Abstract

Tuberculosis, caused by Mycobacterium tuberculosis, is responsible for over two million deaths per year worldwide. Due to its long doubling time (18 h), the microbiological detection of M. tuberculosis by conventional methods takes up to one month, unless the number of bacilli in the biological sample is high enough. Thus, drug resistance assessment requires at least one month for obtaining the primary culture and another month to determine its susceptibility to antimycobacterial drugs. Moreover, for a long time, the lack of genetic tools for mycobacteria has been a barrier for undertaking studies aimed at understanding the mechanisms of drug resistance and drug target identification, being all these topics of utmost importance considering the increase in the number of drug-resistant clones and the few therapeutic options available. Mycobacteriophages are promising as a novel source of genetic elements for mycobacteria manipulation, as well as for the development of versatile, simple, fast and cheap methods for drug resistance assessment of M. tuberculosis clinical isolates. We herein describe the background related to the use of mycobacteriophages, with emphasis placed on their utilization for drug resistance analysis in our country.

Keywords

Mycobacterial genetics, Mycobacteriophages, Diagnostic tools, Tuberculosis