Comparison of PCR/electrospray ionization mass spectrometry and 16S rRNA gene sequencing for identification of microorganisms from clinical sterile body fluid specimens

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Introduction

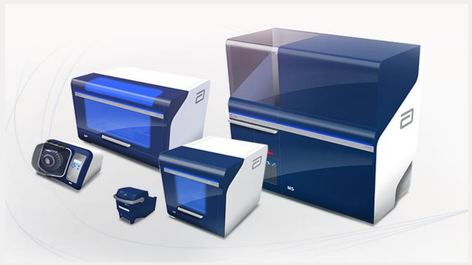
• Early detection and rapid identification of microorganisms is crucial for appropriate management of infections of normally sterile body fluids (SBF) and tissues.

• The aim of the present study was to compare the clinical performance of PCR/electrospray ionization mass spectrometry (PCR/ESI-MS) and 16S rRNA gene sequencing for identification of microorganisms directly from SBF and tissues.

Materials and Methods

• Altogether 44 routine SBF and tissue samples (26 tissue/abscess, 11 pleural, 5 synovial, 2 cerebrospinal fluid) received at the clinical laboratory were included in the study.

Fig 1. IRIDICA PCR/electrospray ionization mass-spectrometry test



• PCR/electrospray ionization mass spectrometry (PCR/ESI-MS) (Fig.1)

• 16S rDNA sequencing carried out with Sanger sequencing

• MecA PCR

Table 1. Comparison of 16S rRNA gene sequencing and PCR/ESI-MS)

16S	IRIDICA
Klebsiella pneumoniae	*Klebsiella pneumoniae*
Proteus mirabilis	*Proteus mirabilis*
Staphylococcus aureus	*Staphylococcus aureus*
Streptococcus mitis-gruppen	*Streptococcus constellatus/gordonii*
Streptococcus mitis-gruppen	*Streptococcus mitis*
Aerococcus urinae	*Aerococcus urinae*
Staphylococcus aureus	*Staphylococcus auerus*
Legionella species	*Legionella longbeachae*
Serratia species	*Serratia marcescens*
Staphylococcus aureus	*Staphylococcus aureus*
Fusobacterium necrophorum	*Fusobacterium necrophorum*
Streptococcus pneumoniae	*Streptococcus pneumoniae*
Aerococcus urinae	Aerococcus urinae
Staphylococcus aureus	Staphylococcus aureus
Fusobacterium necrophorum	Fusobacterium necrophorum
Streptococcus pneumoniae	Streptococcus pneumoniae
Streptococcus pneumoniae/mitis group	Streptococcus pneumoniae samt Streptococcus mitis/pneumoni
Aerococcus urinae	*Aerococcus urinae*
Streptococcus pneumoniae/mitis group	Streptococcus pneumoniae, *Streptococcus mitis/pneumoniae*
Enterococcus species	*F. magna, C. amycolatum, E. cloacae complex, E. faecalis*
P. aeruginosa, E. faecalis	*S. epidermidis, E. faecalis, P. aeruginosa*
Not detected	*Streptococcus pneumoniae*
Not detected	*Staphylococcus auerus*
Not detected	*Streptococcus pneumoniae*
Not detected	*Staphylococcus aureus*
Not detected	*Propionibacterium acnes*
Staphylococcus aureus	*Staphylococcus aureus, mecA pos.*
Dialister pneumosintes, Fusobacterium nucleatur	Bacteria detected - No ID can be provided
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected
Not detected	Not detected

Results

• The PCR/ESI-MS and 16S sequencing could identify 33 and 27 microorganisms, respectively, in 28/45 (62%) and 25/45 (56%) samples, respectively.

• PCR/ESI-MS also detected microorganisms in five samples where the 16S sequencing results were reported as negative. In addition, in two samples PCR/ESI-MS detected additional microorganisms compared to 16S sequencing.

• PCR/ESI-MS could also detect mecA gene in one sample with S. aureus which was later confirmed with mecA PCR.

•In one sample 16S detected two microorganisms whereas the PCR/ESI-MS reported “Bacteria detected - No ID can be provided”.

•In 17/45 samples there was no detection of microorganisms by either method.

•The turn-around time for PCR/ESI-MS and 16S sequencing were 8h and 48h respectively.

Conclusion

• The PCR/ESI-MS is a rapid and reliable method that can be used in microbiological diagnostics of SBF.

• The PCR/ESI-MS has high performance in identification of microorganisms from both mono- and poly-microbial infections in SBF

•The PCR/ESI-MS may have limited specificity in discrimination of Streptococcus mitis and S. pneumoniae.

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