

The diversity of bioaerosols in different environmental scenarios

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1. Project description

Bioaerosols are kinds of biological atmospheric particles, which are directly released from terrestrial and marine ecosystems into the atmosphere (Fröhlich-Nowoisky et al., 2016). Bioaerosols are speculated to impact public health, atmospheric chemistry, nucleation processes, climate, ecosystem development and so on (Haddrell & Thomas, 2017). Aerosol microbiology can interact with oceanic, atmospheric, and terrestrial environments by biogeochemical processes (Zhai et al., 2018). The compositions of biological fractions depend on specific environmental factors. Investigating the diversity of bioaerosols in different scenarios can provide important information of aerosol microbiology changes in temporal and spatial ways. As one of the highest altitude stations, the Jungfraujoch station can provide the unique high altitude and non-polluted air samples to study the specific bioaerosol, which can be an important reference or background samples in the urban bioaerosol research.

In the current work, we collected the airborne particulate matter (PM) and extract the DNA, which was used for 16s rRNA analysis. The unique samples from the Jungfraujoch station were compared with samples from urban environment, especially the heavy polluted city. We expected a unique bioaerosol community from the Jungfraujoch station. This result can also shed light on the research of bioaerosol in the urban environment.

Two kinds of PM samplers were used in the present work (Figure 1). LY2050 (Applied Technical Institute of Liaoyang, China) is a portable PM sampler, which can collect TSP (Total suspended particulate), PM10 and PM2.5 samples. As a medium flow rate sampler, LY2050 was used to collect TSP samples for every day. HighBioTrap (Beijing dBlue Tech, Inc., Beijing, China) is a portable high flow rate sampler to collect PM2.5, which was used to collect PM2.5 every 4 hours in order to check the aerosol microbiology changes during day and night during 22.01. to 25.01. of 2019.

As the PM10 and PM2.5 concentrations at the Jungfraujoch station were extremely low, 0.1-1.8 $\mu\text{g}/\text{m}^3$ (Figure 2), we only select three samples for a preliminary DNA extraction and 16s rRNA sequence analysis.

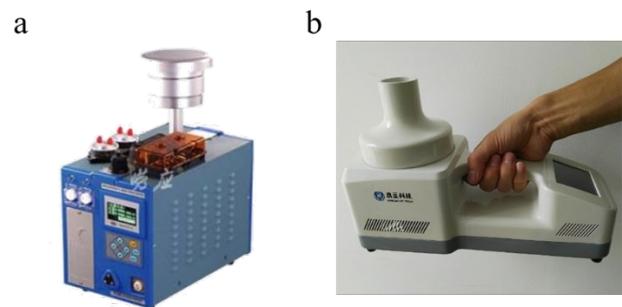


Figure 1. Panel a: LY2050 sampler, the air sampling flow rate is 100L/min (picture comes from www.hbyq.net). Panel b: HighBioTrap sampler, the air sampling flow rate is 1000L/min.

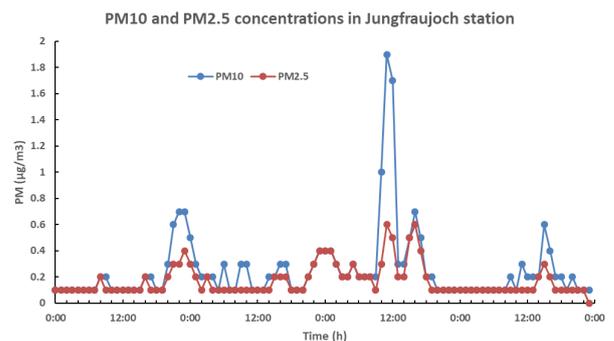


Figure 2. The PM10 and PM2.5 concentrations at the Jungfraujoch station. Data were acquired from Swiss National Air Pollution Monitoring Network (NABEL).

As the result showed in Figure 3, the diversity of bacteria, relative abundance of operational taxonomic unit (OUT, an operational definition used to categorize bacteria based on sequence similarity), was similar with BLA group, which was the blank group in the experiment. This means there were very few microorganisms in the collected samples and it was not possible to distinguish samples from background. Therefore, an optimized sampling plan or experiment need to be considered.

