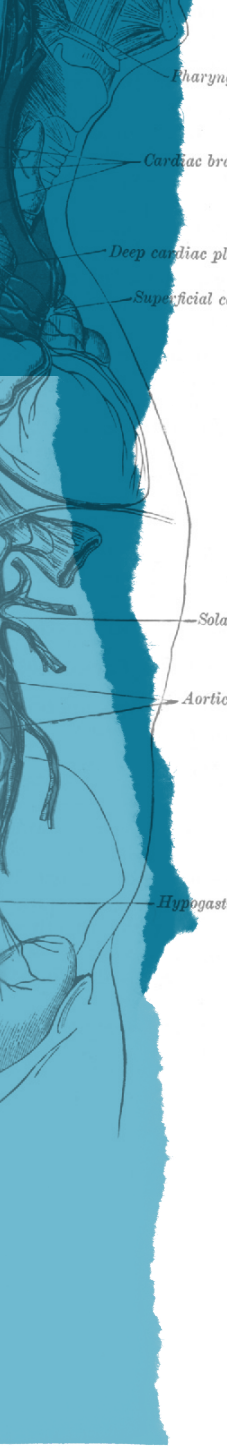

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Lung Microbiota and Pulmonary Function in People with HIV and/or Pneumonia: An Exploratory Study

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ABSTRACT

Introduction: The human lung harbors a diverse microbiota that influences respiratory health. In people living with HIV (PLHIV), chronic inflammation and immunosuppression increase susceptibility to community-acquired pneumonia (CAP) and pulmonary function decline. However, the role of the lung microbiota in these outcomes remains poorly understood. Therefore, we sought to explore the relationship between lung microbiota composition and pulmonary function in PLHIV, with and without CAP.

Methods: We conducted a prospective cohort study in three hospitals in Medellín, Colombia (2016–2018). Adult patients with HIV and/or CAP were included, with respiratory samples and spirometry performed at hospital admission and at six-month follow-up. The subcohort analyzed comprised 12 patients: 5 with HIV+CAP, 3 with CAP, and 4 with HIV. Spirometric parameters (FVC, FEV1, FEV1/FVC, FEF25–75) and microbial diversity (Shannon index, OTUs) were assessed. Lung microbiota profiling was performed by 16S rRNA gene sequencing.

Results: Median age was 58 years, and 66.7% were male. In the HIV+CAP group, *Mycobacterium tuberculosis* was detected in 60% and *Pneumocystis jirovecii* in 40% of cases. From baseline to follow-up, median FEV1 increased from 1.80 L to 2.09 L, and FEF25–75 from 3.13 L/s to 3.00 L/s; FEV1/FVC remained stable (0.82). Median change in Shannon index was 0.5 (IQR: 0.1–1.5), and OTUs –6 (IQR: –40 to 19), indicating individual fluctuations in microbial diversity. The predominant phyla were Firmicutes, Proteobacteria, Fusobacteria, Bacteroidetes, and Actinobacteria. At the genus level, *Streptococcus, Haemophilus, Veillonella, Neisseria*, and *Fusobacterium* were most abundant. In this subcohort of PLHIV and/or CAP patients, changes in pulmonary function coexisted with variability in lung microbiota diversity between admission and follow-up.

Conclusions: The identification of dominant taxa and characterization of their dynamics provides a basis for further studies assessing the interaction between lung microbiota and respiratory impairment in immunocompromised populations.

Keywords: lung microbiota, pulmonary function, HIV, pneumonia.