IDENTIFICATION OF MYCOBACTERIUM SPECIES BY MALDI-TOF MASS SPECTROMETRY IN THE CLINICAL LABORATORY

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Introduction: MALDI-TOF MS method allows the identification of microorganisms by comparison of mass spectra of proteins of the microorganism with a database of known protein reference spectra. The aim of this study was to compare the phenotypic identification of mycobacteria and identification by MALDI-TOF MS in laboratory practice.

Methods: 75 isolates of mycobacteria have been identified by molecular and phenotypic identification methods, and it was compared with the identification by MALDI-TOF MS. For MALDI-TOF MS identification of the material has been processed according to the protocol Bruker Daltonik and the database of Mycobacterial Library v2.0 (Bruker) with 313 reference spectra of mycobacteria was used.

Results: From all the 72 isolates, 71 (98%) were determined in conformity to the genus and the species, or to the complex with both methods. 43 isolates of *Mycobacterium tuberculosis* were identified by MALDI-TOF MS as the *M. tuberculosis* complex with 100% success. 31 isolates (96%) non tuberculosis mycobacteria were consistently identified with both methods to the species level, or to the complex.

Conclusion: MALDI-TOF MS is fast and accurate. Its simplicity, speed and economic availability are ideal for the rapid identification of mycobacteria in a routine laboratory. *Supported* by project KEGA č.032 UK-4/2015.