Airway Microbiota diversity and composition correlates with severity of Chronic Obstructive Pulmonary Disease (COPD)

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Abstract

COPD occurrence is mediated by immune response, environmental factors and microbial dysbiosis. Airway microbiota has been found to be different between healthy people and patients with COPD and these differences could influence disease severity. But, its clinical implications are still unclear. Here, we have explored the airway microbiota of patients with COPD as well as its relations with specific clinical parameters.

40 patients (35?, 67±9y, FEV1pp 33±7, GOLD III-26, IV-14) and 40 healthy controls (34?, 67±12y, FEV1pp 101±19) were recruited and sociodemographic, anthropometric and clinical data were collected. Saliva microbiota was characterised by 16S rRNA sequencing and analysed using Qiime2 pipeline.

Significant differences in airway microbiota composition between patients and healthy people were observed (Fig 1). The microbiota of patients with worse clinical parameters, like lower FEV1pp and SpO2, or with higher number of exacerbations and hospitalisations, clustered separately from less severe. Loss of microbiota diversity correlated with age in patients, but not in healthy people, raising the hypothesis of the cumulative use of antibiotics (by patients) contributing to dysbiosis.

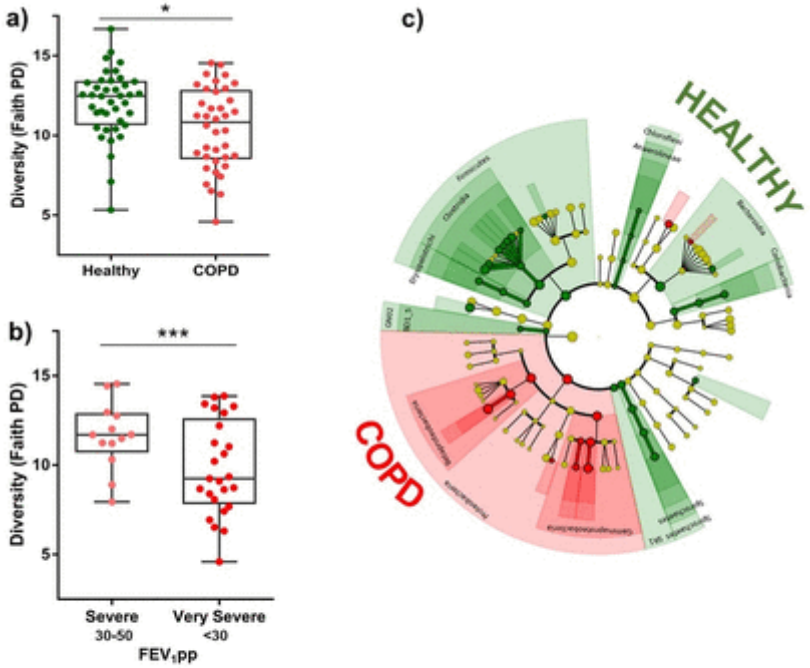

Fig 1 – Diversity and composition of the Airway microbiota and composition is different between healthy and COPD groups. a) The microbiota diversity (estimated as Faith's phylogenetic diversity (PD)) is significantly higher ($p<0.05$) in healthy subjects than in patients. **b)** Estimated alpha diversity, for COPD group according to airway obstruction grade (FEV_1pp). The microbiota from patients with very severe states of airway obstruction is significantly less diverse ($p<0.001$) than in patients with less severe airway obstruction. **c)** The cladogram represents the comparison of COPD and Healthy group's microbiotas. At phylum level, patients' microbiota is enriched in *Proteobacteria*.

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The association between microbiota composition and clinical parameters supports its contribution to COPD trajectory. Future studies should focus on remodelling patients' dysbiotic microbiotas towards healthier ensembles aiming at preventing disease decline.

Footnotes

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