ORAL COMMUNICATION

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Saliva's Microbiota as a biomarker of Chronic Obstructive Pulmonary Disease

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Deviations from the normal composition of the airway microbiota have been proposed to influence Chronic Obstructive Pulmonary Disease (COPD) but this has not been thoroughly explored and their clinical implications are still unclear.

We aimed at exploring saliva's microbiota of patients with COPD and its relation with specific clinical parameters.

Experimental design: Sociodemographic, anthropometric, clinical data and saliva samples were collected from patients with COPD and healthy individuals. Saliva's microbiota was characterized by 16S rRNA sequencing and analysed using Qiime2 pipeline.

Results: 38 patients (33♂, 66±8y, FEV_1pp 33±7, GOLD III-26, IV-12) and 38 healthy controls (33♂, 66±9y, FEV_1pp 103±18) participated. Saliva's microbiota was significantly enriched in *Proteobacteria* (with higher representation of *Neisseria* and *Haemophilus*) and less diverse in COPD than in healthy individuals. Furthermore, loss of microbiota's diversity correlated with disease severity.

Microbiota revealed two major clusters: **Patient I**, comprising 25% of the patients and a larger cluster including the remaining individuals. Additionally, two clusters emerged from the second cluster, **Patient II** (enriched in patients), and **Healthy** (10 healthy individuals).

Microbiota diversity was not different between these latter clusters but was significantly decreased in **Patient I**. *Proteobacteria* was particularly abundant in **Patient I** and **II** and depleted in **Healthy**, whereas *Bacteroidetes* showed the opposite trend. **Patient I** was enriched in more severe, symptomatic and older patients.

These findings support a close association between the microbiota and COPD and open new avenues to promote remodelling of patients' dysbiotic microbiotas aiming at symptom improvement and preventing disease decline.

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