

Evaluation of Accelerate Pheno™ System in a Clinical Setting: Comparison of Identification and Antibiotic Susceptibility Test Results of 224 Prospective Positive Blood Cultures to Standard Laboratory Methods at Detroit Medical Center



Hossein Salimnia, Ph.D.
Wayne State University
Department of Pathology
3901 Beaubien St.
Detroit, MI 48201
Tel. (313) 745-4609
Fax. (313) 993-8765
hsalimni@med.wayne.edu

P. Lephart¹, K.S. Kaye^{2†}, J.M. Pogue³, T. Painter¹, T. Burger^{1‡}, M. Taylor¹, C.C. Cooper², M. Fairfax^{1,4} and H. Salimnia^{1,4}
1. Detroit Medical Center University Laboratories, 2. Infectious Diseases, 3. Pharmacy and 4. Pathology, Wayne State University School of Medicine, Detroit, MI.

INTRODUCTION

Bloodstream infections (BSI) cause more than one million hospitalizations, 258,000 deaths and \$24 billion in hospital costs annually. Rapid organism identification (ID) and antimicrobial susceptibility testing (AST) can guide early appropriate antimicrobial therapy and improve patient outcomes. The Accelerate Pheno™ system identifies common pathogens and provides MICs for multiple antibiotics directly from positive blood cultures in 7 hours. We aimed to evaluate the performance (accuracy) and time to organism ID and AST results of the Accelerate Pheno™ system compared to standard laboratory methods using positive blood cultures collected prospectively from unique patients with suspected BSI.

METHODS

Residual positive blood bottles were tested on the Accelerate Pheno[™] system within 8 hours of positivity using pre-FDA cleared software (1.0) and CLSI 2016 breakpoints. ID sensitivity and specificity and AST essential (EA) and/or categorical agreement (CA) were calculated and compared to our current clinical laboratory methods. The standard methods at the Detroit Medical Center (DMC) consist of a combination of phenotypic, biochemical method and/or MALDI-ToF techniques for organism ID combined with AST via the BD Phoenix[™] Automated Microbiology System. Time to organism ID was also compared to the Verigene® System.

RESULTS

Based on 224 unique prospective positive blood cultures tested, the Accelerate Pheno[™] system, pre-discrepancy testing, showed an overall sensitivity of 93.8% and specificity of 99.7% for pathogen ID compared to our standard methods. For AST, the Accelerate Pheno[™] system showed an overall EA and CA of 96.3% and 94.8%, respectively. Results from organisms/antibiotics not included in the final FDA-cleared version were not included in performance analysis. The average time to ID and AST was about 39 hours faster with the Accelerate Pheno[™] system than with standard methods (Table 4).

CONCLUSION

Rapid ID and AST of bloodstream pathogens allows for rapid transition to targeted therapy which could reduce mortality and unnecessary broad-spectrum antimicrobial exposure. These data showed the ability of the Accelerate Pheno™ system to provide accurate ID in less than 90 minutes, and most importantly, reliable AST results in less than 7 hours from the detection of a positive blood culture; thus decreasing the time to AST results by nearly 2 days compared to standard methods.

ACKNOWLEDGMENTS

The authors would like to thank Robert Mitchell and the staff of the Microbiology laboratory at Detroit Medical Center University laboratories for their help and assistance. This study was supported by a research fund from Accelerate Diagnostics, Inc. Their help with discrepancy testing and analysis of data is highly appreciated.

