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The Diversity of Airborne Bacteria Over the Tibet Plateau Decreased by Taklimakan Dust

Fanli Xue¹ , Zhongwei Huang^{1,2} , Xuefei Huo¹, Qingqing Dong¹ , Zhengpeng Li¹, and Qianqing Gu¹

¹Key Laboratory for Semi-Arid Climate Change of the Ministry of Education, College of Atmospheric Sciences, Lanzhou University, Lanzhou, China, ²Collaborative Innovation Center for Western Ecological Safety, Lanzhou University, Lanzhou, China

Key Points:

- Taklimakan dust alters the community structure and diversity of airborne bacteria in the Tibet Plateau
- The diversity of airborne bacteria in the Tibet Plateau decreased by 42.2% during the dust events
- Taklimakan dust increased 16.4% of potential pathogens and 73.8% of bacterial ice nuclei in the Plateau

Supporting Information:

Supporting Information may be found in the online version of this article.

Correspondence to:

Z. Huang,
huangzhongwei@lzu.edu.cn

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Author Contributions:

Conceptualization: Zhongwei Huang
Data curation: Qingqing Dong
Formal analysis: Fanli Xue, Qingqing Dong
Funding acquisition: Zhongwei Huang
Investigation: Qianqing Gu
Project administration: Zhongwei Huang
Visualization: Fanli Xue
Writing – original draft: Fanli Xue
Writing – review & editing: Zhongwei Huang, Xuefei Huo, Zhengpeng Li

Abstract Taklimakan dust is known to be transported over long distances to the Tibetan Plateau, significantly impacting its climates and ecosystems. However, information on how dust aerosols affect airborne microorganisms is still lacking. In the summer of 2019, we simultaneously collected air samples from the Tibetan Plateau (Ali) and the Taklimakan Desert (Minfeng and Tazhong) and analyzed them using high-throughput DNA sequencing techniques. We found that the diversity of airborne bacteria decreased by 42.2% during dust events. Taklimakan dust contributed $85.4\% \pm 2.1\%$ of airborne bacteria on the Plateau. Moreover, the potential pathogens and bacterial ice nuclei (IN) in the Plateau increased by 16.4% and 73.8%, respectively. Our study provides novel insights into the impact of dust-coated bacteria on the climate and ecosystem across the Tibetan Plateau.

Plain Language Summary To assess the impact of Taklimakan dust (MF and TZ) on airborne bacteria in the Tibetan Plateau, we collected air samples and related environmental data from both the Taklimakan Desert and the Tibetan Plateau. During periods of Taklimakan dust, the Shannon index and Chao1 index of airborne bacteria showed significant decreases of 42.2% and 59.7%, respectively. *Euryarchaeota* may serve as a microbial indicator of dust environments, exhibiting a significant increase of 17.6% in the abundance of *Citrobacter*, *Lactococcus*, *Enterococcus*, and *Acinetobacter*. These findings underscore the pivotal role of Taklimakan dust microorganisms in shaping the structure of aerosol bacterial communities across the Tibetan Plateau. Source tracking revealed that Taklimakan dust contributed $85.4\% \pm 2.1\%$ to the airborne bacterial population in the Tibetan Plateau. The presence of Taklimakan dust led to increases in potential pathogens (16.4%) and ice-nucleation bacteria (73.8%), highlighting the significant impact of this dust on the airborne bacterial community in terms of both health and climate effects within the Tibetan Plateau. This study presents new scientific insights into the impact of Taklimakan dust on airborne bacteria across the Tibetan Plateau.

1. Introduction

Dust aerosols can be transported to the Tibetan Plateau (Dong et al., 2022; Qi et al., 2022; Zhang et al., 2021), exhibiting long-range atmospheric transmission (Huang et al., 2024; Murata & Zhang, 2014; Tang et al., 2018). Different ecosystems harbor distinct microbial communities, such as those found in terrestrial, marine, forested, and industrial environments (Cáliz et al., 2018; Fröhlich-Nowoisky et al., 2016). The short-range and long-range transport of airborne particles in the atmosphere constitutes significant channels that influence the distribution of airborne microorganisms (Maki et al., 2019; Murata & Zhang, 2016). The HYSPLIT model, which stands for Hybrid Single-Particle Lagrangian Integrated Trajectory, is commonly used to demonstrate the paths of air currents (Murata & Zhang, 2016). Dust aerosols transport a substantial quantity of airborne bacteria (Qi et al., 2021, 2023; Tang et al., 2018), facilitating the long-range dispersion of microbial communities along the trajectory of dust plumes (Murata & Zhang, 2016). These recent discoveries have sparked significant scientific interest among climate researchers regarding the climate impact of bioaerosols.

