

Microbial Diversity in the Glacial Ecosystem of Antarctic, Arctic, and Tibetan Plateau: Properties and Response to the Environmental Condition

Birendra Prasad Sharma^{1,2,3}, Subash Adhikari^{2,3,4}, Ganesh Paudel⁵, Namita Paudel Adhikari^{1,2,3*}

¹Key Laboratory of Alpine Ecology and Biodiversity, Institute of Tibetan Plateau Research, Chinese Academy of Sciences, Beijing, China

²Key Laboratory of Tibetan Environment Changes and Land Surface Processes, Institute of Tibetan Plateau Research, Chinese Academy of Sciences, Beijing, China

³University of Chinese Academy of Sciences, Beijing, China

⁴Janapriya Multiple Campus, Tribhuvan University, Pokhara, 33700, Nepal

⁵Institute of Forestry, Tribhuvan University, Pokhara, Nepal

*Corresponding author: n.paudel@itpcas.ac.cn

Article History

Received 16 April 2020

Revised 13 October 2020

Accepted 25 November 2020

Abstract

Microorganisms, as successive members of the food web, play a major role in biological processes. They are found in environments ranging from extremely hot to harsh cold temperatures. Thus, the study of bacterial communities in various ecosystems is of great concern around the world. The glacier is one of the parts of the cryosphere, which is the key component and sensitive indicator of climatic and environmental changes. A glacial ecosystem is a habitat for various microorganisms, i.e., autotrophic and heterotrophic. Different physicochemical parameters like temperature, pH, electrical conductivity, the input of nutrient concentration, precipitation, ions concentrations, etc. influence the microbial diversity in the glacial ecosystem for their metabolic processes. Successive studies of bacterial communities in the Himalayan glacial ecosystem are reliable proxies to know the relationships between microbial biodiversity and climate change since the Himalayan glaciers are free from anthropogenic activities. After the study of the relevant literature, it is clear that the researches

have been carried out in the Polar Regions, and the Tibetan plateau mainly focused on the glacial ecosystem. This review concluded that Proteobacteria, Bacteroidetes, Cyanobacteria, Firmicutes, Verrucomicrobia, and Actinobacteria were the most dominant bacterial phyla via 16S rRNA clone libraries and Illumina MiSeq. Alter in landscapes, nutrient cycles, exposure of light, shifting on the concentration of different elements, glacier retreats were the major components for survival strength of dominant bacterial phyla. However, limited studies on the glacial ecosystem of the Himalayas have been published. Thus, the study of bacterial abundance, diversity, and community in the Himalayas will help plug this research gap.

Keywords: Glacial ecosystem, Glaciers, Illumina MiSeq, Microbial diversity

Introduction

Earth's system comprises five major components, i.e., hydrosphere, atmosphere, biosphere, lithosphere, and cryosphere, that exhibit an imperative role to exchange mass and energy in the whole universe. The cryosphere is the portion of Earth's system which includes a glacier, snow cover, glacier ice, ice sheets, and permafrost (Stocker et al., 2014). A glacier displays the profound indicator of climate change that is globally distributed at low to high latitudes and accumulates the high snowfall. Continuously melting of the glacier due to the variations on different physicochemical characters shows the notable signal of climate change (Liu et al., 2019a) Glaciers occupy approximately 16 million km² (~10 %) of the Earth's total land area, and the remaining 500,000 km² as ice caps, ice fields, and glaciers located at high latitudes above snowlines around the world. These sites are mainly located in the northern hemisphere, i.e., the Arctic, and in the southern hemisphere covers the Tibetan plateau, and sub-Antarctic islands (Shakti et al., 2013). Glaciers harbor different vital ecosystems through the varied microbial communities (Anesio et al., 2009), which support the life of several distinct biomes (Anesio & Laybourn-Parry, 2012; Hodson et al., 2008). Different ecological regions are classified in the glacier ecosystem, which contains disparate habitats for microorganisms but mainly dominated by bacteria, eukarya, and archaea; they are: supraglacial (snow and ice), englacial (ice), subglacial (sediments), proglacial (streams and lakes) and glacier forefields (Anesio & Laybourn-Parry, 2012; Boetius et al., 2015; Hotaling et al., 2017). Microbial life on, in, and underneath of glaciers is generally imposed by a combination of organic and inorganic matters where interactions between bedrocks, sediments, incident solar radiation, and seasonal melting influences the role of the glacier on the downstream level (Lutz et al., 2015; Boetius

et al., 2015; Chuvochina et al., 2011; Hodson et al., 2008).

The surface of glaciers is termed as a supraglacial ecosystem that comprises a heavy range of microbes in their surface snow, ice, cryoconite holes, supraglacial streams, and moraines (Boetius et al., 2015). Due to the strong radiation from the sun and less oxygen from the atmosphere, autotrophic, chemolithotrophic, and heterotrophic bacteria were found. Where heterotrophic bacteria like Proteobacteria, Bacteroidetes, and Actinobacteria dominated in these regions, play a key role in the nutrient cycle (Lutz et al., 2017; Franzetti et al., 2016). The Englacial zone is located a few meters deeper than the supraglacial region. In this habitat, the availability of sun rays and liquid water is low, and only a few nutrient sources are available (Wilhelm et al., 2014). Ribosomal, 16S/genetics (Water Microbiology) (Electronic. That is why a few organisms can survive, and biological activity is likely insignificant compared to other zones (Hodson et al., 2008). The temperate glacial ice transfers in the form of liquid water and passes through the means of drainage channels (fractures and cavities) from the supraglacial surface (Boetius et al., 2015; Lütz-Meindl & Lütz, 2006; Fountain et al., 2005). Viable microorganisms like diverse metabolically active archaeal, bacteria, fungal species, and few viruses are likely found in the basal zone and subglacial region (Butinar et al., 2007). Proglacial lakes are formed by the moraine's damming during glacier retreat, a glacial dam, or melting of glacial ice meets and exceed beyond the glacier terminus, accumulates a large amount of water, nutrients, and microorganisms which affecting microbial composition in lakes due to the variation on different physicochemical parameters (Liu et al., 2017; Jacobsen et al., 2012). Inter connections between microbiological and ecological ventures on, in, or below the glacier directly influence the ecosystem of the glacier-fed stream and lakes, which render the microbial diversity of proglacial streams and lakes geographically diverse (Hotaling et al., 2017; Fellman et al., 2015). Proglacial streams and lakes are the important components of the glacial ecosystem, which strongly controls the geomorphology and ecology of these systems through the connection between glacial processes and downstream levels (Hotaling et al., 2017; O'Neel et al., 2015; Wilhelm et al., 2014). The shifting of elevation (higher to lower or lower to higher) comprises the variations on different environmental parameters like temperature, nutrients, pH, electrical conductivity, etc. indicates the random composition of microbial diversities in glacier habitat (Wilhelm et al., 2013). In polar and alpine lake ecosystem, metabolism processes are restricted by the availability of physicochemical parameters which

play an important regulatory mechanism for the bacterial growth and metabolism (Pomeroy & Wiebe, 2001) where, airborne transport and atmospheric deposition on glacial surfaces is main nutrient matters for the bacterial diversity (Granéli et al., 2004).

