

**Guide to Interpretation of BioFire FilmArray Blood Culture Identification (BCID) Panel**  
**Antimicrobial Stewardship Program, VA Greater Los Angeles Healthcare System**  
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**Introduction:**

The microbiology laboratory is implementing the BioFire FilmArray Blood Culture Identification (BCID) system in order to provide preliminary identification of bloodstream pathogens within an hour of blood cultures turning positive. It is important to note that this system only provides preliminary identification of the organism present and whether or not any of three resistance genes are present; **it does NOT provide antimicrobial susceptibility NOR does it capture all mechanisms of antimicrobial resistance.**

Antimicrobial resistance testing is still performed via standard methodology and can take up to 96 hours to be completed. Certain infections are frequently polymicrobial in nature and the isolation of a single pathogen from the blood culture, while allowing narrowing of therapy, should not result in over-narrowing. Some specific examples of this would include complicated intra-abdominal infections and diabetic foot infections. These infections often involve anaerobes and therapy active against these should generally be included until definitive cultures of the site of infection have returned.

**Table 1: Organism species and antibiotic resistance reported by BioFire FilmArray BCID2 panel:**

Gram+ Bacteria	Gram– Bacteria
<i>Enterococcus faecalis</i>	<i>Acinetobacter baumannii</i>
<i>Enterococcus faecium</i>	<i>Bacteroides fragilis</i>
<i>Listeria monocytogenes</i>	<i>Haemophilus influenzae</i>
<i>Staphylococcus</i>	<i>Neisseria meningitidis</i>
<i>Staphylococcus aureus</i>	<i>Pseudomonas aeruginosa</i>
<i>Staphylococcus epidermidis</i>	Enterobacteriaceae
<i>Staphylococcus lugdunensis</i>	<i>Enterobacter cloacae</i> complex
<i>Streptococcus</i>	<i>Escherichia coli</i>
<i>Streptococcus agalactiae</i>	<i>Klebsiella aerogenes</i>
<i>Streptococcus pyogenes</i>	<i>Klebsiella oxytoca</i>
<i>Streptococcus pneumoniae</i>	<i>Klebsiella pneumoniae</i>
	<i>Proteus</i>
	<i>Salmonella</i>
	<i>Serratia marcescens</i>
	<i>Stenotrophomonas maltophilia</i>
Yeast	Antibiotic Resistance
<i>Candida albicans</i>	<i>mecA/C</i> and MREJ - methicillin resistance

<i>Candida auris</i>	<i>vanA/B</i> - vancomycin resistance
<i>Candida glabrata</i>	IMP, KPC, OXA-48-like, NDM, VIM -
<i>Candida krusei</i>	carbapenem resistance
<i>Candida parapsilosis</i>	<i>mcr-1</i> – colistin resistance
<i>Candida tropicalis</i>	CTX-M – extended-spectrum beta-lactamase
<i>Cryptococcus neoformans/gattii</i>	(most common ESBL gene)

Based on the combination of species identification and presence of antibiotic resistance genes identified above, the GLA Infectious Diseases Section recommends the following empiric therapy (Table 2).

Please note that organisms are listed in alphabetic order, with the exception of all of the *Enterobacteriaceae*, which are listed together. The bacterial family of *Enterobacteriaceae* consists of *E. coli*, *Klebsiella*, *Enterobacter*, *Proteus*, *Serratia* and other related Gram-negative bacteria that can be a part of gut flora. While the BCID panel contains specific primers for *E. coli*, *E. cloacae*, *K. oxytoca*, *K. pneumoniae*, *Proteus*, and *S. marcescens*, the less-specific *Enterobacteriaceae* probe is designed to detect less common species within the family. The antibiotic recommendation is the same whether a specific species probe is positive or just the nonspecific *Enterobacteriaceae* probe.

Similarly, The *Staphylococcus* genus PCR detects many, but not all species of staphylococci including *S. aureus*, *S. epidermidis*, *S. hominis* and others. When *S. aureus* is present, the *Staphylococcus* genus and *S. aureus* species will both be identified, but when a coagulase-negative staphylococcus such as *S. epidermidis* is present, only the *Staphylococcus* genus will be identified.