Numerous studies have demonstrated the significant role of Indian monsoon and westerly circulation in aerosol transport (Qi et al., 2022). The atmospheric circulation can exacerbate the dispersion of microorganisms from various sources, while airborne currents carrying particles and microbes contribute to an amplification in both the concentration and diversity of microbes in downwind regions (Tang et al., 2018). The atmosphere is a dynamic and diverse environment, with airborne microbes forming a highly dynamic assemblage (Cáliz et al., 2018)

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influenced by environmental factors such as temperature (T), relative humidity (RH), wind direction (WD), wind speed (WS), altitude, and air quality concentration (Huang et al., 2023). Understanding the mechanisms of microbial community formation necessitates the identification and characterization of potential sources of airborne microorganisms. The fast expectation-maximization microbial source tracking (FEAST) (Shenhav et al., 2019) tool possesses the capacity to simultaneously and expeditiously assess numerous potential source environments, thereby aiding researchers in unraveling the origins of intricate microbial communities. The climate impact of bioaerosols primarily stems from the capacity of specific airborne microbes to function as cloud condensation nuclei (CCN) and ice nuclei (IN). Common airborne microbes, such as *Pseudomonas*, *Pantoea*, *Erwinia*, and *Xanthomonas*, have the potential to serve as CCN or IN in the process of cloud formation and precipitation (Huang et al., 2021). The long-distance transportation of dust can disrupt the equilibrium of sink environments by introducing a higher proportion of foreign airborne microbes, extremophiles, and potentially pathogenic species (Behzad et al., 2018). During transportation, airborne microorganisms actively participate in atmospheric physical and chemical processes, thereby exerting significant influences on climate and ecosystems.

The Taklamakan Desert is considered an extremely arid region and ranks as the second largest shifting desert globally. The Tibet Plateau is the plateau with the highest altitude in the world. As the “Third Pole” of the Earth, it has a vulnerable ecological environment and is highly sensitive to global climate change. Currently, the research on the long-distance airborne transmission of microorganisms from the Taklamakan Desert to the Tibetan Plateau and its climatic effect is rather scarce. To investigate how Taklimakan dust impact the airborne bacterial population in the Tibetan Plateau, we collected air microbial and environmental data from the Taklimakan dust source area (Tazhong and Minfeng) and the Tibetan Plateau downwind area (ALi) during the same period. Then all collected samples were further analyzed using high-throughput DNA sequencing techniques for obtaining the community structure and diversity of airborne bacteria in the study area. Reveal the quantifiable contribution of Taklamakan dust storms to the climatic impacts on the Tibetan Plateau.

2. Materials and Methods

2.1. Sampling Location and Methods

The sampling sites were located at the Tazhong Meteorological Bureau (38.97°N, 83.65°E, TZ), the Minfeng Meteorological Bureau (37.07°N, 82.70°E, MF), and the Garr Meteorological Bureau (32.50°N, 80.08°E, AL) within the hinterland of the Taklimakan Desert, the southern margin of the Taklimakan Desert, and the Tibetan Plateau, respectively. As shown in Figures 1a and 1b, there were no industrial facilities or high-rise buildings near the sampling locations, reducing potential interference from anthropogenic activities on experimental outcomes. In this research, bioaerosol samples were collected using polycarbonate filters (Whatman 111,106) (Tang et al., 2018), as depicted in Figures 1c–1f. The sampling duration for each sample was 12 hr: from 8:00 to 20:00 for day samples (D), and from 20:00 to 08:00 the following day for night samples (N). A total of 54 valid samples were collected between July 11 and 24 July 2019. For quality control, all filters and filter equipment were autoclaved at 121°C for 120 min prior to sampling. During sampling, gloves and masks were worn, and equipment was disinfected with 75% alcohol. After sampling, the collected samples were stored in a –80°C refrigerator.

2.2. High Throughput Sequencing

For the extraction of genomic DNA from aerosol samples, please refer to Qi et al. (2023). The PCR amplicons underwent high-throughput sequencing using a MiSeq Genome Sequencer with the MiSeq Reagent Kit V2. After sequencing, the original sequences were spliced and subjected to quality control using fastp to eliminate low-quality sequences, labeled sequences, primers, chimeras, etc. Subsequent analysis was conducted on the high-quality sequences after data filtering. Analysis was performed using the Quantitative Insights into Microbial Ecology pipeline (QIIME2) (Almeida et al., 2018) and the SILVA reference database (v132) (Quast et al., 2013). Operational Taxonomic Units (OTUs) were categorized using a similarity threshold of 97%, and species annotations were provided. The data flattening process was conducted to facilitate effective comparison. The original sequences were deposited in the NCBI SRA database (BioProject accession number PRJNA1150353).

