

P1718

Abstract (poster session)

Frontline identification of bacterial isolates using the MALDI Biotyper-system during a resistance surveillance study in a central European area, 2010

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Objectives: The matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry has become a routine microbial identification system. During a multicentre resistance surveillance study conducted by the Paul-Ehrlich-Society between October and December 2010, 8,250 clinical bacterial isolates were identified in a reference laboratory (Antiinfectives Intelligence) using the MALDI Biotyper-system. Three preparation methods are recommended for identification by the manufacturer (Bruker Daltonik, Bremen, Germany). The aim of the present study was to determine which method had to be used for a satisfying identification result. **Methods:** The first preparation method (method 1) describes the direct transfer of bacteria as a thin film to a 96-spot steel-plate, whereas the other methods require a pre-treatment of the bacteria with formic acid (method 2) or formic acid and ethanol (method 3). All strains were initially tested with method 1. Method 2 or 3 were applied if the identification result was not satisfying with method 1 or 2. An identification result was defined as acceptable if the comparison of a bacterial protein spectrum and the reference spectra of the Biotyper data base (3,995 cellular organisms) resulted in an identical species identification in first and second order and if the species were identified additionally with a log score of ≥ 2.0 in first order. **Results:** Eight-thousand-two-hundred and three (99.4%) isolates were identified on species level, whereat 95.5% were directly identified with method 1. Two-hundred-twenty-one (2.7%) and 99 (1.2%) isolates had to be pre-treated with formic acid or formic acid + ethanol, respectively, to achieve a satisfying identification. The identification result was not acceptable for 47 (0.6%) isolates, whereof 34 strains belonged to Enterobacteriaceae species. In 15/47 (31.9%) cases the log score of ≥ 2.0 in first order was failed and 32/47 (68.1%) identification results were not identical in first and second order. Failure of identification of the 34 Enterobacteriaceae could be mainly explained by the non-distinctive classification of the closely related species *Klebsiella oxytoca* and *Raoultella ornithinolytica*. **Conclusion:** The presented data revealed that the MALDI Biotyper-system provided rapid and reliable identification results. Thus, the MALDI-TOF mass spectrometry is a suitable method for bacterial identification in high-throughput surveillance studies.