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Discriminating *Legionella*, atypical mycobacteria and *Acanthamoeba* using a MALDI biotyper

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The genus *Mycobacterium* including more than 100 described species is divided into three subgroups: the *M. tuberculosis* complex, *M. leprae* and NTM – non-tuberculosis mycobacteria. The latter have been isolated from hospitals, water, humid rooms, soil and from the mucosa of humans and animals. NTM can provoke potentially lethal lung infections in children or immunocompromised persons.

Legionella spp. an anaerobic, gram-negative, rod-shaped, non-spore forming bacterium is the causative agent of legionellosis (Legionnaires´ disease). Legionellosis, which represents 4% of community-acquired pneumonia cases worldwide, can have a lethal outcome in 18-20% of cases if untreated. *Legionella* spp. has been isolated from air condition units, swimming pools, ground- and surface water. Legionnaires´ disease is acquired by the inhalation of infectious aerosols.

Acanthamoeba spp., single-celled eukaryotic organisms, can provoke severe infections, including *Acanthamoeba* keratitis, GAE (granulomatous amoebic encephalitis) and infections of the lung and the skin. Acanthamoebae have two life cycle stages – a trophozoite and a cyst – and play a significant role as vectors for bacteria (particularly also *Legionella* spp. and MOTT).

The aim of the present study is the establishment of a reference database for protein mass spectra of *Legionella* spp., NTM and *Acanthamoeba* spp. using MALDI TOF MS (Matrix Assisted Laser Desorption Ionisation Time of Flight Mass Spectrometry) and the MALDI Biotyper software. This reference database is aimed to serve as an essential tool for the identification of *Legionella* spp., NTM and *Acanthamoeba* spp. and furthermore for the detection of *Legionella* spp. and NTM in *Acanthamoeba* spp.

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Zoologisch-Botanische Datenbank/Zoological-Botanical Database

Digitale Literatur/Digital Literature

Zeitschrift/Journal: Berichte des Institutes für Geologie und Paläontologie der Karl-Franzens-Universität Graz

Jahr/Year: 2010

Band/Volume: 15

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