Analytical Performance of the Automated Accelerate Arc™ BC kit and Module for Direct Identification from Positive Blood Cultures using MALDI

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BACKGROUND

When treating sepsis, timely identification (ID) is essential to begin targeting appropriate antimicrobial therapy for the causative pathogen. The Accelerate Arc™ BC kit and module is a fully automated solution for cleaning up positive blood culture samples to enable direct identification using matrix-assisted laser desorption ionization (MALDI). This study assessed performance (reportability and accuracy) of the Accelerate Arc™ BC kit (under development) and module for 20 of the most prevalent species isolated from positive blood cultures using MALDI analysis.

METHODS

- A total of 100 isolates (Table 1) were seeded into BD Bactec™ Plus Aerobic blood culture bottles (Becton Dickinson, BD) and incubated on the BD Bactec™ FX blood culture monitoring system.
- After flagging positive, samples were processed on the Accelerate Arc™ BC kit and module (Arc) at 30 min and 60 min time post-positive (TPP) to simulate a typical clinical laboratory workflow.
- 1 µL of Accelerate Arc™-processed sample was spotted in triplicate for MALDI analysis by both the Bruker Biotyper™ (BD) and Vitek® MS (bioMérieux) systems. Gram-positive samples received 1 µL of formic acid prior to addition of matrix, while gram-negative samples received only matrix.
- Growth from the positive blood culture bottle was used to perform conventional MALDI using the Bruker Biotyper ™ (e.g., from colony growth) as the comparator.
- Reportability was defined as a sample that had at least 1 of 3 spots that resulted in an ID; if >1 spots gave an ID, they had to agree to be considered reportable (Bruker Biotyper ™ = a score of ≥ 1.7; Vitek® MS = any ID).
- Accuracy was defined as ≥1 spot that resulted in an ID for a reportable sample that was in agreement with conventional MALDI ID.

