28th ECCMID EUROPEAN CONGRESS OF CLINICAL MICROBIOLOGY AND INFECTIOUS DISEASES
Madrid, Spain
21 – 24 April 2018

P1788 Comparative evaluation of Accelerate Pheno and Vitek 2 systems for rapid antibiotic susceptibility testing of pathogens in positive blood cultures

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Background: New diagnostic methods are available for rapid identification (ID) and antibiotic susceptibility testing (AST) of microorganisms responsible for bloodstream infections (BSIs). Accelerate Pheno™ system (AXDX) is an automated platform that uses morphokinetic cellular analysis to provide rapid species identification and antibiotic susceptibility directly in positive blood culture (BC) samples. The objective of the present study was to evaluate the performance of AXDX and the older VITEK 2 (VTK) system in comparison with that of conventional ID and AST methods.

Materials/methods: We studied positive BCs from unique BSI patient/episodes in two Italian tertiary care hospitals over a six-month period. BCs were analysed by the AXDX system and by conventional laboratory methods. The last consisted of microscopic observation (MO) by Gram staining, ID by MALDI-TOF MS, and AST by the VTK system. Only the BCs revealing a monomicrobial growth at the MO were submitted to the direct testing with MALDI-TOF MS and VTK for ID and AST, respectively. For all BC isolates, we compare AST results by both AXDX and VTK systems with those of the reference broth microdilution (BMD) method. All comparisons were expressed in terms of essential agreement (EA) and categorical agreement (CA); in the latter case, EUCAST breakpoints (v. 7.1) were used.

Results: One hundred and sixteen BCs were evaluated, 104 (89.6%) of which were monomicrobial. Sixteen isolates failed AXDX ID because eight were off-panel and eight (seven from polymicrobial BCs) failed ID. Therefore, overall species ID agreement between AXDX and MALDI-TOF MS was 93.4% (114/122 isolates). Of 114 isolates, 20 failed to give an AXDX AST result and were excluded from the AST analysis. EAs between AXDX and BMD results and between VTK and BMD results were 91.7% and 90.2%, respectively. CAs between AXDX and BMD results and between VTK and BMD results were 91.2% and 90.1%, respectively. For monomicrobial BCs (n = 86), EAs between AXDX and BMD results and between direct VTK and BMD results were 93.6% and 92.3%; overall CAs were 90.4% and 91.1%, respectively.

Conclusions: Based on these findings, AXDX can be a valid alternative method for rapid identification of antibiotic-resistant BSI microorganisms.