P2345

Abstract (poster session)

The value of MALDI-TOF MS in the identification of clinically relevant anaerobic bacteria

E. Nagy*, S. Backer, M. Kostrzewa, E. Urban (Szeged, HU; Bremen, DE)

Objectives: To evaluate the value of a new MS-based identification system for the frequently isolated, clinically significant anaerobic bacteria, to compare the MALDI-TOF MS results with the results of the regularly used identification kits and to use the 16S rRNA gene sequencing for strains with low log(score) or discrepant results. Methods: Between 2010 and 2011 clinically relevant non-duplicate anaerobic isolates (196) were identified - if possible - by different traditional methods such as growth on different selective media, presumptive identification according to the Wadsworth Manual () and rapid ID 32A ATB and API20 ANA (BioMerieux) kits in the anaerobic reference laboratory of the Institute of Clinical Microbiology of the University of Szeged. Incubation was carried out in an anaerobic chamber (Bactron, USA). Immediately after isolation, an ethanol extraction was carried out on isolated colonies and the stabilized samples were sent to the Bruker Laboratory in Bremen, Germany, where the identification was done by using the standard protocol of the MALDI-TOF MS (Microflex) and the spectra were imported into the Biotyper software (version 2.0). Results: Out of the 196 non-duplicate anaerobic clinical isolates from different genera including Bacteroides, Prevotella, Fusobacterium, Clostridium, Peptostreptococcus, Finegoldia, Propionibacterium and some unidentified Gram-negative and Gram-positive anaerobic bacteria were investigated by MALDI-TOF MS. The threshold of log(score) >2.000 was used for the species level identification and >1.700 for genus level identification. MALDI-TOF MS identified 166 (84.6%) strains at a species level and 184 (93.8%) at a genus level. After 16S rRNA gene sequencing, it turned out that for 10 isolates the species was not included into the database. In cases of discrepant phenotypic identification 16S rRNA gene sequencing supported the MALDI-TOF identification in 97% of the cases. Even species, which are difficult to be distinguished by commercially available identification kits, such as B. fragilis and B. capillosus, were correctly identified. By including newly sequenced anaerobic species from our strain collection into the database, the “missed” results could be minimised. Conclusion: MALDI-TOF MS seems to be a very promising identification method especially in the case of anaerobic bacteria, which need a special culture condition, a longer incubation time to get proper growth and are biochemically often inactive.