau [12] and the Himalayan mountains [13]. The goal of this research is to characterize the microbial diversity of glacial moraines in the Cordillera Vilcanota, Cusco Department, south-

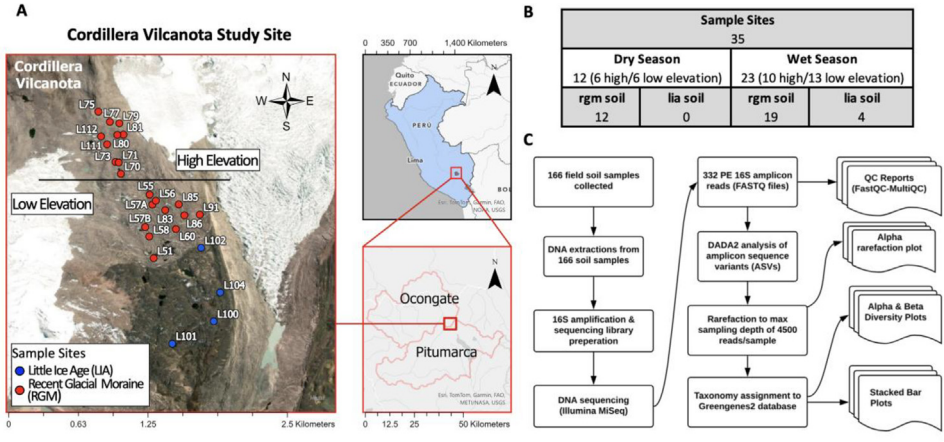

Fig. 1. Overview of sample collection and experimental pipeline. A) Location of collected soil samples, Cordillera Vilcanota, southeastern Peru. B) Overview of sampling variables including season, elevation, and soil age. C) Overview of entire experimental pipeline including the open access bioinformatics analysis using QIIME2 embedded in the DNA Subway graphical user interface.

eastern Peru, in the wet and dry seasons and at different elevations and sediment exposure age groups. While previous studies have measured microbial metagenomics in high elevation glaciers, this is the first public data set detailing microbial diversity of the deglaciated moraines in the Cordillera Vilcanota in southeastern Peru based on seasonal, elevational and soil age differences. These analyses were conducted using Illumina 16S amplicon analysis in tandem with a bioinformatics pipeline exclusively using open access tools to ensure sequence quality and robust metagenomics analysis (Fig. 1). The survey described here is part of an ongoing NSF-funded project hosted by the Cold Spring Harbor Laboratory, DNA Learning Center (CSHL DNALC) and the James Madison University Center for Genome and Metagenome Studies (JMU CGEMS) focused on incorporating metagenomics analysis into undergraduate education. These data will be useful to understand the microbial community underlying initiation of primary succession in recently deglaciated tropical Andean landscapes (Fig. 2).

3. Data Description

To explore seasonal, elevational, and soil age differences in microbial community diversity in soils exposed by recent exposure of a high elevation glacier system, sediment samples were collected from 35 sample sites from the Cordillera Vilcanota of southeastern Peru (Fig 1a-b). Samples were collected during the dry (July 2023) and wet (December 2023) seasons, at “high” (5330–5400 m above sea level) and “low” (5100–5280 masl) elevations, and from Recent Glacial Moraine (RGM) sample sites exposed between ~25–135 years ago, and older sites that remained exposed during the Little Ice Age (LIA) which ended ~1850–1900 in this location following moraine ages as previously studied [14] (Fig 1a–b). Genomic DNA was extracted in duplicate from soil samples using a Qiagen DNEasy PowerSoil Pro kit, and used to create 16S amplicon sequencing libraries as previously demonstrated [15–16]. The Illumina MiSeq sequencing platform was used to generate a total of 3318,970 unprocessed 150 bp paired end (PE) reads from the V3-V4 region of the 16S rRNA gene from the 70 samples yielding 140 FASTQ files. (Table 1). Quality control (QC) and filtering analysis was applied to remove low quality and chimeric sequences yielded a total of 2772,009 PE sequence reads (83.5% of total reads) to be used for a subsequent open access bioinformatics workflow (Table 1; Fig 1c).