Table 1: Identification Performance (n=206 runs)*

Table 1. Identification i enormance (n=200 runs)						
Organism	Sensitivity		Specificity			
Gram-Positive						
Coagulase-negative Staphylococcus spp.	28/31	90.3%	167/169	98.8%		
Enterococcus faecalis	10/11	90.9%	195/195	100%		
Enterococcus faecium	5/5	100%	198/200	99%		
Staphylococcus aureus	47/48	97.9%	152/153	99.3%		
Staphylococcus lugdunensis	0/1	0%	203/203	100%		
Streptococcus spp.	18/19	94.7%	187/187	100%		
Gram-Negative						
Acinetobacter baumannii	0/0	N/A	206/206	100%		
Citrobacter spp.	1/1	100%	204/205	99.5%		
Enterobacter spp.	6/8	75%	197/197	100%		
Escherichia coli	34/34	100%	172/172	100%		
Klebsiella spp.	16/18	88.9%	187/187	100%		
Proteus spp.	7/7	100%	199/199	100%		
Pseudomonas aeruginosa	4/5	80%	201/201	100%		
Serratia marcescens	1/1	100%	205/205	100%		
Yeast						
Candida albicans	1/1	100%	203/203	100%		
Candida glabrata	3/3	100%	199/203	98%		
Overall	181/193	93.8%	3075/3085	99.7%		

*Monomicrobial Meta Call PPV: 97.3%

Table 2: Resistance Phenotype Performance

Combination	Count	CA	VME	ME
Cefoxitin & S. aureus	42	42/42 (100%)	0/26 (0%)	0/16 (0%)
Cefoxitin & CNS	10	8/10 (80%)	1/7 (14.3%)	1/3 (33.3%)
Cefoxitin & S. lugdunensis	0	0/0 (N/A)	0/0 (N/A)	0/0 (N/A)
MLSb & CNS	10	8/10 (80%)	1/6 (16.7%)	1/4 (25%)
MLSb & S. lugdunensis	0	0/0 N/A	0/0 (N/A)	0/0 (N/A

Table 3: Antimicrobial Susceptibility Testing (AST) Performance

Antibiotic	Count	Essential Agreement	Categorical Agreement			
Gram-Positive ^{1,2}						
Ampicillin	11	90.9%	90.8%			
Ceftaroline	0	N/A	N/A			
Daptomycin	64	90.6%	98.4%			
Doxycycline	0	N/A	N/A			
Erythromycin	54	94.4%	94.4%			
Linezolid	65	95.4%	98.5%			
Trimethoprim- Sulfamethoxazole	44	100%	100%			
Vancomycin	65	96.9%	98.5%			
Gram-Negative ^{1,3}						
Amikacin	64	98.4%	98.4%			
Ampicillin- Sulbactam	49	93.9%	75.5%			
Aztreonam	64	93.8%	96.9%			
Cefazolin	46	95.7%	76.1%			
Cefepime	64	96.9%	96.9%			
Ceftazidime	64	90.6%	89.1%			
Ceftriaxone	61	98.4%	98.4%			
Ciprofloxacin	63	100%	96.8%			
Colistin	0	N/A	N/A			
Ertapenem	60	100%	100%			
Gentamicin	64	98.4%	96.9%			
Meropenem	59	98.3%	98.3%			
Minocycline	0	N/A	N/A			
Piperacillin- Tazobactam	62	95.2%	91.9%			
Tobramycin	64	98.4%	93.8%			
Overall	1087	96.3%	94.8%			
Posulte based on CLSI 2016						

¹Results based on CLSI 2016 breakpoints

²3 major errors / 244 S results - 0 very major errors / 5 R results ³1 major error / 655 S results - 5 very major errors / 59 R results

Tillajor offor 7 000 offoodito of vory major offor 7 00 ft roodito

†Currently at Department of Medicine, University of Michigan Medical School, Ann Arbor, MI, U.S.A. ‡Currently at Accelerate Diagnostics, Inc., Tucson, AZ, U.S.A.

