

Chronic environmental radioactivity suppresses microbial diversity and activity in threatened glacier surface ecosystems

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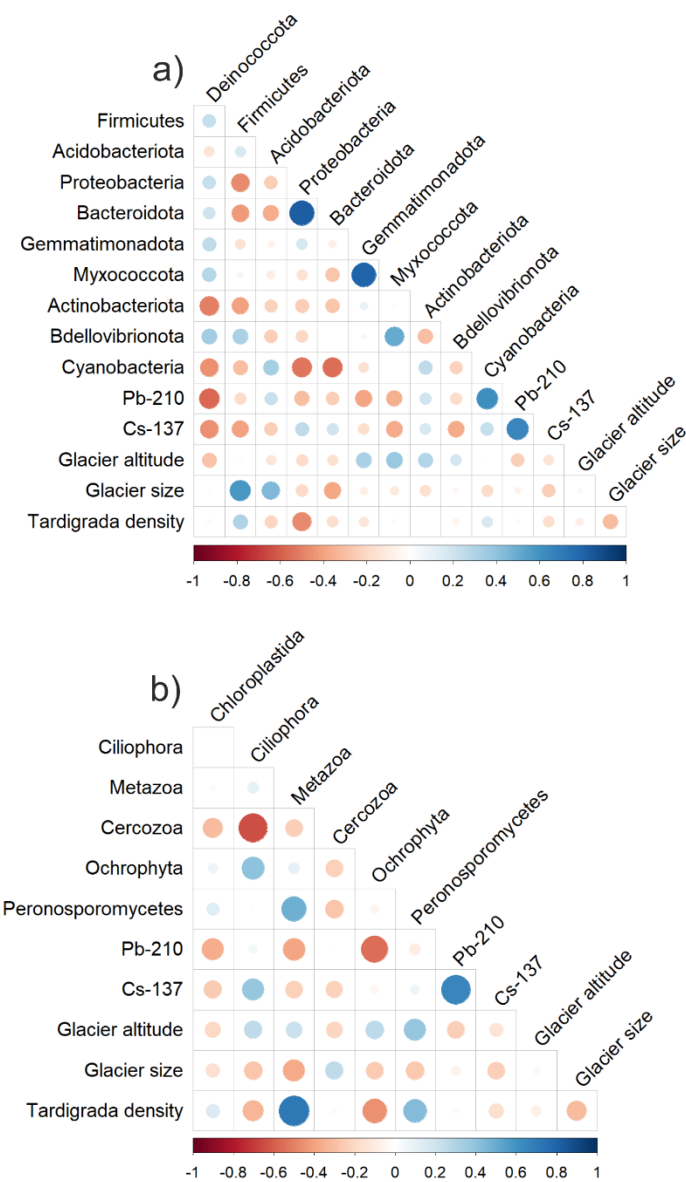
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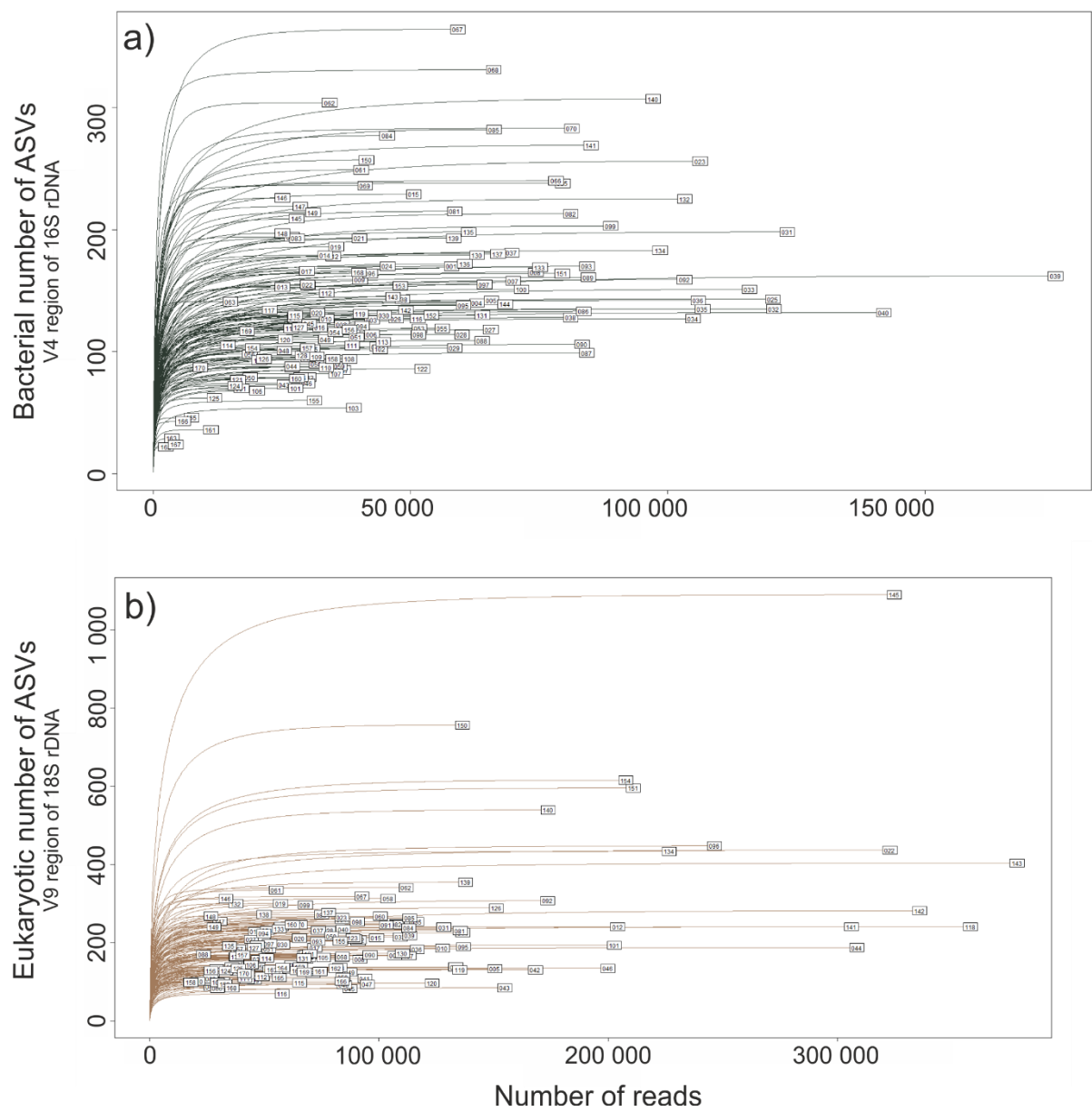
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SUPPLEMENTARY MATERIALS

