



Evaluation of the Accelerate Pheno™ system for direct identification and antimicrobial susceptibility testing from positive blood cultures in bloodstream infections with Gram-negative pathogens

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Disclosure slide

Disclosure of speaker's interests

- Sponsorship or research funding²
- Fee or other (financial) payment³
- Shareholder⁴
- Other relationship, i.e. ...⁵

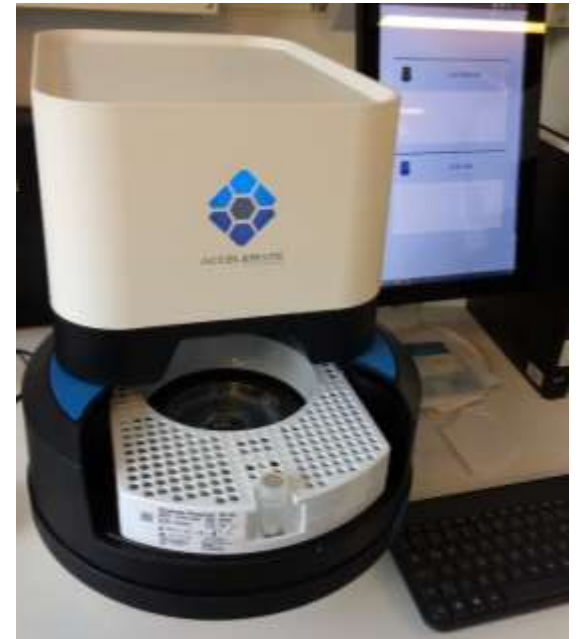
Study period: Accelerate Diagnostics, Inc., Tucson, Arizona, USA provided two systems and the reagents during the study period

Research funding

- DZIF: Deutsches Zentrum für Infektionsforschung (German Center for Infection Research)
- Medizinische Fakultät Tübingen, Germany

Introduction- Accelerate Pheno™ system

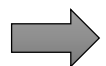
- Automated system for identification and AST from positive blood culture bottles
- Identification result approx. 90 minutes: fluorescence in situ hybridization with probes
- AST result approx. 5 hours: microscopic images of bacterial growth in the presence of the antimicrobial agent -> computed in individual growth curves -> MIC



1. Sample is added to sample vial
2. Cassette is loaded into the machine
3. Reagent cartridge is placed into the machine
4. System is started
5. One sample per system can be tested at a time

Accelerate PhenoTest™ AST panel– Gram-negatives

Identification	Ampicillin- Sulbactam	Piperacillin- Tazobactam	Cefepim	Ceftriaxone	Ertapenem	Meropenem	Amikacin	Gentamicin	Tobramicin	Ciprofloxacin	Colistin
<i>E. coli</i>	X	X	X	X	X	X	X	X	X	X	X
<i>Klebsiella spp.</i>		X	X	X	X	X	X	X	X	X	X
<i>Enterobacter spp.</i>		X	X	X	X	X	X	X	X	X	X
<i>Proteus spp.</i>		X	X	X	X	X	X	X	X	X	
<i>Citrobacter spp.</i>		X	X	X	X	X	X	X	X	X	X
<i>S. marcescens</i>		X	X	X	X	X	X	X	X	X	
<i>P. aeruginosa</i>		X	X			X	X	X	X	X	X
<i>A. baumannii</i>	X	X	X			X	X			X	X



