EV0497
ePoster Viewing
Diagnostic bacteriology – non-culture based, including molecular and MALDI-TOF

What is the actual broadness of the universal panbacterial PCR in diagnostics of infections

Jan Tkadlec[1], Milena Antušková[1], David Jahoda[2], Lucie Šrámková[3], Vilem Rohn[4], Milan Kvapil[5], Dominik Raszka[2], Pavel Drevinek[1]

[1]*2nd Faculty of Medicine, Charles University and Motol University Hospital, Department of Medical Microbiology, Prague, Czech Republic*

[2]*1st Faculty of Medicine, Charles University and Motol University Hospital, 1st Department of Orthopaedics, Prague, Czech Republic*

[3]*2nd Faculty of Medicine, Charles University and Motol University Hospital, Department of Paediatric Haematology and Oncology, Prague, Czech Republic*

[4]*2nd Faculty of Medicine, Charles University and Motol University Hospital, Department of Cardiovascular Surgery, Prague, Czech Republic*

[5]*2nd Faculty of Medicine, Charles University and Motol University Hospital, Department of Internal Medicine, Prague, Czech Republic*

Background: A complementary use of molecular genetic methods in detecting bacterial agents is particularly beneficial in situations where culture based approach fails due to: 1/ its low sensitivity, 2/ the presence of fastidious or unculturable bacteria in the sample, 3/ an ongoing antibiotic therapy or 4/ where it implicits a critical time delay to get a result. While species specific PCRs are designed to identify a unique DNA sequence of single pathogens, broad spectrum molecular assays enable to search through a common DNA region for virtually any bacterial species in the specimens. We aimed to evaluate the usefulness and clinical relevance of the latter approach which we applied to various microbiological materials collected from primary sterile sites.

Material/methods: We examined A/ 119 orthopaedic samples (joint punctures or tissue samples), B/ 155 blood samples of 77 children with haematological disorders, C/ 49 blood samples of 33 internal medicine patients, D/ 29 heart valves because of suspected infectious endocarditis (IE), and E/ 22 cerebrospinal fluid (CSF) samples. Each sample was examined by conventional culture as well as by panbacterial PCR (UMD SelectNA, Molzym, Germany) which was based on detection and nucleotide sequence analysis of a 16S rDNA fragment.

Results: A/ PCR positivity that matched bacterial identification by culture was found in 31 orthopaedic samples. Additional 33 samples were positive only by PCR, with 25 of them (37% of all positive results) being considered clinically significant. B/ Bacterial DNA was detected in 40 blood samples of haematological patients; 19 of them - that were found positive exclusively by PCR (38% of all positivities) - were interpreted as a possible cause of suspected bloodstream infection (BSI). Bacterial identification was confirmed in only 8 of 40 samples by blood culture. Yet blood culture positivity not accompanied by PCR positivity was observed in other 10 samples (20% of all positivities). C/ Concordance between the PCR and culture was observed in 40 of 49 blood samples from internal medicine patients (12 positive, 28 negative; negative predictive value (NPV) 97%). D/ a causative agent of IE was revealed in 20 of 29 valves only by PCR. E/ diagnosis of bacterial meningitis was confirmed by PCR in 3 cases with a culture negative CSF.

Conclusions: The method utilizing a panbacterial PCR can increase a recovery rate, but its meaningful indication as well as interpretation are strictly linked to a type of clinical material under investigation. While it proved to be desirable part or routine microbiological examination for IE and joint infections, false negative results makes it questionable in diagnostics of the BSI. The potential of PCR in BSI can be envisaged in its high NPV as observed especially in the group of adults with suspected BSI.

Supported by AZV15-28157A.