Research Article

A super sandstorm altered the abundance and composition of airborne bacteria in Beijing

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KEYWORDS:
Airborne bacteria
Sandstorm
Bioaerosol
Haze
Pathogen

ABSTRACT

Sandstorm, which injects generous newly emerging microbes into the atmosphere covering cities, adversely affects the air quality in built environments. However, few studies have examined the change of airborne bacteria during severe sandstorm events. In this work, we analyzed the airborne bacteria during one of the strongest sandstorms in East Asia on March 15th, 2021, which affected large areas of China and Mongolia. The characteristics of the sandstorm were compared with those of the subsequent clean and haze days. The composition of the bacterial community of air samples was investigated using quantitative polymerase chain reaction (qPCR) and high-throughput sequencing technology. During the sandstorm, the particle matter (PM) concentration and bacterial richness were extremely high (PM_{2.5}: 207 μg/m³; PM_{10}: 1630 μg/m³; 5700 amplicon sequence variants/m³). In addition, the sandstorm brought 10 pathogenic bacterial genera to the atmosphere, posing a grave hazard to human health. As the sandstorm subsided, small bioaerosols (0.65–1.1 μm) with a similar bacterial community remained suspended in the atmosphere, bringing possible long-lasting health risks.

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Introduction

Bioaerosols are airborne particles of biological origins such as bacteria, fungi, and viruses. Bioaerosols may account for more than 80% of particulate matter (PM) in the atmosphere, and some pathogens can cause diseases and infections (Chen et al., 2022; Fröhlich-Nowoisky et al., 2016; Huffman et al., 2012). The concentration, size distribution, abundance, diversity and transmission of bioaerosols can be easily influenced by global and local atmospheric conditions, either directly or indirectly (Ruiz-Gil et al., 2020). For instance, haze with high-concentration PM_{2.5} (particles with an aerody-
namic diameter smaller than 2.5 μm) contains a large number of bioaerosols, which may lead to respiratory and cardiovascular diseases (Cao et al., 2023; Liu et al., 2021a). Worse, during severe climate changes such as sandstorms, microorganisms attached to the surfaces are forced to resuspend into the atmosphere (Hagivara et al., 2021; Liu et al., 2021b). Though sandstorms typically happen in arid or semi-arid regions, they may transport aerosols hundreds and thousands of kilometers from their origins (Filonchyk, 2022). Consequently, during sandstorms, microorganisms from different ecosystems would be transported and dispersed across great distances, resulting in cross-border environmental pollution (Ichinose et al., 2005) and immune-mediated diseases (Ichinose et al., 2005; Niu et al., 2021). Taking COVID-19 as an example, studies revealed a positive correlation between daily COVID-19 cases/mortality and the rising PM levels during the Saharan sandstorm (Kokkalis et al., 2021; Kutralam-Muniasamy et al., 2021). The longer possible pathogens exist in the air, the greater the harm to people, and the length of time they remain in the air depends on their size and meteorological conditions (Niu et al., 2021; Qiu et al., 2020). It is estimated that PM_{10} (particles with an aerodynamic diameter smaller than 1.0 μm) may remain suspended in the atmosphere for more than 10 days on average (Reche et al., 2018). As sandstorm happen more frequently in cities worldwide, fully understanding the characteristic change of the bioaerosols during sandstorms is important (Liu et al., 2023; Ye et al., 2018).

