

Unraveling the Role of MicroRNAs in Mycobacterium tuberculosis Infection and Disease: Advances and Pitfalls

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Abstract

Tuberculosis (TB) is an infectious disease of extremely high epidemiological burden worldwide that is easily acquired through the inhalation of infected respiratory droplets. The complex pathogenesis of this infection spans from subjects never developing this disease despite intense exposure, to others in which immune containment fails catastrophically and severe or disseminated forms of disease ensue. In recent decades, microRNAs (miRNAs) have gained increasing attention due to their role as gene silencers and because of their altered expression in diverse human diseases, including some infections. Recent research regarding miRNAs and TB has revealed that the expression profile for particular miRNAs clearly changes upon Mycobacterium tuberculosis infection and also varies in the different stages of this disease. However, despite the growing number of studies-some of which have even proposed some miRNAs as potential biomarkers-methodological variations and key differences in relevant factors, such as sex and age, cell type analyzed, M. tuberculosis strain, and antimicrobial therapy status, strongly hinder the comparison of data. In this review, we summarize and discuss the literature and highlight the role of selected miRNAs that have specifically and more consistently been associated with M. tuberculosis infection, together with a discussion of the possible gene and immune regulation pathways involved.

Palabras clave

Palabras clave de autor: [tuberculosis](#); [miRNA](#); [biomarker](#); [Mycobacterium tuberculosis](#); [infection](#); [disease](#)

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