A few studies related to High Throughput Sequencing methods, also called Next-generation sequencing (NGS) in glacier ecosystem which provides a systematic classification of bacterial community composition and diversity as compared to traditional culture and clone library methods in mountain glaciers. This research gap helps to promote the possibility of life on mountain glaciers according to their landscape of biodiversity. It helps to explore microbial biodiversity on glacier's surface and underneath during harsh climatic, atmospheric, or geological conditions.

Nutrients and Environmental Factors

Glaciers, a primary and important water source for many living organisms in the universe which contains different sources of macro/micro-nutrients where microbial activities depend on the concentrations of dissolved organic carbon, nitrogen, and phosphorous (Dubnick et al., 2017; Stibal et al., 2008). This system consists of distinct and well-studied biogeochemical cycles in the surface of the snow, glacier ice, cryoconite holes, supraglacial and proglacial stream/lakes, and sediment (Hodson, 2006). Different researchers studied the glacier explore and highlight their form, role, availabilities, and cycling of nutrients from upstream to downstream (Lawson et al., 2014; Hood et al., 2009). Various microorganisms are present in glacier play a potentially active role in numerous biological and ecological processes through numerous nutrient cycles in the glacial ecosystem (Møller et al., 2013; Moller et al., 2011; Larose et al., 2010a; Larose et al., 2010b; Simon et al., 2009; Hodson et al., 2008). In pristine environmental conditions like low temperature, high solar radiation, pH, less oxygen, strong winds, high altitude, etc. help to stimulate the microbial habitats of biome for functional ecosystem (Hauptmann et al., 2014; Maccario et al., 2014; Larose et al., 2013; Møller et al., 2013). Allochthonous carbon sources help to support the growth of heterotrophic and photosynthetic microorganisms in cryoconite holes (microbial hotspots) using different exogenous organic sources and autochthonous extracellular polymeric substance (EPS) (Hotaling et al., 2017). The energy source for heterotrophic and photoautotrophic organisms is mainly represented by EPS (Cook et al., 2016; Takeuchi et al., 2010).

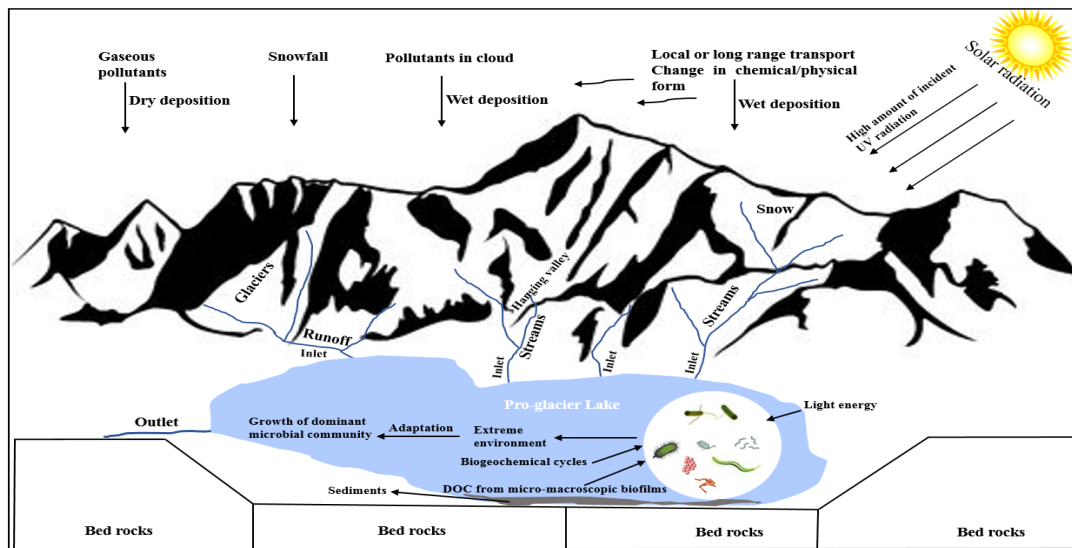
For the activation and functioning in the ecosystem, microorganisms uptake the energy sources from basal melting, which comprises of fine powder of rocks and sedimentary organic

carbon, geothermal energy, and supraglacial input serves as a hotspot for microbial life (Hotaling et al., 2017). Light source plays an imperative role in the glacier ecosystem, but in the absence of light, some chemolithoautotrophs fix the inorganic carbon through the dark fixation at the base of the subglacial region and offer food webs (Christner et al., 2014). The composition of minerals and carbon substrates in bedrock influences the structure and functional activities of a microbial community through redox chemistry with microbial metabolism (Skidmore et al., 2005). Unambiguously, sulfate reduction, sulfate oxidation, nitrate reduction, nitrification, and denitrification occurred in a subglacial zone where the release of methane from the labile carbon source act as the energy sources for microorganisms (Hodson et al., 2005). The glacial ecosystems are geochemically diverse in community composition, which helps to determine through different factors including variations of stream water, electrical conductivity, pH, temperature, seasonal weathering, which affects in physical conditions of glaciers, energy loads in sediment, redox conditions, and many more (Hotaling et al., 2017; Fellman et al., 2014).