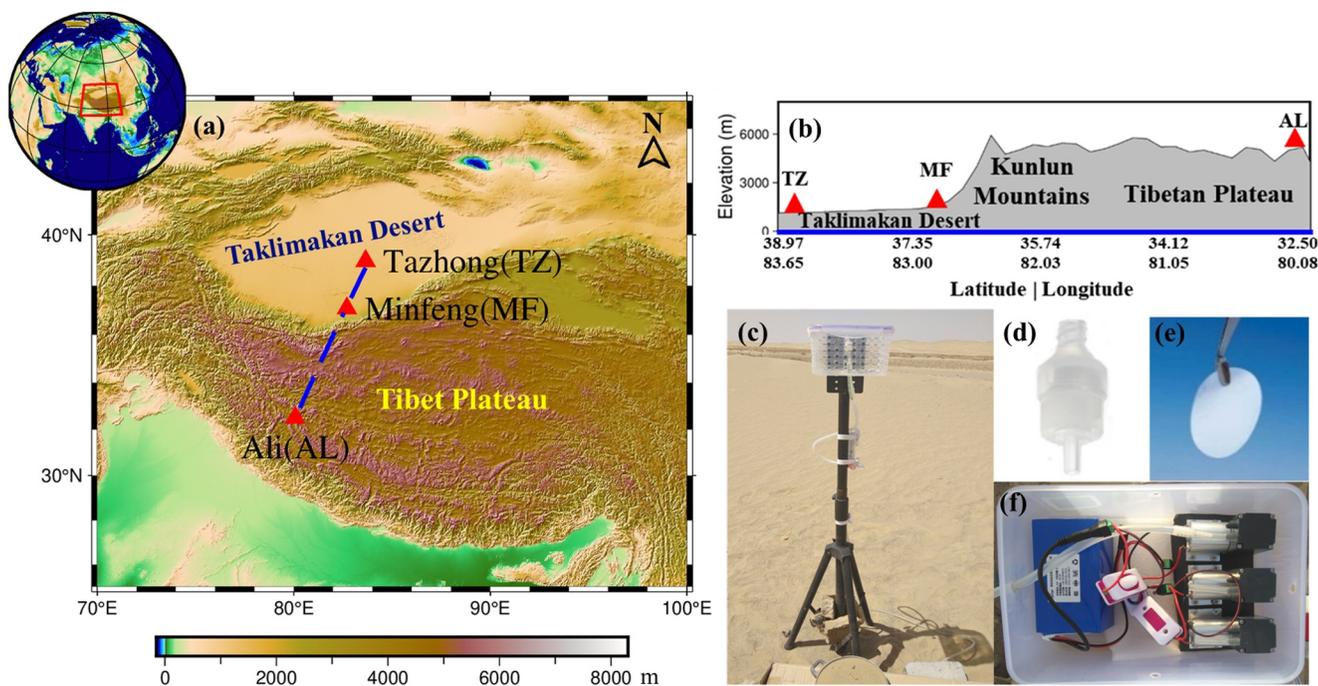


Figure 1. (a) Distribution map of TZ, MF, and AL at sampling sites. (b) Topographic profiles of TZ, MF, and AL sampling sites. (c) Air microbial aerosol sampler. (d) Sample collection filters. (e) Filter membrane with collected sample. (f) Power supply and sampling pump.

2.3. Statistical Analyses

Data processing and visualization were performed using R, Origin, MeteoInfo, and other software. The α -diversity index (Shannon index and Chao1 index) was calculated using the ‘ggplot2’ package in R (Ginestet, 2011; Grunsky, 2002). Principal coordinate analysis (PCoA) was used to confirm the distribution of bacterial communities in TZ, MF, and AL areas. The “Venn” package was utilized for constructing Venn diagrams. Redundancy analysis (RDA) was employed to determine the correlation between airborne bacterial differences and environmental variables. Additionally, the “FEAST” package was used for source tracking analysis (Shenhav et al., 2019; Xue, 2024).

2.4. Other Data

Hourly meteorological data, including temperature, relative humidity, wind direction, and wind speed, were acquired from local monitoring stations (Xue, 2024). In collaboration with the recently launched global data management system by the National Oceanic and Atmospheric Administration, this study utilized MeteoInfo software for visualization (Qi et al., 2022). Additionally, the TrajStat plug-in (Wang et al., 2009) was used to compute the retrograde trajectory of an upper air mass at a height of 500 m.

3. Results

3.1. Classification of the Samples

By conducting backward trajectory analysis (one trajectory per hour) on air samples collected at an altitude of 500 m in the AL region for a duration of 72 hr, we categorized the samples collected from July 18th to 24 July 2019, into four groups based on their trajectory transmission direction. As shown in Figure S1a in Supporting Information S1, the local source (AL_LS), which refers to the air mass that remains in a wandering trajectory at the sampling site for 72 hr, includes isotopes 18D and 18N. The dust source (AL_DS) originates from the Taklimakan Desert in the north and includes isotopes 23D, 23N, 24D, and 24N. The Indian source (AL_IS) represents an air mass influenced by the Southwest Indian seasonal winds and includes isotopes 19D, 19N, 20D, 21N, and 22D. The common source (AL_CS) is influenced by both the dust source and the Indian source and includes isotopes 21D and 22N. According to the 48-hr, 72-hr, and 96-hr backward trajectory analysis of AL dust