Recommendations for some species are dependent on whether certain resistance genes are present:

- The *mecA/C* genes confer resistance to oxacillin. However, for oxacillin resistance to be detected in *S. aureus* (MRSA), both the *mecA/C* gene and the MREJ target (which detects where the gene carrying *mecA/C* integrates into the *S. aureus* genome) need to be detected. The *mecA/C* gene target result is reported when *S. epidermidis* and *S. lugdunensis* are detected. HOWEVER, *mecA/C* is NOT reported when only the *Staphylococcus* target is detected without any other species-specific markers (consistent with less common coagulase-negative staphylococci such as *S. capitis*, *S. hominis*, etc.). It should be noted that >70% of coagulase-negative staphylococci are resistant to oxacillin, so these strains should be presumed to be resistant until susceptibilities return.
- The presence of *vanA/B* indicates resistance to vancomycin. The BCID2 panel only reports *vanA/B* results when *Enterococcus* spp. are found. The GLA Infectious Diseases section recommends empiric therapy with daptomycin for infections when *vanA* or *vanB* (*vanA/B*) positive results are obtained.
- The presence of carbapenemases generally confer resistance to all carbapenems.

At the end of Table 2 are suggestions for empiric therapy when the standard blood culture is positive yet the species-specific BCID assays are negative, based on whether or not a Gram-positive bacterium,

Gram-negative bacterium, yeast, or mold is identified (according to antibiotic resistance detected where relevant).

PLEASE NOTE that this chart should NOT replace clinical judgment, and the Infectious Diseases Consult Service (UCLA virtual pager 89321) is available for further assistance in interpretation. Therapy should be modified when final susceptibility results are available.

**Table 2: Suggested antimicrobial therapy (pending susceptibilities) for organisms identified**

<b><u>Organism Identification by BCID</u></b> <i>(with relevant antibiotic resistance gene results)</i>	<b><u>Suggested therapy pending susceptibilities</u></b> <i>(assuming normal renal function)</i>	<b><u>Comments</u></b>
<b><i>Acinetobacter baumannii</i></b>	Ampicillin-sulbactam 3g IV q4h PLUS minocycline 200mg IV q12h	Mandatory ID consult
<b><i>Bacteroides fragilis</i></b>	Metronidazole, a carbapenem, or beta-lactam/beta-lactamase inhibitor depending on clinical situation	Consider ID consult
<b><i>Candida albicans</i></b>	Micafungin 100mg IV q24h if critically ill or recent azole exposure; otherwise fluconazole 800mg IV x1, then 400mg IV q24h	Mandatory ID consult
<b><i>Candida auris</i></b>	Consult ID	Mandatory ID consult
<b><i>Candida glabrata</i></b>	Micafungin 100mg IV q24h	Mandatory ID consult
<b><i>Candida krusei</i></b>	Micafungin 100mg IV q24h	Mandatory ID consult
<b><i>Candida parapsilosis</i></b>	Fluconazole 800mg IV x1, then 400mg IV q24h	Mandatory ID consult
<b><i>Candida tropicalis</i></b>	Fluconazole 800mg IV x1, then 400mg IV q24h	Mandatory ID consult
<b><i>Cryptococcus neoformans/gattii</i></b>	Consult ID	Mandatory ID consult
<b><i>Enterobacteriaceae AND/OR Escherichia coli, Enterobacter cloacae complex, Klebsiella spp, Proteus, Salmonella, Serratia marcescens</i></b> <b>CARBAPENEMASE NEGATIVE</b>	Ertapenem 1gm IV q24h	Consider ID Consult

