Microbial Diversity Analysis of Surface Snow from Glacier No. 1 at the Headwaters of the Urumqi River, Tianshan Mountains (Postprint)

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Abstract

To investigate the characteristics of snow microbial communities on Urumqi Glacier No. 1 at the headwaters of the Urumqi River in the Tianshan Mountains (hereinafter referred to as "Urumqi Glacier No. 1") and their relationship with climatic and environmental conditions, surface snow samples were collected from this region in spring (April) 2021 at an altitude of 3549 m (TSX1) and in summer (June) at altitudes of 3770 m (TSX2) and 3800 m (TSX3). High-throughput sequencing of the bacterial 16S rDNA V3-V4 region, archaeal 16S rDNA V4-V5 region, and fungal ITS2 region was performed to analyze the diversity of bacteria, archaea, and fungi in the snow samples. The results showed that: (1) Microbial diversity in the surface snow of Urumqi Glacier No. 1 exhibited seasonal differences, with bacterial diversity being higher in spring and lower in summer, while fungal diversity showed the opposite pattern. (2) In terms of species composition, the dominant bacterial phyla were Proteobacteria (58.13%~89.10%) and Bacteroidetes (4.24%~40.74%), and the dominant genera were Flavobacterium (2.32%~33.64%) and Polaromonas (0.01%~24.72%); the dominant archaeal phylum was Thaumarchaeota (38.10%~97.55%), followed by Nanoarchaeaeota (0%~61.90%) and Euryarchaeota (0%~2.82%); the dominant fungal phyla were Ascomycota (7.06%~88.43%) and Monoblepharidomycota (36.21%~40.78%), and the dominant genera were Aspergillus (0.16%~81.04%) and Rhodotorula (0.02%~8.05%). (3) Network interaction analysis revealed that microbial network interactions were dominated by positive correlations (97.3%), with negative correlations accounting for only 2.7%, indicating that interaction relationships tended toward cooperation. (4) The surface snow of Urumqi Glacier No. 1 harbors abundant microorganisms, and seasonal variations in microbial communities reflect the response of microorganisms to atmospheric circulation patterns in different seasons.

Full Text

Abstract

To investigate the microbial community characteristics in surface snow from Glacier No. 1 at the headwaters of Urumqi River, Tianshan Mountains (hereinafter referred to as "Urumqi Glacier No. 1") and their relationship with climate and environment, surface snow samples were collected at altitudes of 3549 m in spring (April, TSX1) and 3770 m (TSX2) and 3800 m (TSX3) in summer (June) 2021. High-throughput sequencing was performed targeting the V3-V4 region of bacterial 16S rDNA, the V4-V5 region of archaeal 16S rDNA, and the ITS2 region of fungi to analyze microbial diversity in the snow samples. The results demonstrated that microbial diversity in surface snow from Urumqi Glacier No. 1 exhibited distinct seasonal patterns, with bacterial diversity being higher in spring and lower in summer, while fungal diversity showed the opposite trend. At the phylum level, the dominant bacteria were Proteobacteria (58.13%–89.10%) and Bacteroidetes (4.24%–40.74%), with Flavobacterium (2.32%–33.64%) and Polaromonas (0.01%–24.72%) as the dominant genera. The dominant archaea was Thaumarchaeota (38.10%–97.55%), followed by Nanoarchaeaeota (0%–61.90%) and Euryarchaeota (0%–2.82%). For fungi, Ascomycota (7.06%–88.43%) and Monoblepharidomycota (36.21%–40.78%) were dominant at the phylum level, while Aspergillus (0.16%–81.04%) and Rhodotorula (0.02%–8.05%) were dominant at the genus level. Network interaction analysis revealed that microbial network interactions were dominated by positive correlations (97.3%), with negative correlations accounting for only 2.7%, indicating that interactive relationships tended toward cooperation. In summary, surface snow from Urumqi Glacier No. 1 harbors rich microbial diversity, and seasonal variations in microbial communities reflect the response of microorganisms to atmospheric circulation in different seasons.

Keywords: Urumqi Glacier No. 1; Tianshan; surface snow; microbial diversity; network interaction analysis

Introduction

Microorganisms in glacial snow and ice serve as indicator organisms for geochemical and climate-environmental changes, with their distribution, abundance, and diversity influenced by climatic and environmental variations in glacial regions [1]. The pigments they contain accelerate glacier melting by reducing surface albedo [2]. Therefore, research on the diversity and function of glacial snow and ice microorganisms holds important theoretical significance in glaciology and ecology, while also reflecting climate and environmental changes with important practical implications.