Table 1
Sample metadata for dataset. Soil age is abbreviated either RGM for Recent Glacial Moraine or LIA for Little Ice Age. The GPS coordinates for each sample location are available in Supplementary Table 1.

SampleID	Sample Site	Season	Soil Age	Elevation	Description	Input Reads	Filtered Reads	% Pass Filter	Feature_Count	SRA accession #
1	L80	dry	RGM	high	L80controldry_1	17,971	14,912	83.0	10,687	SAMN47415363
2	L80	dry	RGM	high	L80controldry_2	8648	7041	81.4	4812	SAMN47415364
5	L75	dry	RGM	high	L75controldry_1	2675	2099	78.5	1541	SAMN47415365
6	L75	dry	RGM	high	L75controldry_2	5557	4508	81.1	3532	SAMN47415366
9	L55	dry	RGM	low	L55controldry_1	21,955	19,466	88.7	14,731	SAMN47415367
10	L55	dry	RGM	low	L55controldry_2	17,212	14,818	86.1	10,944	SAMN47415368
13	L70	dry	RGM	high	L70controldry_1	11,134	9474	85.1	6899	SAMN47415369
14	L70	dry	RGM	high	L70controldry_2	23,544	20,647	87.7	15,888	SAMN47415370
17	L86	dry	RGM	low	L86controldry_1	41,960	35,823	85.4	27,240	SAMN47415371
18	L86	dry	RGM	low	L86controldry_2	57,824	49,106	84.9	38,746	SAMN47415372
21	L71	dry	RGM	high	L71controldry_1	5606	4696	83.8	2944	SAMN47415373
22	L71	dry	RGM	high	L71controldry_2	9643	8328	86.4	6176	SAMN47415374
25	L57B	dry	RGM	low	L57Bcontroldry_1	13,391	10,816	80.8	6681	SAMN47415375
26	L57B	dry	RGM	low	L57Bcontroldry_2	9459	7594	80.3	4528	SAMN47415376
29	L77	dry	RGM	high	L77controldry_1	67,390	55,640	82.6	43,739	SAMN47415377
30	L77	dry	RGM	high	L77controldry_2	42,132	35,036	83.2	26,014	SAMN47415378
33	L81	dry	RGM	high	L81controldry_1	23,921	19,504	81.5	14,928	SAMN47415379
34	L81	dry	RGM	high	L81controldry_2	21,477	17,460	81.3	13,453	SAMN47415380
37	L83	dry	RGM	low	L83controldry_1	22,130	17,458	78.9	11,346	SAMN47415381
38	L83	dry	RGM	low	L83controldry_2	54,585	45,390	83.2	34,115	SAMN47415382
41	L57A	dry	RGM	low	L57Acontroldry_1	40,378	32,367	80.2	24,445	SAMN47415383
42	L57A	dry	RGM	low	L57Acontroldry_2	64,581	51,533	79.8	39,987	SAMN47415384
45	L91	dry	RGM	low	L91controldry_1	87,309	71,082	81.4	57,170	SAMN47415385
46	L91	dry	RGM	low	L91controldry_2	54,561	43,100	79.0	31,223	SAMN47415386
63	L57A	wet	RGM	low	L57Acontrolwet_1	93,352	77,121	82.6	60,202	SAMN47415387
64	L57A	wet	RGM	low	L57Acontrolwet_2	80,290	67,400	83.9	52,923	SAMN47415388
67	L101	wet	LIA	low	L101controlwet_1	45,023	38,060	84.5	23,683	SAMN47415389
68	L101	wet	LIA	low	L101controlwet_2	72,066	59,210	82.2	38,172	SAMN47415390
71	L102	wet	LIA	low	L102controlwet_1	85,900	71,012	82.7	51,992	SAMN47415391
72	L102	wet	LIA	low	L102controlwet_2	85,252	71,696	84.1	53,528	SAMN47415392
75	L91	wet	RGM	low	L91controlwet_1	77,957	68,231	87.5	55,112	SAMN47415393
76	L91	wet	RGM	low	L91controlwet_2	94,685	83,282	88.0	70,949	SAMN47415394
79	L104	wet	LIA	low	L104controlwet_1	76,614	65,491	85.5	50,219	SAMN47415395
80	L104	wet	LIA	low	L104controlwet_2	92,552	80,613	87.1	62,821	SAMN47415396

