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Routine Identification of Clinical Isolates of Anaerobic Bacteria: Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry Performs Better than Conventional Identification Methods

Recently, Justesen et al. (1) compared identification results of the Bruker matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) system and the Shimadzu/SARAMIS system on 290 consecutively collected clinical anaerobic strains. The Bruker system identified 67% of the isolates correctly to the species level, and the Shimadzu system correctly identified 49%. These results are somewhat contradictory to our findings of 2010 (5), with 51% and 61% correct species identifications for Bruker and Shimadzu, respectively. This difference may be explained by the higher percentage of Gram-positive anaerobic cocci (30%) and lower number of *Bacteroides* species in our study (22%) combined with the better performance of the Bruker system on *Bacteroides* species and the better performance of the Shimadzu system on anaerobic Gram-positive cocci (4, 5).

From these and other studies, it can be concluded that MALDI-TOF mass spectrometry (MS) is a promising tool in the identification of anaerobic bacteria but not yet perfect (2, 3, 6). To decide on the implementation of MALDI-TOF MS for the identification of anaerobic bacteria in routine diagnostics, MALDI-TOF MS (Bruker Daltonik, Bremen, Germany) has been compared to conventional methods of identification on 296 consecutive anaerobic clinical isolates collected between January 2010 and February 2011. The most prevalent genera were *Bacteroides* (25%), *Propionibacterium* (15%), *Prevotella* (13%), and *Fusobacterium*, *Clostridium*, and *Actinomyces* (8% each).

The results of MALDI-TOF MS and conventional methods (API Rapid ID 32; bioMérieux, Marcy-l'Étoile, France) were categorized as identical identification to the species level, identical identification to the genus level (if either or both techniques identified to the genus level only), discrepant results, or no reliable MALDI-TOF identification (score of <1.7). Isolates with discrepant results were further investigated by 16S rRNA gene nucleotide sequence analysis. As shown in Table 1, 76% of all isolates were identified to the same genus or species by both methods, whereas discrepant results were found in 11% of the isolates. Of the 25 isolates with discrepant results that were identified by 16S rRNA gene sequencing, 16 major errors were found using conventional methods, while MALDI-TOF MS did not result in major errors. Minor errors were observed 8 and 2 times for conventional methods and MALDI-TOF MS, respectively (chi-square test, $P = 0.009$). Minor errors by MALDI-TOF were *Anaerococcus vaginalis* instead of *Anaerococcus hydrogenalis* and *Fusobacterium nucleatum* and *Fusobacterium naviforme* (duplicate measurement) instead of *F. nucleatum*.

MALDI-TOF results for *Bacteroides* spp., *Clostridium* spp., *Propionibacterium acnes*, *Finegoldia magna*, and *Prevotella* spp. were good. Identification results for *Fusobacterium* spp., non-*acnes Propionibacterium* spp., and *Actinomyces* spp. still need improvement, which is in agreement with observations by other groups (1, 2).

In conclusion, MALDI-TOF MS is superior to conventional techniques for identification of anaerobic bacteria in a clinical setting and can be introduced in the diagnostic routine. Further development of the database will be needed to optimize MALDI-TOF results.

TABLE 1 Results of MALDI-TOF MS and conventional methods

Parameter	No. (%) of isolates
Tested isolates	296
Identical identification to the species level	143 (48)
Identical identification to the genus level	82 (28)
Discrepant results[a]	33 (11)
Correct species identification by MALDI-TOF	21
Correct species identification by conventional methods	1
Correct genus identification by MALDI-TOF	3
No species identification by 16S	3
No 16S performed	5
No reliable MALDI-TOF identification	38 (13)

[a] 16S rRNA gene sequencing as gold standard.

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