The Effect of North Wind on Airborne Microbial Community During Winter in Beijing

Weizhuo Yan, Buying Wang, Changyi Xie, Runlong Cai, Yunfeng Yang, Jingkun Jiang

School of Environment, Tsinghua University, Beijing, China Keywords: Microbial Community, 16S rDNA, Wind, Dust, Snow. Presenting author email: 1121231022@qq.com

Airborne microorganisms are ubiquitous in the atmosphere and may have substantial impacts on atmospheric physics, chemistry, ecosystems and human health. On the other hand, airborne microbes may also be affected by other factors in the atmosphere. However, how microbial community is shaped in the atmosphere remains unclear.

In this study, we examined the response of microbial communities to meteorology parameters, gaseous pollutants and certain chemical components in particulate matter. Twenty-three daily PM_{10} samples were collected in Beijing during the winter of the past three years. Airborne microbial communities were characterized by 16S rDNA sequencing.

It was found that the structure of airborne microbial community in Beijing had a significant change a strong north wind. Moreover, the north wind result in similar changes in microbial community structure in each year. So how the wind affect airborne microbial community?

We assumed that the strong wind could cause more fugitive dust emissions from local place which may contain microorganisms, or that the wind could bring microorganisms from upwind area north of Beijing. To prove these hypothesis, we collected seven fugitive dust samples and went to Baochang, Inner Mongolia which is 230 km northwest from Beijing.

The ground was covered with snow during the whole winter in Baochang. When strong wind blew through Baochang, the number concentration of aerosol particles measured by APS there was one or two orders of magnitude larger than that in Beijing. Thus, the ground covered with snow has the potential to be a source of airborne microorganisms. Four snow samples, two TSP samples and two PM_{10} samples were collected in Baochang.

DNA was extracted from samples collected in Baochang and the fugitive dust samples in Beijing. 16S rDNA sequencing was used to characterize microbial communities. The result may reveal the cause of the changes during strong north wind.

Table 1. The list of genus of bacteria which changed during the strong north wind. Group 1 was the genus of bacteria decrease during the wind. Group 2 was the contrary.

Group 1		Group 2	
Aerococcus	Lactobacillus	Atopobium	Oscillatoria
Bacteroides	Prevotella	Candidatus Solibacter	Rubrobacter
Clostridium	Streptococcus	Chloroflexus	Thermoleophilum
Faecalibacterium	n Fusobacterium	Cytophaga	Microlunatus



Figure 1. The variation trend of relative abundance of each genus of bacteria, wind speed and $PM_{2.5}$ in 2013.



Figure 1. The variation trend of relative abundance of each genus of bacteria, wind speed and PM_{2.5} in 2015.