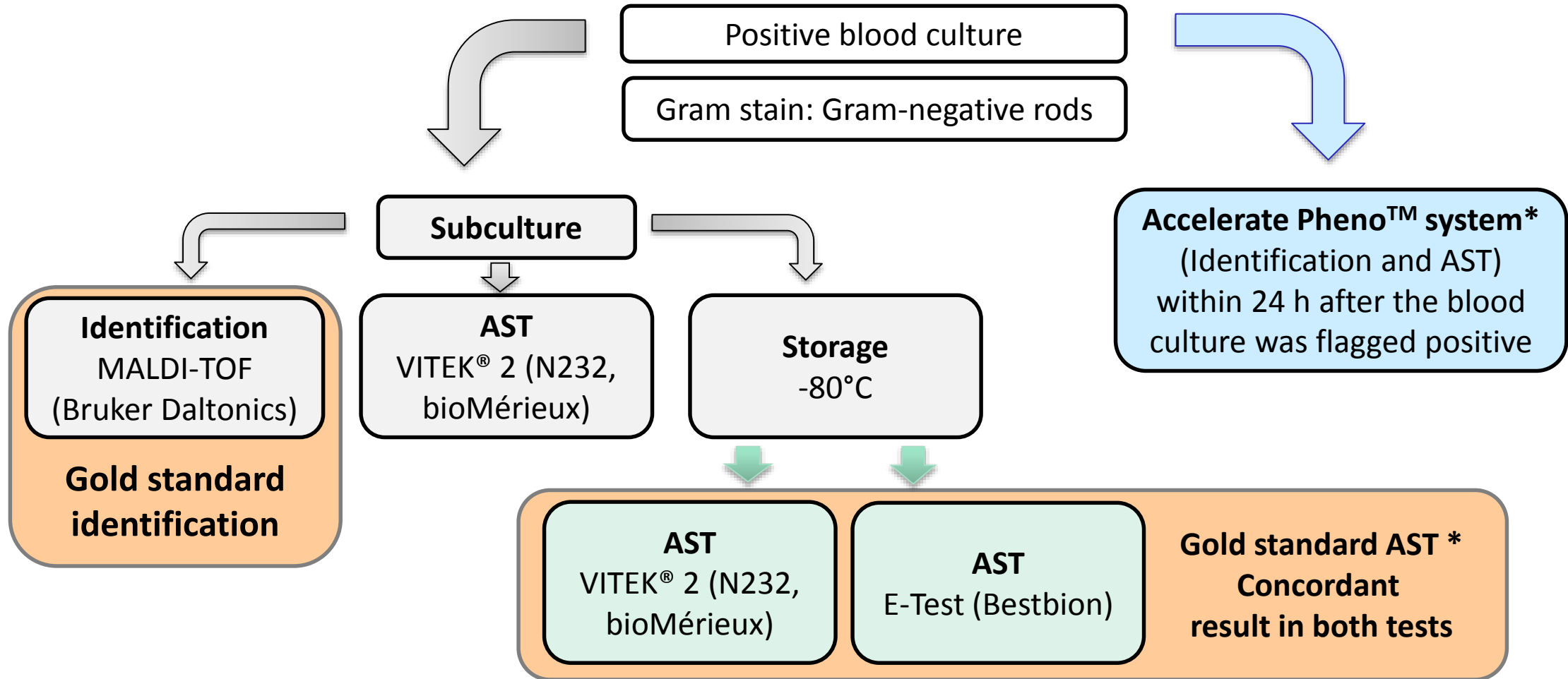
Ceftazidime and aztreonam are included in the new version

Background



- 1500-bed tertiary university hospital and a 340-bed trauma clinic located on same campus
 - Open 7 days per week; 7.30 AM – 5.30 PM; WE 7.30 – 4 PM
 - Low rate of Gram-positive resistant organisms (<1% MRSA; <1% VRE)
- > Focus: Gram-negative organisms

Design of the study



Results - Identification

- 115 Gram-negative blood culture samples were evaluated, including 10 polymicrobial samples
- Correct identification 102 of 115 Gram-negative organisms (88.7%) by the Accelerate Pheno™ system
- 10 organisms were not covered by the Accelerate Pheno™ system identification panel

