

Analytical Validation of the BioFire® Bone and Joint Infection (BJI) Panel:

Identification of Bacteria, Yeast, and Antimicrobial Resistance Genes from Synovial Fluid

N Francis¹, L Barbier², C Dubost², E Billet Hernandez², J Manwaring¹, J Southwick¹, T Dawson¹, J Gann¹, K Ekins¹, J Arce¹, B Flaherty¹, H Durand², C Cantrell³, E Amiot¹

¹BioFire Diagnostics, LLC, Salt Lake City, Utah, USA; ²bioMérieux, SA, Grenoble, France, ³bioMérieux, Durham, NC, USA



Introduction		
The BioFire Bone and Joint Infection (BJI) Panel is a sample-to-answer test for the qualitative detection of nearly 40 different bacteria, yeast, and antimicrobial resistance (AMR) genes in synovial fluid (SF)(Table 1). The panel aims to improve on current culture-based diagnostics, particularly for detection of anaerobes (e.g. <i>Finogoldia magna</i> , <i>Kingella kingae</i> , <i>Parvimonas micra</i> , <i>Peptoniphilus</i> species, and others) in about an hour. Analytical studies were conducted to establish performance characteristics of the panel, including limit of detection (LoD), analytical reactivity and specificity, interference, and reproducibility. In addition, the recommended SF specimen storage conditions were validated.		
Antimicrobial Resistance Genes		
CTX-M <i>mecA/C</i> and MREJ (MRSA) <i>vanA/B</i>	IMP NDM VIM	KPC OXA-48-like
Gram Positive Bacteria		
<i>Anaerococcus prevotii/vaginalis</i> <i>Cutibacterium avidum/granulosum</i> <i>Enterococcus faecium</i> <i>Parvimonas micra</i> <i>Peptostreptococcus anaerobius</i> <i>Staphylococcus lugdunensis</i> <i>Streptococcus agalactiae</i> <i>Streptococcus pyogenes</i>	<i>Clostridium perfringens</i> <i>Enterococcus faecalis</i> <i>Finogoldia magna</i> <i>Peptoniphilus</i> <i>Staphylococcus aureus</i> <i>Streptococcus spp.</i> <i>Streptococcus pneumoniae</i>	
Gram Negative Bacteria		
<i>Bacteroides fragilis</i> <i>Enterobacter cloacae</i> complex <i>Haemophilus influenzae</i> <i>Klebsiella aerogenes</i> <i>Morganella morganii</i> <i>Proteus</i> spp. <i>Salmonella</i> spp.	<i>Citrobacter</i> <i>Escherichia coli</i> <i>Kingella kingae</i> <i>Klebsiella pneumoniae</i> group <i>Neisseria gonorrhoeae</i> <i>Pseudomonas aeruginosa</i> <i>Serratia marcescens</i>	
Yeast		
<i>Candida</i>	<i>Candida albicans</i>	

Limit of Detection		
LoD for each analyte was estimated from serial dilutions and confirmed with ≥95% detection in a minimum of 20 replicates prepared and tested at a known concentration in synovial fluid sample matrix (Table 2).		
- LoD for gram-positive and gram-negative bacteria ranged from: 1.0E+02 CFU/mL - 5.0E+04 CFU/mL (5.3E+02 copies/mL -3.1E+05 copies/mL) - LoD for yeast ranged from: 5.0E+02 CFU/mL - 1.0E+03 CFU/mL (copies/mL not determined (ND) for yeast) - Each AMR gene was confirmed to be reliably detected at the lowest LoD of the applicable host bacteria		
Detection near LoD was achieved in samples stored refrigerated for up to 7 days.		
Analytical Reactivity (Inclusivity)		
Analytical reactivity of each panel assay was assessed via a combination of <i>in silico</i> analysis of sequences available in public databases and testing near LoD. Over 350 isolates were prepared and tested in pooled human synovial fluid.		
The diversity of isolates tested included: - Species, subspecies, and serotypes - AMR gene types - Clinical isolates with known genetic variants (deletions and polymorphisms in the gene targeted by the panel assay)		
Testing and sequence analysis demonstrated that with the exception of rare sequence variants: - Single-species assays are reactive with relevant subspecies and serotypes - Multi-species assays are reactive with the most prevalent and clinically relevant species and subspecies within the indicated genus, complex, or group. - AMR genes are reactive with nearly all characterized AMR gene types		