Numerous studies have reported the dynamic changes in microbial communities associated with meteorological factors and seasonal cycles. Liu et al. [3] investigated microbial abundance, community structure, and their relationship with

seasonal changes in the East Rongbuk Glacier on Mount Everest, finding that microbial quantity and community structure exhibited distinct seasonal characteristics, likely influenced by different water vapor sources in summer and winter. Liu et al. [4] examined seasonal variation patterns of bacteria in the Guoqu Glacier on Geladaindong Peak, revealing that Proteobacteria dominated in summer, while Flavobacterium and Cytophaga were predominant in winter and spring, reflecting bacterial responses to different seasonal atmospheric circulations. Wang [5] analyzed the relationship between bacterial communities in surface snow of Tianshan glaciers and climatic-environmental factors across seasons, showing that bacterial species were fewer in spring and summer (May–August) but more abundant in autumn and winter (September–April), with Arthrobacter and Sphingomonas genera universally present across different seasons.

The snow system of Urumqi Glacier No. 1 is characterized by seasonal temperature fluctuations, intense light, UV radiation, and aerobic conditions. Snow layer thickness varies seasonally, with minimal change in winter but decreasing thickness in summer as temperatures rise, affecting lower snow layers through meltwater percolation [6]. Through deposition processes, snow can connect atmospheric substances and microorganisms with the underlying soil or glacial ice microenvironments, exerting important influences on the glacial ecosystem [7]. In recent years, the climate of Urumqi Glacier No. 1 has become warmer and wetter with global warming, resulting in significant glacial retreat. Accelerated snow melting is continuously replenished by snowfall and precipitation [8]. During the May–August monsoon period, substantial exogenous materials from the arid Central Asian region are transported to Urumqi Glacier No. 1 [9]. Climate change not only alters the original records of chemical components in snow layers but also increases glacial meltwater runoff, thereby affecting downstream ecosystems [10]. Meanwhile, Urumqi Glacier No. 1 has a relatively small area and is located close to urban areas, experiencing severe disturbance from surrounding human activities, such as industrial pollutants from Houxia Town and air pollutants from nearby towns that can enter the glacial region via atmospheric circulation [11]. In summary, the ecology and environment of Urumqi Glacier No. 1 have become extremely vulnerable under the dual impacts of climate change and human activities. Glacial snow serves as an important material for studying glacial climate and environmental changes, with its chemical composition and microbial diversity influenced by surrounding and local microenvironments [12], while microorganisms represent the most sensitive indicator organisms for climate and environmental changes in glacial regions [13]. This study collected surface snow samples from Urumqi Glacier No. 1 in 2021 to analyze bacterial, archaeal, and fungal community composition and explore how glacial surface snow microbial diversity and structure are affected by climate and environmental changes.

1.1 Study Area Overview

Urumqi Glacier No. 1 (43°06 N, 86°49 E) is located in the central Tianshan Mountains, on the north slope of the Karawuqiong Mountain in the middle Tianshan range. The glacier runs northeastward, surrounded by desert and Gobi, and is relatively close to urban areas [Figure 1: see original paper]. The glacier has an elevation range of 4486 m and consists of east and west branches. The region experiences a continental climate primarily influenced by westerly jets, with local valley winds occurring near the surface annually from May to August [14]. According to observation data from the Daxigou Meteorological Station (3593 m), the glacier has an average annual precipitation of 460 mm and average annual temperature of -4.6°C. During 2010–2020, Urumqi Glacier No. 1 showed a warming and wetting trend [15]. Precipitation occurs mainly from May to August, making it a summer-supply glacier [16]. During this period, intensified melting and meltwater infiltration affect lower snow layers [6].

1.2 Sample Collection

Surface snow samples were collected on the shaded aspect of Urumqi Glacier No. 1 in April (spring, TSX1, 3549 m) and June (summer, TSX2 at 3770 m and TSX3 at 3800 m). To avoid contamination, all sampling tools were sterilized, and personnel wore disposable sterile gloves, masks, and clean suits. Three sampling sites were established with 50 cm × 50 cm quadrats, and five replicate samples were collected at each site. To prevent sample contamination and UV exposure, the surface 10 cm of snow was first removed before collecting snow from 10–30 cm depth into sterile polyethylene bottles. Samples were transported in a vehicle-mounted refrigerator and stored at -80°C in the laboratory.