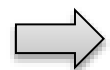
Culture identification (n)	Accelerate Pheno™ ID (n)	Comment
<i>Bacteroides fragilis</i> (3)	no identification (3)	not included in ID panel
<i>Hafnia alvei</i> (1)	no identification (1)	not included in ID panel
<i>Morganella morganii</i> (1)	no identification (1)	not included in ID panel
<i>Acinetobacter radioresistens</i> (1)	no identification (1)	not included in ID panel
<i>Sphingomonas paucimobilis</i> (1)	no identification (1)	not included in ID panel
<i>Moraxella nonliquefaciens</i> (1)	no identification (1)	not included in ID panel
<i>Rhizobium radiobacter</i> (1)	C. glabrata (1)	not included in ID panel, false identification
<i>Serratia rubidaea</i> (1)	S. marcescens (1)	not included in ID panel, false identification
<i>Escherichia coli</i> (1)	E. coli, Klebsiella species (1)	false identification
<i>Klebsiella pneumoniae</i> (2)	no identification (2)	no identification, no AST



In total 102 of 105 (97.1%) correct identifications of organisms included in the panel

Results – Polymicrobial blood stream infections

Culture identification (n)	Accelerate Pheno™ ID (n)	Comment
<i>P. aeruginosa, C. krusei</i>	<i>P. aeruginosa, S. aureus</i>	
<i>E. coli, S. simulans, S. hominis</i>	<i>E. coli</i>	
<i>C. freundii, E. faecalis</i>	<i>Citrobacter species</i>	
<i>E. coli, P. vulgaris, C. freundii</i>	<i>E. coli, Proteus species, Citrobacter species</i>	no AST
<i>S. marcescens, E. faecalis</i>	<i>S. marcescens</i>	
<i>K. pneumoniae, E. faecalis</i>	<i>Klebsiella species, E. faecalis</i>	no AST
<i>E. coli, K. pneumoniae, K. oxytoca, S. lutetiensis</i>	<i>E. coli, Klebsiella species</i>	no AST
<i>K. pneumoniae, E. faecalis</i>	<i>Klebsiella species</i>	
<i>K. pneumoniae, E. coli, E. faecalis, E. casseliflavus</i>	<i>Klebsiella species, E. coli, E. faecalis</i>	no AST
<i>E. coli, E. faecalis</i>	<i>E. coli</i>	



All Gram-negative bacteria were correctly identified in polymicrobial BSI

Results - AST

- AST available for 95/ 104 (91.3 %) strains in which a Gram-negative bacterium was identified by the Accelerate Pheno™ system

Antimicrobial agent	No. of AST results	Category agreement n			Susceptible	Resistant	Discrepancies
		S	R/I	Total (%)			
SAM	66	31	32	63 (95.5)	34	32	3 major
TZP	91	78	6	84 (92.3)	85	6	7 major
FEP	90	73	6/1*	80 (88.9)	83	6/1*	7 minor, 3 major
CRO	85	75	8	83 (97.6)	77	8	2 major
ETP	85	85	0	85 (100)	85	0	-
MEM	94	91	2	93 (98.9)	91	3	-
AMK	95	91	2	93 (97.9)	92	3	1 very major
GEN	94	84	9	93 (98.9)	85	9	1 major
TOB	94	82	10	92 (97.9)	84	10	1 minor, 1 major
CIP	94	69	21	90 (95.7)	73	21	4 minor
CST	88	85	0	85 (96.6)	88	0	3 major
total	976	844	97	941 (96.4)	876	100	14 minor, 20 major, 1 very major

Minor:

S/I, I/R

Major:

False R

(instead of S)

Very major:

False S

(instead of R)



