Analysis of airway microbiome related to particulate matter in patients with chronic obstructive pulmonary disease

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Abstract

Background: Particulate matter (PM) air pollution has been suggested to be associated with chronic obstructive pulmonary disease contributing to global mortality. The aim of this study was to investigate whether PM could induce a dysbiosis in the sputum microbiota.

Methods: The sputum samples were collected 4 times over one year from 100 patients with chronic obstructive pulmonary disease (COPD). We performed 16S rRNA sequencing using DNA isolated from sputum samples. And then we analyzed dynamics of airway microbiota based on PM exposure levels and season.

Results: We found that PM-low exposure group has higher α-diversity in spring season compared to PM-high exposure group. The sputum samples in low exposure group were significantly more abundant with 7 bacterial species including treponema socranskii. In addition, the bacterial community structure in summer significantly differed between samples from other seasons. Bacterial α-diversity in summer is significantly higher than that in spring. We also found that diversity of airway microbiome in PM-low exposure group significantly differed compared to PM-high exposure group among moderate COPD patients.

Conclusions: PM may induce changes in the sputum microbiome depending on exposure levels and seasonal effect. Our results have suggested that airway microbiomes could covary with PM exposure according to seasonal trends.

Keywords: Chronic obstructive pulmonary disease, Particulate matter, Microbiota