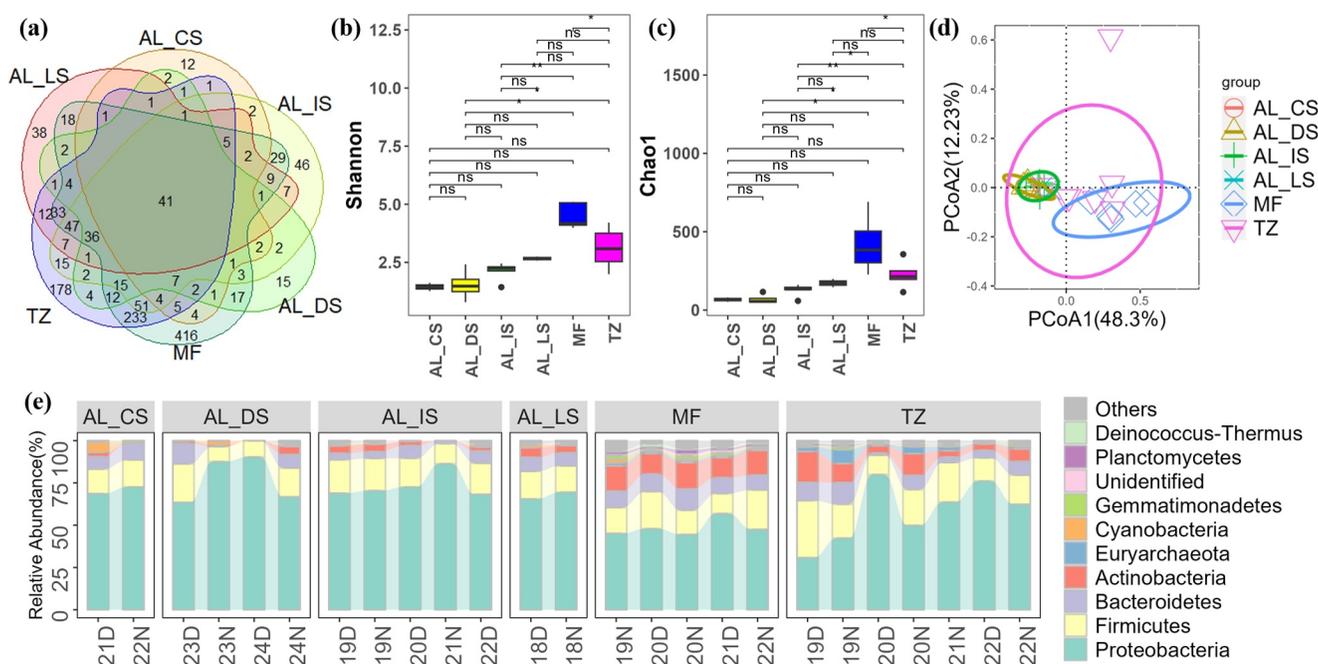


Figure 2. (a) Venn diagram. (b) Shannon index for α -diversity. (c) Chao1 index for α -diversity. (d) PCoA analysis of sample clustering patterns. (e) Bacterial taxonomic composition at the phylum level. Box plots indicate interquartile ranges with medians marked; significance was determined using the Wilcoxon test (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

source samples, we obtained valid samples from MF and TZ from July 19th (daytime) to July 22nd (nighttime) (Figure S1b in Supporting Information S1). Additionally, the occurrence of dust events can be discerned through the analysis of Calipso (Figure S2a in Supporting Information S1) and MERRA-2 (Figures S2b and S2c in Supporting Information S1) satellite data, which yields consistent results with those obtained from backward trajectory analysis.

3.2. Bacterial Diversity in Aerosol Samples

After conducting Illumina-MiSeq high-throughput sequencing and optimizing the process, the abundance of information from all samples in different OTUs was statistically obtained. In total, 2,971 OTUs were identified from the samples, encompassing 54 phyla, 125 classes, 300 orders, 493 families, and 1,393 genera. The Venn diagram allows for the quantification of species that are shared or unique among various samples, visually demonstrating the degree of similarity and overlap in species composition within environmental samples. The Venn diagram in Figure 2a illustrates the distribution of OTUs among different samples under the same sequencing depth. In descending order, the samples with the highest number of OTUs were MF (999), TZ (720), AL_IS (339), AL_LS (267), AL_DS (174), and AL_CS (95). The total number of observed OTUs was 41. The out number of AL_LS is 1.5 times that of AL_DS. In dusty source weather conditions, the out number of AL_LS decreased by 34.8%.

The α -diversity metric serves as an indicator of the microbial community's abundance and variety. In Figures 2b and 2c, the Shannon diversity ranges from 0.8 to 5.1, while the Chao1 index spans from 50.6 to 691.2. The descending order of samples based on their Shannon and Chao1 diversity indices is MF (4.5; 421.4), TZ (3.1; 225.2), AL_LS (2.7; 172.1), AL_IS (2.1; 125.9), AL_DS (1.5; 69.4), and AL_CS (1.4; 66.6). During the dust period, the Shannon index and Chao1 index of airborne bacteria in AL_DS exhibited a significant decrease of 42.2% and 59.7%, respectively, when compared to AL_LS. Furthermore, the diversity indices of MF, TZ, and AL_DS samples showed strong associations with those of AL_LS samples in terms of Shannon and Chao1 measurements. The Shannon and Chao1 indices exhibited similar values in AL_IS samples compared to AL_LS samples, whereas no significant association was found between the Shannon indices of AL_IS and TZ samples. In the PCoA plot (Figure 2d), there were minimal differences among samples from different sources in the AL region, whereas substantial dissimilarities existed between these samples and MF as well as TZ samples.