(*continued on next page*)

Table 1 (*continued*)

SampleID	Sample Site	Season	Soil Age	Elevation	Description	Input Reads	Filtered Reads	% Pass Filter	Feature_Count	SRA accession #
83	L57B	wet	RGM	low	L57Bcontrolwet_1	88,563	74,125	83.7	60,126	SAMN47415397
84	L57B	wet	RGM	low	L57Bcontrolwet_2	108,104	91,842	85.0	75,757	SAMN47415398
87	L56	wet	RGM	low	L56controlwet_1	95,284	76,348	80.1	61,256	SAMN47415399
88	L56	wet	RGM	low	L56controlwet_2	96,936	80,358	82.9	64,675	SAMN47415400
91	L51	wet	RGM	low	L51controlwet_1	84,122	69,447	82.6	50,565	SAMN47415401
92	L51	wet	RGM	low	L51controlwet_2	98,275	83,299	84.8	62,495	SAMN47415402
95	L73	wet	RGM	high	L73controlwet_1	30,591	25,586	83.6	23,508	SAMN47415403
96	L73	wet	RGM	high	L73controlwet_2	15,322	12,726	83.1	10,928	SAMN47415404
99	L86	wet	RGM	low	L86controlwet_1	55,213	45,637	82.7	31,735	SAMN47415405
100	L86	wet	RGM	low	L86controlwet_2	59,169	48,436	81.9	34,620	SAMN47415406
103	L60	wet	RGM	low	L60controlwet_1	33,410	28,902	86.5	22,779	SAMN47415407
104	L60	wet	RGM	low	L60controlwet_2	47,938	41,451	86.5	33,352	SAMN47415408
107	L85	wet	RGM	low	L85controlwet_1	49,282	42,324	85.9	31,397	SAMN47415409
108	L85	wet	RGM	low	L85controlwet_2	68,818	58,756	85.4	44,493	SAMN47415410
111	L111	wet	RGM	high	L111controlwet_1	46,229	37,864	81.9	33,391	SAMN47415411
112	L111	wet	RGM	high	L111controlwet_2	67,231	56,113	83.5	50,753	SAMN47415412
115	L71	wet	RGM	high	L71controlwet_1	35,589	32,237	90.6	27,676	SAMN47415413
116	L71	wet	RGM	high	L71controlwet_2	57,918	51,483	88.9	44,963	SAMN47415414
119	L80	wet	RGM	high	L80controlwet_1	33,342	28,173	84.5	21,534	SAMN47415415
120	L80	wet	RGM	high	L80controlwet_2	50,162	42,274	84.3	33,438	SAMN47415416
123	L79	wet	RGM	high	L79controlwet_1	52,959	43,653	82.4	39,952	SAMN47415417
124	L79	wet	RGM	high	L79controlwet_2	44,139	35,396	80.2	32,030	SAMN47415418
127	L70	wet	RGM	high	L70controlwet_1	4349	3427	78.8	2475	SAMN47415419
128	L70	wet	RGM	high	L70controlwet_2	21,444	18,007	84.0	16,067	SAMN47415420
131	L100	wet	LIA	low	L100controlwet_1	49,682	42,717	86.0	30,991	SAMN47415421
132	L100	wet	LIA	low	L100controlwet_2	53,958	45,725	84.7	32,150	SAMN47415422
135	L58	wet	RGM	low	L58controlwet_1	34,131	27,201	79.7	18,099	SAMN47415423
136	L58	wet	RGM	low	L58controlwet_2	48,973	39,811	81.3	27,491	SAMN47415424
139	L112	wet	RGM	high	L112controlwet_1	32,190	25,964	80.7	20,672	SAMN47415425
140	L112	wet	RGM	high	L112controlwet_2	35,873	28,176	78.5	23,176	SAMN47415426
143	L77	wet	RGM	high	L77controlwet_1	41,235	32,746	79.4	27,449	SAMN47415427
144	L77	wet	RGM	high	L77controlwet_2	56,432	46,585	82.6	39,258	SAMN47415428
147	L75	wet	RGM	high	L75controlwet_1	25,559	21,075	82.5	17,137	SAMN47415429
148	L75	wet	RGM	high	L75controlwet_2	10,311	8306	80.6	6465	SAMN47415430
151	L81	wet	RGM	high	L81controlwet_1	40,809	31,961	78.3	27,609	SAMN47415431
152	L81	wet	RGM	high	L81controlwet_2	16,694	13,864	83.0	11,098	SAMN47415432

