



# Salivary microbiota composition is associated with severe exacerbations

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European Respiratory Journal 2021 58: OA1286; DOI: 10.1183/13993003.congress-2021.OA1286

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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.

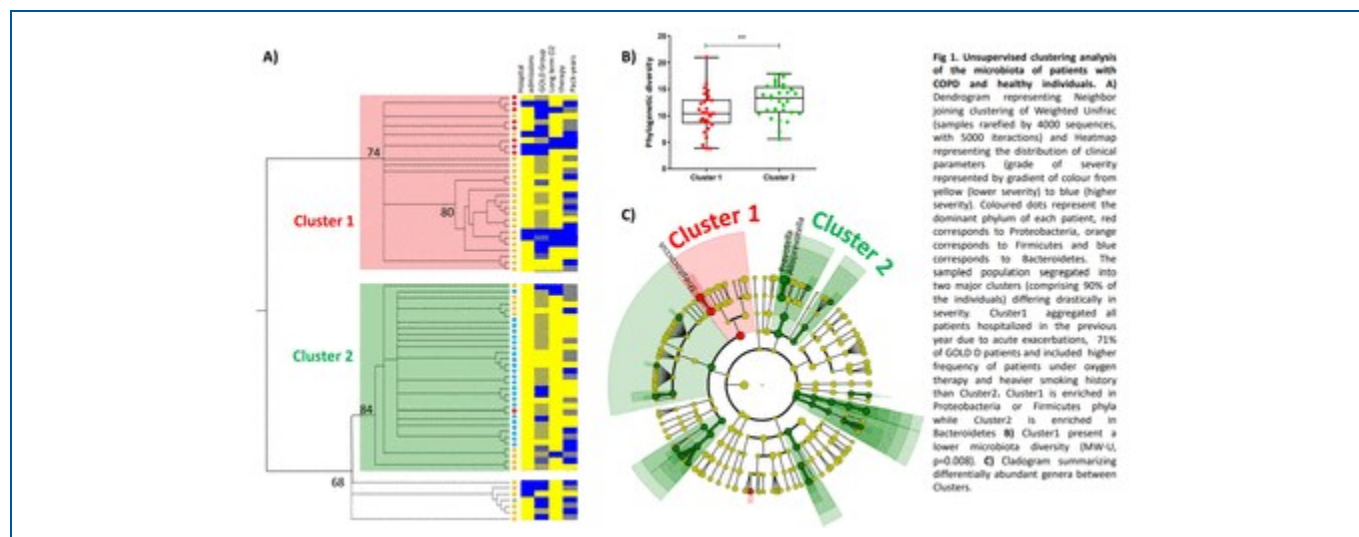
67 patients with COPD (57male, 68±9y, FEV1pp 48±19, GOLD A-12, B-31, C-5, D-19) were characterised based on sociodemographic, anthropometric, clinical data and 16S rRNA profiling of their salivary microbiota. An unsupervised clustering analysis based on patients' beta diversity was performed to query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



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Cite this article as: European Respiratory Journal 2021; 58: Suppl. 65, OA1286.

This abstract was presented at the 2021 ERS International Congress, in session "Prediction of exacerbations in patients with COPD".

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**ISSN**

Print ISSN: 0903-1936  
Online ISSN: 1399-3003

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