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Identification of pathogens in positive blood cultures with the Sepsityper™ kit using the MALDI-TOF MS Axima device and the Saramis database

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Objectives

Blood cultures are still the reference standard in the microbiological diagnosis of sepsis; however, culture depending identification methods are time consuming. Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) has become a valuable tool for rapid identification of cultured microorganisms. To timely improve species identification in positive blood cultures the Sepsityper™ extraction kit (Bruker Daltonics) was introduced. The aim of this study was to evaluate if positive blood culture broth treated with the Sepistyper™ Kit could be successfully analyzed using MALDI-TOF MS AXIMA™ (Shimatzu) and the SARAMIS™ database (bioMérieux).

Methods

Fifty positive blood cultures were made available after routine procedure for the extraction with the Sepsityper™ Kit. Briefly, 1 ml of broth was harvested, treated with lysis buffer and washing buffer and finally the obtained pellet was treated with the standard formic acid extraction protocol. Each extract was spotted four times on the MALDI target. Two non-dried and two dried spots were overlaid with HCCA matrix. After HCCA matrix was dried, samples were measured with MALDI-TOF AXIMA™ and mass spectra were analyzed with the SARAMIS™ database. The data were interpreted according to the manufacturer´s instruction. Out of the two double tested samples (dry and wet), the result with the better score was used for evaluation.

Results

After broth culturing, the routine standard method identified gam-positives, gram-negatives, anaerobes and fungi in 30 (60%), 17 (34%), 2 (4%) and 1 (2%) of the 50 cultures, respectively. Using the Sepsityper™ Kit correct species identification was obtained in 80% (24 of 30) for gram-positives and in 77% (13 of 17) for gram-negatives. Neither *Bacteroides fragilis* nor *Propionibacterium acnes* were identified but *Candida parapsilosis* was correctly identified. Comparing the used procedures, the method of overlaying HCCA matrix after drying gave significant better results ($p<0,001$). Retrospective control of the pellets showed that from the 22% (11 of 50) unidentified samples 82% (9 of 11) did not have a macroscopic visible pellet.

Conclusion

This study indicates, that the Sepsityper™ Kit used together with the MALDI-TOF MS AXIMA™ device and the SARAMIS™ database, has the potential to improve the rapid identification of microorganisms in positive blood cultures in routine diagnostic laboratories.