Numerous studies have investigated ambient bioaerosols under different air pollution levels and climatic conditions, but there are still several unresolved complexities (Li et al., 2020; Xie et al., 2018). Zhen et al. (2017) sampled airborne particles in Beijing for 20 consecutive days throughout each season in 2015. Meteorological factors had a much greater influence on determining airborne bacteria than air pollutants during each season, and variances beyond seasonal variance were all caused by severe meteorological events such as sandstorms and rain. Chen et al. (2021) evaluated the PM_{2.5} bacterial community in Beijing’s suburban atmosphere and found that the microbial community structure at different pollution levels was similar. However, different from the above findings, Li et al. (2015) collected air samples in Xi’an during haze and non-haze days and confirmed that concentrations of viable bacteria and fungi on haze days were much higher than those on non-haze days, and some more allergic and infectious genera can be found during the haze days. Even though China has strictly and successfully controlled air pollution recently, bioaerosols still increase during moderate particle pollution in the winter heating season (Wei et al., 2020; Wu et al., 2021). Many studies focused on bioaerosols during haze episodes instead of sandstorms (Cao et al., 2014; Zhang et al., 2019b). Niu et al. (2021) studied the air samples during a mixed dust and haze period in Beijing but focused on archaea. As bioaerosol influenced by sandstorms varies according to the sandstorm’s origin and intensity, it would be beneficial to study some specific sandstorms to provide additional data and references.

This study investigated airborne bacteria comprehensively during the super sandstorms that affected large areas of China and Mongolia on March 15th, 2021 (Filonchyk, 2022; Yin et al., 2022). The characteristics of airborne bacteria were evaluated by comparing parallel samples taken the day after the sandstorm and another subsequent haze day. Air samples were collected with a six-stage impinger sampler to determine the size distribution, followed by quantitative polymerase chain reaction (qPCR) and high-throughput sequencing of the bacterial 16S rRNA gene region for further quantification and characterization. The processes and factors that affect the composition of airborne bacteria were investigated by statistical analysis. The findings are anticipated to increase our understanding of the unique influences of a severe sandstorm on airborne bacteria and to estimate the potential health risk posed by ambient bioaerosols to people during sandstorm episodes.

1. Materials and methods

1.1. Collection of air samples

Air samples were collected on the roof of a building at Tsinghua University in Beijing, China (116°20’E, 39°56’N; 12 m above ground level). The building is about 500 m away from the nearby main road and far away from the industrial district. Sampling was performed at 2 p.m. on three different typical climate days: March 15th (sandstorm), 16th (after-storm), and 26th (haze), 2021. The daily average meteorological parameters of air pollutants on these days were downloaded from China National Environmental Monitoring Centre (http://www.cnemc.cn) and concluded in Appendix A Table S1.

Air samples were collected with a six-stage Andersen Cascade Impactor (Mingjilianm Instrument and Technology Company, Hebei, China). The aerodynamic diameter of bioaerosols ranged in the six stages: 0.65–1.1 μm, 1.1–2.1 μm, 2.1–3.3 μm, 3.3–4.7 μm, 4.7–7.0 μm, > 7.0 μm, which are named as Rank 1 to 6, respectively. At each stage, a micro disk membrane filter (Jinyou Biotechnology Company, Nanjing, China) with a mean pore size of 0.22 μm was set on a glass culture dish. Before sampling, all sampling tools were sterilized. The sampling flow rate was set at 28.3 L/min by a QT-30 bioaerosol sampling pump (SKC, USA), and each sampling process lasted for 30 min. After sampling, the filters were immediately stored at -40°C.