The growth of a dominant microbial community and richness in proglacial lakes and streams (Fig. 1) seem to depend upon the biological existence of various microbial habitats, sediment, hydrogeochemical sources and limnological compositions (Mojib et al., 2009), different stream characteristics, particular concentrations of Ca, SiO₂ and Fe, specific appearances of local geology and bedrock compositions (Fegel et al., 2016). Differences in various compositions from supraglacial towards proglacial indicate the amount of input that contributes to each source for the bacterial community (Fountain et al., 2005). Physicochemical parameters of surface snow, glacial ice, streamwater (run-off), and biofilms have a remarkable role in colonized the bacterial community across the habitats. Variations of stream water (run-off) along the proglacial possess strong control on the physicochemical parameters like electrical conductivity, pH, and high incident UV radiation (Fellman et al., 2014; Hood et al., 2009). These properties play a highly significant role which influences bacterial diversity along with microbial association even at small magnitudes (Wilhelm et al., 2013). The structural and functional properties of bacterial communities are also linked with the physicochemistry of bacterial taxa (Freimann et al., 2013). Changes in the rate of flow of stream water (run-off), temperature, sediment load, pH, and many more parameters have an important role for the residential and non-residential biota (Hotaling et al., 2017; Sheik et al., 2015; Milner et al., 2010; Brown et al., 2007).

Figure 1

Microbial Diversity in the Proglacial Ecosystem along with the Proglacial Environment



Diversity and Taxonomy of Bacteria in the Proglacial Ecosystems of Different Region
Overview from Polar Region

A study conducted by Amato et al., (2007) revealed ten distinct isolated bacterial strains from snow cover composed of Proteobacteria, Firmicutes, and Actinobacteria by culture-based method from a polythermal glacier in Svalbard (Norway). These bacteria are highly active in the degradation of organic compounds found in surface snow with the ability to metabolize substrates like formate, acetate, and propionate for sustainable growth during the melting season. A study on snow and meltwater on Ny-Å lesund (Svalbard, Norway) by Larose et al., (2010a) using the clone library found Betaproteobacteria, Sphingobacteria, Flavobacteria, Acidobacteria, and Alphaproteobacteria as dominant classes. Both the samples were sampled in the early spring and late spring, which shows the diversity in microbial community composition. The study on bacterial diversity in a glacier foreland of high arctic on Ny-Å lesund (West Spitsbergen, Norway) by Schutte et al., (2010) Bacterial/analysis/genetics</keyword><keyword>Ice Cover/*microbiology</keyword><keyword>RNA, Ribosomal, 16S/genetics</keyword><keyword>Sequence Analysis, DNA/methods</keyword><keyword>*Soil Microbiology</keyword><keyword>Time Factors</keyword></keywords><dates><year>2010</year><pub-dates><date>Mar</date></pub-dates></dates><isbn>1365-294X (Electronic using 454 pyrosequencing of 16S rRNA gene where

Acidobacteria, Chlamydia, Nitrospira, Chloroflexi, Bacteroidetes, Proteobacteria, Firmicutes, Spirochaetes, Actinobacteria, Cyanobacteria, Verrucomicrobia, and Drinococcus-Thermus are identified but Spirosoma, Sphingomonas, Terromonas, Hymenobacter, Gemmatimonas, Brevundimonas, and Sphingopyxis were dominated one. The 454 pyrosequencing and PCR amplification were used by Wilhelm et al., (2013) revealed that Proteobacteria, Bacteroidetes, and Actinobacteria were the dominant bacterial phyla whereas Verrucomicrobia, Nitrospira, and Cyanobacteria were specific to glacial ice and stream water along the main chain of Austrian Alps where bacterial communities exhibit different levels of spatial variation and response to some variation on environmental factors. Peter & Sommaruga (2016) discovered Sphingobacteria, Flavobacteria, and Betaproteobacteria as abundant phyla using the 16S rRNA gene on 454 gene sequencing on the Austrian Central Alps at glacier melting. The study conducted in the Revelva River and the Lake Revvatnet (Southwestern Spitsbergen, Norway) incorporating Illumina Miseq by Kosek et al., (2019) reported that variations on a landscape, nutrients, and the effect on environmental parameters due to seasonal changes helps to fit the phyla like Proteobacteria, Actinobacteria, Bacteroidetes, Firmicutes, Verrucomicrobia, Tenericutes, Cyanobacteria, and Acidobacteria as dominant classes .

Worked out by Mojib et al., (2009) in the different categories of lakes in Schirmacher Oasis (Antarctica) like land-locked, proglacial and epi-shelf lakes was reported that Proteobacteria, Actinobacteria, Bacteroidetes, Fusobacteria, Verrucomicrobia, and Chlorobi show dominant phyla by using culture-independent and culture-dependent methods based upon bacterial 16S rRNA gene analysis. Study of Huang et al., (2013) on East Antarctica through culture-independent bacterial tag encoded FLX Amplicon Pyrosequencing (bTEFAP), clone library, and culture-based analysis targeting the eubacterial 16S rRNA gene. The most dominant bacterial phyla obtained from bTEFAP were Proteobacteria, Bacteroidetes, Actinobacteria, Chloroflexi, Actinobacteria, Firmicutes, Gemmatimonadetes, and Verucomicrobia, whereas Deinococcus-Thermus, Nitrospira, Candidate Division OP10, Planctomycetes, Candidate Division TM7, and Fusobacteria showed comparatively lower abundance in snow meltwater samples. Proteobacteria, Actinobacteria, Bacteroidetes, Fusobacteria, Verrucomicrobia, Chlorobi, and Candidate Division OP as dominant phyla while using the 16S rRNA gene. Hodson et al., (2017) discovered Proteobacteria, Bacteroidetes, Firmicutes, Acidobacteria, Cyanobacteria, Actinobacteria, and Verrucomicrobia were dominant bacterial phyla by using Illumina Miseq in Livingston Island of Maritime Antarctica. Weathering of dust and basal debris is likely to be an important contributing factor for biogeochemical and bacterial habitat.

A study carried out on Taylor Glacier (Antarctica) by Campen et al., (2019) using Illumina Miseq revealed Proteobacteria, Bacteroidetes and Actinobacteria were dominant bacterial phyla. Among the selected sampling sites from the Polar Regions, i.e., Arctic and Antarctica, for the study of abundant phyla using via different biological tools were shown in (Table 1 and 2) respectively.