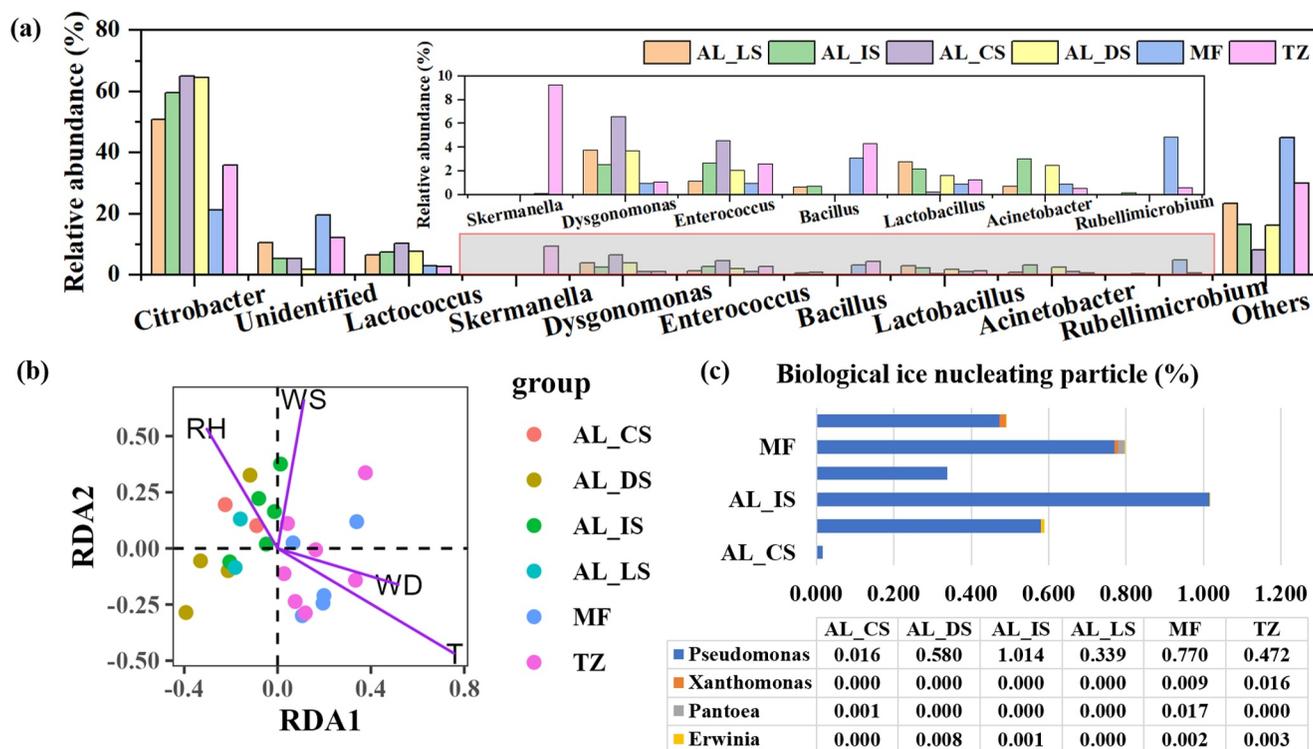


Figure 3. (a) Bacterial taxonomic composition at the genus level. (b) RDA analysis. (c) Relative abundance of IN bacteria at the genus level.

Comparatively speaking, the dissimilarities between TZ and AL samples were minor, while those between MF and AL samples were considerable.

3.3. Bacterial Community Composition and Their Influencing Factors

Differences in community composition can be attributed to the specific ecosystems under investigation. Analysis at the phylum level indicated that *Proteobacteria*, *Firmicutes*, *Bacteroidetes*, and *Actinobacteria* exhibited consistent dominance in all samples from AL, TZ, and MF (Figure 2e). Collectively, these phyla accounted for more than 89.7%. The AL_DS sample exhibited a higher relative abundance of *Proteobacteria* and *Euryarchaeota* compared to the AL_LS sample. The relative abundance of *Proteobacteria* is relatively high in the AL area, with all proportions exceeding 67.5%. Notably, the proportion of *Proteobacteria* in the AL_DS area reaches its peak at 77.0%. This can be primarily attributed to *Citrobacter* being the dominant genus, accounting for a significant relative abundance of 64.5% (Figure 3a). The presence of *Euryarchaeota* was not detected in the AL_LS sample, whereas it was identified in the AL_DS sample. In contrast, the proportions of *Euryarchaeota* in the MF and TZ samples were 1.1% and 2.7%, respectively. In contrast, the highest proportion of *Firmicutes* is observed in the TZ area (20.1%). In contrast, the MF region demonstrates elevated relative abundances of *Bacteroidetes* (10.2%) and *Actinobacteria* (13.8%). Compared to the relative abundance of AL_LS samples, the main phyla exhibiting decreased relative abundance in AL_DS samples were *Firmicutes*, *Actinobacteria*, *Bacteroidetes*, *Gemmatimonadetes*, *Cyanobacteria*, *Planctomycetes*, and *Deinococcus-Thermus*. Collectively, these phyla experienced a total reduction of 8.1%. Specifically, *Actinobacteria* and *Bacteroidetes* demonstrated reductions of 3.2% and 3.0%, respectively. At the genus level, compared to the AL_LS sample, the relative abundance of *Citrobacter* (64.5%), *Lactococcus* (7.6%), *Enterococcus* (2.1%), and *Acinetobacter* (2.5%) was significantly higher in the AL_DS sample, resulting in a total increase of 17.6% for these genera. During the sand and dust period, there was a collective decrease of 1.6% observed in *Skermanella*, *Dysgonomonas*, *Bacillus*, *Lactobacillus*, and *Rubellimicrobium*. Specifically, *Lactobacillus* exhibited a reduction of 1.2%, while *Bacillus* showed a decrease of 0.6%. Moreover, *Skermanella*, *Bacillus*, and *Enterococcus* showed higher relative abundances in TZ and MF samples than in AL samples (Figure 3a), suggesting their resilience in extremely dry conditions.

