

Abstract

Background: Prompt initiation of appropriate antimicrobial therapy of septicemia is associated with improved patient outcomes. Identification and susceptibility testing using conventional methods requires 24 to 72 h. The FilmArray (Biofire) blood culture identification panel (BCID) is a completely automated, high-order multiplex, nested PCR designed to identify 19 bacteria, 5 *Candida* spp. and 4 antibiotic resistance genes (*mecA*, *vanA/B*, and *KPC*) within 1 h directly from positive blood culture bottles. **Methods:** We evaluated the performance of the BCID with 213 consecutive positive blood cultures collected from 178 adult patients. The BCID panel results were available within 2 h of blood culture positivity. The accuracy and time to identification with the BCID panel was compared with the results obtained with conventional MicroScan (Siemens Healthcare) Gram-negative, and Gram-positive combination identification and susceptibility test panels performed on subcultures from positive blood cultures. **Results:** Overall there were 189 monomicrobial positive cultures included in the analysis. BCID provided the correct genus and species for 44 (69%), correct family (*Enterobacteriaceae*) for 7 (11%) and no identification for 13 (20%) (12 not in panel) gram-negative rods. BCID provided the correct genus and species in 48 (47%), correct genus (*Enterococcus* or *Streptococcus* spp.) in 33 (33%) and no identification in 20 (20%) (19 not in panel) gram-positive organisms. BCID provided the correct identification for 23 (96%) of 24 *Candida* spp. There were 27 cultures in which *mecA* was detected by both BCID and conventional methods and 2 in which *mecA* was detected by BCID alone. *VanA/B* was detected in 8 cultures by both methods and 1 in which *vanA/B* was detected by BCID alone. Only one culture contained the *KPC* gene and it was detected by both methods. Mean times from blood culture receipt to identification by BCID and conventional methods were 27 h and 50 h, respectively. There was agreement between BCID and conventional methods for identification in 14 (58%) of 24 polymicrobial cultures. Conventional methods failed to identify 1 organism in 4 and BCID failed to identify ≥1 organism in 7 (5 not in panel) polymicrobial cultures. **Conclusions:** The BCID panel provided rapid, reliable, and clinically actionable results in 82.3% of our positive blood cultures.

Background

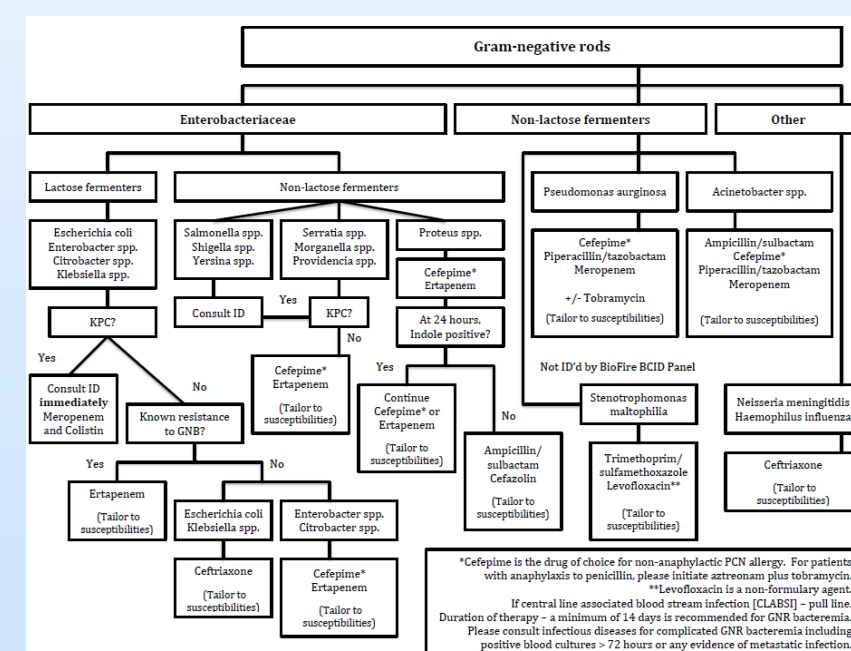
Prompt initiation of appropriate antimicrobial therapy of septicemia is associated with improved patient outcomes. Identification and susceptibility testing using conventional methods requires 24 to 72 h. The FilmArray (Biofire) blood culture identification panel (BCID) is a completely automated, high-order multiplex, nested PCR designed to identify 19 bacteria, 5 *Candida* spp. and 4 antibiotic resistance genes (*mecA*, *vanA/B*, and *KPC*) within 1 h directly from positive blood culture bottles (1, 2).