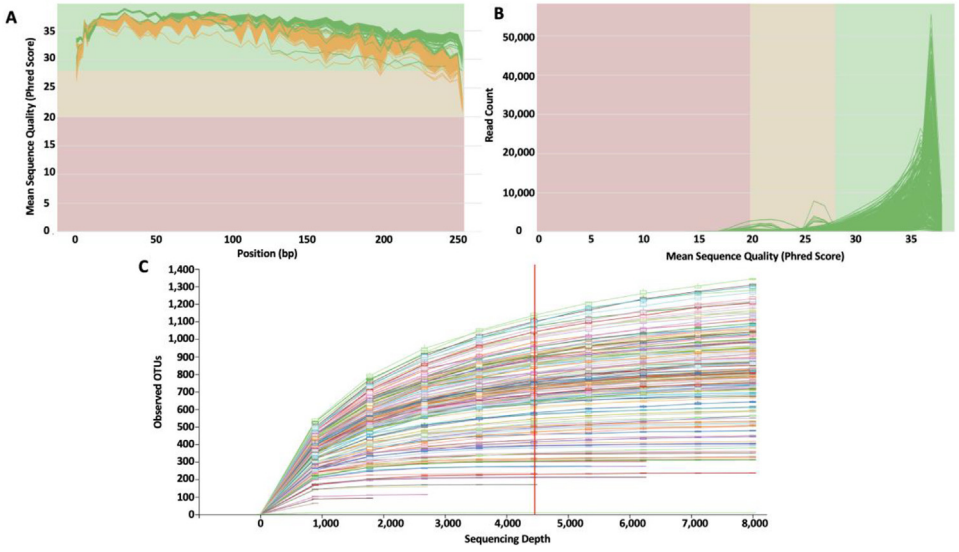

Fig. 2. Overview of sequencing dataset quality. FastQC and MultiQC analysis of raw sequencing reads demonstrates high per base (A) and per sequence (B) quality. C) A sequencing depth of 4500 representative sequences was selected to use for downstream analysis.

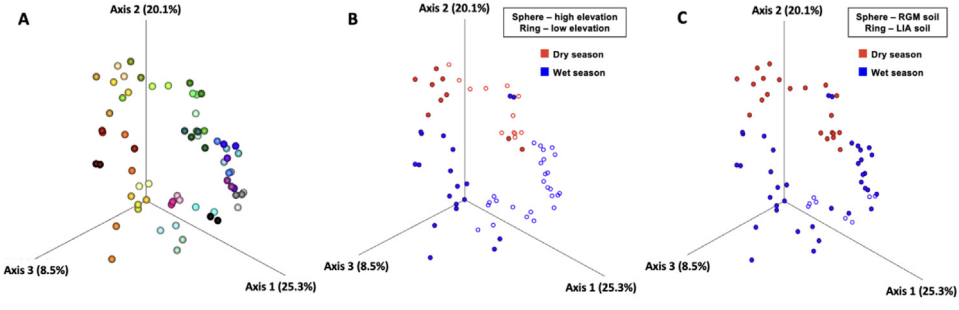

Fig. 3. Inter-sample microbial composition variation analyzed through weighted UniFrac distance matrix Principal Coordinates Analysis (PCoA) demonstrates similar clustering of sample replicate extractions (A), and unique clustering of samples based on season, elevation, and soil age (B-C).

Quality Control of sequencing reads in the 140 FASTQ files was assayed using FastQC and MultiQC analyses [20]. Fig. 1a-b shows that all FASTQ sequencing files have an average per sequence and per base Phred score >20 respectively, a common threshold demonstrating high quality Illumina base calls. High-quality reads were subsequently assigned to amplicon sequence variants (ASVs) and quantified using DADA2 [21] software identifying 2162,930 unique features across the 70 samples (Table 1). Using a sequencing depth of 4500, representative sequences for each sample were aligned and annotated against the SILVA database version 138.2 (Fig 1c). Beta diversity, indicating inter-sample microbial composition variation, was analyzed through Principal Coordinates Analysis (PCoA) using the weighted UniFrac distance matrix based on QIIME2's align-to-tree-mafft-fasttree function [18]. Initial beta diversity assessment demonstrated optimal clustering of sample replicates and clear differences in sample grouping based on season, elevation, and soil age (Fig 3a-c). Initial QC assessment indicates that our data set will be appropriate for studies investigating microbial and plant community establishment in deglaciated moraine landscapes.

