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Abstract (poster session)

MALDI-TOF Mass Spectrometry analysis first time applied to the identification of the pathogenic and non pathogenic spirochetes (*Brachyspira* spp. and *Leptospira* spp.) and benefits of database extension

A. Calderaro*, G. Piccolo, S. Montecchini, M. Buttrini, C. Gorrini, S. Rossi, M.C. Arcangeletti, F. De Conto, M.C. Medici, C. Chezzi (Parma, IT)

Objectives: Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) recently emerged as a first-line method for the accurate identification of bacteria, but to date no application was evaluated for *Brachyspira* spp. and few data are available for *Leptospira* spp. We investigated the potential of MALDI-TOF MS for the rapid identification of isolates of these spirochetes. Methods: In this study, we applied MALDI-TOF MS on human and animal *Brachyspira* and *Leptospira* reference strains in order to look for usability and benefits of supplementing the existing database MALDI Biotyper (Bruker Daltonics) and successively we tested additional strains belonging to a well characterized collection to provide evidence for the usefulness of MALDI-TOF MS for the rapid, cheap and reliable spirochaetal identification. Results: Each *Brachyspira* and *Leptospira* reference strain yielded a protein profile including unique peaks, so that each strain yielded a unique profile. All the obtained protein profiles were found to be reproducible over a second, independent experiment and no differences were observed when strains were from different lots of media. All reference strains profiles were deposited in a database to be used for further blind identification of additional spirochetal isolates from our collection (at present only for *Brachyspira* strains). Each strain yielded an identifiable protein profile with an identification score value >2.0 . The specific peaks differentiating the *Brachyspira* and *Leptospira* species were used for the construction of two separate spectra-based MSP (amin spectrum profile) dendrograms of the reference strains. Conclusion: MALDI-TOF MS is very rapid and only minimal amounts of bacteria are needed, in particular a series of developments including robust and easy-to use software and hardware, a drastically shortening of the time to identification of a positive culture, and even lowering the costs considerably has put the methodology in a central position. Current methods for *Brachyspira* and *Leptospira* identification are time-consuming and costly. On the other hand, MALDI-TOF MS makes it possible to identify field isolates with high accuracy and high speed at low cost. In our hands MALDI-TOF MS has proven to be an accurate identification method and a reliable alternative to genetic-based methods for the identification of *Brachyspira* isolates from both human and animal origin and of *Leptospira* spp. strains