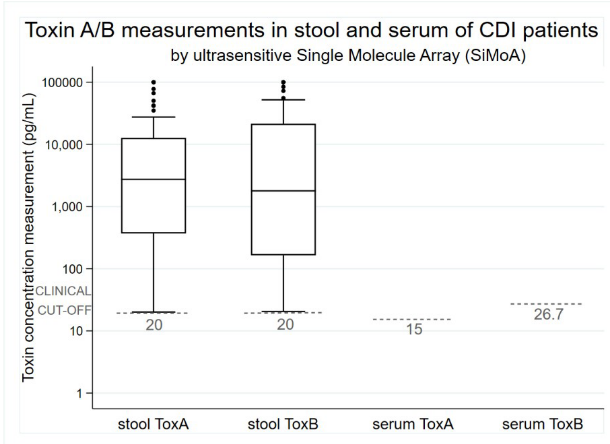
Table 1. Demographics, Baseline Laboratory Values, and Clinical Outcomes for the cohort

Variable	n = 169	
Demographic Information		
Age Median (IQR)	68 (54 – 78)	
Male Gender	90	53.3%
Race		
White	126	74.6%
African American	21	12.4%
Other	18	10.7%
Unknown	4	2.4%
Ethnicity		
Hispanic	9	5.3%
Not Hispanic	144	85.2%
Unknown	16	9.5%
Laboratory Results		
WBC (10^3 cells/µL) Median (IQR)	11.5 (7.4 – 18.6)	
WBC ≥15 x 10^3 cells/µL	61	36.1%
Creatinine (mg/dl) Median (IQR)	1.1 (0.8 – 1.9)	
Creatinine ≥ 1.5 mg/dl	61	36.1%
Albumin (g/dl) Median (IQR)	3 (2.5 – 3.6) n = 152	
Albumin ≤ 3 g/dl	73 (n = 152)	43.2%
027 / NAP1 / B1 strain	17	10.1%
Severe Clinical Outcomes - Total		
ICU admission	24	14.2%
Colectomy	1	0.6%
Death within 40 days	14	8.3%
Severe Clinical Outcomes – Attributed to CDI		
ICU admission	13	7.7%
Colectomy	1	0.6%
Death within 40 days	2	2.4%
Severity Classifications* n = 153		
IDSA Severe	90	74.4%
ESCMID Severe	93	76.9%
Zar *et al* Severe	73	60.3%
Belmares *et al* Severe	23	19.0%

Figure 1. Comparison of TcdA and TcdB concentrations, as measured by Simoa, in serum and stool. Clinical cutoffs are shown: stool, 20 pg/ml for TcdA and for TcdB; serum 15.0 pg/ml for TcdA and is 26.7 pg/ml for TcdB. Signals below these cut-offs are below backgrounds and so negative.



Conclusion: In contrast to earlier published findings which reported on the presence of detectable toxin in the serum of a small number of patients with CDI, our work did not support this observation. Although Simoa is highly sensitive for detection of picogram quantities of TcdA or TcdB it was unable to detect either toxin in serum during CDI. This result does not support the hypothesis that toxemia develops even in severe *C. difficile* infection.

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646. Adapting the modified Carbapenem Inactivation Method to assess for possible beta-lactamase mediated resistance in Piperacillin-Tazobactam resistant/ Ceftriaxone susceptible Escherichia. coli and Klebsiella pneumoniae

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: A cluster of piperacillin-tazobactam resistant/ceftriaxone susceptible *Escherichia coli* and *Klebsiella pneumonaie* bacteremias were noted at our institution. A review of the literature suggested this resistance phenotype was mediated by a beta-lactamase. We sought to further corroborate this phenotypically.

Methods: We adapted the "carbapenem inactivation method" utilizing piperacillin-tazobactam and ceftriaxone discs on all *E. coli* and *K. pneumoniae* isolated from blood and demonstrating piperacillin-tazobactam resistance but with ceftriaxone susceptibility. We utilized pan-susceptible and carbapenem resistance *Enterobacteriaceae* reference strains as well as third generation cephalosporin resistant, piperacillin-tazobactam susceptible isolates as controls.

