A comprehensive dataset of microbial abundance, dissolved organic carbon, and nitrogen in Tibetan Plateau glaciers

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Abstract. Glaciers are recognized as a biome dominated by microorganisms and a reservoir of organic carbon and nutrients. Global warming remarkably increases glacier melting and runoff, which has a significant impact on the carbon and nitrogen cycle of downstream ecosystems. The Tibetan Plateau (TP), dubbed "the water tower of Asia", owns the largest mountain glacial area at mid- and low-latitudes. However, limited data of microbial abundance, organic carbon, and nitrogen in TP glaciers have been reported, which severely hinders our understanding of the regional carbon and nitrogen cycle. This work constructed a new dataset on microbial abundance, dissolved organic carbon (DOC), and total nitrogen (TN) for TP glaciers. In this dataset, there are 5409 records from 12 glaciers for microbial abundance of ice cores and snow pits, and there are 2532 records from 38 glaciers for DOC and TN of five habitats, including ice core, snow pit, surface ice, surface snow, and proglacial runoff. These glaciers cover diverse geographic and climatic regions, where the multiyear average air temperature range from -13.4 °C to 2.9 °C and the multiyear average precipitation range from 76.9 mm to 927.8 mm. This makes the constructed dataset qualified for large-scale researches across the TP. To the best of our knowledge, this is the first dataset of microbial abundance and TN in TP glaciers and also the first dataset of DOC in ice cores on the TP. This new dataset provides important information for the studies on carbon and nitrogen cycle in glacial ecosystems, especially for the assessment of potential impacts of glacier retreat on downstream ecosystems under global warming. The datasets are available from the National Tibetan Plateau/Third Pole Environment Data Center (https://doi.org/10.11888/Cryos.tpdc.271841, Liu, 2021).

1 Introduction

Glaciers are not only an important component of the global climate system, but also recognized as a biome dominated by microorganisms and a reservoir of organic material and nutrients (Anesio and Laybourn-Parry, 2012; Hood et al., 2015).

There exist abundant and active microorganisms in multiple types of habitats such as surface snow and ice, cryoconite holes, proglacial runoff, the englacial ice and subglacial sediments despite the harsh environmental conditions (e.g. sustained low temperature, lack of nutrition and strong radiation) (Anesio et al., 2017; Hodson et al., 2008). These glacial microorganisms play an important role in the carbon cycle of glacial ecosystem and draw increasing attention in recent years (Liu et al., 2016a; Smith et al., 2017; Irvine-Fynn et al., 2021).

Due to the carbon fixation of glacial microorganisms and atmospheric deposition, glaciers are large pools of biologically available carbon and nitrogen, two indispensable elements to life (Hodson et al., 2008; Dubnick et al., 2017), and serve as important material and energy sources for downstream aquatic ecosystems, which is especially important for the nutrient-poor ecosystems like the sparsely vegetated high-alpine valleys and oligotrophic alpine lakes (Hood et al., 2015). Glaciers are also key species pools for downstream aquatic ecosystems and it has been found that the downstream bacterial and fungal communities were significantly affected by glacier-originating taxa (Fell et al., 2021; Liu et al., 2021). Under global climate warming, global glaciers are melting at an accelerating rate. Therefore, the carbon, nitrogen and microorganisms in glaciers are becoming more and more important for downstream ecosystems, and need more investigations and studies (Hood et al., 2009; Singer et al., 2012; Fellman et al., 2015; Wadham et al., 2016).

The Tibetan Plateau (TP), dubbed "the water tower of Asia", owns the largest mountain glacial area at mid- and low-latitudes (Yao et al., 2012). Glaciers on the TP are the sources of large rivers in Asia and thus of great importance for regional environments (Yao et al., 2019). However, due to harsh climate conditions and poor traffic accessibility, there have been limited observations of organic carbon, nitrogen and microorganisms in TP glaciers. In particular, very few such data in ice cores has been published, and even for surface snow and ice data, the spatial coverage is poor (Hood et al., 2015; Liu et al., 2016b). Data scarcity significantly hindered our understanding on the biogeochemical cycle in TP glaciers and the surrounding downstream regions.

In this study, we aim to construct a comprehensive dataset of microorganisms, dissolved organic carbon (DOC), and total nitrogen (TN) in TP glaciers by compiling deep ice-core samples and extensive surface snow and ice samples, which on the one hand can provide fundamental data for analysing the storage, spatial pattern and related drivers of glacier carbon and nitrogen on the TP, and on the other hand can facilitate the researches on glacier biogeochemical cycle and the impact of glacier retreat on downstream ecosystems.

2 Study area

The TP covers an area of about 2.5 million km^2, with an average altitude of more than 4000 m above sea level. Climate over the TP is primarily influenced by the interaction between the Asian monsoon and the westerly wind (Tian et al., 2001). The TP and its surrounding regions contain the largest number of glaciers outside the poles with an area of about 47 thousand km^2 (Yao et al., 2012). These glaciers are important water resources for downstream areas and play a crucial role in regional water supply (Immerzeel et al. 2010). The glaciers on the TP are mainly distributed in the Kunlun, Nyainqntanglha,

Himalayas and Karakoram mountains, and most glaciers are located between 4500-6500 m above sea level (Liu et al., 2015). The glaciers can be divided into three types (Shi et al., 2000): marine glaciers (mainly distributed in the southeast of TP), subcontinental glaciers (mainly distributed in the northeast and southern margin of TP), and the continental glaciers (mainly distributed in the west of TP). Most of the TP glaciers except those in the Karakoram region are experiencing strong retreat under climate warming (Yao et al., 2012; Wang et al., 2021).

3 Sample distribution and laboratory measurements

3.1 Sample distribution

In this study, 5409 microbial abundance samples from 12 glaciers across the TP were collected as shown in Fig. 1(a), including 5210 ice core samples from 7 glaciers and 199 snow-pit samples from 7 glaciers. For DOC and TN, 2532 samples from 38 glaciers were collected as shown in Fig. 1(b), including 1625 ice core samples from 7 glaciers, 180 surface ice samples from 17 glaciers, 100 snow pit samples from 4 glaciers, 254 surface snow samples from 28 glaciers, and 397 runoff samples from 16 glaciers.

The sampled glaciers covered diverse climate conditions. The multiyear average air temperature ranged from -13.4 ℃ (the Guliya glacier) to 2.9 ℃ (the Zhuxigou glacier), and the multiyear average precipitation ranged from 76.9 mm (the No.15 glacier) to 927.8 mm (the 24K glacier). These conditions cover the main types of environments for glaciers on the TP, which made the dataset comprehensive and representative.

3.2 Sample distribution

Ice cores were drilled from the accumulation zones of nine glaciers to depths from 11 to 173 m (Fig. 1). Both microbial abundance and DOC/TN samples were collected in five glaciers (i.e. Muztagh Ata (MSTG), Cuopugou (CPG), Zuoqiupu (ZQP), Noijin Kangsang (NJKS), and East Rongbuk (ERB)), there were only microbial abundance samples in the Laohugou (LHG) and Geladandong (GLDD) glacier, and there were only DOC and TN samples in the Muji (MJ) and Dunde (DD) glacier. The MJ, MSTG, LHG, DD, and GLDD glacier are mainly influenced by the westerly, while the CPG, ZQP, NJKS, and ERB glacier are strongly influenced by monsoon. The samples were transported frozen to the laboratory.

