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Abstract (poster session)

Dysbiosis of the lung bacterial community in patients with stable chronic obstructive pulmonary disease

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Objectives: There has been considerable controversy about the role of lower respiratory tract bacteria in the pathogenesis and exacerbation of chronic obstructive pulmonary disease (COPD). Aim of this study was to investigate the lower respiratory tract microbioma of stable COPD patients, smokers, and healthy non-smokers subjects in order to identify microbial pathogens potentially associated with COPD. **Methods:** Sputum was induced in 6 COPD patients, 4 smokers, and 3 healthy non-smoker controls. An aliquot of each specimen was subjected to microscopic examination and bacteriological culture, while another was used for deep sequencing of the 16S rRNA gene by using the 454 Life Sciences FLX system. About 10,000 good-quality reads per sample were obtained. Sequences were processed using the RDP Multiclassifier for taxonomic classification of bacteria phyla and genera. **Results:** The composition of the microbioma in sputum samples varied widely among subjects, while it was relatively stable during time in the same subject, and included several genera from 10 bacterial phyla. *Pseudomonas*, *Streptococcus* and *Haemophilus* genera accounted for a large percentage of sequences in some patients with COPD, while *Neisseria* and *Streptococcus* genera were abundant in smokers. These genera were absent or rarely detected in healthy subjects. A "core microbioma" composed of bacteria common to all sputum samples was identified that included *Prevotella*, *Streptococcus*, *Leptotrichia*, *Veilonella*, *Fusobacterium*, *Actinomyces*, *Rothia*, *Porphyromonas*, and *Neisseria* (cutoff >1% of sequences), while some genera were specific to patient groups (e.g., *Gemella* and *Granulicatella*, detected in COPD patients and smokers). Conventional microscopy and culturing analyses did not represent the microbial diversity identified by deep sequencing. **Conclusions:** *Pseudomonas*, *Streptococcus*, *Haemophilus*, and *Neisseria* genera were the most abundant bacteria in the deep airways microbioma of COPD patients and smokers, but not in healthy subjects, and could contribute to COPD symptoms and severe exacerbations. A "core microbioma" including aerobic and anaerobic bacteria, common to all sputum samples, was identified and considered as normal lung flora. The dysbiosis of the lung bacterial community could provide the constant inflammatory stimulus observed in stable COPD patients.