Results: 96% of the piperacillin-tazobactam resistant, ceftriaxone susceptible strains demonstrated the capacity to degrade the piperacillin-tazobactam discs while 100% spared the ceftriaxone discs. 75% of the piperacillin-tazobactam susceptible, ceftriaxone resistant control strains spared the piperacillin-tazobactam discs while degrading the ceftriaxone discs.

Conclusion: The resistance phenotype observed is due to beta-lactamase production and the modified carbapenem inactivation method can be adapted to probe for other beta-lactamases. Further study is required to definitively identify which beta-lactamase is responsible.

Disclosures: **All Authors**: No reported disclosures

647. Adoption of the updated fluoroquinolones breakpoints for Gram negative bacteria in clinical microbiology laboratories

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Despite the multiple safety warnings related to fluoroquinolones (FQs) treatment, their use remains unavoidable in several occasions due to their broad spectrum of coverage including activity against multi-drug resistant glucose non-fermenting Gram-negative bacteria such as *Pseudomonas* spp., and high oral bioavailability. The Clinical and Laboratory Standards Institute (CLSI) has lowered the FQs minimal inhibitory concentrations (MICs) breakpoints for *Salmonella* spp. in 2012 and 2013, and for the *Enterobacterales* and *P. aeruginosa* in 2019. We aim to explore the number of hospitals that adopted the revised breakpoints.

Methods: We conducted a cross-sectional phone-based survey querying the 43 microbiology laboratories that serve 100% of the acute care and long-term hospitals in Connecticut to determine use of revised FQs MIC breakpoints for Gram-negative bacteria.

Results: Six laboratories refer antimicrobial susceptibility testing to another local hospital microbiology laboratory or to a national reference laboratory. Thus, we obtained information about the study question from a total of 37 microbiology laboratories. Eight laboratories (21.6%) were affiliated to university hospitals and 29 (78.4%) were community-based. Microscan Beckman coulter MicroScan was the most common antimicrobial susceptibility test method used in 15 (40.6%) microbiology laboratories followed by BioMérieux Vitek 2 in 13 (35.1%) laboratories. Four laboratories (10.8%) only adopted the revised CLSI FQs breakpoints for *Enterobacterales, P. aeruginosa*, and *Salmonella* spp, 5 (13.5%) implemented the revised breakpoints for *Enterobacterales* and *P. aeruginosa* but not for *Salmonella* spp., and 8 (21.6%) laboratories adopted the revised CLSI breakpoints for *Salmonella* spp. but not for *Enterobacterales* and *P. aeruginosa*.

Conclusion: The use of outdated CLSI breakpoints for FQs against Gram-negative bacteria remains common in the microbiology laboratories. There is an urgent need to mitigate the impact of using the outdated FQs breakpoints and reporting false susceptibility to FQs.

Disclosures: **All Authors**: No reported disclosures

648. BioFire® FilmArray® Pneumonia plus Panel Performance Evaluation: A Multicenter, International Collaborative Study

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EME Evaluation Program Collaborative

Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Classical methods to identify causes of community acquired, healthcare and ventilator associated pneumonia can be insensitive and slow, leading to unnecessary or inappropriate antimicrobial therapy. The BioFire® FilmArray®

Pneumonia *plus* Panel (PN*plus*) detects 15 bacteria (in semi-quantitative log bin values from 10^4 to > 10^7), 7 antibiotic resistance markers (mecA/C/MREJ, CTX-M, KPC, VIM, IMP, NDM, OXA-48 like), 3 atypical bacteria (AB), and 8 viral classes directly from bronchoalveolar lavage (BAL)-like and sputum-like specimens (including endotracheal aspirates) in about 1 hr. This study compared PN*plus* results to standard of care testing (SOC).

Methods: 2476 samples (1234 BAL-like; 1242 sputum-like) were tested at 52 laboratories from 13 European countries and Israel by PN*plus* and SOC. SOC varied by site and physician prescription. Pathogen detection rates were compared. PN*plus* bin values and SOC descriptive or numerical quantities were evaluated for 1297 bacterial detections.