Snow pits were digged at the accumulation zones of seven glaciers (Fig 1). Both microbial abundance and DOC/TN samples were collected in the GLDD, Zhadang (ZD), Palon No.4 (PL4), and ERB glacier, and there were only microbial abundance samples in the DD, Mengdagangri (MDGR), and Yala glacier. Fourteen snow pits in total were sampled for microbial abundance measurement, including six at the ZD glacier during April, May, June, August, September and October in 2006, two at the MDGR glacier during 2006 and 2007, two at different altitudes at the PL4 glacier, and one for each at the DD, GLDD, ERB, and Yala glacier, respectively. Four snow pits were sampled for DOC and TN concentration measurement with one snow pit in each glacier among GLDD, ZD, PL4 and ERB. At each pit, snow was sampled from top to bottom at 5 or 10 cm interval using steel scoop.
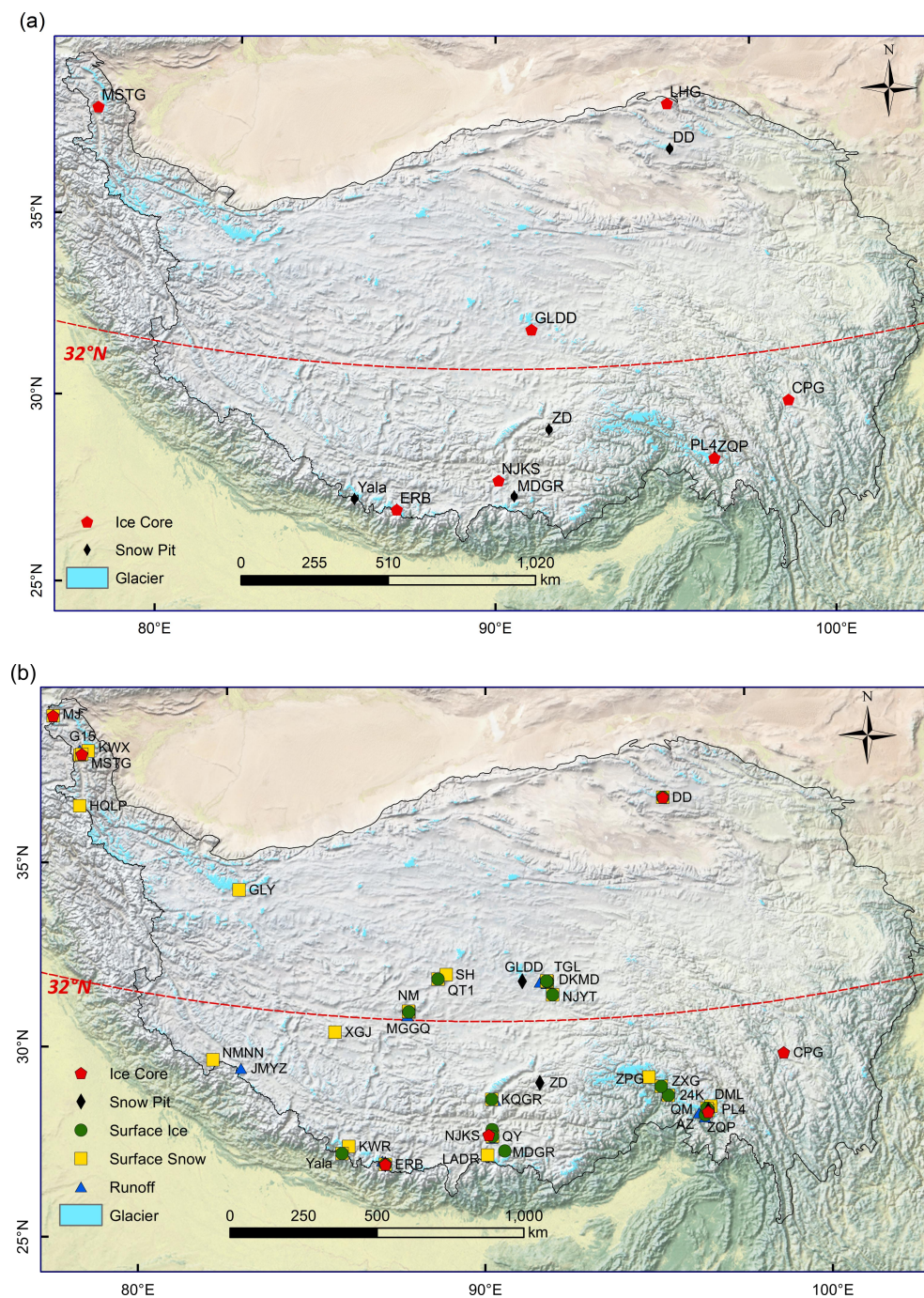
Figure 1: Location of sampled glaciers for microbial abundance (a), DOC and TN (b) on the Tibetan Plateau. The abbreviations of glacier names were labelled in the map and the full names were available in the supplement.
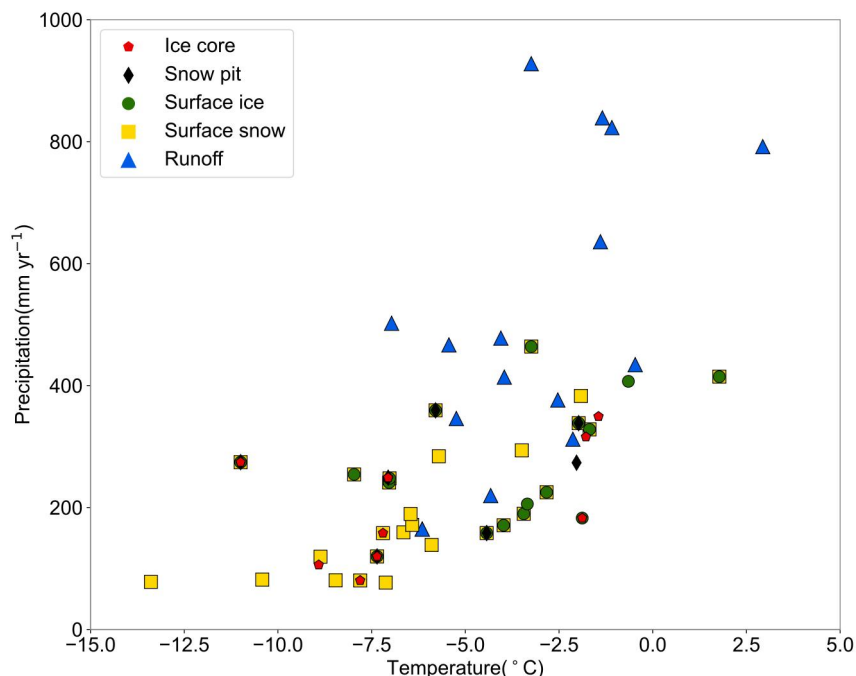
Figure 2: Muti-year average air temperature and precipitation of sampled glaciers.

Surface snow (within 10 cm deep) were sampled using steel scoop at different altitudes from ablation to accumulation zone in 28 glaciers for DOC and TN concentration measurement. Surface ice samples were collected with a precleaned ice axe at the ablation zones in 17 glaciers. Ice and snow samples were stored in well-sealed WhirlPak bags (WhirlPak®, Nasco, USA) and transported to laboratory under frozen conditions.

Water samples were collected from proglacial runoff of 16 glaciers using 100 mL polycarbonate bottles pre-cleaned using 1% HCl (Nalgene, USA). Totally eight sets of 24-h water samples were collected at six glaciers (i.e. MSTG, Tanggula Longxiazailongba (TGL), Qiangtang No.1 (QT1), Qiangyong (QY), Tonkmadi (DKMD), and PL4) to investigate the diurnal variation of conductivity, pH, DOC, NO3- and TN of water. Water samples were transported in a dark container with ice keeping cold. In the laboratory, samples were kept in dark and frozen at -20°C until analysis.

