A novel system for microbial identification and susceptibility testing directly from clinical blood culture samples

PETRA LÜTHJE, MÅNS ULLBERG, VOLKAN ÖZENCI; KAROLINSKA UNIVERSITY HOSPITAL AND KAROLINSKA INSTITUTET, STOCKHOLM, SWEDEN

Introduction

The fully automated Accelerate Pheno™ System identifies microbial pathogens and performs antimicrobial susceptibility testing (AST) directly from positive blood culture bottles within 1 ½ and 7 hours, respectively.

Aim of the study

The aim of the study was to evaluate the performance of the Accelerate Pheno™ system on clinical samples using standard methods as reference.

Conclusion

- The Accelerate Pheno™ system was easily operated.
- Identification results should be interpreted in conjunction with Gram stain.
- AST using SW1.2 produced reliable results.

Results – Identification

- Results from the Accelerate Pheno™ System were obtained for 98/108 (91%) blood culture bottles with a total of 105 microorganisms
- Out of 105 microorganisms, 54/59 (92%) Gram-negative and 36/46 (78%) Gram-positive isolates were detected and correctly identified by the Accelerate Pheno™ System (Table 2)

Table 2. Identification results for 105 isolates.

Gram stain	*n*= (•)				
Gram- rods	59 (58)	54		5	
Gram+ cocci in chains	20 (8)	11	1	3	5
Gram+ cocci in clusters	26 (25)	23	1	2	

- Number of isolates (number included in the AST panel)
- Correct identification, including off-panel species (“no ID”)
- Correct genus level identification for off-panel species
- Not detected/ no identification for on-panel species
- False identification

Results – Antimicrobial susceptibility testing

- AST was completed for 49/58 (84%) Gram-negative and 25/33 (78%) Gram-positive isolates eligible to AST
- No very major errors were observed
- For **Gram-positive species**, full categorical agreement was achieved for *Enterococcus* spp. (ampicillin, linezolid, vancomycin; *n*=5) and *Staphylococcus* spp. (FOX screen, erythromycin, linezolid; *n*=20); minor errors were observed for 4/9 CoNS spp. and trimethoprim-sulfamethoxazole.
- For **Gram-negative species**, categorical agreement with disc diffusion for amikacin, ertapenem, ciprofloxacin, gentamicin and meropenem was 96-100%.
- Categorical agreement with microbroth dilution for ceftazidime, piperacillin-tazobactam and aztreonam increased to >90% when applying software SW1.2 (Figure 1).

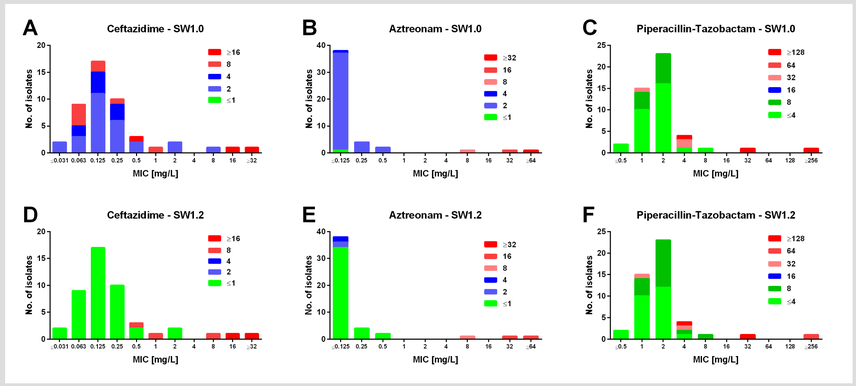

Figure 1. Improved AST for Enterobacteriaceae using SW1.2. (A-C) Initial results with SW1.0 for samples directly from blood culture bottles; **(D-F)** isolates were re-analyzed with SW1.2 from simulated blood cultures. Results from the Accelerate Pheno™ System were compared to MIC-values determined by broth microdilution (x-axis); ■ sensitive, ■ intermediate, ■ resistant.

Table 1. Identification and AST panel SW1.0.

Gram-positive	Gram-negative
S. aureus	*E. coli*
S. lugdunensis	*Klebsiella* species
CoNS species	*Enterobacter* species
E. faecalis	*Proteus* species
E. faecium	*Citrobacter* species
Streptococcus species	*S. marcescens*
S. pneumoniae	*P. aeruginosa*
S. agalactiae	*A. baumannii*

- Included in AST panel
- Identification only

Materials and Methods

All clinical samples (*n*=108) were analyzed with the **Accelerate Pheno™ System SW1.0** (Table 1).

47/49 Gram-negative isolates were grown in simulated blood cultures and re-analyzed with **SW1.2.**

- Identification: Fluorescence *in situ* hybridisation
- AST: Morphokinetic cellular analysis of bacterial growth

Standard methods served as reference.

- Identification: MALDI-TOF MS, Vitek2
- AST: Disc diffusion, broth microdilution for ceftazidime, aztreonam and piperacillin-tazobactam; breakpoints according to EUCAST version 6.0 were applied