

Role of non-coding RNAs in tuberculosis and their potential for clinical applications

ABSTRACT

Tuberculosis (TB), caused by *Mycobacterium tuberculosis* (Mtb), remains the leading cause of mortality due to infectious diseases, only surpassed in 2020 by COVID-19. Despite the development in diagnostics, therapeutics, and evaluation of new vaccines for TB, this infectious disease remains uncontrollable due to the emergence of multidrug-resistant (MDR) and extremely drug-resistant (XDR) TB, among other factors. The development in transcriptomics (RNomics) has enabled the study of gene expression in TB. It is considered that non-coding RNAs (ncRNAs) from host [microRNAs (miRNAs)] and Mtb [small RNAs (sRNAs)] are important elements in TB pathogenesis, immune resistance, and susceptibility. Many studies have shown the importance of host miRNAs in regulating immune response against Mtb via in vitro and in vivo mice models. The bacterial sRNAs play a major role in survival, adaptation, and virulence. Here, we review the characterization and function of host and bacteria ncRNAs in TB and their potential use in clinical applications as diagnostic, prognostic, and therapeutic biomarkers