3.3 Laboratory measurements

Each ice core was cut into 5-10 cm long sections in a -20 °C clean room. After cutting away the outer 1-2 cm annulus with knife, the inner ice was used. Knife and containers were pre-cleaned using 1% HCl and filter water. Snow and ice were melted overnight and the meltwater were aliquoted into 20 mL glass bottles. The glass bottles were leached using 1% HCl, rinsed by deionized water for 3 times and combusted (450 °C for > 3 h) before use.

Flow cytometry combined with the nucleic acid stain is a fast, accurate, quantitative and reproducible technique for counting the number of bacteria (Hammes et al., 2008; Prest et al., 2013), which was used for the enumeration of bacteria in this study.

1.98 mL of meltwater was fixed with glutaraldehyde (final concentration: 1%), stored at 4 °C, and analysed within 8 hours after staining with SYBR Green I (Marie et al., 1997). SYBR Green I is the standard dye used in the analysis of various environments to distinguish bacteria from abiotic particles (Van Nevel et al., 2017; Mao et al., 2022). Staining could capture inorganic particulates and result in false positives, which were mitigated by the following experimental controls in this study:1) if particulates were large, they would have been removed in the filtering step before analysis; 2) fixed gating could distinguish inorganic background and bacteria (Prest et al., 2013). Samples were processed on an EPICS ALTRA II flow cytometer (Beckman Coulter, USA) (Liu et al., 2016a). Duplicate samples were measured with a relative standard deviation lower than 10%. Flow cytometry data were collected and analysed with CytoWin 4.31 software.

The DOC and TN concentrations were measured with a TOC-Lcph (Shimadzu Corp., Japan) following standard methods (Greenberg et al., 1992). Concentrations of ions were measured using a Dionex ion Chromatograph System 2000 (Dionex Corp, USA) as previously described (Liu et al., 2016a). The in-situ conductivity and pH of proglacial runoff were measured with the YSI EXO2 Water Quality Sonde.

4 Data description of microbial abundance

4.1 Snow pit

The microbial abundance in snow pits of the seven sampled glaciers (i.e.) ranged from 212 to 721 305 cells mL^{-1}, and the mean microbial abundance values were 2 117, 8 664, 218 305, 12 479, 14 442, 64 515, and 12 401 cells mL^{-1} for DD, GLDD, ZD, PL4, MDGR, Yala, and ERB, respectively. The range of these measurements was consistent with the results of existing researches using the flow cytometer method (e.g. 3.7-25.0×10^4 cells mL^{-1} in the Kuytun 51 Glacier, Tianshan Mountains; Xiang et al., 2009; on the order of 10^3 to 10^5 cells mL^{-1} in the alpine snowpack; Lazzaro et al., 2015; Fillinger et al., 2021). Fig. 3(a) shows the spatial distribution of log(microbial abundance) for sampled snow pits averaged in each glacier. Generally, there were lower microbial abundance in the westerly region than in the monsoon region. The DD glacier, located in the northeast of the TP, had the lowest microbial abundance (i.e. 2 177 cells mL^{-1}), while the ZD glacier, located in the south of the TP, had the highest abundance (i.e. 218 305 cells mL^{-1}), which was 100 times higher as that in DD. Figure 4 shows the variation of log(microbial abundance) with depth in each snow pit, but no consistent patterns were found.
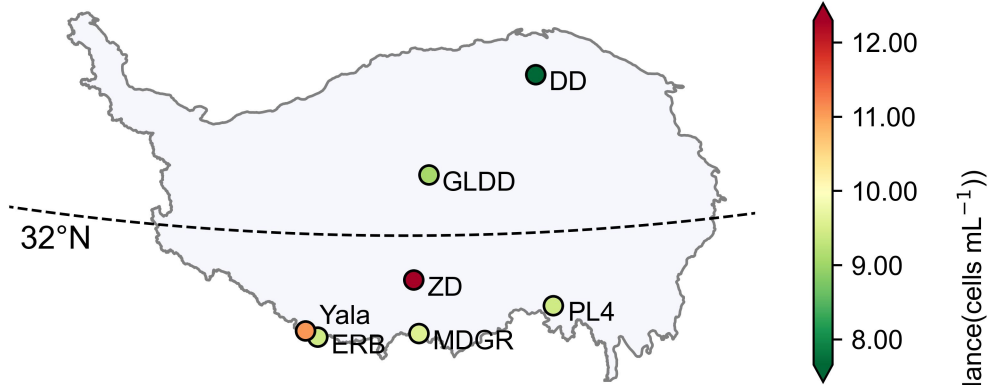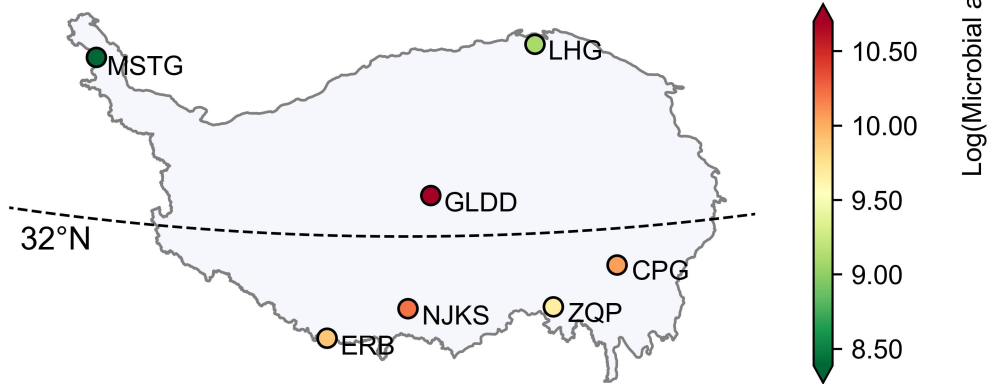
Figure 3: The spatial distribution of log(microbial abundance) for sampled snow pits (a) and ice cores (b) averaged in each glacier.