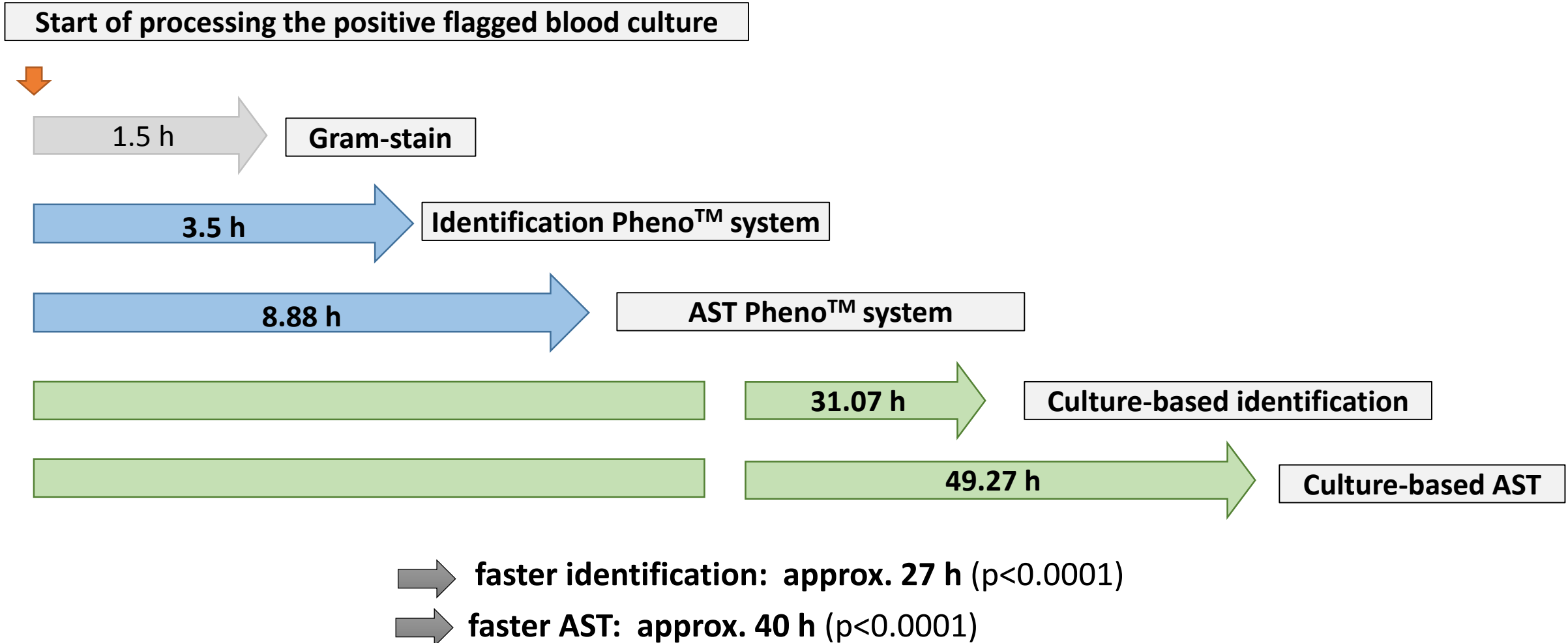
Category agreement 96.4% of AST measurements

Marschal et al. JCM, in press

Results –MDR *P. aeruginosa*

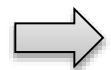
Organism		TZP		FEP		MEM		AMK		GEN		TOB		CIP		CST	
<i>P. aeruginosa</i>	Accelerate	128	R	32	R	>=16	R	>=128	R	>=32	R	>=32	R	>=8	R	<=0,5	S
	E-Test	>256	R	96	R	>32	R	24	R	>256	R	>256	R	>32	R	2	S
<i>P. aeruginosa</i>	Accelerate	128	R	32	R	4	I	<=4	S	16	R	16	R	>=8	R	<=0,5	S
	E-Test	>256	R	>256	R	>32	R	16	I	>256	R	>256	R	>32	R	1,5	S
<i>P. aeruginosa</i>	Accelerate	128	R	32	R	>=16	R	>=128	R	16	R	>=32	R	>=8	R	<=0,5	S
	E-Test	12	S	24	R	>32	R	24	R	16	R	24	R	>32	R	0,75	S

Median time to result



Conclusion

- Accelerate Pheno™ system was easy to perform with little hands-on time, however no high through-put possible at the moment
- Correct identification was obtained for 97.1% Gram-negative organisms included in the panel, 88.7% for the all samples
- For the AST 96.3 % of category agreement was observed
- Reduction in time to result
- Further studies are needed to evaluate the clinical impact in different settings



Valuable tool for rapid blood culture diagnostics for selected patients

Thank you for your attention



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**Matthias Marschal
Johanna Bachmeier
Philipp Oberhettinger
Matthias Willmann
Ingo Autenrieth
&
Diagnostic Team**