Figure 1. Workflow

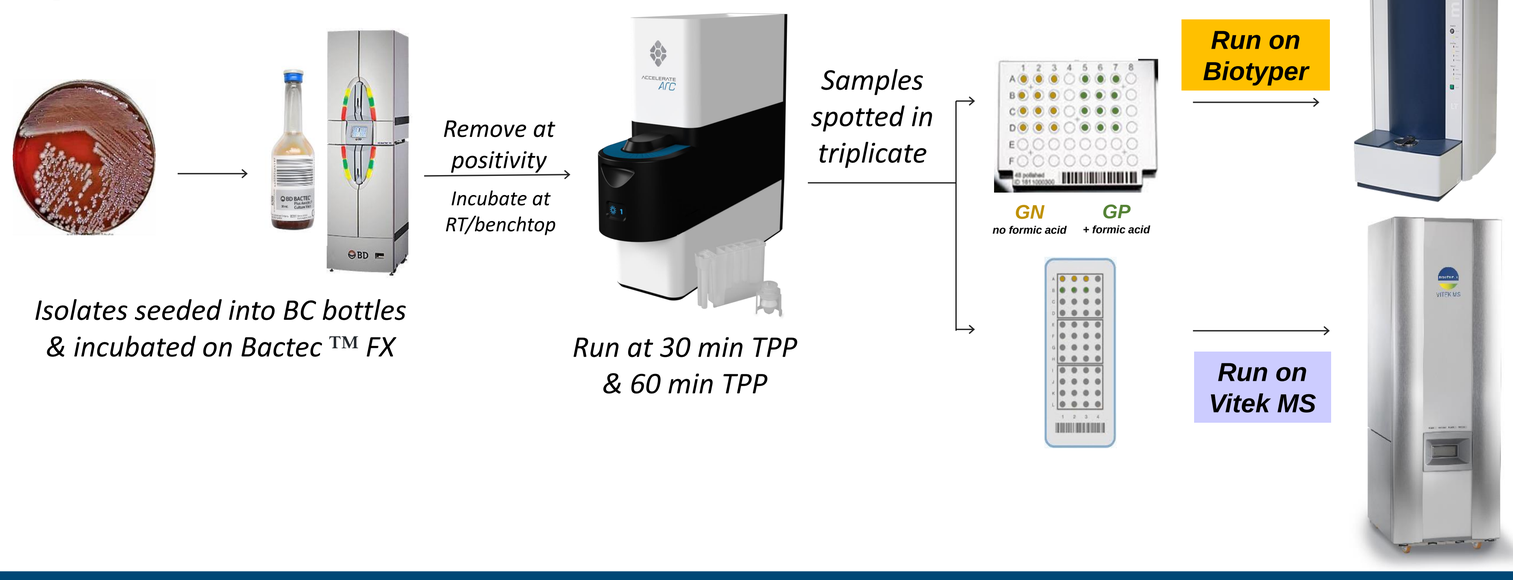

Table 1. List of organisms tested

	Species	# Tested
Gram negative	*Acinetobacter baumannii*	5
	Citrobacter freundii	6
	Citrobacter koseri	4
	Enterobacter cloacae complex	5
	Escherichia coli	6
	Klebsiella aerogenes	5
	Klebsiella oxytoca	5
	Klebsiella pneumoniae	5
	Pseudomonas aeruginosa	6
	Proteus mirabilis	5
	Proteus vulgaris	5
	Serratia marcescens	5
Gram positive	*Enterococcus faecalis*	5
	Enterococcus faecium	5
	Staphylococcus aureus	6
	Staphylococcus epidermidis	6
	Staphylococcus lugdunensis	4
	Streptococcus agalactiae	4
	Streptococcus pneumoniae	4
	Streptococcus pyogenes	4

RESULTS & CONCLUSIONS

Table 2. Reportability and Accuracy by Organism Group[1]

Organism Group	Bruker Biotyper™		Vitek® MS	
	Reportability	Accuracy	Reportability	Accuracy
Gram-negative (n=12 species)	*94%* (116/124)	*100%* (116/116)	*67%* (83/124)	*92%* (76/83)
Gram-positive (n=8 species)	*79%* (60/76)	*100%* (60/60)	*71%* (54/76)	*98%* (53/54)
All organisms (n=20 species)	*88%* (176/200)	*100%* (176/176)	*69%* (137/200)	*94%* (129/137)

[1]Data is combined from 30 m & 60 m TPP runs

Table 3. Reportability and Accuracy by Species[1]

Organism		Bruker Biotyper™		Vitek® MS	
		Reportability	Accuracy	Reportability	Accuracy
Gram negative	*E. coli*[2]	*100%*	*100%*	*83%*	*100%*
	E. cloacae	*100%*	*100%*	*90%*	*89%*
	K. pneumoniae[2]	*100%*	*100%*	*100%*	*100%*
	K. oxytoca	*100%*	*100%*	*60%*	*100%*
	P. mirabilis	*100%*	*100%*	*90%*	*100%*
	P. vulgaris	*100%*	*100%*	*30%*	*66%*
	C. freundii	*92%*	*100%*	*30%*	*67%*
	A. baumannii	*90%*	*100%*	*40%*	*100%*
	K. aerogenes	*90%*	*100%*	*100%*	*83%*
	C. koseri	*88%*	*100%*	*40%*	*75%*
	P. aeruginosa[2]	*83%*	*100%*	*92%*	*100%*
	S. marcescens	*80%*	*100%*	*40%*	*100%*
Gram positive	*S. epidermidis*[2]	*100%*	*100%*	*100%*	*100%*
	S. agalactiae	*100%*	*100%*	*80%*	*100%*
	E. faecium[2]	*90%*	*100%*	*100%*	*100%*
	S. aureus[2]	*83%*	*100%*	*83%*	*100%*
	E. faecalis	*80%*	*100%*	*80%*	*100%*
	S. pyogenes	*75%*	*100%*	*13%*	*100%*
	S. lugdunensis	*50%*	*100%*	*38%*	*100%*
	S. pneumoniae	*35%*	*100%*	*50%*	*67%*

[1]Data is combined from 30 m & 60 m TPP runs; [2]6 most common bloodstream pathogens in original abstract data

- Overall, Arc-processed samples enabled robust reportability and accuracy for 20 bloodstream pathogens on the Bruker Biotyper and Vitek MS systems.
  - Combined reportability across all tested organisms (n=20) was lower for Vitek MS compared to the original data for the 6 most common bloodstream pathogens. This was primarily due to the addition of streptococci and less prevalent gram-negative bacilli (e.g. *P. vulgaris* and *Citrobacter* spp.). Another possibility is instability of some samples post-spotting due to a limitation in the study design where Vitek MS slides were run at an off-site laboratory. However, this would need to be investigated further to rule this out.
  - Out of 200 runs, 2 (1%) had to be repeated due to a technical failure with the instrument.
  - This study was designed to test an equal number of isolates for each of the 20 species evaluated. As a result, overall reportability may vary depending on actual organism prevalence.
- Compared to conventional MALDI, Arc-processed samples had overall agreement of 100% on the Bruker Biotyper and 94% on the Vitek MS.
  - Inaccurate calls on the Vitek MS were either inaccurate to species level but accurate to genus level (e.g. *C. freundii* called as *C. braakii*) or could be mitigated by correlation with gram stain (e.g., *E. cloacae* complex called as *S. capitis*) (data not shown).

ACKNOWLEDGEMENTS

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Accelerate Arc™ module is US-IVD and the BC kit is currently US-RUO