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EVALUATION OF THE ACCELERATE PHENO™ SYSTEM FOR THE DIAGNOSIS OF BLOOD STREAM INFECTIONS (BSI)

G. Giuliani, M. Re, L. Re, C. Rescaldani, L. Manolia R. Ottaviano.
Laboratory Medicine and Microbiology Unit – ASST-Rhodense, Rho, Milan, Italy

Sistema Socio Sanitario
Regione Lombardia
ASST Rhodense

ABSTRACT

Diagnosis of bloodstream infections (BSIs) is one of the most critical functions of microbiology laboratories and time-to-results is a milestone. For the great majority of etiologic agents of BSIs, conventional blood culture methods provide results within 48 hours and thanks to modern automated continuous-monitoring blood culture systems the incubation for more than 5 days seldom is required. Thanks to recent advances in molecular biology, several PCR-based methods for the diagnosis of BSIs directly from whole blood - such as PCR MagicPlex, Sepsi Test, SeptiFast, VYOO, PCR/ESI-MS, and PlexID - has been proposed to speed the determination of the etiological agent and give a result within 6 – 8 hours. These methods are limited by the very low number of circulating microbes during paucibacterial infections. Other methods are blood culture dependent (e.g. MALDI-TOF, FISH, Xpert MRSA/SA BC, StaphSR assay, StaphPlex, FilmArray, Verigene, and Prove-it Sepsis) and provide a result within 1 – 5 hours. In the context of blood culture dependent methods, we evaluated the performance of Accelerate Pheno system (APs) in BSIs with both Gram-negative and Gram-positive bacteria in comparison with conventional culture-based identification and AST methods.

OBJECTIVES

Objectives:

1. To evaluate the performance of APs in terms of correct identification of bacteria;
2. To evaluate the performance of APs in terms of AST results;
3. To evaluate the adaptability/flexibility of APs in our processes of bacterial diagnosis.

METHODS

The Accelerate Pheno system (Accelerate Diagnostics, USA) is a fully automated test system capable of performing identification and AST directly from positive blood cultures within approximately 7 h. The system combines gel electrofiltration and fluorescence *in situ hybridization for bacterial identification, as well as automated* microscopy for analyzing bacterial growth rates and for extrapolating MIC values. APs results were compared with current laboratory ID (BD™ Bruker MALDI-TOF) from both blood culture (rapid-ID) and pure colonies (standard-ID), as well as AST (BD Phoenix™).

RESULTS

On a total of 48 BSIs of which 29 Gram-negative (22 *Escherichia coli*, 4 *Klebsiella pneumoniae*, 2 *Acinetobacter baumannii* and 1 *Bacteroides ovatus*), 18 Gram-positive (6 *Staphylococcus aureus*, 6 *Staphylococcus epidermidis*, 4 *Enterococcus faecium* and 2 *Enterococcus faecalis*) and 1 polymicrobial (*Pseudomonas aeruginosa*/*Enterococcus faecalis*), APs provided 95.8% correct identification. In 2 specimens, the APs could not provide identification of which 1 case with an organism not covered by APs panel (*B. ovatus*) and in the polymicrobial episode APs could provide a partial identification for *E. faecalis* but not for *P. aeruginosa*. APs provided AST results in 28 Gram-negative BSIs (100%) and 18 Gram-positive BSIs (100%). A total of 414 AST of which 324 Gram-negative and 90 Gram-positive were produced and compared to the culture-based AST results of Phoenix. The overall category agreement was 96.9% for Gram-negative and 97.7% for Gram-positive isolates. A low CA was observed for amikacin (92.8%), cefepime (92.8%), aztreonam (92.3%), vancomycin (88.9%) and piperacillin-tazobactam (85.7%). Minor, major and very major discrepancies for Gram-negative and Gram-positive (parentheses) were detected in 1.8% (0%), 0.6% (2.2%), 0.6% (0%), respectively. Major discrepancies were observed for vancomycin and piperacillin-tazobactam. The median ID run time was 1.5h for APs, 1.5h for rapid-ID and 18h for standard-ID. The median ID/AST run time was 7h for APs and 46h for cultured-based AST.

CONCLUSIONS

Our study demonstrated that APs identifies organisms 16.5h before cultured-based identification. APs AST results were available 39h earlier compared to conventional culture-based AST. These results indicate that APs could be a useful tool for the diagnosis of BSI.

Analysis of the results demonstrated that APs allows the identification of microorganisms directly from the broth-culture, minimizing both the times of the bacterial identification and AST results. By this way, the clinicians can apply a targeted therapy in a timely manner and the rate of morbidity and mortality of the septic patients can be reduced.

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