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Oral Session
PCR and other molecular tests directly on blood: what is new?

FIELD EVALUATION OF THE NEW QUICKFISH™ ASSAYS FOR THE RAPID DIAGNOSIS OF SEPSIS

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Objectives. The rapid identification of pathogens responsible for sepsis is a majorgoal to administrate a targeted therapy and to reduce patient mortality rates.In our laboratory about 90 cases of sepsis per months were detected, mainlycaused by staphylococci and Gram negative bacteria.

Peptidenucleic acid fluorescence *in situ*hybridization (PNA FISH) is a molecular diagnostic tool for the rapididentification (about 2 hours) of pathogens directly from positive bloodcultures (BC), currently used in our laboratory and, on the basis of theavailable panel used, able to distinguish between *Staphylococcus aureus* (SA) and other coagulase-negativestaphylococci (CNS), between *Enterococcusfaecalis* (EF) and other enterococci (OE), between *Escherichia coli* (EC), *Klebsiellapneumoniae* (KP) and *Pseudomonasaeruginosa* (PA), between *Candidaalbicans*/*C. parapsilosis*, *C. tropicalis* and *C. glabrata*/*C. krusei*.

Arecent evolution of PNA FISH, the *Quick*FISH™assay (AdvanDx) uses a faster (about 20 minutes) and simpler protocol atpresent limited to bacteria. The aim of this study was to evaluate the SA/CNS andthe EC/KP/PA *Quick*FISH™ assays on positive blood culture detected in our laboratory in thefirst month of use, as compared to conventional cultures and subsequentMALDI-TOF MS identification methods.

Methods. In a period of 1 month 109 cases of sepsis were detected, on a total of860 analysed samples belonging to 373 patients. Onthe basis of the Gram stain microscopy result, from 60 positive bloodculture bottles (Bactec FX, BD) (1 bottle perpatient) the *Quick*FISH™ assays were applied selecting the appropriate panel. Thesamples were then cultured using standard techniques and the identification ofgrown microorganisms were performed by MALDI-TOF MS and biochemicalidentifications by traditional assays when needed for discordant results.

Results. On all 60 positive BC, *Quick*FISH™showed a 100% agreement with the identification by other methods (6 SA, 30 CNS,2 SA+CNS, 12 EC, 4 KP, 2 PA and 4 negative). The *Quick*FISH™ assay provided species identification in average 1 dayearlier in the case ofmonomicrobial infections and 2 days for polymicrobialinfections than the other methods.

Conclusion. In the first month of use *Quick*FISH™demonstrated to be an excellent tool for the rapid identification of mainpathogens directly on blood culture, improving the PNA FISH method in terms of rapidity and ease of handlingand reducing significantly the reporting time as compared to other methods(MALDI-TOF MS performed on conventional cultures) with a positive impact forthe appropriate management of the patient and the administration of a targetedtherapy.