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Identification of previously unknown bacterial species by MALDI-TOF MS

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Background: In clinical microbiology, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) has become an important means of bacterial identification, enabling faster reporting of culture results. The database entries for micro-organisms used in MALDI-TOF MS are based on 16S rRNA gene sequencing, which makes this technique comparable to molecular identification techniques. As a result, more pathogenic microorganisms are identified correctly compared to conventional biochemical methods and new emerging human pathogens have been identified as well. We assessed the merit of MALDI-TOF MS identifications of previously unidentified species and their implications for accurate and relevant reporting.

Material/methods: In four microbiology laboratories in The Netherlands, using the Bruker MALDI Biotyper® system or the bioMérieux VITEK® MS system, MALDI-TOF MS results of previously unknown bacterial species were collected retrospectively. We studied the clinical relevance of these isolates to the specific patient and in general, by consulting medical records and published case reports.

Results: Many new, clinically relevant species of both Gram-positive and Gram-negative bacteria were identified by the two MALDI-TOF MS systems. Examples are: *Aerococcus sanguinicola* causing urinary tract infection, *Weeksella virosa* isolated from an external ear canal, and *Neisseria zoodegmatis* and *Wohlfahrtiimonas chitiniclastica* from infected wounds. According to literature, the clinical relevancy of detected species such as *Alloscardovia omnicolens* and *Bacteroides denticanum* is still not clear. The ability to identify more pathogens than before and generally far more easier than before, especially colonies previously considered as commensal flora, leads to a higher workload in the laboratory. Moreover, standardized antimicrobial susceptibility testing methods including breakpoints are not yet available for all relevant species.

Conclusions: Bacterial identification by MALDI-TOF MS is not only much faster than conventional methods, but contributes to the detection of previously unknown pathogens as well. In an era of increasing numbers of immunocompromised patients and subsequent more complex bacterial

cultures, this is of great value. However, more research is needed to determine the clinical relevancy of certain species and to supplement standardized susceptibility testing guidelines.