Supplementary Figure 1. Pearson correlation between the relative abundance of bacteria (a) and eukaryotes (b) and the activity concentration of ^{137}Cs and ^{210}Pb .



Supplementary Figure 2. Rarefaction curves for bacterial (A) and eukaryotic (B) ASVs across samples.



Supplementary Table 1. The results of quality assurance for reference material CRM IAEA-447 (INTERNATIONAL ATOMIC ENERGY AGENCY, Certified Reference Material Certificate IAEA-447, IAEA, Vienna, 1-7 pp.).

Reference material/standard (reference date)	²¹⁰ Pb (Bq kg ⁻¹)		¹³⁷ Cs (Bq kg ⁻¹)	
	measured	certified	measured	certified
IAEA 447 (2021-03-01)	324 ± 4	306 ± 15 ^a	306 ± 13	328 ± 8 ^a
IAEA 447 (2021-12-17)	308 ± 11	306 ± 15 ^a	318 ± 10	328 ± 8 ^a

^aIAEA, 2004

Supplementary Table 2. Primers used for amplification of the V4 region 16S rDNA V4 and the V9 region of 18S rDNA.

Region	Primer pair	References
V4 16S rDNA	V4F (5'-CGATCAGCAGCCGCGGTAATA-3') V4R (5'-GGACTACCAGGGTATCTAA-3')	Makowska et al. (2020) Therese et al. (1998)
V9 18S rDNA	1391F (5'-GTACACACCGCCCGTC-3') EukBr (5'-TGATCCTTCTGCAGGTTCACCTAC-3')	Lane (1991) Medlin et al. (1988)

Supplementary Table 3. Loss of amplicon reads through data processing.

Region	Input reads	Passed quality filtering	Passed denoising	Passed chimera removal	Passed post denoising QC
V4 of 16S rDNA	34 997 235	16 557 237(-52.7 %)	16 270 630 (-1.7 %)	14 329 326 (-11.9 %)	7 697 760 (-46.3 %)
V9 of 18S rDNA	23 863 449	21 684 498 (-9.1 %)	21 627 713 (-0.3 %)	21 220 134 (-1.9 %)	20 857 593 (-1.7 %)

Supplementary Table 4. List of KEGG pathways analysed in this study, including pathway codes, names, and functional categories (DNA repair or metabolism and stress response).

Pathway	KEGG code	Mechanism category	Abbreviation
Base excision repair	ko03410	DNA repair	BER
Nucleotide excision repair	ko03420	DNA repair	NER
Mismatch repair	ko03430	DNA repair	MMR
Homologous recombination	ko03440	DNA repair	HR
Non-homologous end joining	ko03450	DNA repair	NHEJ
Pentose phosphate pathway (NADPH)	ko00030	Metabolism & stress response	PPP
Glutathione metabolism	ko00480	Metabolism & stress response	GSH
Selenocompound metabolism	ko00450	Metabolism & stress response	Se metabolism
Protein folding	ko04141	Metabolism & stress response	Protein folding
Protein processing	ko04142	Metabolism & stress response	Protein processing
ABC transporters	ko02010	Metabolism & stress response	ABC transporters
Two-component system	ko02020	Metabolism & stress response	Two-component
DNA replication	ko03030	Metabolism & stress response	DNA replication
Bacterial translation	ko03010	Metabolism & stress response	Translation
Central carbon metabolism	ko00010	Metabolism & stress response	Glycolysis

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