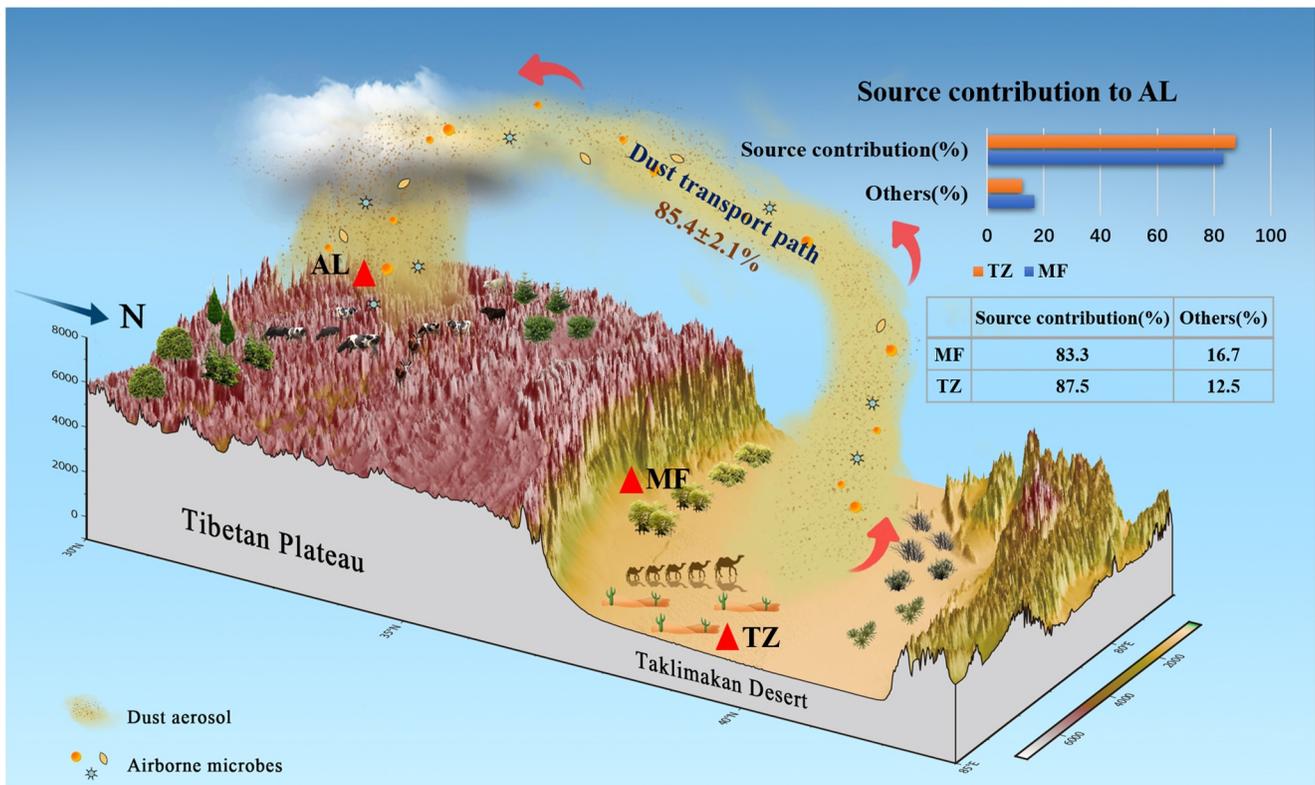


Figure 4. Schematic diagram illustrating the transport mechanism of airborne bacteria from the Taklimakan Desert to the Tibetan Plateau.

Pathogens present in the atmosphere can be disseminated through atmospheric circulation, thereby amplifying their potential health hazards. Among the top 10 genera in terms of relative abundance, the AL_DS samples exhibited a predominant presence of potential airborne pathogens, primarily *Citrobacter* (64.5%), *Enterococcus* (2.1%), and *Acinetobacter* (2.5%). The combined relative abundance of these genera in the AL_DS samples was 69.1% (Figure 3a), representing a significant increase of 16.4% compared to the AL_LS samples' proportion of 52.6%. The RDA analysis elucidates the impact of meteorological factors on the dominant phyla of airborne bacterial communities in AL, TZ, and MF. As depicted in Figure 3b, temperature exerts the most significant influence, followed by WS, RH, and WD on microbial diversity in these regions. RH exhibits a negative correlation with bacterial community diversity in the air, while temperature, WS, and WD display positive correlations with airborne bacterial diversity. The abundances of *Pseudomonas*, *Pantoea*, *Erwinia*, and *Xanthomonas* were subjected to statistical analysis in this study (Figure 3c). The IN abundances for AL_LS, AL_DS, MF, and TZ samples were determined as 0.3%, 0.6%, 0.8%, and 0.5% respectively. The results of source tracking (Figure 4) demonstrated that the airborne bacteria in the AL area were predominantly contributed by MF and TZ, accounting for 83.3% and 87.5%, respectively, with an average contribution rate of $85.4\% \pm 2.1\%$.