<b><i>Enterobacteriaceae</i> AND/OR <i>Escherichia coli</i>, <i>Enterobacter cloacae</i> complex, <i>Klebsiella</i> spp, <i>Proteus</i>, <i>Salmonella</i>, <i>Serratia marcescens</i> KPC, OXA-48-LIKE POSITIVE</b>	Ceftazidime-avibactam 2.5g IV q8h	Mandatory ID consult
<b><i>Enterobacteriaceae</i> AND/OR <i>Escherichia coli</i>, <i>Enterobacter cloacae</i> complex, <i>Klebsiella</i> spp, <i>Proteus</i>, <i>Salmonella</i>, <i>Serratia marcescens</i> NDM, VIM, IMP POSITIVE</b>	CONSULT INFECTIOUS DISEASES	Mandatory ID consult
<b><i>Enterococcus</i> spp: <i>vanA/B</i> NEGATIVE <i>vanA/B</i> POSITIVE</b>	Vancomycin IV (trough 15-20) Daptomycin 8-10 mg/kg IV q24h	Consult ID Consult ID
<b><i>Haemophilus influenzae</i></b>	Ceftriaxone 2gm IV q24h	
<b><i>Listeria monocytogenes</i></b>	Ampicillin 2gm IV q4h	Consult ID
<b><i>Neisseria meningitidis</i></b>	Ceftriaxone 2gm IV q12h	Consult ID
<b><i>Pseudomonas aeruginosa</i></b>	CONSULT INFECTIOUS DISEASES	Mandatory ID consult
<b><i>Stenotrophomonas maltophilia</i></b>	Trimethoprim-sulfamethoxazole 5 mg/kg IV q12h (dosed according to trimethoprim component) PLUS levofloxacin 750mg IV q24h	Mandatory ID consult
<b><i>Staphylococcus</i> genus AND POSITIVE <i>S. aureus</i> species result <i>mecA/C</i> + MREJ NEG <i>mecA/C</i> + MREJ POS</b>	Oxacillin 2gm IV q4h Vancomycin IV (trough 15-20)	MSSA (mandatory ID consult) MRSA (mandatory ID consult)
<b><i>Staphylococcus</i> genus AND POSITIVE <i>S. lugdunensis</i> species result <i>mecA/C</i> NEGATIVE <i>mecA/C</i> POSITIVE</b>	Oxacillin 2gm IV q4h Vancomycin IV (trough 15-20)	Consult ID: <i>S. lugdunensis</i> is rarely a contaminant
<b><i>Staphylococcus</i> genus AND POSITIVE <i>S. epidermidis</i> species result <i>mecA/C</i> NEGATIVE <i>mecA/C</i> POSITIVE</b>	SEE COMMENTS→  Oxacillin 2gm IV q4h Vancomycin IV (trough 15-20)	May be a contaminant (especially if isolated from only one set of multiple blood culture bottles)

<b><i>Staphylococcus</i> genus and NEGATIVE <i>S. aureus</i>, <i>S. epidermidis</i>, and <i>S. lugdunensis</i> species result</b>	SEE COMMENTS→  Vancomycin IV (trough 15-20)	Result suggests less-common coagulase-negative staphylococcus (may be contaminant, especially if isolated from only one of multiple blood culture bottles). NOTE: <i>mecA/C</i> gene target is not reported for these isolates; assume methicillin resistance pending susceptibilities
<b><i>Streptococcus agalactiae</i>*</b>	Penicillin 3-4 million units IV q4h	Consult ID (especially in setting of suspected endocarditis or diabetic foot infection)
<b><i>Streptococcus pneumoniae</i>*</b>	Ceftriaxone 2gm IV q24h -add vancomycin IV (trough 15-20 mg/dL) and increase to ceftriaxone 2gm IV Q12H if CNS infection suspected	
<b><i>Streptococcus pyogenes</i>*</b>	Penicillin 3-4 million units IV q4h -add clindamycin 900mg IV q8h if necrotizing fasciitis is suspected)	
<b><i>Streptococcus</i> genus and all <i>Streptococcus agalactiae/pneumoniae/pyogenes</i> species results NEGATIVE</b>	Ceftriaxone 2gm IV q24h	
<b>Positive blood culture growth but NO species detected by BCID (with relevant antibiotic BCID resistance gene results)</b>	<b><u>Suggested therapy pending susceptibilities</u></b> (assuming normal renal function)	<b><u>Comments</u></b>
<b>Gram-positive bacterium in culture, no species ID by BCID</b>	Vancomycin IV (trough 15-20)	Consult ID
<b>Gram-negative bacterium in culture, no species ID by BCID CARBAPENEMASE NEGATIVE  KPC, OXA-48-LIKE POSITIVE</b>	Meropenem 1g IV q8h  Ceftazidime-avibactam 2.5g IV q8h	Consult ID  Mandatory ID consult

