Abstract

Strictly aerobic bacteria *Mycobacterium (M.) tuberculosis* (Mtb) belongs to the group of *M. tuberculosis* complex. It is a cause of worldwide spread disease – tuberculosis (TBC), which is being a threat even in the 21st century and claims 1.5 million lives every year (85). It is mainly a threat for socially disadvantaged groups. Source of these mycobacteria is almost always contagious person, rarely contagious animal. The disease almost always first affects respiratory tract, in later stages it can affect any other body organ. The cellular type of immunologic response dominates and so in the indirect diagnostics there is the use of the antibodies being problematic. Skin tests which were used for the testing of the cellular immunologic response in the past are being currently replaced by so-called IGRA tests. In contrast to the most bacteria, *Mtb* diagnostics proves to be difficult. This is caused mainly by the long reproductive time which leads to prolonged cultivation time. To speed up the cultivation metabolic cultivation methods are used.

In the direct diagnostics the microscopic and cultivation techniques still play the main role, help of methods of molecular biology can be used as well. Simple PCR methods enable fast mycobacteria identification, however their use in direct proof brings higher incidence of false positive results. Molecular genetic methods enabling precise identification of source of the infection e.g. fingerprinting are being employed in the epidemiology. Out of the newest methods the next generation sequencing (NGS) method is now available to the scientists. NGS lowered price and time required for the whole mycobacterium genome sequencing. New methods of sequencing are employed in the mycobacterium research and bring new knowledge among others about genes responsible for mycobacterium resistance to antituberculotics.

**Key words:** *Mycobacterium tuberculosis, Mycobacterium tuberculosis* complex, tuberculosis, diagnostic, PCR, MTD