4. Discussion

The Taklimakan Desert is an extremely arid ecosystem, while the Tibetan Plateau, the highest plateau globally, is highly sensitive to climate change. Source tracking results (Figure 4) demonstrated that the contribution of Taklimakan dust to airborne bacteria on the Tibetan Plateau was estimated at $85.4\% \pm 2.1\%$. The transport of the Taklimakan dust source to the Tibetan Plateau through backward trajectory is influenced by both the westerlies and the underlying surface characteristics, as evidenced in Figure S1a in Supporting Information S1 and Figure 4. Arid atmospheric conditions, intense ultraviolet radiation, and low nutrient levels create heightened selective pressure on airborne bacteria, potentially reducing bacterial diversity (Huang et al., 2023; Qi et al., 2023). Moreover, westerly winds predominantly traverse simplistic ecosystems such as deserts and sparsely vegetated grasslands, further diminishing airborne bacterial community richness.

The compositions of bacterial communities in the air are influenced by both the origin of the air mass (Tang et al., 2018) and the ecosystems traversed by the air mass (Fröhlich-Nowoisky et al., 2016). The AL region is recognized as a transitional zone influenced alternately by the Indian monsoon and prevailing westerly winds (Yao et al., 2013). The AL samples exhibited a negative correlation with temperature and wind direction (Figure 3b), suggesting that air mass sources from different directions may exhibit significant variations in the composition of the AL community. However, during the sampling period, the prevailing westerly wind and Indian monsoon alternately governed the atmospheric conditions above the AL region, resulting in a north-south movement pattern. Consequently, the ecological environments encountered were exclusively situated around the Tibetan Plateau, resulting in minimal variations in community composition across different air mass sources. This observation suggests that the predominant bacteria found in AL samples may originate from the surrounding environment of the Tibetan Plateau. The diversity of MF and TZ sample species is evident in the Venn diagram, with the surrounding areas of the Taklimakan experiencing frequent sandstorms during summer (Ma et al., 2020). This observation suggests a substantial influx of airborne microorganisms carried by dust particles. In contrast to AL_LS, *Euryarchaeota* emerged from nonexistence in AL_DS samples, with the proportions of *Euryarchaeota* being 1.1% and 2.7% in MF and TZ samples, respectively. Dust exposure significantly influenced *Euryarchaeota*, making it a characteristic bacterium in both MF and TZ samples. Besides, *Euryarchaeota* is frequently observed thriving under extreme salinity conditions. Consequently, the presence of *Euryarchaeota* can serve as a reliable indicator for characterizing the Taklimakan dust community composition. Identifying *Euryarchaeota* in AL_DS samples suggests that the Tibetan Plateau has been influenced by deposition events originating from the Taklimakan Desert. Compared to AL_LS samples, AL_DS samples showed a 17.6% increase in the abundance of *Citrobacter*, *Lactococcus*, *Enterococcus*, and *Acinetobacter*. Additionally, MF and TZ samples exhibited a positive correlation with WD, indicating predominant influence by westerly air masses. The aggregation of bacterial communities in aerosols is attributed to atmospheric circulation, confirming that Taklimakan dust-borne microbes shape the bacterial community composition within the Tibetan Plateau region.

The bacterial diversity in the atmosphere is influenced by different air mass sources (Fröhlich-Nowoisky et al., 2016). The α -diversity, measured by the Shannon index and Chao1 index, reflects the variation in airborne bacterial communities across different spatial orientations. The high altitude of the Tibetan Plateau, characterized by lower temperatures, reduced allochthonous inputs of organic matter, and intense solar radiation, favors the selection of bacterial species that exhibit resilience to harsh environmental conditions (Qi et al., 2021). During the Taklimakan dust period, the Shannon index and Chao1 index of airborne bacteria in the Tibetan Plateau decreased significantly by 42.2% and 59.7%, respectively. The Shannon diversity and Chao1 indices of the aerosol samples were significantly higher in arid regions than in semi-arid regions (Qi et al., 2023). The highest α diversity was observed in the MF region, likely due to the higher vegetation and human population density, which contribute to the abundance of airborne microbes (Zhang et al., 2024). Analysis of the Shannon diversity and Chao1 index for MF samples confirms their higher diversity and richness compared to AL_DS samples. AL_LS samples also exhibited higher diversity than DS samples, though no significant correlation was found with MF and TZ samples. These findings highlight notable dissimilarities in microbial populations between AL_LS samples and MF/TZ samples. The continuous availability of local resources makes AL_LS the most diverse and resource-rich region, such as numerous lakes in the Tibetan Plateau (Zhang et al., 2017). Before reaching the sampling site, arid atmospheric conditions and intense ultraviolet radiation likely reduce bacterial diversity by preferentially transmitting certain airborne microbes (Qi et al., 2022). AL_DS exhibits the lowest diversity and richness due to selective airborne bacterial populations under ultraviolet radiation and arid conditions (Pan et al., 2021), thereby constraining atmospheric bacterial diversity. Consequently, the atmospheric milieu hampers the proliferation and propagation of microbial communities, while dust-mediated transport further diminishes airborne microbial diversity across the Tibetan Plateau. The MF and TZ samples showed a positive correlation with T and WD, suggesting selective transmission of airborne microorganisms. Wilcoxon test analysis revealed no significant differences in the Shannon index and Chao1 index between AL_DS samples and MF/TZ samples ($P < 0.05$), indicating a significant association between the AL dust period and both MF and TZ. This supports the notion that Taklimakan dust negatively affects bacterial diversity in the AL region.