Results: 13 samples (0.5%) gave invalid PN*plus* results. 3278 bacteria in PN*plus* were detected by PN*plus* and/or SOC. SOC detected 1878 bacteria (57.1%) compared to 3128 bacteria (95.8%) for PN*plus* (p=< 0.0001). SOC detected 73 AB (70.9%) and 134 viruses (21.1%), PN*plus* detected 93 AB (90.3%) and 618 viruses (97.9%) (p=< 0.0001). Mean number of analytes/sample detected by PN*plus* and SOC were 1.99 and 1.44, respectively. PN*plus* bin values were less than SOC, equal to SOC or greater than SOC in 5.9%, 25.4% and 69.6% of results, respectively. PN*plus* values were on average > 1 log than SOC values (58.5% 1-2 logs; 11.0% 3-4 logs). PN*plus* identified 98.2% of MRSA and SOC 55.6%. All gram-negative resistance markers were detected at least once. PN*plus* and SOC results were fully concordant (positive or negative) or partially concordant for 49.1% and 26.4% of samples, respectively.

Conclusion: PN*plus* detected significantly more potential pathogens than SOC. Lack of routine SOC viral testing was a missed opportunity to define the cause of pneumonia. Semi-quantification may assist in understanding the significance of the pathogens detected. Pathogen and resistance marker detection in about 1 hr could dramatically impact antimicrobial use and enhance patient outcomes.

Disclosures: Christine C. Ginocchio, PhD, MT(ASCP), bioMerieux (Employee) bioMerieux (Employee, Shareholder) Barbara Mauerhofer, Pharmacist, bioMerieux (Employee) Cory Rindlisbacher, n/a, BioFire Diagnostics (Employee) Carolina Garcia, BS, bioMerieux (Employee)

649. Clinical Implementation of a Rapid Susceptibility Testing Procedure, Directly From a Positive Blood Culture Using the Vitek®2 System on Gram Negative Rods

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: The national average of identification and susceptibility for organisms isolated from positive blood culture to final susceptibility based on growth on solid media is 48 hours. The goal of this research was to prove that the Vitek®2 (bioMérieux, Inc.) system can provide an accurate and reliable susceptibility result directly from positive blood culture for Gram negative rods and reduce the turnaround time (TAT) from positive blood culture to the final susceptibility.

Methods: An FDA-modified validation procedure was performed on positive blood cultures directly from the bottle to the VITEK®2 System for susceptibility testing. The protocol tested and validated an aliquot of 50uL of blood directly from the positive bottle into 10 mL of saline (1:200). The solution was vortexed and 3mL were placed in the VITEK®2 test tube. This protocol was intended only for Gram negative rods using the AST-GN70, AST-GN81 & AST-GN801 cards. This protocol followed the CLSI M52 and M100 guidelines.

Results: 515 organisms from clinical blood culture samples from July 2018 to October 2019 were evaluated. Organisms included, but were not limited to: *E. coli, K. pneumoniae, Enterobacter spp.*, and *P. aeruginosa, Proteus spp., Salmonella spp., Acinetobacter spp., and S. maltophilia.* There were 5,201 drug/bug combinations. AdventHealth Orlando achieved an essential agreement of 99.32% (n=5,166), minor error 0.74% (n=39) major error 0.02% (n=1) and very major error 0.49% (n=2). A 100% agreement was achieved on detection of ESBL, CRE, and MDR organisms.

Conclusion: Rapid direct blood culture protocol using the VITEK®2 System and the AST-GN cards is accurate, reliable and can be performed with less than 1 minute hands-on time. The protocol can be implemented in any laboratory at no additional costs or modification where the current VITEK®2 AST-GN panels are in use. This protocol was clinically implemented at AdventHealth Orlando on July 15, 2019. Compared with the national average of 72 hours, the TAT obtained during this study was 23 hours from positive blood culture to final susceptibility, a significant reduction of 25 hours. The authors encourage bioMérieux Inc. to evaluate and explore the opportunity to expand the use of the VITEK®2 system for this application with the appropriate clinical trial.

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650. Clinical Performance Evaluation of Virtuo Blood Culture System in a Tertiary Care Hospital

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Bloodstream infections are a major cause of morbidity and mortality. BACT/ALERT VIRTUO (VIRTUO) blood culture system is an automated, closed system used with resin-containing media which may enhance the growth of microorganisms. Our objective was to assess the real-world performance of the VIRTUO system.

Methods: We retrospectively reviewed all blood cultures performed between January-December 2018 (VersaTREK) and January-December 2019 (VIRTUO) at a 1250-bed academic medical center. Blood culture positivity rates, contamination rates, and time from collection to arrival in the laboratory were compared pre- versus post-VIRTUO implementation. Contamination was defined as a single blood culture with common skin microbiota.