Assay	LoD (CFU/mL)	LoD (copies/mL)	Assay	LoD (CFU/mL)	LoD (copies/mL)
Gram Positive Bacteria			Gram Negative Bacteria		
<i>Anaerococcus prevotii/vaginalis</i>	1.0E+04	4.8E+04	<i>Bacteroides fragilis</i>	1.0E+03	1.1E+03
<i>Clostridium perfringens</i>	5.0E+02	1.3E+03	<i>Citrobacter</i>	1.0E+03	4.7E+03
<i>Cutibacterium avidum/granulosum</i>	3.4E+04	5.0E+04	<i>Enterobacter cloacae</i> complex	5.0E+04	1.3E+05
<i>Enterococcus faecalis</i>	2.1E+03	5.0E+03	<i>Escherichia coli</i>	5.0E+02	6.0E+03
<i>Enterococcus faecium</i>	1.0E+03	1.2E+03	<i>Haemophilus influenzae</i>	5.0E+02	6.9E+02
<i>Finogoldia magna</i>	1.0E+04	3.1E+05	<i>Kingella kingae</i>	1.0E+03	3.4E+03
<i>Parvimonas micra</i>	1.0E+03	4.8E+03	<i>Klebsiella aerogenes</i>	5.0E+03	7.5E+03
<i>Peptoniphilus</i>	1.1E+04	4.0E+04	<i>Klebsiella pneumoniae</i> group	1.0E+04	1.6E+04
<i>Peptostreptococcus anaerobius</i>	1.0E+04	1.6E+04	<i>Morganella morganii</i>	1.0E+03	2.2E+03
<i>Staphylococcus aureus</i>	1.0E+02	4.2E+03	<i>Neisseria gonorrhoeae</i>	1.0E+02	2.2E+03
<i>Staphylococcus lugdunensis</i>	1.0E+03	2.6E+03	<i>Proteus</i> spp.	1.0E+03	5.2E+03
<i>Streptococcus</i> spp.	1.0E+05	2.5E+05	<i>Pseudomonas aeruginosa</i>	1.0E+04	1.3E+04
<i>Streptococcus agalactiae</i>	1.0E+04	1.9E+04	<i>Salmonella</i> spp.	5.0E+02	1.6E+03
<i>Streptococcus pneumoniae</i>	1.0E+02	5.3E+02	<i>Serratia marcescens</i>	5.0E+03	1.1E+04
<i>Streptococcus pyogenes</i>	5.0E+03	8.9E+03	Yeast		
			<i>Candida</i>	1.0E+03	ND
			<i>Candida albicans</i>	5.0E+02	ND

Table 2. Limit of Detection (LoD) for Bone and Joint Infection Analytes

Precision (Reproducibility)	
The precision (reproducibility) of detection was assessed in a multi-variable study that evaluated: concentration (negative, low positive, and moderate or high positive), test site (3), test day (5), operator (2 per site), instrument/system (BioFire® FilmArray® 2.0 and BioFire® FilmArray® Torch) and kit lot (3). Positive samples included a representative subset of gram-positive and gram-negative bacteria, <i>Candida</i> yeast, and AMR genes.	

- For positive samples:
- Agreement with the expected detected result was 98.3% - 100%
- For negative samples:
- Agreement with the expected not detected result was 99.6% - 100%

Overall, in 420 replicate tests, panel agreement with the expected detection result was 99.9% between runs, days, sites, operators, systems, and lots.

Analytical Specificity (Exclusivity)		
Over 420 microorganisms were tested at high titer (>10 ⁸ CFU/mL for bacteria, >10 ⁶ CFU/mL for yeast, and >10 ⁵ units/mL for viruses and parasites) to evaluate assay specificity. Isolate testing included all on-panel species as well as off-panel phylogenetic near-neighbors and other commensal, pathogenic, or environmental species (including viruses and parasites) that could be present in synovial fluid.		
Few instances of cross reactivity and false-positive results were observed. Most non-specific interactions are between closely-related species, such as:		
<i>Anaerococcus prevotii/vaginalis</i>: other <i>Anaerococcus</i> species <i>Bacteroides fragilis</i>: <i>Bacteroides xylanisolvens</i> <i>Clostridium perfringens</i>: <i>Clostridium cadaveris</i> and <i>C. fallax</i> <i>Escherichia coli</i>: <i>Escherichia albertii</i>, <i>E. fergusonii</i>, and <i>Shigella</i> species <i>Staphylococcus aureus</i>: <i>Staphylococcus argenteus</i> and <i>S. schweitzeri</i>		
Interference		
Thirty-eight substances, including endogenous, exogenous, technique specific substances, and ten potentially competing microorganisms were evaluated at high concentration in contrived multi-analyte samples prepared in synovial fluid. No interference was observed for samples containing the substances and microorganisms listed in Table 3.		
Substance Tested		
Endogenous	Exogenous	Competing Microorganisms
Blood Cholesterol C-reactive protein Fibrinogen Lactate Monosodium urate/ Uric Acid Calcium phosphate Calcium oxalate Bilirubin White Blood Cells Rheumatoid Factor Type II collagen	Acetaminophen Salicylic Acid Ibuprofen Capsaicin Cream Salicylate Cream Camphor Balm Arnica Gel Nystatin Fluconazole Mupirocin Ceftriaxone Vancomycin	Clindamycin Triple antibiotic ointment Hydrocortisone Hyaluronic acid Lidocaine Cobalt ions Chromium ions Ultra-High M.W. Polyethylene Polymethyl Methacrylate Bone Cement Iohexol
	Ethanol Bleach	Povidone-iodine K2-EDTA
		<i>Streptococcus pyogenes</i> <i>Escherichia coli</i> <i>Finogoldia magna</i> <i>Candida albicans</i> <i>Cutibacterium acnes</i> <i>Staphylococcus epidermidis</i> <i>Corynebacterium striatum</i> <i>Cryptococcus neoformans</i> Parvovirus B19 Chikungunya virus

Table 3. Substances Evaluated for Interference with BJI Panel

Conclusions	
The BioFire BJI Panel is a robust, accurate, and easy-to-use multiplex PCR test capable of detecting many relevant aerobic and anaerobic bacteria, yeast, and AMR genes in synovial fluid specimens. Rapid and reliable molecular detection of BJI analytes, particularly for challenging anaerobic species may aid in the timely diagnosis and effective management of bone and joint infections.	

This poster contains data regarding the BioFire BJI Panel which has not yet been reviewed or approved by regulatory agencies for in vitro diagnostic use.

Table 1. BioFire Bone and Joint Infection Panel Analytes

Contact Information:
Nick Francis
BioFire Diagnostics, LLC
515 Colorow Drive, SLC, UT 84115
nick.francis@biofiredx.com