1.3 Microbial Collection from Snow Samples

Snow samples were melted in the dark at 4°C. From each melted sample, 500 mL of meltwater was filtered through 0.22 m polyethersulfone membranes to collect microorganisms. The membranes were stored at -80°C and transported on dry ice for high-throughput sequencing.

1.4 DNA Extraction and PCR Amplification

Genomic DNA was extracted from the membranes using the SEQ Advanced Water DNA Kit (Thermo), with quality and concentration quantified via agarose gel electrophoresis and Qubit 2.0 fluorometer (Invitrogen). Using 50 ng of template DNA, the V3-V4 region of bacterial 16S rDNA was amplified with primers ACTCCTACGGGAGGCAGCA and GGACTACHVGGGTWTCTAAT [17]; the V4-V5 region of archaeal 16S rDNA was amplified with primers Arch519F (CAGCCGCCGCGGTAA) and Arch915R (GTGCTCCCCCGCCAATTCCT) [18]; and the fungal ITS2 region was amplified with primers ITS3-F (GCATCGATGAAGAACGCAGC) and ITS4-R (TCCTCCGCTTATTGATATGC) [19]. All primers included barcodes. PCR reactions (50 L) contained 25 L of 2×

Premix Taq, 1 L each of forward and reverse primers, and nuclease-free water. Amplification conditions were: initial denaturation at 95°C for 5 min, followed by 30 cycles of 95°C for 30 s, 55°C for 30 s, and 72°C for 30 s, with a final extension at 72°C for 10 min. Negative controls using sterile deionized water instead of template DNA were included.

1.5 Library Construction and Sequencing

Amplicon libraries were constructed using the NEBNext Ultra II DNA Library Prep Kit for Illumina (New England Biolabs, USA) following standard protocols. The libraries were sequenced on the Illumina NovaSeq 6000 platform using PE150 mode. The bacterial, archaeal, and fungal sequencing data have been deposited in the National Center for Biotechnology Information (NCBI) under BioProject accession PRJNA872833.

1.6 Data Processing and Analysis

Raw sequences were quality-filtered to remove low-quality reads, short reads (<16 bp), and chimeras, yielding high-quality clean tags. These were clustered into operational taxonomic units (OTUs) at 97% similarity using UPARSE [20]. Representative sequences were aligned against the SILVA database (for bacteria and archaea) and Unite database (for fungi) for taxonomic annotation. Alpha diversity indices (Shannon, Simpson, Chao1) were calculated using the psych package in R to assess richness and diversity. Spearman correlation matrices were generated at the genus level to determine inter-species relationships, with significance thresholds set at $P \leq 0.05$. Network visualization was performed using Gephi V.0.9.6 software [21].

2 Results

2.1 Microbial Sequencing Data and Rarefaction Curves

High-throughput sequencing yielded 228–297 effective sequences for bacteria, 103–334 for archaea, and 228–297 for fungi across samples. Rarefaction curves for bacteria (FIGURE:2a), archaea (FIGURE:2b), and fungi (FIGURE:2c) approached saturation, indicating that sequencing captured the majority of microbial diversity. The three snow samples shared 6.34% of bacterial OTUs, with the highest number of unique OTUs in TSX1. Alpha diversity indices (TABLE:1) showed that bacterial diversity was higher in spring samples than summer samples, and higher at high altitude than low altitude within the summer samples.

2.2 Bacterial Diversity Analysis

A total of 11 bacterial phyla were identified across all samples (FIGURE:3). The dominant phyla were Proteobacteria (89.10% in TSX1, 58.13% in TSX2, 56.56% in TSX3) and Bacteroidetes (4.24% in TSX1, 40.74% in TSX2, 32.47% in TSX3). At the class level, Alphaproteobacteria (63.65% in TSX1, 35.31%

in TSX2, 40.74% in TSX3) and Bacteroidia (5.31% in TSX1, 56.56% in TSX2, 61.17% in TSX3) were dominant. At the genus level, 228–297 genera were identified, with dominant genera including Brevundimonas (11.90% in TSX1, 12.44% in TSX2), Stenotrophomonas (9.95% in TSX1), Sphingomonas (6.99% in TSX1, 8.64% in TSX2), Methylobacterium (2.32%–33.64% across samples), Ralstonia (0.01%–24.72%), Flavobacterium (7.06%–88.43%), Polaromonas (0.16%–81.04%), Rhodoferax (0.02%–8.05%), and Massilia (0.79%–4.41%). Unclassified genera accounted for 4.85%–26.73%.

