A breath of Beijing air gets metagenomics treatment

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A woman wearing a face mask walks on an overpass in Beijing on January 16, 2014

(Phys.org) —A Friday report in *Nature News* handles a well-publicized topic, the air quality in Beijing. That may seem like rather old news, but the Friday report has new information on the city's troubling air quality. Scientists were looking for information about the potential for pathogens and allergens in Beijing's air and they turned to "metagenomics" as their

study tool. The research team described what they were seeking in their paper, "Inhalable Microorganisms in Beijing's PM2.5 and PM10 Pollutants during a Severe Smog Event," for *Environmental Science & Technology*. "While the physical and chemical properties of PM pollutants have been extensively studied, much less is known about the inhalable microorganisms. Most existing data on airborne microbial communities using 16S or 18S rRNA gene sequencing to categorize bacteria or fungi into the family or genus levels do not provide information on their allergenic and pathogenic potentials. Here we employed metagenomic methods to analyze the microbial composition of Beijing's PM pollutants during a severe January smog event."

They took 14 air samples over seven consecutive days. Using genome sequencing, they found about 1,300 different microbial species in the heavy smog period of early last year. The scientists compared their results with a large gene database. What about their findings? Most of the microbes they found were benign but a few were responsible for allergies and respiratory disease. As *Nature News* reported, the most abundant species identified was Geodermatophilus obscurus, That is a common soil bacterium. Streptococcus pneumonia, however, was also part of the brew, which can cause pneumonia, along with Aspergillus fumigatus, a fungal allergen, and other bacteria typically found in faeces. "Our results," wrote the researchers, "suggested that the majority of the inhalable microorganisms were soil-associated and nonpathogenic to humans. Nevertheless, the sequences of several respiratory microbial allergens and pathogens were identified and their relative abundance appeared to have increased with increased concentrations of PM pollution."

The authors suggested that their findings may provide an important reference for environmental scientists, health workers and city planners. The researchers also suggested, according to *Nature News*, that clinical studies explore signs of the same microbes in the sputum of patients with

respiratory tract infections, to assess whether smoggier days lead to more infections.

Metagenomics, which can analyze microbial communities regardless of the ability of member organisms to be cultured in the laboratory, is recognized as a powerful approach. *Nature Reviews* also describes metagenomics as "based on the genomic analysis of microbial DNA that is extracted directly from communities in environmental samples."

More information: *Environmental Science & Technology* paper: pubs.acs.org/doi/abs/10.1021/es4048472
Nature News story: www.nature.com/news/beijing-sm … -of-microbes-1.14640