1.2. DNA extraction and high-throughput gene sequencing for bacteria

Genomic DNA from all air samples was extracted by the cetyltrimethylammonium bromide (CTAB) method, and the DNA was stored at -80°C before further analysis (Jiang et al., 2015). Bacterial abundance was determined by qPCR of the 16S rRNA gene. The amplification of PCR was carried out on a Bio-Rad CFX96 Touch Real-Time PCR Detection System (Bio-Rad, USA) with primers 341F 5′-(CTTACGGGNGGCWGCAG)-3′ and 806R 5′-(GGACTACHVGGGTWTCTAAAT)-3′. The DNA of each sample was diluted to 1 ng/μL with PCR-grade water before configuring the reaction mixture. PCR reactions were performed in a 30 μL mixture, which contained 15 μL of High-Fidelity PCR Master Mix (New England Biolabs, USA), ~ 15 μL of PCR-grade water, 0.2 μmol/L of forward and reverse primers,
and approximately 10 ng of template DNA. The reaction conditions were as follows: pre-degeneration at 95°C for 1 min, denaturation at 95°C for 10 sec, annealing at 50°C for 30 sec, extension at 72°C for 30 sec, with a total of 30 cycles, and then a final extension step at 72°C for 5 min. The PCR products were mixed with the same volume of 1× loading buffer containing SYBR Green (Synergy Brands) and were analyzed via 2% agarose gel electrophoresis. The products were used to prepare the Illumina DNA library after the purification using TIANgel Purification Kit (TIANGEN Biotech, China). Sequencing libraries were generated using TIANSeq Fast DNA Library Prep Kit (TIANGEN Biotech, China). Libraries were assessed for quality with the Qubit® 2.0 Fluorometer (Thermo Scientific) and Agilent Bioanalyzer 2100 system. Finally, the library was sequenced using the 2 × 250 bp paired-end reads.

### 1.3. Analysis of sequencing data

Sequences were processed using QIIME 2 (Quantitative Insights Into Microbial Ecology 2, 2022.5) with slight modifications (Bolyen et al., 2019). After the Demux plugin and the primers cutting with the Cutadapt plugin, raw sequences were then operated using the DADA2 (Divisive Amplitude Denoising Algorithm 2) to obtain the chimera-free sequences (Callahan et al., 2016). After the DADA2 operation, amplicon sequence variants (ASVs) were gained, corresponding to sequences clustered with a 100% similarity. To ensure the comparability of species diversity among samples, all samples were normalized to the same sequencing depth. The even read number of all 18 samples was 33,680 with 6610 ASVs after normalization. Bacterial species annotation was performed using the SILVA rRNA database (Quast et al., 2013).

### 1.4. Statistical analysis

Alpha diversity is used to analyze the complexity of sample species diversity through 4 indices, including Simpson, ACE, Chao1, and Shannon (McMurdie and Holmes, 2013). A higher value for each index indicates a higher microbial diversity (Grice et al., 2009). Community diversity refers to the consistency of species distribution in a sample. These indices were calculated with QIIME2. Beta diversity analysis was used to assess sample differences in species complexity. Principal Coordinate Analysis (PCoA) based on the Bray-Curtis dissimilarity and the Jaccard index was conducted to visualize the differences among airborne bacterial communities of air samples. The two-dimensional PCoA results were displayed using QIIME2. Canonical correlation analysis (CCA) carried out by CANOCO 4.5 software was used to show the correlation between airborne bacterial communities and ambient meteorological parameters.

### 2. Results

#### 2.1. Particulate matter and airborne bacterial ASVs

The whole 18 samples were divided into three groups depending on the weather: sandstorm, after-storm and haze. Every ASV indicates one possible independent bacterium species. Thus, the number of ASVs obtained from each group can estimate the richness of bacterial species. As shown in Fig. 1a, the ASV numbers on the sandstorm, after-storm, and haze days were 5700, 2515, and 2992, respectively. The detailed ASV data of all samples are concluded in Appendix A Sheet S1. The FM2.5 and PM10 mass concentrations on the sandstorm day were 207 μg/m³ and 1630 μg/m³, respectively. The concentration of PM10 on the sandstorm day was significantly higher than that on the day after the sandstorm (177 μg/m³) and the haze day (157 μg/m³). Besides, the concentration of PM2.5 on the day after the sandstorm (37 μg/m³) was significantly lower than that on haze day (136 μg/m³) and sandstorm day (207 μg/m³). The overall PM pollutant conditions of North China on the sandstorm day, the day after the sandstorm and the haze day could be consulted by a real-time air pollutant database (http://tapdata.org.cn) as shown in Fig. 1bd (Geng et al., 2021; Xiao et al., 2021). The three graphs display how a sandstorm hit North China and faded away, and a haze occurred. As is shown in Fig. 1a, the number of ASVs is positively related to particulate matter concentration. The results agree with similar research (Niu et al., 2021; Xie et al., 2018). Since bioaerosols constitute substantial parts of airborne PM, the high PM concentration can indicate high bacterial community richness and bioaerosol concentration.