Table 1

Summary Table of the Arctic Region

Arctic	Sampling site	Biological tools	Abundant phyla	References
Arctic	Kongsvegen glacier	Culture-based	Proteobacteria, Firmicutes Actinobacteria	Amato et al., 2007
Arctic	Svalbard (Norway)	Clone library	Betaproteobacteria, Sphingobacteria, Flavobacteria, Acidobacteria Alphaproteobacteria	Larose et al., 2010a
Arctic	Midre Lovén glacier	Clone library and 454 pyrosequencing	Spirosoma, Sphingomonas, Terromonas, Hymenobacter, Gemmatimonas, Brevundimonas Sphingopyxis Proteobacteria,	Schütte et al., 2010
Arctic	The Austrian Central Alps	PCR amplification and 454 pyrosequencing	Bacteroidetes, Actinobacteria, Verrucomicrobia, Nitrospira Cyanobacteria	Wilhelm et al., 2013
Arctic	Fasel fad lakes (Austrian Central Alps)	Clone library and 454 pyrosequencing	Sphingobacteria, Flavobacteria, Betaproteobacteria	Peter & Sommaruga, 2016

Arctic	Southwestern Spitsbergen (Norway)	Illumina MiSeq	Proteobacteria, Actinobacteria, Bacteroidetes, Firmicutes, Verrucomicrobia, Tenericutes, Cyanobacteria, Acidobacteria	Kosek et al., 2019
--------	-----------------------------------	----------------	---	--------------------

Table 2*Summary Table of the Antarctica Region*

Region	Sampling site	Biological tools	Abundant phyla	References
Antarctica	Schirmacher Oasis	Culture-based and Clone library	Proteobacteria, Actinobacteria, Bacteroidetes, Fusobacteria, Verrucomicrobia, Chlorobi	Mojib et al., 2009
Antarctica	East Antarctica (Lake Tawani)	Clone library and Culture-based	Proteobacteria, Actinobacteria, Bacteroidetes, Fusobacteria, Verrucomicrobia, Chlorobi Candidate Division OP	Huang et al., 2013
Antarctica	Livingston Island	Illumina Miseq	Proteobacteria, Bacteroidetes, Firmicutes, Acidobacteria, Cyanobacteria, Actinobacteria, Verrucomicrobia	Hodson et al., 2017
Antarctica	Taylor Glacier	Illumina Miseq	Proteobacteria, Bacteroidetes, Actinobacteria	Campen et al., 2019

Overview from the Third Pole Region

The third pole region covers the Tibetan plateau, and adjoining sites consists of high

mountains and snow covers with an average of 100,000 km² and 46000 glaciers and called Asia's water tower, supporting the livelihood of about 1.3 billion people (Adhikari et al., 2019a; 2019b, Adhikari et al., 2020; Zhang et al., 2015; Yao et al., 2012). An early study in glacier meltwater on the East Rongbuk Glacier (Mt. Everest) revealed that Proteobacteria (Alpha, Beta, and Gamma), Actinobacteria, and Firmicutes as a dominant phylum using 16S rRNA gene sequencing (Liu et al., 2009) 350 m on the East Rongbuk Glacier, Mount Everest

Extremophiles

89-99

13

1

Bacteria/genetics/growth & development/*isolation & purification

Base Sequence

DNA Primers

Microscopy, Electron, Transmission

Nepal

Phylogeny

Polymerase Chain Reaction

RNA, Ribosomal, 16S/genetics

Species Specificity

*Water Microbiology

2009

Jan

1433-4909 (Electronic. The research carried out on bacterial diversity by Liu et al., (2011) concerned about microbial diversity of three different environments, i.e., surface snow, glacial stream, and moraine lake in Yala glacier (Nepal). Moraine Lake and stream environment were dominated by Bacteroidetes, Betaproteobacteria, followed by Actinobacteria using 16S rRNA gene clone library and flow cytometry. This showed the variations in microbial patterns in different ecosystems where nutrient availability is the major factor. A study of Srinivas et al., (2011) in proglacial soil from Kafni glacier (India) by using the 16S rRNA gene clone library reported that phyla Proteobacteria, Bacteroidetes, Actinobacteria, Chloroflexi, Spirochaetae, Tenericutes, and Verrucomicrobia were abundant ones. A study in vertical variation in large stratified lake Nam Co (Central Tibet) by Liu et al., (2016) revealed Actinobacteria, Proteobacteria, followed by Cyanobacteria and Firmicutes were dominant phyla using 454 pyrosequencing which indicated that bacterial abundance (BA) decreased along with depth while the viral abundance increased. A study of Liu et al., (2017) in the alpine glacial-fed lake from Western Tibet (Kalakuli) using 16S rRNA gene-based Illumina MiSeq sequencing reported Actinobacteria, Proteobacteria, Verrucomicrobia, Firmicutes, and Planctomycetes as dominant phyla, which shows the bacterial diversity was significantly affected by the ratio of water nutrients (TN and DOC) but bacterial community compositions were significantly correlated with both biotic and abiotic elements of BA, temperature, and

pH. Bacteriological study in a glacial-fed Tibetan lake conducted by Liu et al., (2019a) using 16S rRNA gene sequencing and Illumina MiSeq observed that Bacteroidetes, Actinobacteria, Proteobacteria (Alpha and Beta), Firmicutes, and Cyanobacteria were dominant phyla in lake samples. Proteobacteria showed comparatively higher abundance in glacial melting (summer) time, where temperature and conductivity show a strong correlation with bacterial community composition. An investigation on bacterial diversity and abundance due to elevation pattern in mountain streams (Gangrigabu, Southeast Tibet) by Liu et al., (2019b) in the southeast of Tibetan Plateau using Illumina MiSeq showed that Proteobacteria (Alpha, Beta, and Gamma), Bacteroidetes, Actinobacteria, and Acidobacteria were dominant phyla. While all of these phyla were decreased with elevation but the bacterial phyla of Acidobacteria tend to decrease with increasing elevation. (Table 3) shows a summary among the sampling sites selected from the Third pole region for the study of abundant phyla using different biological methods.

