DNA markers for tuberculosis diagnosis

ABSTRACT

Tuberculosis (TB), caused by *Mycobacterium tuberculosis* complex (MTBC), is an infectious disease with more than 10.4 million cases and 1.7 million deaths reported worldwide in 2016. The classical methods for detection and differentiation of mycobacteria are: acid-fast microscopy (Ziehl-Neelsen staining), culture, and biochemical methods. However, the microbial phenotypic characterization is time-consuming and laborious. Thus, fast, easy, and sensitive nucleic acid amplification tests (NAATs) have been developed based on specific DNA markers, which are commercially available for TB diagnosis. Despite these developments, the disease remains uncontrollable. The identification and differentiation among MTBC members with the use of NAATs remains challenging due, among other factors, to the high degree of homology within the members and mutations, which hinders the identification of specific target sequences in the genome with potential impact in the diagnosis and treatment outcomes. *In silico* methods provide predictive identification of many new target genes/fragments/regions that can specifically be used to identify species/strains, which have not been fully explored. This review focused on DNA markers useful for MTBC detection, species identification and antibiotic resistance determination. The use of DNA targets with new technological approaches will help to develop NAATs applicable to all levels of the health system, mainly in low resource areas, which urgently need customized methods to their specific conditions.