<b>NDM, VIM, IMP POSITIVE</b>	CONSULT INFECTIOUS DISEASES	Mandatory ID consult
<b>Yeast in culture, no species ID by BCID</b>	Voriconazole 6mg/kg IV q12h x2 doses, then 4mg/kg IV q12h	Mandatory ID consult
<b>Mold in culture, no species ID by BCID</b>	Liposomal amphotericin B 5mg/kg IV q24h	Consult ID

\*The *Enterobacteriaceae* family assay and the *Streptococcus* genus assays may be negative in the setting of a specific species being positive; this does not mean that the species assay is incorrect (just that the assay is designed to pick up less common species). Furthermore, not all species are detected by the genus-specific assays for *Enterococcus*, *Staphylococcus*, *Streptococcus*, and the family specific assay for *Enterobacteriaceae*. Pathogens detected and not detected with each assay are tabulated below in Table 3.

**Table 3: Pathogens detected and not detected by genus/family-specific assays**

<b>Genus-Specific Assay</b>	<b>Pathogens Detected</b>	<b>Pathogens NOT Detected</b>
<i>Enterococcus</i> genus	<i>E. faecium</i> , <i>E. faecalis</i> , <i>E. avium</i> , <i>E. casseliflavus</i> , <i>E. durans</i> , <i>E. gallinarium</i> , <i>E. hirae</i> , <i>E. dispar</i> (reduced sensitivity), <i>E. saccharolyticus</i> (reduced sensitivity)	<i>E. raffinosus</i>
<i>Staphylococcus</i> genus	<i>S. aureus</i> , <i>S. caprae</i> , <i>S. cohnii</i> , <i>S. epidermidis</i> , <i>S. haemolyticus</i> , <i>S. hominis</i> , <i>S. lugdunensis</i> , <i>S. xylosus</i> Detected but with reduced sensitivity: <i>S. capitis</i> , <i>S. pasteurii</i> , <i>S. saprophyticus</i> , <i>S. simulans</i> , <i>S. warneri</i>	<i>S. auricularis</i> , <i>S. carnosus</i> , <i>S. lentus</i> , <i>S. pettenkoferi</i> , <i>S. pseudointermedius</i> , <i>S. schleiferi</i> , <i>S. sciuri</i>
<i>Streptococcus</i> genus	<i>S. anginosus</i> , <i>S. bovis</i> , <i>S. constellatus</i> , <i>S. dysgalactiae</i> , <i>S. equinus</i> , <i>S. gallolyticus</i> , <i>S. gordonii</i> , <i>S. intermedius</i> , <i>S. mitis</i> , <i>S. mutans</i> , <i>S. oralis</i> , <i>S. parasanguinis</i> , <i>S. pseudopneumoniae</i> , <i>S. salivarius</i> , <i>S. sanguinis</i>	
<i>Enterobacteriaceae</i> genus	<i>Cedaceae</i> spp., <i>Citrobacter</i> spp., <i>Cronobacter</i> spp., <i>Enterobacter</i> spp., <i>Escherichia</i> spp., <i>Klebsiella</i> spp., <i>Kluyvera</i> spp., <i>Leclercia</i> , <i>adecarboxylata</i> , <i>Proteus</i> spp.,	<i>Morganella morganii</i> , <i>Providencia</i> spp., <i>Rahnella</i> spp., <i>Serratia liquefaciens</i> , <i>Serratia plymuthica</i> ,

	<p><i>Raoutella</i> spp., <i>Salmonella</i> spp., <i>Shigella</i> spp., <i>Serratia marcescens</i>, <i>Serratia ficaria</i>, <i>Serratia entomophila</i>, <i>Yokenella regensbergi</i></p> <p>Detected but with reduced sensitivity: <i>Edwardsiella</i> spp., <i>Enterobacter</i> <i>gergoviae</i>, <i>Hafnia alvei</i>, <i>Pantoea</i> spp., <i>Salmonella bongori</i> spp., <i>Serratia</i> <i>fonticola</i>, <i>Serratia odorifera</i>, <i>Serratia</i> <i>rubidaee</i></p>	<p><i>Tatumella ptyseos</i>, <i>Yersinia enterocolitica</i></p>
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