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, FEV1 pp 33±7, GOLD III-26, IV-12) and 38 healthy controls (33♂, 66±9y, FEV1 pp 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.

Acknowledgments: This work was funded by Programa Operacional de Competitividade e Internacionalização - COMPETE, through Fundo Europeu de Desenvolvimento Regional - FEDER (POCI-01-0145-FEDER-028806 and POCI-01-0145-FEDER-007628), Fundação para a Ciência e Tecnologia - FCT (PTDC/DTP-PIC/2284/2014 and PTDC/SAU-SER/28806/2017) and under the project UID/BIM/04501/2013 and UID/BIM/04501/2019. SD was supported by Grant SFRH/BD/140908/2018 from FCT.