

The Impact of Mycobacterial Infections on Lung Microbiota Composition

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DESCRIPTION

The human respiratory tract is home to a complex ecosystem of microorganisms known as the lung microbiota. While traditionally thought to be sterile, recent advances in sequencing technology have revealed that the lungs harbour a diverse community of bacteria, viruses, and fungi. This intricate microbial landscape plays a crucial role in respiratory health and disease. One area of particular interest is the impact of mycobacterial infections, such as Tuberculosis (TB) and Non-Tuberculous Mycobacteria (NTM) infections, on lung microbiota composition. This article explores the dynamic relationship between mycobacterial infections and the lung microbiota, shedding light on its implications for respiratory health.

The lung microbiota

Until relatively recently, the lungs were considered a sterile environment. However, the advent of high-throughput sequencing technologies has revolutionized our understanding of the lung microbiota. Researchers now appreciate that the lungs are not devoid of microorganisms but rather host a diverse and dynamic community of bacteria.

The lung microbiota is distinct from the oral and gut microbiota, with lower bacterial diversity. *Prevotella*, *Streptococcus*, and *Veillonella* are among the commonly found genera in healthy lungs. The composition and stability of the lung microbiota are influenced by various factors, including age, environment, and underlying respiratory conditions.

Mycobacterial infections

Mycobacterial infections, particularly TB and NTM infections remain significant global health challenges. *Mycobacterium tuberculosis*, the causative agent of TB, infects approximately 10 million people each year and is a leading cause of mortality worldwide. NTM infections, caused by various Non-Tuberculous Mycobacteria species, are also on the rise and primarily affect individuals with underlying lung diseases.

Impact on lung microbiota composition

Shifts in microbial diversity: Mycobacterial infections can lead to shifts in lung microbiota composition. Studies have shown alterations in bacterial diversity and the relative abundance of specific taxa in infected individuals compared to healthy controls.

Disease severity: The severity of mycobacterial infections can influence the extent of lung microbiota disruption. Severe TB cases often exhibit more significant alterations in microbiota composition.

Persistence of alterations: In some cases, the changes in lung microbiota composition induced by mycobacterial infections can persist even after successful treatment, contributing to long-term respiratory health issues.

Immune response: The host's immune response to mycobacterial infections, characterized by inflammation and the recruitment of immune cells, can further shape the lung microbiota by creating a microenvironment conducive to specific microbial communities.

Clinical implications

Understanding the impact of mycobacterial infections on lung microbiota composition has several clinical implications:

Treatment response: The composition of the lung microbiota may influence an individual's response to mycobacterial infection treatment. Reshaping the microbiota to a healthier state could potentially enhance treatment outcomes.

Disease severity prediction: Analysing lung microbiota composition could help predict the severity of mycobacterial infections, allowing for more tailored treatment strategies.

Recurrence risk: Persistent alterations in lung microbiota composition may increase the risk of mycobacterial infection recurrence. Targeted interventions to restore a balanced microbiota could be explored to reduce this risk.

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Secondary infections: Changes in the lung microbiota resulting from mycobacterial infections may also influence susceptibility to secondary respiratory infections, such as pneumonia or fungal infections.

Research challenges and future directions

While research into the impact of mycobacterial infections on lung microbiota composition is advancing, several challenges remain:

Causality vs. association: Determining whether the observed alterations in lung microbiota are causally linked to mycobacterial infections or merely associated with the disease is complex. Longitudinal studies and experimental models are needed to establish causality.

Individual variability: The lung microbiota exhibits significant individual variability, making it challenging to define a "healthy" microbiota and assess deviations from it.

Treatment strategies: Developing effective strategies to modulate the lung microbiota to improve treatment outcomes and prevent recurrence is an active area of research but remains challenging.

Standardization: Standardizing methods for studying the lung microbiota, including sampling techniques and sequencing

protocols, is crucial for meaningful comparisons between studies.

CONCLUSION

The interaction between mycobacterial infections and lung microbiota composition is a burgeoning field of research with significant clinical implications. Understanding how these infections disrupt the delicate microbial balance in the lungs and how these disruptions affect disease outcomes is a complex endeavour. As researchers delve deeper into this intricate relationship, they aim to harness this knowledge to develop treatments that are more effective, predict disease severity, and improve the long-term respiratory health of individuals affected by mycobacterial infections. The pulmonary microbiota, formerly an enigmatic entity concealed within the respiratory tract, is progressively assuming a pivotal role in the mitigation of respiratory pathologies. With continued research and collaboration between microbiologists, immunologists, and clinicians, we are on the brink of unlocking its potential to transform the diagnosis and treatment of mycobacterial infections and other lung-related conditions.