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Microbial aerosol characteristics in highly polluted and near-pristine environments featuring different climatic conditions

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Abstract There is an increasing interest in understanding ambient bioaerosols due to their roles both in health and in climate. Here, we deployed an Ultraviolet Aerodynamic Particle Sizer to monitor viable (fluorescent) bioaerosol concentration levels at city centers (highly polluted) and their corresponding suburbs (near pristine) (total 40 locations) in 11 provinces featuring different climate zones in China between July 16 and 28, 2013. The concentration levels of viable bioaerosol particles (BioPM) of >0.5 μm were measured, and corresponding percentages of BioPM% (biological fraction of total PM) and $BioPM_{2.5}$% (biological fraction of $PM_{2.5}$) in particulate matter (PM) and BioPM, respectively, were determined. For some key cities, indoor viable bioaerosol levels were also obtained. In addition, bacterial structures of the air samples collected across these monitoring locations were studied using pyrosequencing. BioPM concentration levels ranged from 2.1×10^4 to $2.4 \times 10^5/m^3$ for city centers [BioPM% = 6.4 % (±6.3 %)] and 0.5×10^4 to $4.7 \times 10^5/m^3$ for suburbs [BioPM% = 10 % (±8.7 %)]. Distinctive bioaerosol size distribution patterns were observed for different climate zones, e.g., some had fluorescence peaks at 3 μm, while the majority had peaks at 1 μm. Ambient bacterial aerosol community structures were also found different for different geophysical locations. Results suggest that there was a poor overall relationship between PM and BioPM across 40 monitoring locations ($R^2 = 0.081$, two-tailed P value = 0.07435). Generally, city centers had higher PM concentrations than suburbs, but not BioPM and BioPM%. Indoor bioaerosol levels were found at least tenfold higher than those corresponding outdoors. *Bacillus* was observed to dominate the bacterial aerosol community in the air sample.

Keywords Viable bioaerosol · Bacteria · Air pollution · Climate · China

Kai Wei, Yunhao Zheng, and Jing Li have contributed equally to this work.

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1 Introduction

Biological aerosols, commonly referred to bioaerosols, are ubiquitous in the atmosphere. They not only impact human health [1], but also affect atmospheric chemistry and cloud formation by acting as ice nuclei (IN) [2]. For example, bioaerosol particles can more efficiently catalyze the

formation of ice at higher temperature than non-biological ones [3]. Among all the microbial species, the *Pseudomonas* strains are the most commonly found bacteria to act as CCN [4]. Attributed to a special complex surface protein [5], the bacterium is able to initiate the ice formation at a temperature of approximately 10 °C higher than that required otherwise for those non-biological origins [6]. These atmospheric effects of bioaerosols are increasingly being explored in many parts of the world in recent decades.

Apart from the adverse health effects, the microbial fraction of bioaerosol particles (bacteria and fungi), especially the metabolically active ones, can play an important role in atmospheric oxidization, degradation of chemical pollutants, organic carbon contribution as well as interfacial chemistry [2, 7–9]. Studies indicated that the majority of bacteria present in cloud water are viable and metabolically active [7, 8], which could directly modify atmosphere chemistry [2]. Ariya et al. [9] showed that various bacteria and fungi isolated from rain and cloud water can degrade carboxylic acids effectively, especially the dicarboxylic acids in the atmospheric aqueous phase. Carboxylic acid is an oxidative product of organic matter in the air which can contribute to the formation of secondary organic aerosol (SOA) [10, 11]. SOA is known to play a very important role in climate through direct and indirect forcing [12]. Vaïtilingom et al. [13] isolated three strains of *Pseudomonas*, one *Sphingomonas*, and one yeast from cloud water, and they found that formate, acetate, and succinate could be degraded by these microorganisms in aqueous phase at higher temperatures than those otherwise required for non-biological particles. In other words, through the oxidization process, bacteria and fungi can indirectly influence the climate.

Ambient bioaerosols are emitted from various sources, e.g., sea, land, forest, agriculture, animals, and humans, but they can be also transported regionally and globally. Jones and Harrison [14] indicated that biological materials present on the land surfaces in the form of pollen, fungal spores, bacteria, viruses, or debris of plant and animal matter consists of 25 % (in mass) of the total airborne particulate. Heald and Spracklen [15] investigated bioaerosol emission rates at four continents and found that bioaerosol concentrations peaked in July, August, and September for North America, Europe, Asia, but for South America the bioaerosol levels remained consistent and high throughout the entire year compared to the other continents. Recently, Huffman et al. [16] found that fluorescent biological aerosol particles (viable bioaerosol particles) had an average concentration of $7.3 \times 10^4/m^3$, accounting for 24 % of the total particle number and 47 % of total mass in a pristine environment. The bioaerosol emission pattern was previously attributed to two possible reasons: heating of the ground by sunrise and settlement of particles from higher atmospheric layers during late night before sunrise [17–19]. Jones and Harrison [14] summarized that meteorological variables play an important role in the initial release of biological material and their subsequent airborne dispersal, while temperature and water availability influence the emission source and control the release of some fungal spores. Brodie et al. [20] revealed that the atmosphere harbors a significant amount of bacteria including many human pathogen neighbors. Recently, Cao et al. [21] indicated that increased particulate matter (PM) pollution resulted in increased bioaerosol concentration and allergenic materials in Beijing. Li et al. [22] indicated that air samples collected from the automobile air conditioning systems in Beijing contained more than 400 unique bacteria including human pathogens as well as pathogenic fungi species. In addition, air samples collected in Beijing appeared to have more bacterial diversity than other places such as Haikou and Guangzhou in southern China [22]. Clearly, the bioaerosol level and composition varied with monitoring locations and atmospheric parameters.

The chemical characteristics of PM in ambient air have been subjected to extensive studies in modern China; however, little information exists for its biological components (bioaerosols). Herein, we employed a viable bioaerosol sensor to study bioaerosol dynamics across many parts of China. We monitored the bioaerosol levels in major cities (highly polluted) and their suburbs (less polluted) (total 40 locations) in 11 provinces (7 different climate zones) of China. For certain selected locations, indoor bioaerosol levels were also measured. In addition, we employed the automobile air conditioning filter method developed in our previous work and high-throughput gene sequence to study the bacterial community structures in major cities of China. Results obtained here can help answer the following three questions: (1) What are bioaerosol concentration levels and compositions in many parts of China under different climatic conditions? (2) How different are bioaerosol levels indoors compared to those outdoors? (3) Are there any differences in bioaerosol concentration between locations with high PM pollution and those near-pristine environments?

2 Materials and methods

In this work, an Ultraviolet Aerodynamic Particle Sizer (UV-APS; TSI, Inc., Shoreview, Minnesota), a bioaerosol sensor, was employed to study the viable bioaerosol concentration and size distribution across major parts of China as shown in Fig. 1 between July 16 and 28, 2013. The UV-APS detects the size distribution and concentration level of viable bioaerosol particles by measuring the intrinsic