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Lung Microbiota in Tuberculosis. There are No Small Roles, Only Small Actors

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Abstract

After receiving less attention compared to other body sites, the study of the lung microbiota has started to emerge during the past few years. It is still unclear if changes in the lung microbiota composition are associated with pulmonary Tuberculosis (TB). The limited number of studies on the sputum microbiota on TB patients and controls available so far has reported somewhat contradictory results. This could be due to technological difficulties related to obtaining reliable samples as compared to other body niches, or due to differences in the geographical origin of these samples. Despite the inconsistencies, they do suggest that the lung microbiota in TB patients differs from healthy individuals. Understanding the composition of the lung microbiota in health and comparing it to that of pulmonary TB cases may elicit clues into the pathogenesis of Mycobacterium tuberculosis infection at the pulmonary alveolus, and may help design treatment options for TB with potential direct benefits for patients and public health.

Keywords Lung; Microbiota; Tuberculosis

Introduction

Previously considered sterile and void of any microbial communities, the lungs have been recently found to harbor a resident microbiota [1]. Identification of the composition of the lung microbiome has shown that it overlaps with that of the oropharyngeal cavity [2]. New studies on lung microbiota abnormalities associated with multiple respiratory diseases, including tuberculosis have started to emerge [3-5].

A few recent studies have shown changes in the lung microbiota related to pulmonary tuberculosis [6,7]. Inconsistencies across studies and sampling methodologies, however, have prevented a definitive understanding of how the lung microbiota changes with tuberculosis [6,7].

Geographic differences between the studies, and inherent immunogenetic factors, may partially explain these contrasting results. Better controlled and larger studies, as well as meta-analyses, are needed to elucidate the role of these changes in Mycobacterium tuberculosis (Mtb) infection and TB therapy, and to identify an overrepresentation and/or underrepresentation of particular species in TB patients and controls. Lung bacterial samples can be obtained through induced sputum or lung secretions that carry the risk of oral contamination. Bronchoalveolar lavage is a more credible, but invasive option [7]. So far only one study has used this approach [8].

No study has directly examined the impact of antibiotics or anti-TB treatment on taxa abundance or composition. This contrasts the scenario of research for diseases affecting gut flora. Although tuberculosis is treatable, antibiotic-resistant tuberculosis is a growing global concern. This has triggered a fervent search for new antibiotics and alternative approaches to fighting tuberculosis [9].

Studying how Mtb infection and its treatment alter the lung's microbiota could open the door for a potential role of probiotics in TB treatment and prevention [10,11]. Changes in the microbiota composition do not only occur at the alveolar level but in other niches. Changes in the gut microbiota may appear as the most important as this represents the biggest niche for commensal bacteria in the human body, and it has been shown to interact with the lung [3,12,13].

The microbiome, through microbial products and immunomodulators released upon recognition of commensals and pathogens by immune cells could have an impact in the inflammatory response in the lung. Antibiotic usage, while effectively targeting Mtb do cause considerable damage to the commensal bacteria [14,15].

The design of methods to keep environmental conditions that favor the growth and maintenance of healthy microbial communities though prebiotics and probiotics [16] along with correction of immune dysregulation caused by the disease (Figure 1), could provide a better outcome in the treatment of TB.

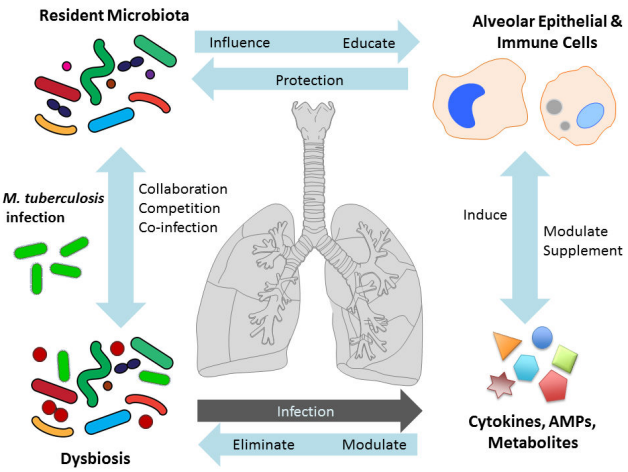

Figure 1: The different roles of the lung microbiota in tuberculosis.

Disclosure statements

Author declares no conflict of interest.

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