4. Experimental Design, Materials and Methods

4.1. Study site and field sampling

Soil samples were collected from 35 sites within a glacier forefield in the Cordillera Vilcanota (−13.7547, −71.0851), Cusco Department, southeastern Peru during the wet (December) and dry (July) season of 2023. Geographic coordinates for the sampling sites are available in the supplementary material (Table S1). We avoided sampling inside plant patches or water features. Sites were selected along an elevational gradient from 5100 to 5400 masl from glacial moraine deposits that were previously dated to ∼25–135 years ago, and older sites that remained exposed during the Little Ice Age (LIA) which ended ∼1850–1900 in this location (14). Soils were sampled at 3–4 points at each site to a depth of 4 cm with a flame-sterilized trowel and stored in sealed, sterile bags on ice in the field and then frozen until DNA extraction. Two replicate DNA extractions were completed from homogenized soils samples from each site, yielding 70 study samples.

4.2. DNA extraction and 16S amplicon sequencing

DNA extractions were performed from 0.4 g of each soil samples using the Qiagen DNeasy PowerSoil kit (Hilden, Germany) following the manufacturer's protocols and DNA concentrations were measured with a Qubit 3.0 fluorometer (Thermo Fisher Scientific, MA, USA). Plant material such as roots and rocks were excluded from subsampled soil. 16S amplification and library preparation was performed at the James Madison University Center for Genome and Metagenome Studies (CGEMS). Pooled 16S amplicons were sequenced on the Illumina (San Diego, CA, USA) MiniSeq platform. The V4 region of the bacterial 16 s rRNA gene was amplified and barcoded for each sample using primers developed by Kozich et al. [17]. Samples were screened for successful amplification on an agarose gel and pooled. A double-sided bead clean-up was carried out to remove primer-dimers and a low amount of off-target larger PCR products. Quality and concentration of the pooled library was checked using a Bioanalyzer (Agilent, Santa Clara, CA, USA) and NEB's Library Quant Kit for Illumina. The library was then sequenced on a MiniSeq using a mid-output reagent cartridge. Before loading, the library was combined with Ilumina's PhiX control (30:70 16s:PhiX) to ensure a high-quality run despite the low diversity of the 16 s library. A dual indexing strategy was used with these primers as previously demonstrated by Senn and colleagues: Forward: GTGCCAGCMGCCGCGGTAA. Reverse: GGACTACHVGGGTWTCTAAT [15].

4.3. Bioinformatics analyses

The graphical user interface DNA Subway Purple Line was used to run the QIIME2 version 2 2017.4 16S rRNA gene amplicon sequencing pipeline [18].This pipeline includes FastQC app version 0.11.2 [19], MultiQC version 1.26 [20],DADA2 app version 2021.11.02 [21] and emperor plots for raw sequencing ready QC, ASV analysis and beta diversity analyses respectively as previously reported [16,17].

Limitations

Not applicable

Ethics Statement

The authors have reviewed the ethical requirements and confirm that this work does not involve human subjects, animal experiments or any data collected from social media platforms.

CRediT Author Statement

Kelsey E. Reider: conceptualization, investigation, methodology, writing, supervision, project administration, funding acquisition; **Clayton Fannin:** formal analysis, software, visualization, data curation, writing; **Kiersten A. Hannah:** investigation, formal analysis, software, visualization, data curation, writing; **Anthony R. Gelona III:** investigation, data curation, writing; **Carly Anderson:** investigation, data curation, writing; **Karen Barnard-Kubow:** investigation, methodology, formal analysis, software, visualization, data curation, writing; **Ray A. Enke:** conceptualization, methodology, writing, supervision, funding acquisition.

Data Availability

16S Soil Metagenome Dataset from a Retreating Glaciers Area in the High Tropical Andes Mountains (Original data) (NCBI SRA).