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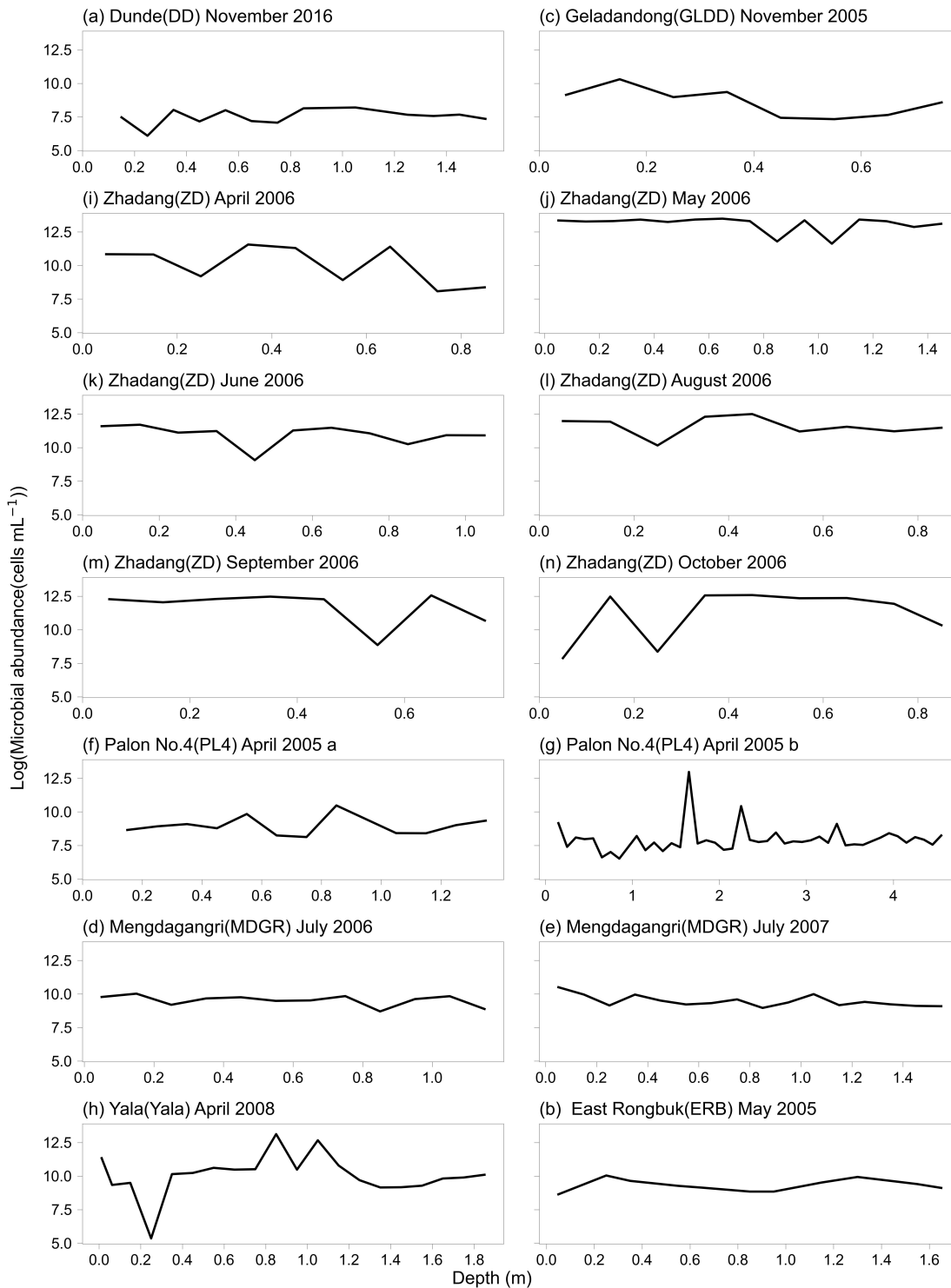
Figure 4: The variation of log(microbial abundance) with depth in each sampled snow pit.

4.2 Ice core

Bacteria in glacier are originated from atmospheric deposition, and it has been reported that microorganisms originating from the Saharan Desert have been found thousands of kilometers away in the Caribbean and European Alps (Kellogg et al., 2006). The deposited microorganisms are subjected to a range of post-depositional environmental selection processes (Chen et al., 2021), until they are buried by snow and eventually frozen in the ice core. The microbial abundance in ice cores of the seven sampled glaciers had a wide range from 63 to 1 130 080 cells mL^{-1}, and the mean microbial abundance values were 4 389, 8 617, 44 318, 23 311, 15 648, 27 330, and 19 656 cells mL^{-1} for MSTG, LHG, GLDD, CPG, ZQP, NJKS, and ERB, respectively. These values generally fell in the range of existing researches using the flow cytometer method (e.g. on the order of 10^4 to 10^7 in the GISP2 Greenland ice core; Miteva et al., 2009; 6.53×10^3 - 2.89×10^5 cells mL^{-1} in the West Antarctic Ice Sheet Divide ice core; Santibanez et al., 2016). The spatial distribution of average log(microbial abundance) in each ice core was shown in Fig. 3(b). Two ice cores in the north (i.e. MSTG and LHG) had obvious lower microbial abundance (i.e. 4 389 and 8 958 cells mL^{-1}, respectively) than those in the south where the microbial abundance was at least 15 688 cells mL^{-1}. Fig. 4 showed the variation of log(microbial abundance) along depth in each ice core. The microbial abundance in ice cores in the CPG and NJKS glacier had decreasing trends with depth, while that in the MSTG glacier had an increasing trend. There existed low-frequency fluctuations for the microbial abundance in ice cores in the ERB, GLDD, and LHG glacier, and there were mainly high-frequency fluctuations in the ZQP glacier.
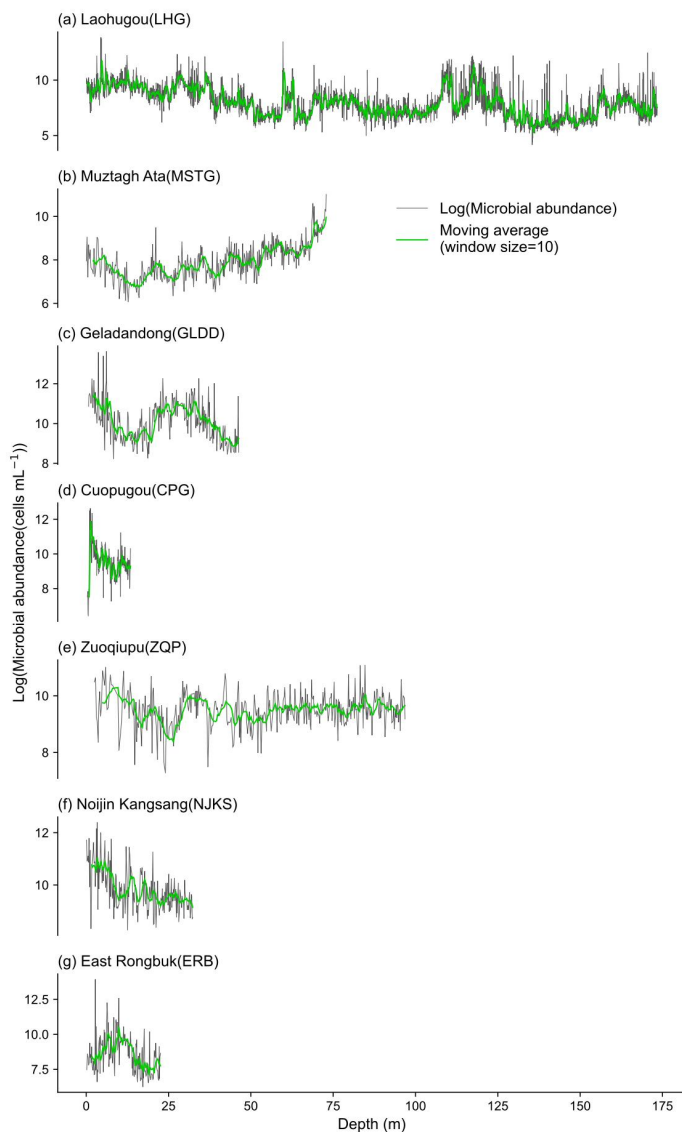
Figure 5: The variation of log(microbial abundance) along depth in seven ice cores. The window size used in the moving average method was 10.

