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Microbiome diversity in the bronchial tracts of patients with chronic obstructive pulmonary disease.

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Abstract

Culture of bacteria from **bronchial** secretions in respiratory **patients** has low sensitivity and does not allow for complete assessment of microbial **diversity** across different **bronchial** compartments. In addition, a significant number of clinical studies are based on sputum samples, and it is not known to what extent they describe the real **diversity** of the mucosa. In order to identify previously unrecognized lower airway bacteria and to investigate the complexity and distribution of microbiota in **patients** with **chronic obstructive pulmonary disease** (COPD), we performed PCR amplification and pyrosequencing of the 16S rRNA gene in **patients** not showing signs or symptoms of infection. Four types of respiratory samples (sputum, **bronchial** aspirate, bronchoalveolar lavage, and **bronchial** mucosa) were taken from each individual, obtaining on average >1,000 16S rRNA sequences per sample. The total number of genera per patient was >100, showing a high **diversity**, with Streptococcus, Prevotella, Moraxella, Haemophilus, Acinetobacter, Fusobacterium, and Neisseria being the most commonly identified. Sputum samples showed significantly lower **diversity** than the other three sample types. Lower-**bronchial**-tree samples, i.e., bronchoalveolar lavage and **bronchial** mucosa, showed a very similar bacterial compositions in contrast to sputum and **bronchial** aspirate samples. Thus, sputum and **bronchial** aspirate samples are upper **bronchial** tree samples that are not representative of the lower **bronchial** mucosa flora, and bronchoalveolar lavage samples showed the results closest to those for the **bronchial** mucosa. Our data confirm that the **bronchial** tree is not sterile in COPD **patients** and support the existence a different microbiota in the upper and lower compartments.

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