

The Lung and Gut Microbiota in Pulmonary Tuberculosis: A Systematic Review

Rouhollah Abdolhamidi^{1*}, Samira Tarashi², Sara Ahmadi Badi², Arfa Moshiri^{3,4}, Seyed Davar Siadat²

*(Rouhollah Abdolhamidi) ramidofficial@gmail.com

¹ Pharmaceutical Sciences Research Center, Pharmaceutical Sciences Branch, Islamic Azad university, Tehran, Iran

² Microbiology Research Center, Pasteur Institute of Iran

³ Gastroenterology and Liver Diseases Research Center, Research Institute for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences

⁴ Laboratory of Experimental Therapies in Oncology, IRCCS Istituto Giannina Gaslini

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Tuberculosis (TB) is an infectious disease which historically described as one of the most significant troublesome issues in human health. TB needs robust and efficient control strategies and evaluation of lung and gut microbiota can be very important in this regard. Since, the disruption of the normal community of lung and gut microbiota impact on the pathogenesis of *Mycobacterium tuberculosis*.

The current provides a review of the most important lung and gut microbiota detected in the standard sample types of TB infection. Therefore, several databases, Scopus, Medline, and Embase, Cochrane library for English published articles were evaluated.

Only few studies compared the interaction between lung and gut microbiota derived from TB patients and healthy controls. *M. tuberculosis* is known as one of the most important pathogens that rapidly colonizes after dysbiosis of lung microbiota. Similarly, dysbiosis of gut microbiota also influences the development of TB. Moreover, it is currently unclear how dysbiosis could progress TB infection but a strong viewpoint indicates dysbiosis of lung and gut microbiota is associated with the alteration of immune responses and development of TB infection. The gut-lung axis is introduced as a regulatory influence of gut microbiota on lung immunity. Some of the crucial lung bacterial mechanisms involved in TB progression have been related to *Klebsiella*, *Stenotrophomonas*, *Pseudomonas*, *Neisseria*, *Streptococcus*, *Prevotella*, *Veillonella*, *Rothia*, *Sphingomonas*, *Acinetobacter*, *Leuconostoc* and *Lactobacillus*. On the other hand, the most important related gut bacterial mechanisms in TB progression have been associated to *Bacteroides*, *Escherichia*, *Shigella*, *Fusobacterium*, *Faecalibacterium*, *Collinsella*, *Streptococcus*, *Prevotella* and *Roseburia*. Almost all the selected studies indicated the microbiota diversity by high throughput 16S rDNA gene sequencing.

Given existing evidence of dysbiosis of lung and gut microbiota and the link between them and immune system in TB development has become a crucial topic for future biomedical research. Ultimately, such studies can revolutionize the current view on treatment and control strategies and deepens the understanding of different microbiota effects on TB infection.