2.3 Archaeal Diversity Analysis

Archaeal OTU analysis (FIGURE:4) revealed that 10.71% of OTUs were shared among samples, with the highest number of unique OTUs in TSX3. Alpha diversity indices (TABLE:1) indicated higher archaeal diversity in summer samples than spring samples, and higher diversity at lower altitude within summer samples. At the phylum level, Thaumarchaeota dominated all samples (97.55% in TSX1, 38.10% in TSX2, 61.90% in TSX3), followed by Nanoarchaeaeota (0% in TSX1, 61.90% in TSX2, 36.21% in TSX3) and Euryarchaeota (0% in TSX1, 0.09% in TSX2, 2.45% in TSX3). At the class level, Nitrososphaeria (97.55% in TSX1, 38.10% in TSX2, 61.90% in TSX3) and Woesearchaeia (2.45% in TSX3) were identified. At the genus level, Candidatus Nitrososphaera from Thaumarchaeota was present in all samples (0.79%–4.41%), while Candidatus Nitrosocaldus was found only in TSX3 (0.09%–2.67%). Methanobrevibacter (Methanobacteria) was detected exclusively in TSX2 at 1.61% relative abundance. Unclassified archaea accounted for 0.98% of sequences.

2.4 Fungal Diversity Analysis

Fungal OTU analysis showed that 76.19%–95.56% of OTUs were shared among samples, with the highest number of unique OTUs in TSX3. Alpha diversity indices (TABLE:1) revealed higher fungal diversity in summer samples than spring samples. A total of 11 fungal phyla were identified (FIGURE:5). Ascomycota was dominant (88.43% in TSX1, 10.10% in TSX2, 7.06% in TSX3), followed by Monoblepharidomycota (36.21% in TSX2, 40.78% in TSX3). Basidiomycota and Chytridiomycota were also present at lower abundances. At the class level, Dothideomycetes (82.11% in TSX1, 3.88% in TSX2, 2.20% in TSX3), Eurotiomycetes (14.97% in TSX1, 7.93% in TSX2, 10.62% in TSX3), and Monoblepharidomycetes (36.21% in TSX2, 40.78% in TSX3) were dominant. At the genus level, Aspergillus (81.04% in TSX1, 0.08% in TSX2, 0.27% in TSX3) and Rhodotorula (0.02%–8.02% across samples) were dominant, with Cystobasidium also present (0.01%–2.23%). Unclassified genera accounted for 47.56%–41.08% of sequences.

2.5 Microbial Co-occurrence Network

Spearman correlation analysis at the genus level was used to construct interaction networks among bacteria, archaea, and fungi (FIGURE:6). The network

was dominated by positive correlations (97.3%), with negative correlations comprising only 2.7%, indicating cooperative rather than competitive relationships. The bacterial network contained the most nodes and edges, suggesting more complex ecological interactions among bacteria. The network comprised three independent sub-networks: bacteria-bacteria, bacteria-fungi, and fungi-fungi interactions.

3 Discussion

Alpha diversity results revealed significant seasonal differences in microbial diversity between spring and summer in surface snow from Urumqi Glacier No. 1. Bacterial diversity and richness were higher in spring, as indicated by higher Chao1 and Shannon indices and more bacterial taxa identified. In contrast, TSX2 and TSX3 showed lower bacterial diversity and uneven richness distribution, with extremely high ecological dominance of Proteobacteria and Bacteroidetes (combined relative abundance near 100%). Fungal diversity was higher in summer samples, with TSX2 and TSX3 showing significantly higher Chao1 and Shannon indices than TSX1. These findings align with reports from the East Rongbuk Glacier on Mount Everest, where bacterial diversity negatively correlated with temperature [3], possibly related to the growth characteristics of cold-adapted bacterial communities. Additionally, influenced by westerly jets and dust storms, large quantities of bacteria are transported via atmosphere and dust deposition into the glacial region in spring, contributing to increased bacterial diversity. Higher fungal diversity in summer is associated with rising temperatures and extended daylight favorable for fungal growth [22].