Table 3

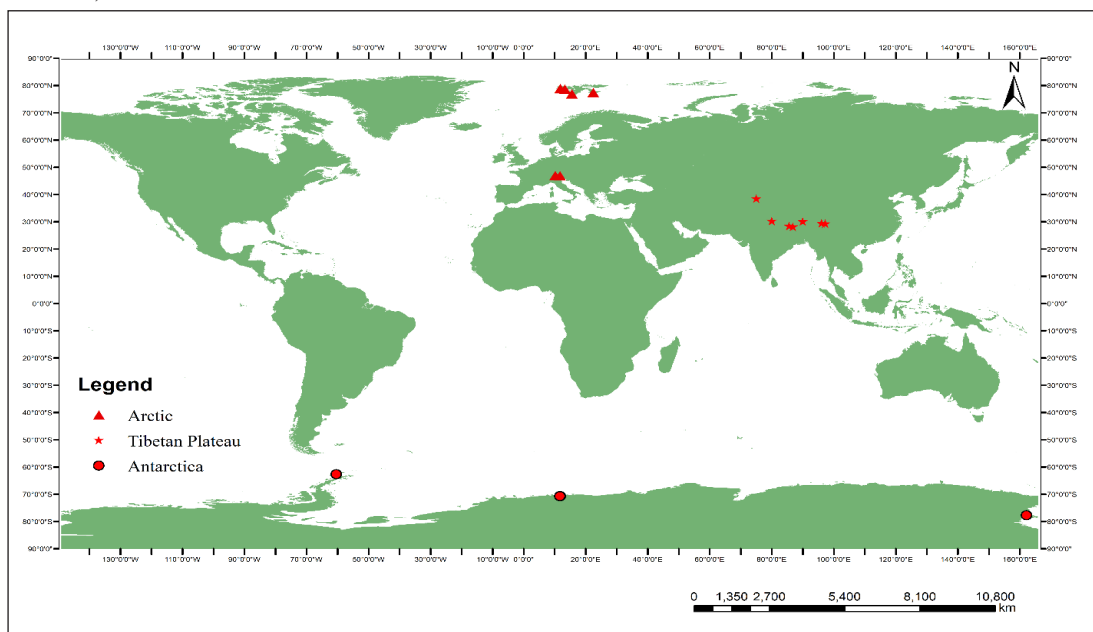
Summary Table of Third Pole Regions

Region	Sampling site	Biological tools	Abundant phyla	References
Tibetan Plateau	East Rongbuk glacier (Mt. Everest)	Clone library	Proteobacteria (Alpha, Beta, and Gamma), Actinobacteria Firmicutes	Liu et al., 2009
Tibetan Plateau	Yala glacier (Nepal)	Clone library and flow cytometry	Bacteroidetes, Betaproteobacteria, Actinobacteria	Liu et al., 2011
Tibetan Plateau	Kafni Glacier(India)	Clone library	Proteobacteria, Bacteroidetes, Actinobacteria, Chloroflexi, Spirochaetae, Tenericutes Verrucomicrobia	Srinivas et al., 2011
Tibetan Plateau	Lake Nam Co (Central Tibet)	454 pyrosequencing	Actinobacteria, Proteobacteria, Cyanobacteria Firmicutes	Liu et al., 2016

Tibetan Plateau	Lake Ranwu	Clone library and Illumina MiSeq	Bacteroidetes, Actinobacteria, Proteobacteria (Alpha and Beta), Firmicutes, Cyanobacteria	Liu et al., 2019a
Tibetan Plateau	Gangrigabu mountain (Southeast Tibet)	Illumina Miseq	Proteobacteria (Alpha, Beta, and Gamma), Bacteroidetes, Actinobacteria, Acidobacteria	Liu et al., 2019b

Figure 2

Global Study of Microbial Diversity in the Glacial Ecosystem (Antarctic, Arctic, and Tibetan Plateau)



Conclusion

Although having different significant research carried out in the various fields on the Earth’s surface, but mountain glaciers are one of the most understudied areas, which tend to bring an

endangered and rapid change on the Earth's topography and ecosystems, among them glacial ecosystem was underestimated. It is particularly interesting that deep mountain lakes occur at the base of glacier terminus and that these rapidly developed hydrological systems provide a unique opportunity to study the initial formation, colonization and, growth of microbial diversity in the glacial environment. This review will contribute to extending the role of microbial diversity that how microbial community will shifts the resources like nutrients and different cycling processes, i.e., nitrogen, sulfur, and carbon from glaciers on, within, and beneath of glaciers. From these, we can know that how these resources from glaciers affect the downstream ecosystems. This review concluded that Proteobacteria, Bacteroidetes, Cyanobacteria, Firmicutes, Verrucomicrobia, and Actinobacteria were the most dominant bacterial phyla. Such bacteria have a strong affinity to environmental parameters such as nutrients, temperature, radiation, electrical conductivity, pH, discharge volume of stream, and sediment load. The aforementioned dominant bacterial phyla showed a strong ability for survival in atypical conditions. Different biological approaches were used to revealed diverse results in bacterial communities. For the general approach to reviewing bacterial communities from Polar region and Third pole regions using 16S rRNA clone libraries and Illumina MiSeq from published papers. As we know, mountain glaciers accumulate the snowfall and exceed seasonal melting where different factors linked to climate change may favor significantly altering landscapes, nutrients, exposure of light, shifting the concentrations of different elements, and much more association which is interconnected with glaciers helps to alter the bacterial diversity, ecosystems, and their functions. Polar Regions and Third Pole regions are located in high altitudes and experience climate change, which contains diverse bacterial communities. Thus, high coverage biological analysis tools need to be used to study the exact picture of microbial diversity and community compositions.

Mountain glaciers are the key components of varied ecosystems with different physicochemical aspects where microbial diversity plays a dominant role in it. Global warming brings changes in the role of geo-microbiological, biogeochemical, and ecological processes in the habitats of different bacterial communities. Since mountain glaciers are at a high risk of climate change-induced global warming, microbiological studies in mountain glaciers need to be prioritized. Similarly, methodologies also need to be optimized; our review uncovered that most of the studies were primarily focused on traditional culture methods and 16S rRNA clone library; besides these, we did not found the new types of emerging technologies like NGS tools were applied to finding the different results in the bacterial community. The NGS technique

allows the sequencing of DNA and RNA much more quickly than other ones to get a better result on specific bacterial groups and their relationships with environmental parameters. Moreover, all regions like the Arctic, Antarctic, Greenland, and Tibetan Plateau were located in the high elevated zone, which is immaculate, influences, and affected by climate change where the microbial community cannot remain unaffected. If we use the latest high coverage methods like NGS and other technologies, which help to expose the significantly different results and bacterial shifts from the previous studies in those regions.