#### 2.2. Airborne bacterial composition

The top ten phyla across all 18 samples and their relative abundances are shown in Fig. 2a. The original taxonomy data of all samples at the phylum level are concluded in Appendix A Sheet S2. Overall, the top four phyla in the bacterial 16S rRNA libraries of the after-storm group are: Proteobacteria (47.2%), Actinobacteria (15.9%), Firmicutes (14.4%), and Bacteroidetes (15.0%), comprising > 92% of all reads. Changes in bacterial community structure with bioaerosol size seem not obvious in the after-storm group. The relative abundance of dominant bacterial taxa that shows significant changes with size will be discussed later. As for the haze group, the top four phyla are still Proteobacteria (51.6%), Actinobacteria (13.4%), Firmicutes (13.7%), and Bacteroidetes (12.9%), which comprise > 91% of all reads. It can be indicated that when there is haze and relatively high PM concentration in the atmosphere, the relative abundance of Proteobacteria will increase with that of Actinobacteria, Firmicutes, and Bacteroidetes decrease. However, the relative abundance changes between the two groups at the phylum level are apparent, the biggest of which lies in Proteobacteria (4.4%). It is worth noting that the fifth abundant phyla, Cyanobacteria, ranged from 1.6% to 5.0% when the weather changed to haze. The bacterial community composition of the sandstorm group becomes complicated. The collective top four phyla in after-storm and haze groups: Proteobacteria (27.8%), Actinobacteria (19.1%), Firmicutes (18.9%), and Bacteroidetes (8.7%) only comprised 74.5% of all reads in the sandstorm group. It can be indicated that some bacteria are more abundant as a result of the sandstorm, such as Cyanobacteria (9.1% in sandstorm, > 5.0% in haze, > 1.6% in after-storm group), Chloroflexi (5.2% in sandstorm, > 1.4% in after-storm group), Acidobacteria (3.3% in sandstorm, > 0.06% in after-storm group), Gemmatimonadota (2.5% in sandstorm, > 0.05% in after-storm group), and Planctomycetota
Fig. 1 – (a) Average mass concentration of PM$_{2.5}$ and PM$_{10}$ on the sandstorm day, the day after the sandstorm and the haze day, and the number of ASVs obtained from the air samples. The average PM$_{2.5}$ concentration on (b) the sandstorm day, (c) the day after the sandstorm, and (d) the haze day over North China. The green points on the map marked the sampling location. The PM$_{2.5}$ data were gained from http://tapdata.org.cn.

Fig. 2 – Relative abundance of airborne bacteria from 18 samples collected (a) at the phylum level and (b) at the genus level on the sandstorm day, the day after the sandstorm, and the haze day. S, A, and H are sandstorm, after-storm, and haze days.
Fig. 3 – Alpha diversity of the air samples was estimated by (a) Shannon, (b) Simpson, (c) Chao1, and (d) ACE indices in the sandstorm, after-storm and haze groups. ** indicates that the difference between concentrations is statistically significant (p < 0.05).

(1.8% in sandstorm, > 0.06% in after-storm group). Considering the larger number of species annotated in the sandstorm group (Fig. 1a), more bacteria must belong to those expanding phyla like Cyanobacteria attached to airborne dust during the sandstorm. Besides, there are larger differences in bacterial composition between different bioaerosol size ranges in the sandstorm, in contrast with the other groups. The reason may be that the size distribution of PM in the sandstorm differed from that in the haze and after-storm groups.

