

# Evaluation of Accelerate-Pheno™ system, an automated Identification and Phenotypic Antibiotic Susceptibility Testing (AST) in Hospital Universitario de la Princesa.

Zurita-Cruz, Nelly Daniela; Gómez-de-Frutos, Sara; Llorca, Laura; Fernández-Caso, Belén; Soler-Maniega, Tamara; De las Cuevas, Carmen; Cardeñoso, Laura.

## Background

The aim of this study was to evaluate the Accelerate-Pheno™ System (Accelerate Diagnostics, Inc.), a rapid and automated identification (ID) and phenotypic Antibiotic Susceptibility Testing (AST) system, comparing with ID by MALDI-TOF MS™ system (Bruker-Daltonics) directly from positive blood cultures (BC) and AST obtained by MicroScan™ Walkaway™ system (Beckman-Coulter)

## Material and methods

We selected 75 positives BC to evaluate the rapid ID obtained with Accelerate-Pheno™ System by Fluorescent *in situ* hybridization (FISH), comparing with ID by MALDI-TOF MS™ system (Bruker-Daltonics), both directly from positive BC. Results from both rapid identification methods were compared with our culture-based Gold Standard ID after 18-24 hours.

The rapid phenotypic AST with minimal inhibitory concentration (MIC) by Accelerate-Pheno™ System directly from 60 positive BC, 22% (n=13) Gram-positive cocci (12 *Staphylococcus* sp and 1 *Enterococcus* spp) and 78% (n=47) Gram-negative bacilli (44 enterobacteriaceae and 3 *P. aeruginosa*) were compared with MicroScan™ Walkaway™ system results, obtained subculture (gold standar), to analyze the categorical concordance.

	Total positive BC	Gold Standard ID MicroScan™ (%)	Accelerate-Pheno™ (%)	MALDI-TOF MS™ direct from BC (%)
Monomicrobial Bacteremia	70	70 (100)	65 (93)	61 (87)
Polymicrobial Bacteremia	5	5 (100)	4 (80)	0
Total positive Blood Cultures identification	75	75	69 (92)	61 (81)

Table 1) Identification results obtained by MALDI-TOF MS™ directly from BC and Accelerate-Pheno™ system

## Results

### Identification Concordance:

ID by Accelerate-Pheno™ system was succesfull for 92% (n=65) BC: In one case ID was not possible because the pathogen isolated (*Salmonella* sp) is not included in the ID panel. It is noteworthy that Accelerate-Pheno™ system was able to correctly identify the microorganisms isolated in 80% (n=4) of the polymicrobial bacteremia.

Identification by MALDI-TOF MS™ directly from BC was succesfull for 81% (n=61) of samples. None of polymicrobial bacteremia was successful identified.

The time required for identification was 1.5 h for both methods. Results are shown in Table 1.

### AST Categorical Concordance:

Comparison between AST by Accelerate-Pheno™ and MicroScan™ Walkaway™ system shown a Categorical Concordance of 97.5% for Gram-positive cocci and 90.4% for Gram-negative bacilli. Detailed results are shown in Table 2.

Results from the MicroScan™ Walkaway™ system were obtained in 36-48 h, while those from the Accelerate-Pheno™ System delayed just 7 h.

	Gram negative bacilli									
	AMG	CTX	PTZ	CFTZ	CFP	ETP	MPN	CIP	COL	
Categorical concordance (%)	44(93)	31(71)	43(92)	27(88)	45(96)	43(98)	45(96)	42(90)	9(90)	
Minor errors (%)	4(2,8)	0	0	2(6)	0	1(2)	0	3(6)	0	
Mayor errors (%)	2(1,4)	9(20)	1(2)	1(3)	1(2)	0	2(4)	1(2)	0	
Very mayor errors (%)	4(2,8)	4(9)	3(6)	1(3)	1(2)	0	0	1(2)	1(10)	
Saphylococcus aureus and coagulase-negative staphylococcus							Enterococcus sp			
	CFX	VAN	LZD	DPT	STX		AMP	VAN	LZD	
Categorical concordance (%)	8(89)	12(100)	9(100)	12(100)	11(92)		1(100)	1(100)	1(100)	
Minor errors (%)	0	0	0	0	0		0	0	0	
Mayor errors(%)	1(11)	0	0	0	9(82)		0	0	0	
Very mayor errors (%)	0	0	0	0	2(18)		0	0	0	

Table 2. Categorical Concordance between AST obtained by Accelerate-Pheno™ System and MicroScan™ Walkaway™ system. AMG (aminoglycosides); CTX (cefotaxime); PTZ (piperacillin/tazobactam) CFTZ (ceftazidime); CFP (cefepime); ETP (ertapenem); MPN (meropenem); CIP (ciprofloxacin); COL (colistin); CFX (cefoxitine); VAN (vancomycin); LZD (linezolid); DPT (daptomycin); STX (cotrimoxazole); AMP (ampicillin)

## Conclusion

The Accelerate-Pheno™ system shown good results identifying pathogens directly from positive BC, including polymicrobial bacteremia, in 1.5 h and offered a phenotypic AST with MIC in 7 h. Using this new technology, physicians could receive this information at least 28 hours early to optimize antimicrobial treatment for patients with severe BSI or sepsis.