5 Data description of DOC and TN

5.1 Ice core

Organic carbon and nitrogen in ice cores can be both from both allochthonous or autochthonous sources. It has been reported that the wet DOC deposition ranged from 47 to 330 mg C m^{-2} y^{-1} (Yan et al., 2020) and the wet N deposition ranged from 44 to 155 mg N m^{-2} y^{-1} on the TP (Liu et al., 2015). In addition, microbial carbon fixation has also been reported in glacier

The DOC concentrations in ice core samples ranged from 0.005 to 5.05 mg L^{-1} with an average value of 0.54±0.38 mg L^{-1}. These values are larger than the englacial DOC concentrations in global mountain glaciers reported by Hood et al. (2015) (0.01 to 1.20 mg L^{-1}, 0.29±0.03 mg L^{-1} on average), which may be related to the higher aerosol concentration in the area around the TP (Spracklen et al., 2011). The TN concentrations ranged from 0.001 to 1.15 mg L^{-1} with an average value of 0.24±0.16 mg L^{-1}. Fig. 6 shows the variation of DOC and TN concentrations along vertical profiles in ice cores of the MSTG and ERB glacier. Generally, there are decreasing trends of DOC and TN with depth, suggesting that atmospheric deposition has been increasing in recent years. There exist large inter-annual variations in the serial data with some occasional large values, which may be related to historical large sand storms.
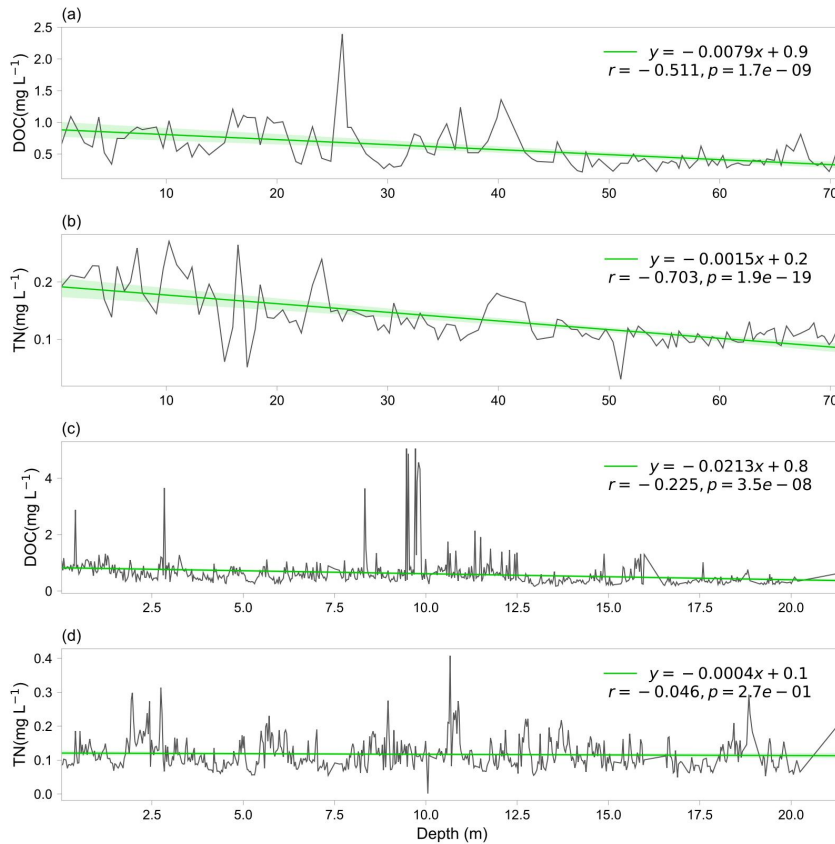
Figure 6: Variation of DOC (a, c) and TN (b, d) concentrations along vertical profiles in ice cores of the MSTG (Muztagh Ata) glacier (a, b) and the ERB (East Rongbuk) glacier (c,d).

5.2 Surface ice, surface snow and snow pit

The DOC concentrations ranged from 0.08 to 9.0 mg L^{-1} (0.89±1.05 mg L^{-1}), from 0.12 to 11.65 mg L^{-1} (1.19±1.78 mg L^{-1}), and from 0.05 to 16.15 mg L^{-1} (0.72±1.71 mg L^{-1}) in surface ice, surface snow, and snow pits, respectively. These values are comparable to the DOC concentrations of surface ice in four TP glaciers reported by Liu et al. (2016b) (i.e. 1.01±0.22 mg L^{-1}), and those of surface snow (mean values ranging from 0.16 to 1.17 mg L^{-1}) and snow pits (mean values ranging from 0.21 to 0.81 mg L^{-1}) in TP glaciers summarized by Gao et al. (2020). The TN concentrations ranged from 0.01 to 1.88 mg L^{-1} (0.19±0.22 mg L^{-1}), from 0.07 to 3.06 mg L^{-1} (0.34±0.35 mg L^{-1}), and from 0.02 to 0.84 mg L^{-1} (0.15±0.15 mg L^{-1}) in surface ice, surface snow, and snow pits, respectively. Fig. 7 shows the spatial distribution of DOC and TN concentrations for surface snow and surface ice. For the DOC concentrations of surface snow, there is a decreasing pattern from south to north in the monsoon dominant region (i.e. located on the south the 32°N). The DOC and TN concentrations in the westerly and monsoon regions were not significantly different according to the Mann Whitney U test. The differences of TN concentrations between the two regions were evident with higher values in the westerly region although the Mann Whitney U test was not significant with a p value of 0.056.
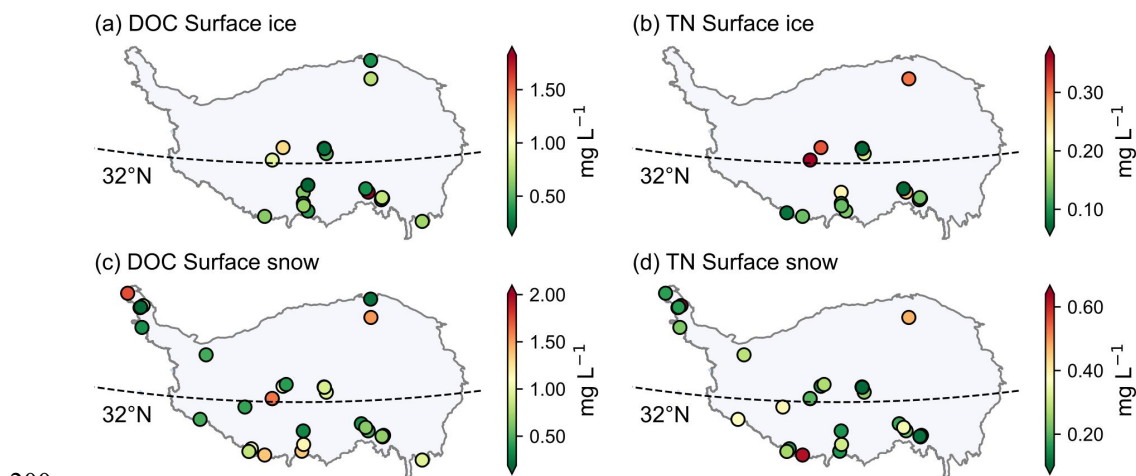
Figure 7: The spatial distribution of DOC (a, c) and TN (b, d) concentrations for surface ice (a, b) and surface snow (c, d).

5.3 Runoff

The DOC concentrations ranged from 0.16 to 4.94 mg L^{-1} (0.79±0.68 mg L^{-1}) in proglacial runoff, which are consistent with the range from 42 glaciers worldwide (0.10 - 3.40 mg L^{-1}) summarized by Li et al. (2017). The TN concentration range from 0.05 to 2.3 mg L^{-1} (0.29±0.22 mg L^{-1}). The runoff water is alkaline with pH values ranging from 7.3 to 12.4 (9.10±0.88). Fig. 8 shows the spatial distribution of DOC, TN, NO$_3^-$ concentrations and pH for proglacial runoff on the TP. For the DOC concentrations of runoff, there is decreasing trend from west to east. There were significant differences in the TN and NO$_3^-$ concentrations of runoff between the westerly and monsoon regions with p values less than 0.01 according to the Mann

Whitney U test and the values in the westerly region were higher. The pH values in the westerly region were also larger in
the westerly region than in the monsoon region although the Mann Whitney U test was not significant with a p value of 0.07.