At the genus level, there are 661 groups found across all the samples. The top twenty genera are shown in Fig. 2b. The original taxonomy data of all genus-level samples are concluded in Appendix A Sheet S3. In the after-storm group, Sphingomonas is the most abundant genus (17.3%), followed by Bacteroides (10.5%). The same composition occurs in the haze group, with Sphingomonas at 23.9% and Bacteroides at 9.1%. In the sandstorm group, with more genera in total, the abundance of Sphingomonas and Bacteroides shrinks to 9.7% and 4.0%. On the other hand, there are some bacteria more abundant as a result of the sandstorm, such as Microcystis (8.9% in sandstorm, > 1.5% in after-storm group), Bifidobacterium (4.8% in sandstorm, > 2.1% in after-storm group), Faecalibacterium (3.2% in sandstorm, > 0.1% in after-storm group) and Subdoligranulum (2.5% in sandstorm, > 0.07% in after-storm group). Staphylococcus, Corynebacterium, and Pseudomonas among the abundant genus were also observed in Middle East dust storms (Amarloei et al., 2020). On the species level, Pseudomonas kluvysepensis, an endemic species from Khuvsgul Lake, Khuvsgul province, Mongolia, was detected only in samples on the sandstorm day, which confirmed that the sandstorm carried bacteria from the source and changed the local bioaerosol composition (Ara et al., 2011). In conclusion, the sandstorm can significantly change the community structure of bioaerosols in terms of quantity and type, and the influences are far greater than those of the haze.

2.3. Airborne bacterial diversity

Four different indices are concluded to assess the alpha diversity of the three groups, as shown in Fig. 3. Chao1 and ACE indices express the richness of the bacterial community, while Shannon and Simpson indices account for both richness and evenness. The Shannon index estimates that the airborne bacterial community in the sandstorm is far richer and more even than the after-storm (p = 0.010) and haze groups (p = 0.005). The other three indices met the result of the Shannon index quite well. The alpha diversity on the haze day is slightly lower than on the day after the sandstorm. The severe sandstorm had just faded away on the day after the sandstorm, and some parts of the sandstorm remained in the atmosphere. Although the concentration of PM2.5 on that day was 37 μg/m^3, which was quite a low level, the concentration of PM10 was still 177 μg/m^3, even higher than that on the haze day (157 μg/m^3). Under the combined effects of the sandstorm residuals and high PM10 concentration, it is reasonable that the after-storm day has a slightly higher alpha diversity than the haze day.

Principle coordinate analysis (PCoA) was performed to assess the clustering and potential separation of airborne bac-
Fig. 4 – Principal coordinate analysis (PCoA) plots of airborne bacterial beta diversity of the 18 samples based on (a) Bray-Curtis dissimilarity and (b) Jaccard index. The numbers 1–6 represent the size range of the samples: 0.65–1.1 μm, 1.1–2.1 μm, 2.1–3.3 μm, 3.3–4.7 μm, 4.7–7.0 μm, > 7.0 μm, respectively. For example, S1 is short for the 0.65–1.1 μm sample in the sandstorm group and A2 for the 1.1–2.1 μm sample in the after-storm group.

