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Salivary microbiota composition is associated with severe exacerbations

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Abstract

People with COPD present microbiota dysbiosis. Clinical implications of this finding are still unknown and need validation.

Here, we tested the association between salivary microbiota and COPD and its ability to discriminate different types of patients.

67 patients with COPD (57male, 68±9y, FEV1pp 48±19, GOLD A-12, B-31, C-5, D-19) were characterised based on sociodemographic, anthropometric, clinical data and 16S rRNA profiling of their salivary microbiota. An unsupervised clustering analysis based on patients' beta diversity was performed to query its relationship with the disease.

Two major clusters (comprising 90% of individuals) differing drastically in severity were observed. Cluster1 aggregated all patients hospitalized in the previous year due to acute exacerbations, 71% of GOLD D patients and included a higher frequency of patients under oxygen therapy and heavier smoking history than Cluster 2 (Fig 1A).

Furthermore, Cluster1 had a lower microbiota diversity (MW-U, p=0.008) (Fig 1B) and was enriched in Proteobacteria or Firmicutes, particularly Streptococcus. In contrast, Cluster2 was significantly enriched in

Bacteroidetes, particularly Alloprevotella and Prevotella (Fig 1C).

Saliva's microbiota showed a strong association with COPD, especially in terms of severe exacerbations, supporting the use of salivary microbiota for further studies in this population.

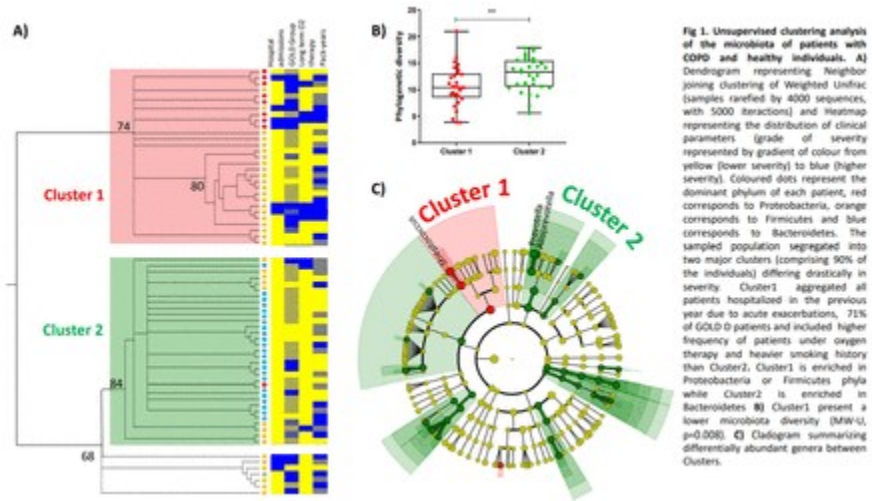

Fig 1. Unsupervised clustering analysis of the microbiota of patients with COPD and healthy individuals. A) Dendrogram representing Neighbor joining clustering of Weighted Unifrac (samples rarefied by 4000 sequences, with 5000 iteractions) and Heatmap representing the distribution of clinical parameters (grade of severity represented by gradient of colour from yellow (lower severity) to blue (higher severity). Coloured dots represent the dominant phylum of each patient, red corresponds to Proteobacteria, orange corresponds to Firmicutes and blue corresponds to Bacteroidetes. The sampled population segregated into two major clusters (comprising 90% of the individuals) differing drastically in severity. Cluster1 aggregated all patients hospitalized in the previous year due to acute exacerbations, 71% of GOLD D patients and included higher frequency of patients under oxygen therapy and heavier smoking history than Cluster2. Cluster1 is enriched in Proteobacteria or Firmicutes phyla while Cluster2 is enriched in Bacteroidetes **B)** Cluster1 present a lower microbiota diversity (MW-U, p=0.008). **C)** Cladogram summarizing differentially abundant genera between Clusters.

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COPD Mirobiome/Microbiota COPD - mechanism

Footnotes

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