Fig. 9 shows the diurnal variation of DOC, TN, NO₃⁻, and conductivity in proglacial runoff of the Qiangyong glacier. There
did not exist obvious patterns in the diurnal curve of DOC, while there were obvious unimodal patterns for TN, NO₃⁻, and
conductivity. These observations are very helpful for biogeochemical studies at fine temporal resolutions.
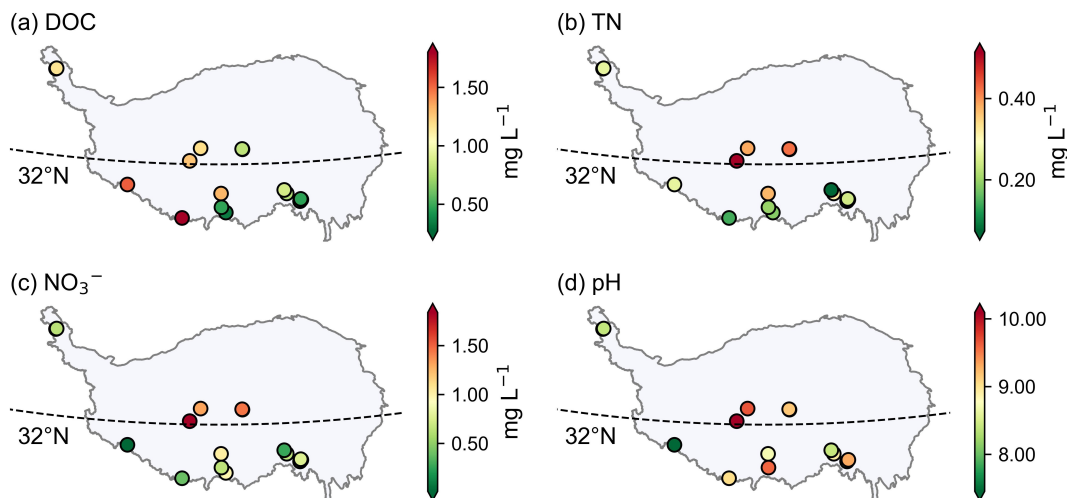
Figure 8: The spatial distribution of DOC (a), TN (b), NO₃⁻ (c) concentrations and pH (d) for proglacial runoff on the
Tibetan Plateau.
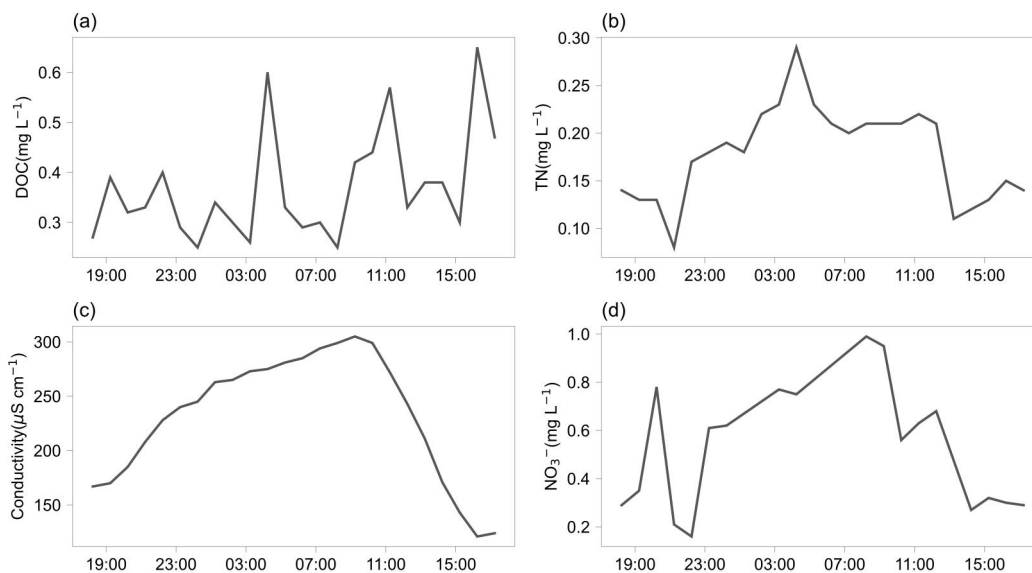
Figure 9: The 24-h time series of DOC (a), TN (b), conductivity (c), and NO₃⁻(d) in proglacial runoff of the Qiangyong glacier.

5.4 Comparison among different habitats

220   Considering that observations of DOC and TN concentrations were available in all the five main glacial habitats (i.e. ice core, snow pits, surface ice, surface snow, and proglacial runoff), differences among glacial habitats were compared. The boxplots of different types of samples showed that the DOC and TN concentrations in ice cores were lower than those in surface ice (Fig. 10). The Mann-Whitney-Wilcoxon test showed the difference was significant for DOC with a p value of 0.02 and not significant for TN with a p value of 0.24. The DOC and TN concentrations were also lower in snow pits than in surface snow.

225   The difference was not significant for DOC with a p value of 0.19 and was significant for TN with a p value of 0.03. The DOC and TN concentrations in proglacial runoff were similar to those in surface snow.
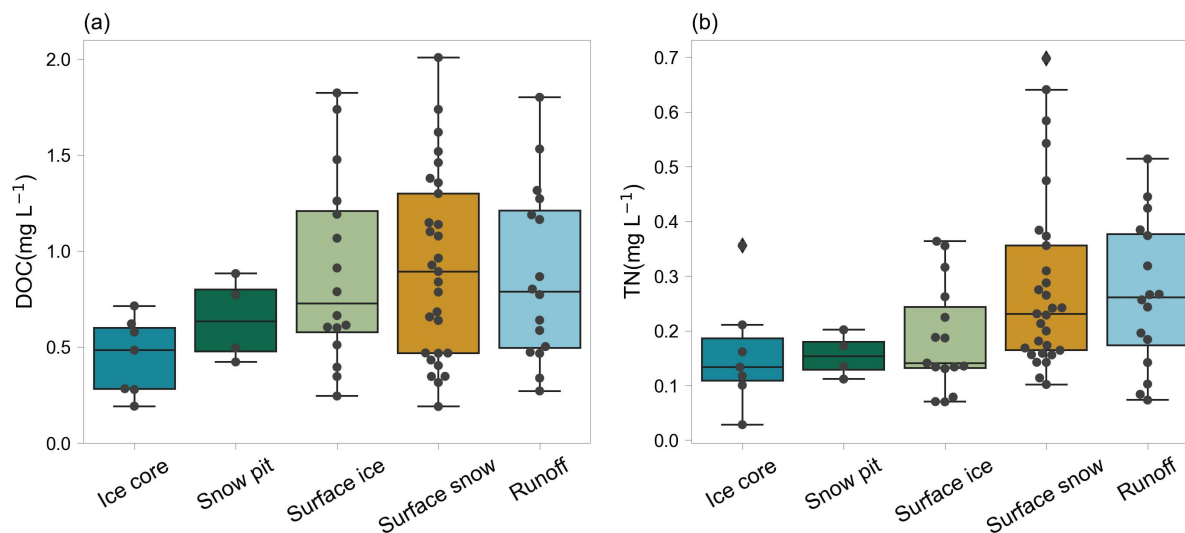
Figure 10: The boxplots of the DOC (a) and TN (b) concentrations in five main glacial habitats on the Tibetan Plateau.

6 Data availability

230   The dataset of microbial abundance, DOC and TN in ice core, snow pit, surface ice and snow from the Tibetan Plateau glaciers are accessible at the National Tibetan Plateau/Third Pole Environment Data Center (https://doi.org/10.11888/Cryos.tpdc.271841, Liu, 2021).

