

Comparison of the Phoenix™ Automated Microbiology System to the Dade-MicroScan WalkAway-40 for Identification of Clinical Bacterial Isolates

F. MARCO, A. JURADO, M.T. JIMÉNEZ DE ANTA

Servei de Microbiologia. Institut Clinic d'Infeccions i Immunologia. IDIBAPS. Hospital Clinic Universitari. Barcelona, Spain

REVISED ABSTRACT

■ **OBJECTIVES:** The Phoenix™ System (BD Diagnostic Systems, Sparks, Maryland, USA), a rapid automated ID/AST system, was compared to the Dade-MicroScan WalkAway-40 System (Dade-MicroScan, W. Sacramento, California, USA) for accuracy of identification (ID) of fresh clinical laboratory isolates as well as a Challenge Set of selected stock strains.

METHODS: A total of 327 bacterial isolates, comprised of 191 gram-negative bacilli (GNB) and 136 gram-positive cocci (GPC) (27 *Staphylococcus aureus*, 53 coagulase-negative staphylococci, 45 enterococci and 11 streptococci), was evaluated in both the Phoenix (PHX) and MicroScan (MSC) systems. Inoculum suspensions were prepared following manufacturer's instructions. Standard commercially available PHX and MS ID/AST panels were inoculated and incubated following each manufacturer's procedure. If required, supplemental tests were used to determine a final ID. Results from both systems were compared for genus / species agreement, and discrepancies were arbitrated using a third system, API (bioMérieux, France).

RESULTS: The overall rate of agreement between the PHX and MS systems for species level ID was 95.8% and 96.3% for GNB and GPC, respectively. *Enterococcus* and *Streptococcus* species both achieved a 100% rate of species level agreement. The genus level agreement was > 99% overall. Arbitration of the 8 GNB disagreements resolved with 7 in agreement with the Phoenix ID. For the 5 GPC disagreements, 3 resolved in agreement with Phoenix. Supplemental manual ID tests were required for 4 GNB strains (2.1%) with MSC, while PHX required additional tests for 2 GNB strains (1.0%). In addition, PHX correctly identified 60 /63 (95.8%) of *Staphylococcus* species as beta-lactamase producing strains.

CONCLUSIONS: The Phoenix Automated Microbiology System provides a high level of agreement to the MicroScan WalkAway System for identification of gram-negative and gram-positive clinical isolates.



INTRODUCTION

The identification of gram-negative and gram-positive clinical bacteria represents the largest proportion of identification tests performed in an average clinical microbiology laboratory. Automation of these tests can reduce the human workload of the laboratory. Rapid identification test systems can have a beneficial impact on patient welfare through directed therapy. Clinical laboratories are under more and more pressure to increase labor efficiency while providing timely and medically useful information to the medical staff. These laboratorians are, thus, considering the purchase of new systems offering enhanced levels of automation and more rapid test results. However, in making such a purchase decision, the accuracy identification and susceptibility testing is crucial for laboratories evaluate. For without accuracy the advantages of automation and rapid test results are lost in regards to patient care.

In this study, we evaluated a new automated identification (ID) and antimicrobial susceptibility test (AST), Phoenix, for accuracy of identification of some commonly isolated gram-negative and gram-positive bacteria.

METHODS AND MATERIALS

Bacterial Isolates

A combination of fresh clinical isolates and some frozen stock cultures were tested including 191 gram-negative and 136 gram-positive bacteria. The gram-negative bacteria included a representative sample of Enterobacteriaceae and *Aeromonas* species in our hospital. *Pseudomonas* and other non fermentative bacteria were not included because it is our laboratory practice to test these organisms with other systems (Sensititre, API and other manual tests). The gram-positive bacteria included a routine mix of Staphylococci, Enterococci and Streptococci. gram-positive bacilli were not included because it is our laboratory practice to test these organisms with other systems (Sensititre and manual tests such as serology).