References

- Adhikari, N. P., Adhikari, S., & Paudel, G. (2019a). Bacterial diversity in aquatic ecosystems over the central Himalayas, Nepal: Progress and future perspectives. *Janapriya Journal of Interdisciplinary Studies*, 8(2019), 200–211. <https://doi.org/10.3126/jjis.v8i0.27319>
- Adhikari, S., Zhang, F., Zeng, C., Tripathee, L., Adhikari, N. P., Xu, J., & Wang, G. (2020). Precipitation chemistry and stable isotopic characteristics at Wengguo in the northern slopes of the Himalayas. *Journal of Atmospheric Chemistry*, 76(4), 289–313. <https://doi.org/https://doi.org/10.1007/s10874-020-09399-1>
- Adhikari, N. P., Adhikari, S., Liu, X., Shen, L., & Gu, Z. (2019b). Bacterial diversity in Alpine Lakes: A review from the third pole region. *Journal of Earth Science*, 30(2), 387–396. doi:10.1007/s12583-018-1206-5
- Amato, P., Hennebelle, R., Magand, O., Sancelme, M., Delort, A. M., Barbante, C., & Ferrari, C. (2007). Bacterial characterization of the snow cover at Spitzberg, Svalbard. *FEMS Microbiol Ecol*, 59(2), 255–264. doi:10.1111/j.1574-6941.2006.00198
- Anesio, A. M., Hodson, A. J., Fritz, A., Psenner, R., & Sattler, B. (2009). High microbial activity on glaciers: Importance to the global carbon cycle. *Global Change Biology*, 15(4), 955–960. doi:10.1111/j.1365-2486.2008.01758.x
- Anesio, A. M., & Laybourn-Parry, J. (2012). Glaciers and ice sheets as a biome. *Trends in Ecology & Evolution*, 27(4), 219–225. doi:10.1016/j.tree.2011.09.012
- Boetius, A., Anesio, A. M., Deming, J. W., Mikucki, J. A., & Rapp, J. Z. (2015). Microbial ecology of the cryosphere: Sea ice and glacial habitats. *Nat Rev Microbiol*, 13(11), 677–690. doi:10.1038/nrmicro3522
- Brown, L. E., Hannah, D. M., & Milner, A. M. (2007). Vulnerability of alpine stream biodiversity to shrinking glaciers and snowpacks. *Global Change Biology*, 13(5), 958–966.

- Butinar, L., Spencer-Martins, I., & Gunde-Cimerman, N. (2007). Yeasts in high Arctic glaciers: The discovery of a new habitat for eukaryotic microorganisms. *Antonie Van Leeuwenhoek*, *91*(3), 277-289. doi:10.1007/s10482-006-9117-3
- Campen, R., Kowalski, J., Lyons, W. B., Tulaczyk, S., Dachwald, B., Pettit, E., . . . Mikucki, J. A. (2019). Microbial diversity of an Antarctic subglacial community and high-resolution replicate sampling inform hydrological connectivity in a polar desert. *Environ Microbiol*, *21*(7), 2290-2306. doi:10.1111/1462-2920.14607
- Christner, B. C., Priscu, J. C., Achberger, A. M., Barbante, C., Carter, S. P., Christianson, K., Skidmore, M. L. (2014). A microbial ecosystem beneath the West Antarctic ice sheet. *Nature*, *512*(7514), 310-313.
- Chuvochina, M., Alekhina, I., Normand, P., Petit, J.-R., & Bulat, S. (2011). Three events of Saharan dust deposition on the Mont Blanc glacier associated with different snow-colonizing bacterial phylotypes. *Microbiology*, *80*(1), 125-131.
- Cook, J. M., Edwards, A., Bulling, M., Mur, L. A., Cook, S., Gokul, J. K., Irvine-Fynn, T. D. (2016). Metabolome-mediated biocryomorphic evolution promotes carbon fixation in Greenlandic cryoconite holes. *Environ Microbiol*, *18*(12), 4674-4686. doi:10.1111/1462-2920.13349
- Dubnick, A., Wadham, J., Tranter, M., Sharp, M., Orwin, J., Barker, J., Fitzsimons, S. (2017). Trickle or treat: The dynamics of nutrient export from polar glaciers. *Hydrological Processes*, *31*(9), 1776-1789. doi:10.1002/hyp.11149
- Fegel, T. S., Baron, J. S., Fountain, A. G., Johnson, G. F., & Hall, E. K. (2016). The differing biogeochemical and microbial signatures of glaciers and rock glaciers. *Journal of Geophysical Research: Biogeosciences*, *121*(3), 919-932. doi:10.1002/2015jg003236
- Fellman, J. B., Hood, E., Raymond, P. A., Hudson, J., Bozeman, M., & Arimitsu, M. (2015). Evidence for the assimilation of ancient glacier organic carbon in a proglacial stream food web. *Limnology and Oceanography*, *60*(4), 1118-1128. doi:10.1002/lno.10088
- Fellman, J. B., Nagorski, S., Pyare, S., Vermilyea, A. W., Scott, D., & Hood, E. (2014). Stream temperature response to variable glacier coverage in coastal watersheds of Southeast Alaska. *Hydrological Processes*, *28*(4), 2062-2073. doi:10.1002/hyp.9742
- Fountain, A. G., Jacobel, R. W., Schlichting, R., & Jansson, P. (2005). Fractures as the main pathways of water flow in temperate glaciers. *Nature*, *433*(7026), 618-621.
- Franzetti, A., Tagliaferri, I., Gandolfi, I., Bestetti, G., Minora, U., Mayer, C., . . . Ambrosini, R. (2016). Light-dependent microbial metabolisms drive carbon fluxes on glacier surfaces.