3. Discussion

3.1. Airborne potential pathogens change

On the species level, 22 kinds of bacteria species were confirmed to be human pathogens, according to the literature. The relative abundance of the pathogenic bacteria species in the three groups was concluded in Fig. 5. B. longum was the most abundant pathogenetic species detected and was discovered in all groups, which can cause human sepsis and peri-tonitis (Esaiaassen et al., 2017). The sandstorm increased the relative abundance from 0.4% to 0.7% compared to the after-storm group, which was a remarkable abundance change for such a single species. B. fragilis and P. bivia were the other two species found in all groups. B. fragilis results in most anaerobic peritoneal infections and bacteremia, and P. bivia can cause pelvic inflammatory disease. The relative abundances of B. fragilis and P. bivia in the after-storm group were higher than those in the sandstorm and haze group. The reason was that there were much more bacteria species on the sandstorm and haze day. The sandstorm newly brought B. bifidum, R. mucilaginos, C. jeikeium, T. forsythia and L. garvieae into the atmosphere. The relative abundance of these species was relatively low (under 0.01%), but they were able to cause bacteremia, sepsis, endocarditis or become opportunistic pathogens sometimes (Fefer et al., 1998; Nolan et al., 2020; Pardo et al., 2020). The haze newly brought B. bifidum, L. buccalis, M. abscessus, A. schindleri, D. pneumosintes, C. ureolyticus, and O. ulei with increasing particle concentration compared to the after-storm group. These species were confirmed to be related to neutropenia, lung diseases, central nervous system infections, endodontic infec-
Moreover, cardia, storm detected the potential species detected in the study. The distinction of level, between different samples was accurately. It is because the specificity of the hypervariable regions on the 16S rRNA can only distinguish a few bacteria on the species level, which is the limitation of the technology. Gene reads obtained after 16S rRNA sequencing can tell the difference in most bacteria on the genus level. As shown in Fig. 2, 98.73% of the gene reads were annotated on the phylum level and 85.84% on the genus level. Therefore, possible pathogens on the genus level need further study.

To understand the change of airborne bacterial pathogens during the sandstorm more comprehensively, we used the annotation results on the genus level to make predictions. The bacterial genera which included pathogenic species were identified as potential pathogens. The potential pathogens on the genus level from all the samples in the three groups were found according to the literature and finally concluded in Fig. 6. Thirty-four pathogens were detected from samples collected on the day after the sandstorm and thirty-five on the haze day. However, during the sandstorm, the number of pathogens increased to 44. Nocardia, Bilophila, Leptotrichia, Gordonia, Aerococcus, Cupriavidus, Mycobacterium, Enterobacter, Clostridium_sensu_stricto_8 and Prevotellaceae_NK3B31_group were distinctively found during sandstorm compared to the day after the sandstorm. Moreover, except for Nocardia, Leptotrichia, and Gordonia, the other seven pathogens were not detected on the haze day.

The newly occurring pathogens during sandstorms can affect human health in many ways. For instance, Nocardia infection is mostly exogenous, and N. asteroides, one kind of Nocardia species, can lead to serious human pneumonia (Brown-Elliott et al., 2006). Leptotrichia and Gordonia species like L. buccalis and G. rubripertincta are generally regarded as opportunistic pathogens (Soekkhee et al., 2001; Verma et al., 2006). Enterobacter is also an opportunistic pathogen. (Maguvu and Bezuindenhou, 2021). Aerococcus species like A. urinae have been known to cause invasive infections like endocarditis in hospital settings (Senneby et al., 2012). M. leprae and M. tuberculosis of the Mycobacterium genus can cause leprosy and tuberculosis, respectively, which are severe infectious diseases (Horne and Skerrett, 2019).

Although most of these newly emerged pathogens during the sandstorm were less than 0.01% of the total bacterial community, this does not mean a significant health risk was not posed. For example, even if the 16S rRNA copies were evened, the data still suggest at least 330 pathogenic Mycobacterium 16S rRNA copies/m³ during the sandstorm, and even low doses (1 CFU) of Mycobacterium can elicit infection (Ferguson et al., 2021). The data of gene copies obtained and discussed in this study may not be directly equal to the living pathogens, but the PM mass concentration can help to indicate the possible living microorganisms in the bioaerosols. For instance, Yuan et al. sampled and cultured the airborne bacteria during a dust event when the PM₁₀ was 652 µg/m³.

Fig. 5 – Pathogenic bacteria species successfully annotated after 16S rRNA sequencing on the sandstorm day, the day after the sandstorm, and the haze day. The full names of the species are listed in Appendix A Table S2.