The dominant bacteria in Urumqi Glacier No. 1 snow included Proteobacteria, Bacteroidetes, and Actinobacteria, with Alphaproteobacteria as the main class and Deltaproteobacteria and Betaproteobacteria as secondary classes. These bacteria have been reported as dominant in other glaciers, such as on the north slope of Mount Everest [23] and Svalbard [24], indicating their widespread distribution and stable relative abundance in glacial environments. Dominant genera included Brevundimonas, Stenotrophomonas, Sphingomonas, Methylobacterium, Ralstonia, Flavobacterium, Polaromonas, Rhodoferax, and Massilia, which have been previously reported as dominant in Tianshan glacial snow [25], suggesting stable spatial distribution. Seasonal differences in dominant genera between spring and summer likely reflect different climatic influences: spring communities are primarily affected by dust sources, while summer communities are influenced by precipitation and increased melting.

Archaeal communities included Thaumarchaeota, Nanoarchaeaeota, and Euryarchaeota. Thaumarchaeota are typical ammonia-oxidizing archaea that play important roles in nitrogen cycling in terrestrial habitats [26], suggesting their involvement in glacial nitrogen cycling. Euryarchaeota included Halobacteria and Methanobacteria, which participate in methane production and anaerobic methane oxidation in glaciers, holding significance in global biogeochemical cycles [27, 28]. Nanoarchaeota were also identified, though their functional roles

remain poorly characterized. Higher archaeal diversity in summer may be attributed to the fact that the most abundant archaea at both phylum and genus levels are ammonia-oxidizing archaea, whose metabolic rates decrease at lower temperatures [29], resulting in reduced abundance in spring.

A total of 11 fungal phyla were identified, with Ascomycota and Monoblepharidomycota showing high relative abundance. Ascomycota has been reported as a dominant fungus in Greenland ice cores [30] and various glacial environments [31], playing roles in plant interactions [32] and soil succession [33]. The class Lecanoromycetes (Ascomycota) showed high relative abundance across samples and is associated with lichen formation [34]. Monoblepharidomycota is commonly found in soil and plants [35], though its ecological function in glaciers remains unknown. The dominant fungal genera Aspergillus and Rhodotorula are both cold-tolerant. Aspergillus can degrade hydrocarbons at low temperatures [36], while Rhodotorula produces various cold-adapted enzymes, withstands extreme climates [37], and degrades lignin and cellulose more efficiently than bacteria [38], playing an important role in glacial carbon cycling.

Microbial correlation network analysis revealed that most nodes in the Urumqi Glacier No. 1 network showed mutualistic interactions, driven primarily by nutrient availability. This suggests that in the harsh glacial environment, microorganisms tend toward cooperative relationships, which is more conducive to survival. Bacteria comprised the largest proportion of the microbial community, with relatively stable community structure, and their direct or indirect interactions with fungi and archaea may promote community resilience.

This study identified numerous cold-adapted microorganisms from Urumqi Glacier No. 1 surface snow. Cold-adapted bacteria included Proteobacteria (Brevundimonas, Polaromonas, Sphingomonas), Bacteroidetes (Flavobacterium), Actinobacteria (Cryobacterium, Arthrobacter, Hymenobacter), Firmicutes (Bacillus, Paenibacillus), and others found in various cold environments [39, 40]. Cold-adapted fungi included Basidiomycota (Cryptococcus, Rhodotorula, Sporobolomyces, Cystobasidium, Dioszegia, Vishniacozyma) and Ascomycota (Penicillium, Alternaria), which are also distributed in Urumqi Glacier permafrost [41] and Greenland ice [42]. Alpine glaciers represent major habitats for cold-adapted microorganisms, which play important roles in nutrient cycling and organic matter mineralization [43] and have evolved various cold-adaptation strategies with significant potential for environmental, agricultural, and industrial applications [44].

4 Conclusion

The diversity of bacteria and fungi in surface snow from Urumqi Glacier No. 1 is affected by seasonal changes. Bacterial diversity is higher in spring and lower in summer, with Proteobacteria dominating in spring and Bacteroidetes in summer. Fungal diversity is higher in summer and lower in spring, with Monoblepharidomycota dominating in summer and Ascomycota in spring. Archaea

including Thaumarchaeota, Euryarchaeota, and Nanoarchaeaeota were identified in both seasons. The high microbial diversity in Urumqi Glacier No. 1 surface snow reflects seasonal responses to atmospheric circulation and climate change, with spring communities influenced by dust and summer communities by melting. Co-occurrence network analysis revealed predominantly mutualistic interactions among microbial groups, suggesting that cooperative relationships are more advantageous for microbial survival in the harsh glacial environment.

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Note: Figure translations are in progress. See original paper for figures.