Table 4: Comparison of Time to ID and AST

	Average Time to ID	Average Time to AST
Accelerate Pheno™ System	1.4 h	6.7 h
Verigene System	2.0 - 2.5 h	N/A
MALDI-TOF	33.9 h	N/A
Standard Methods ID / BD Phoenix Automated Microbiology System	40.3 h	45.5 h

Figure 1: Categorical Time Difference to ID Results for Culture vs. Accelerate Pheno™ System

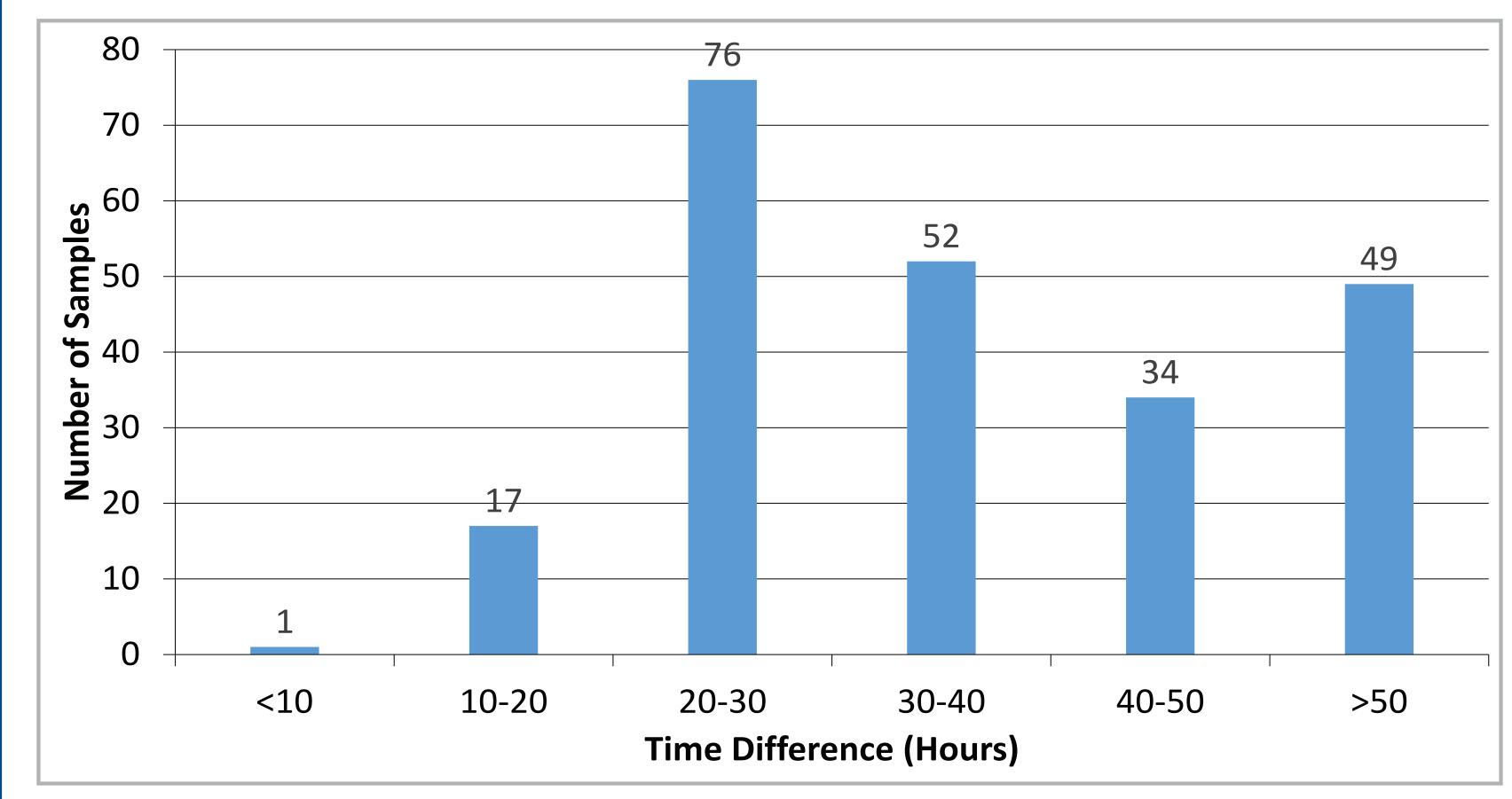


Figure 2: Categorical Time Difference to AST Results for Culture vs. Accelerate Pheno™ System