7 Conclusions

We constructed a new dataset of microbial abundance, DOC and TN for glaciers on the TP, comprising 5,409 microbial
235   abundance data from 12 glaciers and 2,532 DOC and TN data from 38 glaciers. The sampled glaciers cover diverse geographic and climatic regions, which makes it qualified for large-scale researches across the TP. This systematic dataset

can provide important information for the studies on carbon and nitrogen cycle in glacial ecosystems, their response to global climate change, and their impact on downstream ecosystems such as glacier-feed streams and lakes. The time series data of microbial abundance in ice cores can be used as an indicator of past climate change, and the spatial distribution of DOC and TN data can be used to estimate the storage and spatial distribution of glacier carbon and nitrogen, which are essential inputs for biogeochemical models of the glacial ecosystems. Considering its broad spatial and temporal coverage, this dataset can serve as an important data source for forecasting the impact of warming on glacial carbon cycle at regional and even global scales.

Author contributions

YL and JL designed the study and wrote the manuscript. PF and JL compiled and analysed the dataset. YL, BG, MJ, PL, GM, BX, and SK performed field sampling and experimental measurement. All authors contributed to the writing and editing of this paper.

Competing interests

The authors declare that they have no conflict of interest.

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References

Anesio, A. M. and Laybourn-Parry, J.: Glaciers and ice sheets as a biome, Trends Ecol. Evol., 27, 219-225, doi: 10.1016/j.tree.2011.09.012, 2012.

Anesio, A. M., Lutz, S., Chrismas, N. A. M., and Benning, L. G.: The microbiome of glaciers and ice sheets, npj Biofilms Microbiomes, 3, 1-11, doi:10.1038/s41522-017-0019-0, 2017.

Chen, Y., Liu, K., Liu, Y., Vick-Majors, T. J., Wang, F., and Ji, M.: Temporal variation in glacier snowpack bacterial communities mediated by nitrogen, Cryosph. Discuss., 2021, 1–23, https://doi.org/10.5194/tc-2021-215, 2021.

Dubnick, A., Wadham, J., Tranter, M., Sharp, M., Orwin, J., Barker, J., Bagshaw, E., and Fitzsimons, S.: Trickle or treat: The dynamics of nutrient export from polar glaciers, Hydrol. Process., 31, 1776-1789, https://doi.org/10.1002/hyp.11149, 2017.

Egge, E., Elferink, S., Vaulot, D., John, U., Bratbak, G., Larsen, A., and Edvardsen, B.: An 18S V4 rRNA metabarcoding

265   dataset of protist diversity in the Atlantic inflow to the Arctic Ocean, through the year and down to 1000 m depth, Earth Syst. Sci. Data, 13, 4913–4928, https://doi.org/10.5194/essd-13-4913-2021, 2021.

Fell, S. C., Carrivick, J. L., Cauvy-Frauinié, S., Crespo-Pérez, V., Hood, E., Randall, K. C., Nicholass, K. J. M., Tiegs, S. D., Dumbrell, A. J., and Brown, L. E.: Fungal decomposition of river organic matter accelerated by decreasing glacier cover, Nat. Clim. Chang., 11, 349-353, https://doi.org/10.1038/s41558-021-01004-x, 2021.

270   Fellman, J. B., Hood, E., Raymond, P. A., Hudson, J., Bozeman, M., and Arimitsu, M.: Evidence for the assimilation of ancient glacier organic carbon in a proglacial stream food web, Limnol. Oceanogr., 60, 1118-1128, https://doi.org/10.1002/lno.10088, 2015.

Fillinger, L., Hürkamp, K., Stumpp, C., Weber, N., Forster, D., Hausmann, B., Schultz, L., and Griebler, C.: Spatial and Annual Variation in Microbial Abundance, Community Composition, and Diversity Associated With Alpine Surface Snow,

275   Front. Microbiol., https://www.frontiersin.org/article/10.3389/fmicb.2021.781904, 2021.

Gao, T., Kang, S., Zhang, Y., Sprenger, M., Wang, F., Du, W., Wang, X., and Wang, X.: Characterization, sources and transport of dissolved organic carbon and nitrogen from a glacier in the Central Asia, Sci. Total Environ., 725, 138346, https://doi.org/https://doi.org/10.1016/j.scitotenv.2020.138346, 2020.

Greenberg Arnold, E. and Clesceri Lenore, S.: Standard methods for the examination of water and wastewater. USA:

280   American Public Health Association, 1992.

Hammes, F., Berney, M., Wang, Y., Vital, M., Köster, O., and Egli, T.: Flow-cytometric total bacterial cell counts as a descriptive microbiological parameter for drinking water treatment processes, Water Res., 42, 269–277, https://doi.org/https://doi.org/10.1016/j.watres.2007.07.009, 2008.

Hodson, A., Anesio, A. M., Tranter, M., Fountain, A., Osborn, M., Priscu, J., Laybourn-Parry, J., and Sattler, B.: Glacial

285   ecosystems, Ecol. Monogr., 78, 41-67, https://doi.org/10.1890/07-0187.1, 2008.

Hood, E., Battin, T. J., Fellman, J., O'Neel, S., and Spencer, R. G. M.: Storage and release of organic carbon from glaciers and ice sheets, Nat. Geosci., 8, 91-96, https://doi.org/10.1038/ngeo2331, 2015.

Hood, E., Fellman, J., Spencer, R. G. M., Hernes, P. J., Edwards, R., D'Amore, D., and Scott, D.: Glaciers as a source of ancient and labile organic matter to the marine environment, Nature, 462, 1044-1047, https://doi.org/10.1038/nature08580,

290   2009.

Immerzeel, W. W., van Beek, L. P. H., and Bierkens, M. F. P.: Climate Change Will Affect the Asian Water Towers, Science, 328, 1382, https://doi.org/10.1126/science.1183188, 2010.

Irvine-Fynn, T. D. L., Edwards, A., Stevens, I. T., Mitchell, A. C., Bunting, P., Box, J. E., Cameron, K. A., Cook, J. M., Naegeli, K., Rassner, S. M. E., Ryan, J. C., Stibal, M., Williamson, C. J., and Hubbard, A.: Storage and export of microbial

295   biomass across the western Greenland Ice Sheet, Nat. Commun., 12, 3960, https://doi.org/10.1038/s41467-021-24040-9, 2021.

Kellogg, C. A. and Griffin, D. W.: Aerobiology and the global transport of desert dust, Trends in Ecology & Evolution, 21, 638–644, https://doi.org/10.1016/j.tree.2006.07.004, 2006.

Lazzaro, A., Wismer, A., Schneebeli, M., Erny, I., and Zeyer, J.: Microbial abundance and community structure in a melting
300   alpine snowpack, Extremophiles, 19, 631–642, https://doi.org/10.1007/s00792-015-0744-3, 2015.

Li, X., Ding, Y., Xu, J., He, X., Han, T., Kang, S., Wu, Q., Mika, S., Yu, Z., and Li, Q.: Importance of Mountain Glaciers as a Source of Dissolved Organic Carbon, 123, 2123–2134, https://doi.org/https://doi.org/10.1029/2017JF004333, 2018.

Liu, K., Liu, Y., Hu, A., Wang, F., Zhang, Z., Yan, Q., Ji, M., and Vick-Majors, T. J.: Fate of glacier surface snow-originating bacteria in the glacier-fed hydrologic continuums, Environ. Microbiol., 23, 6450-6462,
305   https://doi.org/10.1111/1462-2920.15788, 2021.

Liu, S., Yao, X., Guo, W., Xu, J., Shangguan, D., Wei., J., Bao., W., and Wu., L.: The contemporary glaciers in China based on the Second Chinese Glacier Inventory, Acta Geographica Sinica, 70, 3-16, 2015. (in Chinese)

Liu, Y.: Dataset of microbial abundance, dissolved organic carbon, and total nitrogen in Tibetan Plateau glaciers, National Tibetan Plateau Data Center, https://doi.org/10.11888/Cryos.tpdc.271841, 2021.