Methods

We evaluated the performance of the BCID with 213 consecutive positive blood cultures (bioMérieux standard aerobic and anaerobic bottles) collected from 178 adult patients. The BCID panel results were available within 2 h of blood culture positivity around the clock. BCID panel results were called to clinicians with the Gram stain results. A link to pathogen-specific treatment algorithms developed by our Antimicrobial Stewardship program was available to all clinicians in the electronic medical record. See example below. In addition, BCID results were used by an infectious disease pharmacist to assess appropriateness of therapy and recommend changes if needed.

The accuracy and time to identification with the BCID panel was compared with the results obtained with conventional MicroScan (Siemens Healthcare) Gram-negative, and Gram-positive combination identification and susceptibility test panels performed on subcultures from positive blood cultures. The only other rapid identification and susceptibility test methods deployed at the time were direct tube coagulase and subcultures to MRSA chromogenic medium for gram positive cocci in clusters. The comparator methods for *Candida* spp. included *C. albicans* screen, rapid trehalose assimilation and RapID Yeast Plus tests (Remel) and morphology on corn meal agar as appropriate.

Gram Negative Rod Treatment Algorithm



Results

Identification	CM+/BCID+	CM+/BCID-	CM-/BCID+
Gram negative			
<i>E. coli</i>	19	0	0
<i>K. pneumoniae</i>	11	0	0
<i>P. aeruginosa</i>	7	0	0
<i>E. cloacae</i>	4	1	0
<i>P. mirabilis</i>	3	0	0
<i>A. baumannii</i>	2	0	0
<i>C. freundii</i>	1	0	0
<i>C. koseri</i>	1	0	0
<i>E. gergoviae</i>	1	0	0
<i>H. influenzae</i>	1	0	0
<i>S. typhimurium</i>	1	0	0
Subtotal	51	1	0

Identification	CM+/BCID+	CM+/BCID-	CM-/BCID+
Gram positive			
<i>S. aureus</i>	26	0	0
<i>Enterococcus</i> spp.	18	0	0
Coagulase-negative staphylococci	12	0	0
Alpha-hemolytic streptococci	6	0	0
<i>S. pneumoniae</i>	5	0	0
<i>S. pyogenes</i>	3	0	0
<i>S. agalactiae</i>	2	0	0
Microaerophilic streptococci (A/C/I)	2	1	0
<i>Streptococcus</i> , Group G	2	0	0
<i>S. mitis</i>	2	0	0
<i>S. bovis</i>	1	0	0
<i>S. salivarius</i>	1	0	0
<i>S. lugdunensis</i>	1	0	0
Subtotal	81	1	0

Identification	CM+/BCID+	CM+/BCID-	CM-/BCID+
Yeast			
<i>C. albicans</i>	17	0	0
<i>C. glabrata</i>	5	1	0
<i>C. parapsilosis</i>	1	0	0
Subtotal	23	1	0

Identification	CM+/BCID-
Gram positive not in BCID panel	
<i>Micrococcus</i> spp.	8
<i>Aerococcus</i> spp.	3
<i>Bacillus</i> spp.	3
<i>Granulicatella</i> sp.	1
<i>Corynebacterium</i> sp.	1
<i>Clostridium</i> sp.	1
<i>Weissella confusa</i>	1
<i>Lactobacillus</i> sp.	1
Subtotal	19

Identification	CM+/BCID-
Gram negative not in BCID panel	
<i>Acinetobacter lwoffii</i>	3
<i>Alcaligenes</i> sp.	1
<i>Burkholderia cepacia</i>	2
<i>Stenotrophomonas maltophilia</i>	1
<i>Fusobacterium nucleatum</i>	1
<i>Morganella morganii</i>	1
<i>Moraxella catharralis</i>	1
<i>Neisseria</i> spp.	2
Subtotal	12

Resistance Gene	CM+/BCID+	CM+/BCID-	CM-/BCID+	CM-/BCID-
<i>mecA</i>	27	0	2 (CNS)	13
<i>vanA/vanB</i>	8	0	1	9
<i>KPC</i>	1	0	0	49

Key to Tables

CM, Conventional methods; Red, Only genus or family level identification provided by BCID