The Indian monsoon and westerly winds transport airborne microbes from various sources (Qi et al., 2022), further facilitating their dispersion. Investigating the impact of Taklimakan dust on the health and climate of the Tibetan Plateau is of significant scientific importance. These findings underscore the significant impact of Taklimakan dust on air microorganism levels in the Tibet Plateau under westerly wind conditions. For the top 10

genera in terms of relative abundance, there was a significant increase in *Citrobacter*, *Enterococcus*, and *Acinetobacter* levels in AL_DS samples compared to AL_LS samples. *Citrobacter* is an infrequent yet significant pathogen associated with neonatal meningitis and infections. *Enterococci* are typically prominent pathogens responsible for abdominal and pelvic infections (Zhang et al., 2024). *Acinetobacter* can be found in diverse natural environments, harboring a wide range of causative agents for nosocomial infections, including pneumonia (Hartzell et al., 2007). These genera, potential airborne pathogens, can cause various infectious diseases, including respiratory tract infections, and are commonly found in soil, water, and food sources. The relative abundance of these genera in AL_DS samples accounted for 69.1% (Figure 3a), a 16.4% increase compared to AL_LS samples (52.6%). Quantitative results revealed that Taklimakan dust contributed to the dissemination of potential pathogens on the Tibetan Plateau, exceeding 16.4%. These airborne pathogens, capable of spreading through atmospheric circulation, increase health risks (Triadó-Margarit et al., 2022).

The climate impact of bioaerosols primarily arises from airborne microbes (such as *Pseudomonas*, *Pantoea*, *Erwinia*, and *Xanthomonas*) serving as CCN and IN (Huang et al., 2021). The formation of IN is initiated by the amalgamation of biological particles with mineral dust, amplifying the impact of dust storms on cloud and precipitation formation (Behzad et al., 2018; Hoose et al., 2010; Huang et al., 2021; Twohy et al., 2009). Statistical analysis of IN in this study (Figure 3c) revealed IN abundance of 0.8% and 0.5% in MF and TZ samples, respectively, with AL_DS samples showing a significant increase by 73.8% compared to AL_LS samples (0.6% vs. 0.3%). This suggests that dust particles and airborne bacteria enhance ice nucleation, potentially leading to increased rainfall on the Tibetan Plateau. These microbes actively participate in cloud condensation processes, influencing precipitation events and the hydrological cycle, and thus affecting regional and global climatic patterns (Huang et al., 2023). Westerly dust facilitates the transportation of airborne microbes to the Tibetan Plateau, augmenting ice nucleation and potentially increasing precipitation in this region. Prolonged drought in desert regions decreases plant litter, leading to reduced plant cover and soil roughness. This increase in surface reflectivity diminishes precipitation, exacerbating drought conditions within these arid areas (Tariq et al., 2024).

5. Conclusions

This study investigates the influence of Taklimakan dust (MF and TZ) on the presence of airborne bacteria in the Tibetan Plateau (AL). The results demonstrate that the diversity of airborne bacteria on the Tibetan Plateau is diminished by the deposition of Taklimakan dust. Source tracking analysis determined that approximately $85.4\% \pm 2.1\%$ of airborne bacteria on the Tibetan Plateau originate from Taklimakan dust. *Euryarchaeota* could potentially serve as a key bacterial indicator within the Taklimakan dust community composition. Compared to the AL_LS community, AL_DS samples exhibited a significant increase of 17.6% in the populations of *Citrobacter*, *Lactococcus*, *Enterococcus*, and *Acinetobacter*, indicating the substantial influence of airborne microbes transported by Taklimakan dust on the bacterial community composition in the Tibetan Plateau. AL_DS samples showed a 16.4% increase in the abundance of potential pathogenic bacteria and a remarkable 73.8% increase in ice nucleation bacteria compared to the AL_LS community. This study provides novel insights into the impact of airborne bacteria transported by Taklimakan dust on the bacterial abundance and community composition in the Tibetan Plateau region.

Data Availability Statement

The Quantitative Insights into Microbial Ecology pipeline (QIIME2) (Almeida et al., 2018) and the SILVA reference database (v132) (Quast et al., 2013) employed a 97% similarity threshold to classify Operational Taxonomic Units (OTUs) and provided species annotations. The original sequence was deposited in the NCBI SRA database (BioProject accession number PRJNA1150353; <https://www.ncbi.nlm.nih.gov/bioproject/1150353>). Data processing and visualization were performed using R language, Origin and MeteInfo software (Ginestet, 2011; Grunsky, 2002). The “FEAST” package has been uploaded to <https://doi.org/10.5281/zenodo.14031069>. In conjunction with the global data management system released by the National Oceanic and Atmospheric Administration (NOAA) (<ftp://arlftp.arlhq.noaa.gov/pub/archives/gdas1>), this research employs MeteInfo software visualization. Additionally, TrajStat plug-in is utilized to compute the retrograde trajectory of an upper air mass at a height of 500m (Wang et al., 2009). The hourly meteorological data, including temperature (T), relative humidity (RH), wind direction (WD), and wind speed (WS), are acquired from local monitoring stations (<https://doi.org/10.5281/zenodo.14031069>).

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