- ISME J*, 10(12), 2984-2988. doi:10.1038/ismej.2016.72
- Freimann, R., Burgmann, H., Findlay, S. E., & Robinson, C. T. (2013). Bacterial structures and ecosystem functions in glaciated floodplains: contemporary states and potential future shifts. *ISME J*, 7(12), 2361-2373. doi:10.1038/ismej.2013.114
- Granéli, W., Carlsson, P., & Bertilsson, S. (2004). Bacterial abundance, production and organic carbon limitation in the Southern Ocean (39–62°S, 4–14°E) during the austral summer 1997/1998. *Deep Sea Research Part II: Topical Studies in Oceanography*, 51(22-24), 2569-2582. doi:10.1016/j.dsr2.2001.01.003
- Hauptmann, A. L., Stibal, M., Bælum, J., Sicheritz-Pontén, T., Brunak, S., Bowman, J. S., . Blom, N. (2014). Bacterial diversity in snow on North Pole ice floes. *Extremophiles*, 18(6), 945-951.
- Hodson, A. (2006). Biogeochemistry of snowmelt in an Antarctic glacial ecosystem. *Water Resources Research*, 42(11). doi:10.1029/2005wr004311
- Hodson, A., Anesio, A. M., Tranter, M., Fountain, A., Osborn, M., Priscu, J., . Sattler, B. (2008). Glacial ecosystems. *Ecological Monographs*, 78(1), 41-67.
- Hodson, A. J., Mumford, P. N., Kohler, J., & Wynn, P. M. (2005). The high Arctic glacial ecosystem: new insights from nutrient budgets. *Biogeochemistry*, 72(2), 233-256. doi:10.1007/s10533-004-0362-0
- Hodson, A. J., Nowak, A., Cook, J., Sabacka, M., Wharfe, E. S., Pearce, D. A., Vieira, G. (2017). Microbes influence the biogeochemical and optical properties of maritime Antarctic snow. *Journal of Geophysical Research: Biogeosciences*, 122(6), 1456-1470. doi:10.1002/2016jg003694
- Hood, E., Fellman, J., Spencer, R. G., Hernes, P. J., Edwards, R., D'Amore, D., & Scott, D. (2009). Glaciers as a source of ancient and labile organic matter to the marine environment. *Nature*, 462(7276), 1044-1047. doi:10.1038/nature08580
- Hotaling, S., Hood, E., & Hamilton, T. L. (2017). Microbial ecology of mountain glacier ecosystems: biodiversity, ecological connections and implications of a warming climate. *Environ Microbiol*, 19(8), 2935-2948. doi:10.1111/1462-2920.13766
- Huang, J. P., Swain, A. K., Thacker, R. W., Ravindra, R., Andersen, D. T., & Bej, A. K. (2013). Bacterial diversity of the rock-water interface in an East Antarctic freshwater ecosystem, Lake Tawani (P). *Aquatic Biosystems*, 9(1), 4.
- Jacobsen, D., Milner, A. M., Brown, L. E., & Dangles, O. (2012). Biodiversity under threat in glacier-fed river systems. *Nature Climate Change*, 2(5), 361-364. doi:10.1038/

nclimate1435

- Kosek, K., Luczkiewicz, A., Koziol, K., Jankowska, K., Ruman, M., & Polkowska, Z. (2019). Environmental characteristics of a tundra river system in Svalbard. Part 1: Bacterial abundance, community structure and nutrient levels. *Sci Total Environ*, *653*, 1571-1584. doi:10.1016/j.scitotenv.2018.11.378
- Larose, C., Berger, S., Ferrari, C., Navarro, E., Dommergue, A., Schneider, D., & Vogel, T. M. (2010a). Microbial sequences retrieved from environmental samples from seasonal Arctic snow and meltwater from Svalbard, Norway. *Extremophiles*, *14*(2), 205-212.
- Larose, C., Dommergue, A., De Angelis, M., Cossa, D., Averty, B., Maruszczak, N., Ferrari, C. (2010b). Springtime changes in snow chemistry lead to new insights into mercury methylation in the Arctic. *Geochimica et Cosmochimica Acta*, *74*(22), 6263-6275. doi:10.1016/j.gca.2010.08.043
- Larose, C., Dommergue, A., & Vogel, T. M. (2013). Microbial nitrogen cycling in Arctic snowpacks. *Environmental Research Letters*, *8*(3), 035004. doi:10.1088/1748-9326/8/3/035004
- Lawson, E. C., Bhatia, M. P., Wadham, J. L., & Kujawinski, E. B. (2014). Continuous summer export of nitrogen-rich organic matter from the Greenland Ice Sheet inferred by ultrahigh resolution mass spectrometry. *Environ Sci Technol*, *48*(24), 14248-14257. doi:10.1021/es501732h
- Liu, K., Liu, Y., Han, B. P., Xu, B., Zhu, L., Ju, J., Xiong, J. (2019a). Bacterial community changes in a glacial-fed Tibetan lake are correlated with glacial melting. *Sci Total Environ*, *651*(Pt 2), 2059-2067. doi:10.1016/j.scitotenv.2018.10.104
- Liu, K., Yao, T., Liu, Y., Xu, B., Hu, A., & Chen, Y. (2019b). Elevational patterns of abundant and rare bacterial diversity and composition in mountain streams in the southeast of the Tibetan Plateau. *Science China Earth Sciences*, *62*(5), 853-862. doi:10.1007/s11430-018-9316-6
- Liu, K., Liu, Y., Jiao, N., Xu, B., Gu, Z., Xing, T., & Xiong, J. (2017). Bacterial community composition and diversity in Kalakuli, an alpine glacial-fed lake in Muztagh Ata of the westernmost Tibetan Plateau. *FEMS Microbiol Ecol*, *93*(7). doi:10.1093/femsec/fix085
- Liu, K., Liu, Y., Jiao, N., Zhu, L., Wang, J., Hu, A., & Liu, X. (2016). Vertical variation of bacterial community in Nam Co, a large stratified lake in central Tibetan Plateau. *Antonie Van Leeuwenhoek*, *109*(10), 1323-1335. doi:10.1007/s10482-016-0731-4
- Liu, Y., Yao, T., Jiao, N., Kang, S., Huang, S., Li, Q., Liu, X. (2009). Culturable bacteria in