Acknowledgements

This work was supported by funding from NSF grants #1821657 and DBI #2217840. The research, sample export, and sample import were authorized by R.D. 135-2023-MIDDAGRI-SERFOR-DGGSPFFS-DGSPF, 003931-SERFOR, and USDA P330-21-00210. We thank Steven K. Schmidt, Felipe Crispin Condori, Wilian Crispin Jancco, and the park guards and management of ACR Ausangate for their assistance.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Supplementary Materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2026.112758.

References

[1] K. Barnard-Kubow, 16S Soil Metagenome Dataset from a Retreating Glaciers Area in the High Tropical Andes Mountains. NCBI SRA, 2025.
[2] M. Huss, et al., Toward mountains without permanent snow and ice, Earth's Future 5 (2017) 418–435.
[3] A.M. Milner, et al., Glacier shrinkage driving global changes in downstream systems, Proc. Natl. Acad. Sci. U.S.A. 114 (2017) 9770–9778.
[4] W.W. Immerzeel, et al., Importance and vulnerability of the world's water towers, Nature 577 (2020) 364–369.
[5] J.L. Darcy, et al., Phosphorus, not nitrogen, limits plants and microbial primary producers following glacial retreat, Sci. Adv. 4 (2018) eaaq0942.

[6] S. Cauvy-Fraunié, O. Dangles, A global synthesis of biodiversity responses to glacier retreat, Nat. Ecol. Evol. 3 (2019) 1675–1685.
[7] A.J. Pain, J.B. Martin, E.E. Martin, J.T. Salinas-Reyes, C. Bennett, Glacial retreat converts exposed landscapes from net carbon sinks to sources, Commun. Earth. Environ. 6 (2025) 424.
[8] J.A. Bradley, J.S. Singarayer, A.M. Anesio, Microbial community dynamics in the forefield of glaciers, Proc. R. Soc. B. 281 (2014) 20140882.
[9] F. Cuesta, et al., New land in the Neotropics: a review of biotic community, ecosystem, and landscape transformations in the face of climate and glacier change, Reg. Environ. Chang. 19 (2019) 1623–1642.
[10] D.R. Nemergut, et al., Microbial community succession in an unvegetated, recently deglaciated soil, Microb. Ecol. 53 (2007) 110–122.
[11] K.E. Reider, et al., Wild Andean camelids promote rapid ecosystem development after glacier retreat, Sci. Rep. 14 (2024).
[12] Y. Liu, et al., Salinity drives archaeal distribution patterns in high altitude lake sediments on the Tibetan Plateau, FEMS. Microbiol. Ecol. 92 (2016).
[13] S. Ciccazzo, Dynamic of Bacterial Community Colonization in High-Altitude Mountain Environments, University of Milan, 2014.
[14] T.A. Seimon, et al., Long-term monitoring of tropical alpine habitat change, Andean anurans, and chytrid fungus in the Cordillera Vilcanota, Peru: results from a decade of study, Ecol. Evol. 7 (2017) 1527–1540.
[15] S. Senn, et al., The functional biogeography of eDNA metacommunities in the post-fire landscape of the Angeles national forest, Microorganisms 10 (2022) 1218.
[16] S. Senn, et al., De Novo Leaf transcriptome assembly and metagenomic studies of coast Live Oak (Quercus agrifolia), Appl. Microbiol. 5 (2025) 24.
[17] J.J. Kozich, S.L. Westcott, N.T. Baxter, S.K. Highlander, P.D. Schloss, Development of a dual-index sequencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq illumina sequencing platform, Appl. Environ. Microbiol. 79 (2013) 5112–5120.
[18] E. Bolyen, et al., Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2, Nat. Biotechnol. 37 (2019) 852–857.
[19] S. Andrews, FastQC, Babraham Bioinformatics, Babraham Institute, 2010.
[20] P. Ewels, M. Magnusson, S. Lundin, M. Käller, MultiQC: summarize analysis results for multiple tools and samples in a single report, Bioinformatics 32 (2016) 3047–3048.
[21] B.J. Callahan, et al., DADA2: high-resolution sample inference from Illumina amplicon data, Nat. Meth. 13 (2016) 581–583.