Identification	Polymicrobial Cultures	
	Detected by:	
	CM	BCID
VRE, <i>P. aeruginosa</i>	1, 1	1, 1
<i>Enterococcus</i> , AHS, NHS, <i>P. aeruginosa</i>	0, 1, 1, 1	1, 1, 1, 1
MRSA, <i>Bacillus</i> sp., <i>E. coli</i> , <i>H. influenzae</i> , <i>Corynebacterium</i> sp., AHS	1, 1, 1, 0, 1, 1	1, X, 1, 1, X, 1
<i>Enterococcus</i> , <i>E. coli</i>	1, 1	1, 1
<i>C. glabrata</i> , CNS	1, 1	1, 1
<i>Abiotrophia</i> sp., AHS	1, 1	X, 0
AHS, NHS	1, 1	1, 1
<i>K. pneumoniae</i> , <i>P. aeruginosa</i>	1, 0	1, 1
<i>C. albicans</i> , <i>C. glabrata</i>	1, 1	1, 1
VRE, MRSA, <i>P. aeruginosa</i> , <i>C. glabrata</i> , <i>C. albicans</i> , AHS	1, 1, 1, 1, 1	1, 1, 1, 1, 1
<i>P. mirabilis</i> , <i>Lactobacillus</i> sp.	1, 1	1, X
<i>K. pneumoniae</i> , <i>S. marcescens</i>	1, 1	1, 1
<i>Enterococcus</i> , <i>S. pneumoniae</i>	1, 0	1, 1
<i>B. fragilis</i> , <i>Peptostreptococcus</i> sp.	1, 1	X, X
<i>A. lwoffii</i> , <i>Corynebacterium</i> sp.	1, 1	X, X
<i>C. parapsilosis</i> , CNS	1, 1	1, 1
NHS, AHS	1, 1	1, 1
<i>Enterococcus</i> , CNS, <i>C. glabrata</i>	1, 1, 1	1, 1, 1
<i>Enterococcus</i> , <i>E. gergoviae</i>	1, 1	1, 1
<i>K. pneumoniae</i> , <i>P. mirabilis</i> , <i>S. marcescens</i>	1, 1, 1	1, 1, 1
CNS, <i>Enterococcus</i>	1, 1	1, 0
<i>Enterococcus</i> , <i>Corynebacterium</i> sp.	1, 1	1, X
MRSA, <i>E. coli</i> , <i>P. mirabilis</i>	1, 1, 1	1, 1, 1
MSSA, <i>S. pneumoniae</i>	1, 1	1, 1
Subtotal	24	24

Key: 1, detected; 0, not detected; and X, not in BCID panel

Results Summary

Overall there were 189 monomicrobial positive cultures included in the analysis. BCID provided the correct genus and species for 44 (69%), correct family (*Enterobacteriaceae*) for 7 (11%) and no identification for 13 (20%) (12 not in panel) gram-negative rods. BCID provided the correct genus and species in 48 (47%), correct genus (*Enterococcus* or *Streptococcus* spp.) in 33 (33%) and no identification in 20 (20%) (19 not in panel) gram-positive organisms. BCID provided the correct identification for 23 (96%) of 24 *Candida* spp. There were 27 cultures in which *mecA* was detected by both BCID and conventional methods and 2 in which *mecA* was detected by BCID alone. *VanA/B* was detected in 8 cultures by both methods and 1 in which *vanA/B* was detected by BCID alone. Only one culture contained the *KPC* gene and it was detected by both methods. Mean times from blood culture receipt to identification by BCID and conventional methods were 27 h and 50 h, respectively. There was agreement between BCID and conventional methods for identification in 14 (58%) of 24 polymicrobial cultures. Conventional methods failed to identify 1 organism in 4 and BCID failed to identify ≥1 organism in 7 (5 not in panel) polymicrobial cultures.

Conclusions

The BCID panel provided rapid, reliable, and clinically actionable results in 82.3% of our positive blood cultures. The ease of use, speed, and comprehensive coverage of pathogens and inclusion of key antibiotic resistance genes offer great opportunities for laboratories to provide information that will positively impact patient care.

References

- Blaschke AJ et al. 2012. Rapid identification of pathogens from positive blood cultures by multiplex polymerase chain reaction using the FilmArray system. *Diag. Microbiol. Inf. Dis.* 74:349-355.
- Altun O, Almuhayawi M, Ulberg M, Ozenci V. 2013. Clinical evaluation of the FilmArray blood culture identification panel in identification of bacteria and yeasts from positive blood culture bottles. *J. Clin. Microbiol.* 51:4130-4136.