Phoenix

(BD Diagnostic Systems, Sparks, MD): gram-negative panels NMIC/ID-1 [Cat no.448506] and gram-positive panels PMIC/ID-1 [Cat no.448502] were used. Phoenix panels were tested strictly following manufacturer's instructions. Briefly, blood agar plates were inoculated with the test cultures and were incubated for 18-24 hours at 35°C. Isolated colonies were used to prepare a suspension of the bacteria in the Phoenix ID

broth. The suspension was adjusted to match a 0.5 MacFarland standard using the BD CrystalSpec nephelometer. Panels were auto-inoculated by pouring the ID suspension into the ID port of the panel. After closing, the panels were logged and loaded into the instrument. The instrument automatically incubated and optically scanned the panels at 20 min intervals. An ID result was considered final as soon as a probability of >90% was reached. PHX software version was 1.06.

MicroScan

Overnight panels were used for all testing. Prompt inoculation procedures were strictly followed. Panels were incubated and interpreted in the MicroScan WalkAway 40 system. The panels were additionally read visually to verify the results. MSC software version was 23.11-ISN.102 W/A 23.10-ISN.104.

Arbitration

If discrepancy was detected, additional testing was performed with the API system or in some cases with manual conventional tests (including serology for *Shigella* and *Salmonella*).

Table 1
Comparison of Phoenix (PHX) to MicroScan (MSC) for 191 gram-negative Strains

ID Name	ORG CODE	ID AGREEMENT			ID DISAGREEMENT		
		# Tested	PHX=MSC	%	#	PHX favored by Arbitration	MSC favored by Arbitration
<i>Aeromonas hydrophila</i> group ¹	AERMHYDGR	3	2	67%	1	1	
<i>Aeromonas sobria</i> ²	AERMVERS	1		0%	1	1	
<i>Citrobacter braakii</i> ³	CITBRA	3		0%	3	3	
<i>Citrobacter freundii</i>	CITFRE	4	4	100%			
<i>Citrobacter koseri</i>	CITKOS	9	9	100%			
<i>Enterobacter aerogenes</i>	ENTBAER	10	10	100%			
<i>Enterobacter cloacae</i>	ENTBCLO	19	19	100%			
<i>Escherichia coli</i>	ESCCOL	19	19	100%			
<i>Klebsiella oxytoca</i>	KLEOXY	15	15	100%			
<i>Klebsiella pneumoniae</i>	KLEPNEP	22	22	100%			
<i>Morganella morganii</i>	MORGMOR	17	17	100%			
<i>Proteus mirabilis</i>	PROTMIR	20	20	100%			
<i>Proteus vulgaris</i>	PROTVUL	4	4	100%			
<i>Providencia stuartii</i>	PROVSTU	5	5	100%			
<i>Salmonella</i> species	SALSPE	18	18	100%			
<i>Serratia liquefaciens</i>	SERLIQ	1		0%	1		1
<i>Serratia marcescens</i>	SERMAR	15	15	100%			
<i>Shigella flexneri</i> ⁴	SHIFLE	3	1	33%	2	2	
<i>Shigella sonnei</i>	SHISON	2	2	100%			
<i>Yersinia enterocolitica</i>	YERENT	1	1	100%			
Total		191	183	95.8%	8	7	1

Key:

*1 1 strain MSC ID = *V. fluvialis* (Genus level ID error)

*2 1 strain *Aeromonas* species in MSC - OK to the genus level ID

*3 *Citrobacter braakii* not in MSC database all identified in MSC as *C. freundii*

*4 1/2 MSC ID = *Shigella* species (OK genus level ID), the other strain MSC ID = *E. coli* (Genus level Error); Confirmed *Shigella* by serology

RESULTS

The results of the performance of the PHX system in comparison to MSC for clinical routine isolates and some stock cultures of gram-negative and gram-positive bacteria are shown in Tables 1 and 2. The concordance of PHX compared with MSC was 95.8% and 96.3% for each group, respectively:

- Of the 191 gram-negative strains the PHX and MSC systems coincided for 183 strains. Of the 8 discordant results 7 were arbitrated in favor of PHX and 1 was in favor of MSC. MSC identified 3 *C. braakii* as *C. freundii* probably because *C. braakii* is not in the MSC database. Of the 4 *Aeromonas* strains MSC correctly identified two isolates, one to the genus level and misidentified the other as a *Vibrio fluvialis*, while PHX correctly identified all 4. Of the 5 *Shigella* strains MSC

correctly identified three isolates, one to the genus level and misidentified the other as an *E. coli*, while PHX correctly identified all 5. The only *Serratia liquefaciens* included in this study was misidentified in Phoenix as a *S. marcescens*.

- Of the 136 gram-positive strains the PHX and MSC systems coincided for 130 strains. Of the 5 discordant results 3 were arbitrated in favor of PHX and 2 were in favor of MSC. MSC misidentified 3 clinically important Staphylococci and PHX misidentified two strains. A new PHX software version (containing revised algorithms to improve this issue) was used to retest the 2 misidentified strains, yielding correct identification in both cases.

Table 2
Comparison of Phoenix (PHX) to MicroScan (MSC) for 136 gram-negative Strains

ID Name	ORG CODE	ID AGREEMENT			ID DISAGREEMENT		
		# Tested	PHX=MSC	%	#	PHX favored by Arbitration	MSC favored by Arbitration
<i>Enterococcus casseliflavus/gallinarum</i> group	ENTCCASGAL	4	4	100%			
<i>Enterococcus faecalis</i>	ENTFAA	21	21	100%			
<i>Enterococcus faecium</i>	ENCTFAI	19	19	100%			
<i>Enterococcus hirae/avium</i> gp	ENTCHIRFAI	1	1	100%			
<i>Staphylococcus aureus</i>	STAAUE	17	17	100%			
<i>Staphylococcus aureus</i> Methicillin Resistant	STAAUEMR	10	10	100%			
<i>Staphylococcus epidermis</i>	STAEPI	18	18	100%			
<i>Staphylococcus haemolyticus</i> ¹	STAHAE	15	14	93%	1	1	
<i>Staphylococcus hominis</i>	STAHOM	1	1	100%			
<i>Staphylococcus lugdunensis</i> ²	STALUG	10	7	70%	3	2	1
<i>Staphylococcus saprophyticus</i> ³	STASAP	8	7	88%	1		1
<i>Staphylococcus sciuri</i>	STASCI	1	1	100%			
<i>Streptococcus agalactiae</i>	STRAGA	9	9	100%			
<i>Streptococcus pyogenes</i>	STRPYO	2	2	100%			
Total Enterococcus		45	45	100%	0	0	0
Total Staphylococcus		80	75	94%	5	3	2
Total Streptococcus		11	11	100%	0	0	0
Overall Total		136	131	96.3%	5	3	2

Key:

*1 1 strain MSC = *S. simulans*

*2 Strain 1: PHX = *S. lugdunensis* & MSC = *S. haemolyticus*. Strain 2: PHX = *S. Lugdunensis* & MSC = *S. hominis*. Strain 3: PHX = *S. haemolyticus* & MSC = *S. lugdunensis*

*3 1 strain PHX ID = *S. aureus*

CONCLUSIONS

For gram-negatives resolution of discrepancies raised the performance of PHX from 95.8% concordance with MSC to 99.5% including arbitration.

For gram-positives resolution of discrepancies raised the performance of PHX from 96.3% concordance with MSC to 98.5% including arbitration. PHX performance was further improved to 100% by re-running discrepant *Staphylococcus* isolates with the newer PHX software version 2.02.

The Phoenix Automated Microbiology System provides a high level of agreement to the MicroScan WalkAway System for identification of gram-negative and gram-positive clinical isolates.