Fig. 6 – The stacked plot of relative abundance of potential bacterial pathogens of 18 samples in the sandstorm, after-storm, and haze groups. A to E in the inner circle refers to the groups at the phylum level: Actinomycetota (A), Bacillota (B), Bacteroidota (C), Pseudomonadota (D), and others (E), respectively. Every stacked bar in the graph represents the abundance percentage of one pathogen in a group. The labels around the graph are abbreviations for pathogens, and the comparison table is listed as Appendix A Table S3.
in Beijing, and they found that the bacterial concentration reached $1 \times 10^8$ cells/m$^3$ (Yuan et al., 2017). Considering the sandstorm brought an extremely high PM concentration, the absolute values of airborne bacterial pathogens can be much higher. Therefore, we gave a qualitative explanation of the potential bacterial-induced risks during this sandstorm in this work. Furthermore, the results can provide considerable data reference for quantifying the bacterial-induced human risks during sandstorm in future study.

3.2. Difference in airborne pathogens from literature

Compared with other research on atmospheric bioaerosols, it is the same that the concentrations of viable airborne bacteria or bacterial 16S rRNA gene abundances during the haze and sandstorm days are much higher than on the non-haze days and non-sandstorm days. However, there are many differences in the airborne bacterial composition. For instance, Zhang et al. (2019a) studied the microbial activity in PM$_{2.5}$ under slight and moderate pollution in Beijing. They detected six pathogenic bacteria (Rickettsia, Erysipelothrix, Prevotella, Strep-tococcus, Shigella, and Brucella) from PM$_{2.5}$ samples. Only Prevotella is common in our research. The first reason for the difference may be that they sampled the air in a pre-urban village with mountains and a lake, while we sampled the air in an urban district. Besides, the identification of pathogenic bacteria may be different. In this study, the opportunistic pathogens were all included, so the number of pathogens on haze day was larger than that in Zhang et al. (2019a)’s research. Pathogens like Sphingomonas and Bacillus also increased during Asian dust events in 2018, Beijing (Park et al., 2018). At the phylum level, Deinococcota, Cyanobacteria, Proteobacteria and Actinobacteria were the main bacterial types in the Asian dust area according to the literature, with agreed with Fig. 2 (Maki et al., 2015).

On the other hand, Cao et al. (2014) suggested that the relative abundance of several respiratory allergens and pathogens appeared to increase with increasing PM concentrations on hazy days during a severe smog event in Beijing, which agreed with this research. This research revealed some newly-found pathogenic bacteria during a super sandstorm from Mongolia. The results must differ from those on haze days because the atmospheric environment has changed. However, there are some limitations of this research. The sandstorm lasted a short time, so the air samples seemed insufficient. Long-term observation and analysis of the after-storm and haze days should be made to complete the comparison with the sandstorm samples in future studies.

4. Conclusions

This study provided a detailed analysis of airborne bacteria on a super sandstorm that affected large areas of China and Mongolia on March 15th, 2021. During the sandstorm, the PM concentration and bacterial richness (PM$_{2.5}$: 207 µg/m$^3$; PM$_{10}$: 1630 µg/m$^3$; 5700 ASVs/m$^3$) soared to extremely high levels in comparison to both non-sandstorm days (PM$_{2.5}$: 37 µg/m$^3$; PM$_{10}$: 177 µg/m$^3$; 2515 ASVs/m$^3$) and the haze day (PM$_{2.5}$: 136 µg/m$^3$; PM$_{10}$: 157 µg/m$^3$; 2992 ASVs/m$^3$). In addition, the sandstorm newly introduced 10 pathogenic bacterial genera to the atmosphere, which can pose a severe threat to human health. As the sandstorm subsided, bioaerosols of smaller diameters (0.65–1.1 µm) would remain suspended in the atmosphere. In conclusion, the study helps us understand how a severe sandstorm strikes the residential environment in atmospheric bacterial composition. Considering the great concern of bioaerosol transmission and the complexity of the frequent global sandstorm events, the results of this study will shed new light on the unique influences of the sandstorm on airborne bacteria and assess the potential health risk of ambient bioaerosols on humans during sandstorm episodes.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

This work was supported by the National Natural Science Foundation of China (No. 52078269).

Appendix A Supplementary data

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.jes.2023.07.029.

REFERENCES