310   Liu, Y., Priscu, J. C., Yao, T., Vick-Majors, T. J., Xu, B., Jiao, N., Santibáñez, P., Huang, S., Wang, N., Greenwood, M., Michaud, A. B., Kang, S., Wang, J., Gao, Q., and Yang, Y.: Bacterial responses to environmental change on the Tibetan Plateau over the past half century, Environ. Microbiol., 18, 1930-1941, https://doi.org/10.1111/1462-2920.13115, 2016a.

Liu, Y., Xu, J., Kang, S., Li, X., and Li, Y.: Storage of dissolved organic carbon in Chinese glaciers, J. Glaciol., 62, 402-406, https://doi.org/10.1017/jog.2016.47, 2016b.

315   Liu, Y. W., Xu-Ri, Wang, Y. S., Pan, Y. P., and Piao, S. L.: Wet deposition of atmospheric inorganic nitrogen at five remote sites in the Tibetan Plateau, Atmos. Chem. Phys., 15, 11683–11700, https://doi.org/10.5194/acp-15-11683-2015, 2015.

Mao, G., Ji, M., Xu, B., Liu, Y., and Jiao, N.: Variation of High and Low Nucleic Acid-Content Bacteria in Tibetan Ice Cores and Their Relationship to Black Carbon, Front. Microbiol., 13, https://www.frontiersin.org/article/10.3389/fmicb.2022.844432, 2022.

320   Marie, D., Partensky, F., Jacquet, S., and Vaulot, D.: Enumeration and cell cycle analysis of natural populations of marine picoplankton by flow cytometry using the nucleic acid stain SYBR Green I, Appl. Environ. Microbiol., 63, 186-193, 1997.

Prest, E. I., Hammes, F., Kötzsch, S., van Loosdrecht, M. C. M., and Vrouwenvelder, J. S.: Monitoring microbiological changes in drinking water systems using a fast and reproducible flow cytometric method, Water Res., 47, 7131-7142, https://doi.org/https://doi.org/10.1016/j.watres.2013.07.051, 2013.

325   Santibanez, P. A., Mcconnell, J. R., and Priscu, J. C.: A flow cytometric method to measure prokaryotic records in ice cores: an example from the West Antarctic Ice Sheet Divide drilling site, J. Glaciol., 62, 655 – 673, https://doi.org/DOI: 10.1017/jog.2016.50, 2016.

Shi., Y. and Liu., S.: Estimation of the response of Chinese glaciers to global warming in the 21st century, Science Bulletin, 45, 434-438, 2000. (in Chinese)

330   Singer, G. A., Fasching, C., Wilhelm, L., Niggemann, J., Steier, P., Dittmar, T., and Battin, T. J.: Biogeochemically diverse organic matter in Alpine glaciers and its downstream fate, Nat. Geosci., 5, 710-714, https://doi.org/10.1038/ngeo1581, 2012.

Smith, H. J., Foster, R. A., McKnight, D. M., Lisle, J. T., Littmann, S., Kuypers, M. M. M., and Foreman, C. M.: Microbial formation of labile organic carbon in Antarctic glacial environments, 10, 356–359, https://doi.org/10.1038/ngeo2925, 2017.

Spracklen, D. V, Jimenez, J. L., Carslaw, K. S., Worsnop, D. R., Evans, M. J., Mann, G. W., Zhang, Q., Canagaratna, M. R.,

335   Allan, J., Coe, H., McFiggans, G., Rap, A., and Forster, P.: Aerosol mass spectrometer constraint on the global secondary organic aerosol budget, 11, 12109–12136, https://doi.org/10.5194/acp-11-12109-2011, 2011.

Telling, J., Anesio, A. M., Tranter, M., Irvine-Fynn, T., Hodson, A., Butler, C., and Wadham, J.: Nitrogen fixation on Arctic glaciers, Svalbard, J. Geophys. Res. Biogeosciences, 116, https://doi.org/https://doi.org/10.1029/2010JG001632, 2011.

Tian, L., Masson-Delmotte, V., Stievenard, M., Yao, T., and Jouzel, J.: Tibetan Plateau summer monsoon northward extent

340   revealed by measurements of water stable isotopes, J. Geophys. Res. Atmos., 106, 28081-28088, 2001.

Wadham, J. L., Hawkings, J., Telling, J., Chandler, D., Alcock, J., O'Donnell, E., Kaur, P., Bagshaw, E., Tranter, M., Tedstone, A., and Nienow, P.: Sources, cycling and export of nitrogen on the Greenland Ice Sheet, 13, 6339-6352, https://doi.org/10.5194/bg-13-6339-2016, 2016.

Van Nevel, S., Koetzsch, S., Proctor, C. R., Besmer, M. D., Prest, E. I., Vrouwenvelder, J. S., Knezev, A., Boon, N., and

345   Hammes, F.: Flow cytometric bacterial cell counts challenge conventional heterotrophic plate counts for routine microbiological drinking water monitoring, Water Res., 113, 191-206, https://doi.org/https://doi.org/10.1016/j.watres.2017.01.065, 2017.

Wang, Q., Yi, S., and Sun, W.: Continuous Estimates of Glacier Mass Balance in High Mountain Asia Based on ICESat-1,2 and GRACE/GRACE Follow-On Data, Geophys. Res. Lett., 48, e2020GL090954, https://doi.org/10.1029/2020GL090954,

350   2021.

Xiang, S.-R., Shang, T.-C., Chen, Y., Jing, Z.-F., and Yao, T.: Changes in diversity and biomass of bacteria along a shallow snow pit from Kuytun 51 Glacier, Tianshan Mountains, China, J. Geophys. Res. Biogeosciences, 114, https://doi.org/10.1029/2008JG000864, 2009.

Yan, F., Wang, P., Kang, S., Chen, P., Hu, Z., Han, X., Sillanpää, M., and Li, C.: High particulate carbon deposition in

355   Lhasa—a typical city in the Himalayan–Tibetan Plateau due to local contributions, Chemosphere, 247, 125843, https://doi.org/https://doi.org/10.1016/j.chemosphere.2020.125843, 2020.

Yao, T., Thompson, L., Yang, W., Yu, W., Gao, Y., Guo, X., Yang, X., Duan, K., Zhao, H., Xu, B., Pu, J., Lu, A., Xiang, Y., Kattel, D. B., and Joswiak, D.: Different glacier status with atmospheric circulations in Tibetan Plateau and surroundings, Nat. Clim. Chang., 2, 663-667, https://doi.org/10.1038/nclimate1580, 2012.

360   Yao, T., Xue, Y., Chen, D., Chen, F., Thompson, L., Cui, P., Koike, T., Lau, W. K.-M., Lettenmaier, D., and Mosbrugger, V.: Recent third pole's rapid warming accompanies cryospheric melt and water cycle intensification and interactions between monsoon and environment: Multidisciplinary approach with observations, modeling, and analysis, Bull. Am. Meteorol. Soc., 100, 423-444, https://doi.org/10.1175/BAMS-D-17-0057.1, 2019.

Zhang, Y., Kang, S., Wei, D., Luo, X., Wang, Z., and Gao, T.: Sink or source? Methane and carbon dioxide emissions from

365 cryoconite holes, subglacial sediments, and proglacial river runoff during intensive glacier melting on the Tibetan Plateau, Fundam. Res., 1, 232–239, https://doi.org/https://doi.org/10.1016/j.fmre.2021.04.005, 2021.