

Whole-Cell Matrix-Assisted Laser Desorption Ionization Time-Of-Flight Mass Spectrometry Applications in Medical Microbiology

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Matrix assisted laser desorption/ionisation time of flight mass spectrometry (MALDI-TOF MS) has been introduced several years ago as a new method for bacterial identification [1,2]. Since a couple of years a variety of studies have been investigated the accuracy of a MALDI-TOF MS-based identification of grown colonies [3,4,5,6]. Since proteomic profiles were compared to a database, the accuracy of the identification results on the database used [7,8]. For most identification approaches, protein peaks in the mass-to charge ratio of 2000 to 10000 Da were used, most of them thought to represent ribosomal protein peaks. The results of commercial databases are believed to be very high in accuracy. Nevertheless, an independent protein profile deposition possibility and further optimization strategies [9,10] are desirable in order to improve these databases independently of the manufacturer. Therefore studies with focus on the accuracy of identification of rare bacteria, fungi and other organisms are highly appreciated.

The direct identification of bacteria from materials such as urine and blood culture has also been published and introduced in some diagnostic laboratories [11,12,13,14]. Even though the accuracy seems to be lower compared to that of direct identification, studies investigating the direct identification approach from various clinical specimens are welcome.

A few "proof of principle" studies have been published with regard to MALDI-TOF MS and an epidemiological application [15,16]. In addition, other techniques, such as Raman-spectroscopy [17,18] or the PlexID® system, have been described. The accuracy and more important, the possibilities and limitation has been often only scarcely investigated.

Whether these technologies are suitable to identify certain pathogenicity factors [19,20,21] or resistance [22,23,24] is current ongoing research in medical microbiology. Since any kind of information beside species information would have a great impact on infectious diseases treatment and therapy; this will be a challenge to solve in the next years and in addition, the detection of outstanding resistant organisms, such as *carbapenemase* –producing *enterobacteriaceae* and other threat of the next century [25]. Methods that directly identify underlying resistance mechanisms are needed and will be of peculiar importance.

Studies with a clear hypothesis and a well-organized study structure are highly appreciated even in cases of a negative result.

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