

# INVESTIGATION OF THE RESPIRATORY MICROBIOME IN TUBERCULOSIS PATIENTS IN LITHUANIA

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Tuberculosis (TB) remains a major global health concern despite advances in treatment and prevention. Lithuania has one of the highest TB and drug-resistant TB rates in the European Union, underscoring the need for improved understanding of disease drivers [1]. Increasing evidence suggests that the respiratory tract microbiome may act as an ecological barrier or facilitator of *Mycobacterium tuberculosis* colonization [2]. Therefore, investigating lung microbiome composition may provide critical insight into TB susceptibility and progression.

This study aimed to analyze microbiota composition in sputum and oral swab samples using full-length 16S rRNA gene sequencing. Non-invasive and painless, sputum samples are commonly used to examine the microbiome of the lower respiratory tract. A total of 97 sputum samples obtained from patients with TB and other chronic lung diseases (CLD) were analyzed. Additionally, 18 paired oral swab samples were included to assess potential connection between respiratory tract microbiota from different areas.

The sputum microbiome of CLD patients was characterized by lower diversity and a higher proportion of *Pseudomonadota* bacteria, a pattern consistent with dysbiosis. In contrast, TB patients exhibited comparatively greater bacterial diversity. No significant differences in microbiome composition or diversity were observed between drug-sensitive and drug-resistant TB. In the majority of samples, the sputum microbiome differed from that of the oral cavity. Similarities observed between sputum and oral microbiomes may reflect not only the introduction of oral microorganisms during sampling but also the biological continuity between the upper and lower respiratory tracts.

In conclusion, these preliminary findings indicate that sputum is a suitable and informative sample for respiratory tract microbiome studies, and that TB and CLD patients exhibit distinct patterns of microbiome dysbiosis. These results provide a foundation for future research investigating the role of the respiratory tract microbiome in TB pathogenesis and progression.

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[1] "Tuberculosis surveillance and monitoring in Europe 2025 - 2023 data," European Centre for Disease Prevention and Control, Mar. 24, 2025. <https://www.ecdc.europa.eu/en/publications-data/tuberculosis-surveillance-and-monitoring-europe-2025-2023-data>

[2] T. Shah, Z. Shah, Z. Baloch, and X. Cui, "The role of microbiota in respiratory health and diseases, particularly in tuberculosis," *Biomedicine & Pharmacotherapy*, vol. 143, p. 112108, Sep. 2021, doi: 10.1016/j.biopha.2021.112108.