- glacial meltwater at 6,350 m on the East Rongbuk Glacier, Mount Everest. *Extremophiles*, 13(1), 89-99. doi:10.1007/s00792-008-0200-8
- Liu, Y., Yao, T., Jiao, N., Tian, L., Hu, A., Yu, W., & Li, S. (2011). Microbial diversity in the snow, a moraine lake and a stream in Himalayan glacier. *Extremophiles*, 15(3), 411.
- Lütz-Meindl, U., & Lütz, C. (2006). Analysis of element accumulation in cell wall attached and intracellular particles of snow algae by EELS and ESI. *Micron*, 37(5), 452-458. doi:10.1016/j.micron.2005.11.004
- Lutz, S., Anesio, A. M., Edwards, A., & Benning, L. G. (2015). Microbial diversity on Icelandic glaciers and ice caps. *Frontiers in Microbiology*, 6. doi:10.3389/fmicb.2015.00307
- Lutz, S., Anesio, A. M., Edwards, A., & Benning, L. G. (2017). Linking microbial diversity and functionality of arctic glacial surface habitats. *Environ Microbiol*, 19(2), 551-565. doi:10.1111/1462-2920.13494
- Maccario, L., Vogel, T. M., & Larose, C. (2014). Potential drivers of microbial community structure and function in Arctic spring snow. *Frontiers in Microbiology*, 5, 413.
- Milner, A. M., Brittain, J. E., Brown, L. E., & Hannah, D. M. (2010). Water sources and habitat of Alpine streams. 6, 175-191. doi:10.1007/978-3-540-88275-6_9
- Mojib, N., Huang, J., Hoover, R., Pikuta, E., Storrie-Lombardi, M., Sattler, B., Bej, A. (2009). *Diversity of bacterial communities in the lakes of Schirmacher Oasis, Antarctica* (Vol. 7441): SPIE.
- Moller, A. K., Barkay, T., Abu Al-Soud, W., Sorensen, S. J., Skov, H., & Kroer, N. (2011). Diversity and characterization of mercury-resistant bacteria in snow, freshwater and sea-ice brine from the High Arctic. *FEMS Microbiol Ecol*, 75(3), 390-401. doi:10.1111/j.1574-6941.2010.01016.x
- Møller, A. K., Søborg, D. A., Abu Al-Soud, W., Sørensen, S. J., & Kroer, N. (2013). Bacterial community structure in high-Arctic snow and freshwater as revealed by pyrosequencing of 16S rRNA genes and cultivation. *Polar Research*, 32(1), 17390. doi:10.3402/polar.v32i0.17390
- O'Neel, S., Hood, E., Bidlack, A. L., Fleming, S. W., Arimitsu, M. L., Arendt, A., Pyare, S. (2015). Icefield-to-ocean linkages across the Northern Pacific coastal temperate rainforest ecosystem. *BioScience*, 65(5), 499-512. doi:10.1093/biosci/biv027
- Peter, H., & Sommaruga, R. (2016). Shifts in diversity and function of lake bacterial communities upon glacier retreat. *ISME J*, 10(7), 1545-1554. doi:10.1038/ismej.2015.245
- Pomeroy, L. R., & Wiebe, W. J. (2001). Temperature and substrates as interactive limiting

- factors for marine heterotrophic bacteria. *Aquatic Microbial Ecology*, 23(2), 187-204.
- Schutte, U. M., Abdo, Z., Foster, J., Ravel, J., Bunge, J., Solheim, B., & Forney, L. J. (2010). Bacterial diversity in a glacier foreland of the high Arctic. *Mol Ecol*, 19 Suppl 1, 54-66. doi:10.1111/j.1365-294X.2009.04479.x
- Shakti, P., Pradhananga, D., Ma, W., & Wang, P. (2013). An overview of Glaciers distribution in the Nepal Himalaya. *Hydro Nepal: Journal of Water, Energy and Environment*, 13, 20-27.
- Sheik, C. S., Stevenson, E. I., Den Uyl, P. A., Arendt, C. A., Aciego, S. M., & Dick, G. J. (2015). Microbial communities of the Lemon Creek Glacier show subtle structural variation yet stable phylogenetic composition over space and time. *Front Microbiol*, 6, 495. doi:10.3389/fmicb.2015.00495
- Simon, C., Wiezer, A., Strittmatter, A. W., & Daniel, R. (2009). Phylogenetic diversity and metabolic potential revealed in a Glacier Ice Metagenome. *Applied and Environmental Microbiology*, 75(23), 7519-7526. doi:10.1128/aem.00946-09
- Skidmore, M., Anderson, S. P., Sharp, M., Foght, J., & Lanoil, B. D. (2005). Comparison of microbial community compositions of two subglacial environments reveals a possible role for microbes in chemical weathering processes. *Appl Environ Microbiol*, 71(11), 6986-6997. doi:10.1128/AEM.71.11.6986-6997.2005
- Srinivas, T., Singh, S., Pradhan, S., Pratibha, M., Kishore, K. H., Singh, A. K., Shivaji, S. (2011). Comparison of bacterial diversity in proglacial soil from Kafni Glacier, Himalayan Mountain ranges, India, with the bacterial diversity of other glaciers in the world. *Extremophiles*, 15(6), 673.
- Stibal, M., Tranter, M., Telling, J., & Benning, L. G. (2008). Speciation, phase association and potential bioavailability of phosphorus on a Svalbard glacier. *Biogeochemistry*, 90(1), 1-13. doi:10.1007/s10533-008-9226-3
- Stocker, T. F., Qin, D., Plattner, G.-K., Tignor, M. M., Allen, S. K., Boschung, J., & Midgley, P. M. (2014). Climate change 2013: The physical science basis. contribution of working group I to the fifth assessment report of IPCC the intergovernmental panel on climate change: Cambridge University Press.
- Takeuchi, N., Nishiyama, H., & Li, Z. (2010). Structure and formation process of cryoconite granules on Ürümqi glacier No. 1, Tien Shan, China. *Annals of Glaciology*, 51(56), 9-14.
- Wilhelm, L., Besemer, K., Fasching, C., Urich, T., Singer, G. A., Quince, C., & Battin, T. J.

- (2014). Rare but active taxa contribute to community dynamics of benthic biofilms in glacier-fed streams. *Environ Microbiol*, 16(8), 2514-2524. doi:10.1111/1462-2920.12392
- Wilhelm, L., Singer, G. A., Fasching, C., Battin, T. J., & Besemer, K. (2013). Microbial biodiversity in glacier-fed streams. *ISME J*, 7(8), 1651-1660. doi:10.1038/ismej.2013.44
- Yao, T., Thompson, L. G., Mosbrugger, V., Zhang, F., Ma, Y., Luo, T., & Fayziev, R. (2012). Third pole environment (TPE). *Environmental Development*, 3, 52-64. doi:10.1016/j.envdev.2012.04.002
- Zhang, G., Yao, T., Xie, H., Wang, W., & Yang, W. (2015). An inventory of glacial lakes in the third pole region and their changes in response to global warming. *Global and Planetary Change*, 131, 148-157. doi:10.1016/j.gloplacha.2015.05.013