Results: A total of 101803 blood cultures were performed during the study period: 48969 (48.1%) were processed with VersaTREK system and 52834 (51.9%) with VIRTUO system. A decreased median time from collection until arrival to the laboratory was seen post-implementation (2.0 pre- vs. 0.8 hours post-implementation, p< 0.001). The positivity rate increased from 3987 (8.1%) pre-implementation to 6141 (11.6%) post-implementation (p < 0.001) (Table and Figure). *Staphylococcus aureus* was the most frequently isolated species for both periods and had higher recovery rate with the VIRTUO system (717 (1.5%) pre- vs. 1764 (3.3%) post-implementation, p< 0.001). Higher recovery rate was also noted for other *Staphylococcus* spp. in the post-implementation period (985 (2.0%) pre- vs. 1644 (3.1%) post-implementation, p< 0.001). No difference in the organism recovery rate was noted for *Streptococcus* spp., *Enterococcus faecium, E. faecalis*, *Pseudomonas aeruginosa*, *Enterobacterales*, and *Candida* spp. The inpatient contamination rate was higher post-implementation (1.5% pre- vs. 1.9% post-implementation, p < 0.001).

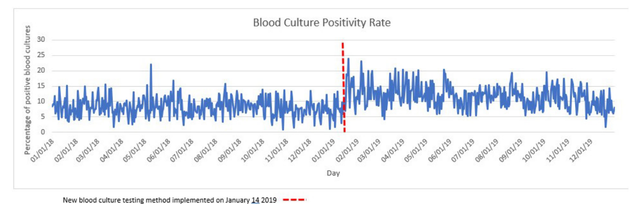
Comparison of blood culture positivity rate pre- vs. post-implementation, by culture location

Table. Comparison of blood culture positivity rate pre- vs. post-implementation, by culture location

	Entire study period		Pre-implementation 1/1/2018 to 1/13/2019		Post-implementation 1/14/2019 to 12/13/2019		*p*
	Total	Positive result	Total	Positive result	Total	Positive result	
All locations	101803	10128 (10.0%)	48969	3987 (8.1%)	52834	6141 (11.6%)	<0.001
Inpatient location	71621	6580 (9.2%)	36972	2627 (7.1%)	34649	3953 (11.4%)	<0.001
Emergency dept.	15023	2111 (14.1%)	6225	809 (13.0%)	8798	1302 (14.8%)	0.002
Outpatient location	15159	1437 (9.5%)	5772	551 (9.6%)	9387	886 (9.4%)	0.826

Daily positivity rate for blood cultures processed at BJH during the study period

Figure. Daily positivity rate for blood cultures processed at BJH during the study period



Conclusion: The VIRTUO system showed a higher rate of positive blood cultures compared to the VersaTREK system primarily from a higher detection of *Staphylococcus* spp. Further studies are needed to assess whether an increased rate of positive blood cultures is associated with changes in management and clinical outcomes.

Disclosures: **All Authors**: No reported disclosures

651. Comparative Analysis Between Bacterial And Fungal Malignant Otitis Externa

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Session: P-25. Diagnostics: Bacteriology/mycobacteriology

Background: Malignant otitis externa is a fatal infection of the external ear and temporal bone. *Pseudomonas aeruginosa* is the most common causative organism, while fungi are a rare cause of malignant otitis externa. We aimed to compare the clinical, therapeutic and evolutionary features between bacterial and fungal malignant otitis externa.

Methods: We conducted a retrospective study including all patients hospitalized for malignant otitis externa in the infectious diseases department between 2000 and 2018.

Results: Overall, we encountered 82 cases of malignant otitis externa, among which there were 54 cases (65.9%) of bacterial malignant otitis externa (BMO) and 28 cases (34.1%) of fungal malignant otitis externa (FMO). The males were predominant among BMO cases (57.4% vs 50%; p=0.5). Patients with FMO were significantly older (70±9 years vs 61±10 years; p< 0.001) and had medical history of diabetes mellitus more frequently (96.4% vs 77.8%; p=0.03). The use of topical corticosteroids was significantly more reported among FMO cases (28.6% vs 5.6%; p=0.006). Otalgia (96.4% vs 81.5%), otorrhea (75% vs 66.7%) and cephalalgia (46.4% vs 42.6%) were the