POSTER COMMUNICATION

04

Impact of pulmonary rehabilitation on the airway microbiota of patients with COPD

Bárbara Andrade[1], Sara Miranda[2,3], Célia Freitas[2,4], Ana Catarina Sousa[5,6,7], Carla Valente[8], Catarina Almeida[1,3], Alda Marques[2,3], Ana Sousa[1,3]

[1]Department of Medical Sciences, Institute for Biomedicine, University of Aveiro, Aveiro, Portugal
[2]Lab3R – Respiratory Research and Rehabilitation Laboratory, School of Health Sciences, University of Aveiro, Aveiro, Portugal.
[3]iBiMED – Institute of Biomedicine, University of Aveiro, Aveiro, Portugal
[4]Center for Health Technology and Services Research (CINTESIS)/ University of Porto
[5]CNRS LabEx DRIIHM; CNRS- INEE- ECCOREV (Unité FR3098); OHMi Estarreja-OHM Bassin Minier de Provence; France
[6]CICECO, University of Aveiro, Portugal
[7]CICS-UBI, University of Beira Interior, Portugal
[8]Department of Pneumology, Centro Hospitalar do Baixo Vouga, E.P.E

Chronic Obstructive Pulmonary Disease (COPD) is the third worldwide leading cause of mortality. Pulmonary Rehabilitation (PR), a comprehensive intervention that comprises exercise training, education and psychosocial support, is the most cost-effective therapy for patients with COPD.

Exercise training increases ventilation and oxygen uptake, which most likely influences airway microbiota. However, whether this has a role on the positive impact of PR on COPD is still unclear. This study aims to contribute for answering this question by following the impact of PR on the microbiota of 25 patients with COPD (19♂, 73±6y, FEV1pp 48±15) over a period of ~9 months (~3 months before PR, 3 months during PR and 3 months after PR) and of 5 patients not submitted to PR (5♂, 75±6y, FEV1pp 48±13) for a period of 6 months. Sociodemographic, anthropometric, clinical data and saliva samples (once a month) were collected. Saliva microbiota was characterised by 16S rRNA sequencing and analysed using QIIME2 pipeline.

A preliminary analysis of 6 patients (6♂, 72±3y, FEV1pp 46±19) showed that, after PR, the microbiota composition did not converge to a similar composition. Instead, samples collected in different time points from the same patient were more similar amongst themselves than among different patients.
Pooled analysis of the 6 patients showed a significant increase in Neisseria genus from Pre-PR to PR, suggesting that PR contributes to microbiota modulation. Whether this change is related to patients' health status improvement will be the focus of future studies.

Acknowledgments: This work is part of a project entitled "PRISMA - Pulmonary Rehabilitation: a response for patients with COPD in an InduStrialized environment and its implication on lung MicrobiotA", ref. OHM-E/2018/ 1912, funded by LabEx DRIIHM, International Observatory Hommes-Milieux of Estarreja.