2142. Comparison of Molecular-Based vs. Conventional Culture-Based Screening Methods for Detection of Carriers of Extended-Spectrum β-Lactamases (ESBL) and Carbapenemases-Producing *Enterobacteriaceae* (CPE)

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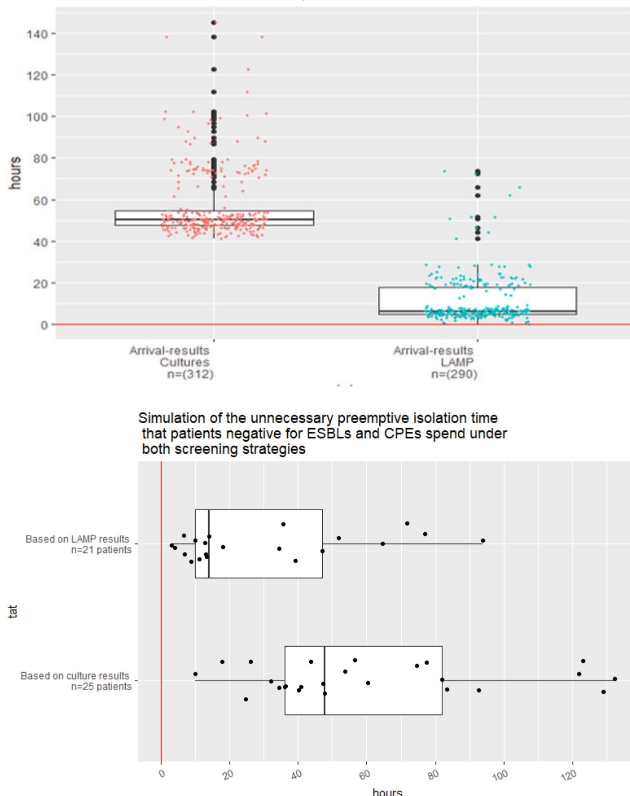
Background. Active surveillance and contact precautions may prevent cross-transmission of ESBL-producing *Enterobacteriaceae* and CPE. Culture-based methods delaying results might increase risk of cross-transmission, and lead to unnecessary preemptive contact precautions. This observational cohort study compared rapid Loop-Mediated Isothermal Amplification (LAMP) assays to conventional culture-based methods for ESBL and CPE screening of critically ill patients.

Methods. This study was conducted in the adult ICUs at Geneva University Hospitals. We collected consecutive rectal ESwabs routinely performed, either for admission screening of high-risk patients or once weekly routine screening of all patients hospitalized in the ICU. Eazyplex® SuperBug CRE system (Amplex Biosystems) assays were performed directly on rectal Eswabs according to the manufacturer's instructions. For the conventional culture-based method, we used chromID® ESBL agar (ESBL) coupled with chromID®OXA-48. Discordant specimens were retested using disk diffusion tests and the same LAMP assay on isolates. Microbiological turn-around times (TAT; from the reception in the laboratory to result notification) were collected.

Results. Overall, 290 rectal ESwabs were analyzed. ESBL and CPE prevalence were 16.7% and 1.0%, respectively. Three discordant isolates could not be further investigated and considered as LAMP false positive. Adjusted analytical performances were for CPE: 100% (95IC 100–100%) sensitivity, 99.6% (99.0–100%) specificity, 75% (32.6–100%) PPV, and 100% (100–100%) NPV, and for ESBL: 85% (73.9–96.1%) sensitivity, 98.8% (97.4–100%) specificity, 91.9% (83.1–100%) PPV, and 97.6% (95.7–99.5%) NPV. A decrease in TAT was observed when comparing LAMP screening assay against conventional method (50.3 hours vs. 6.2 hours; Figure 1). Figure 2 shows time reductions comparing both screening strategies.

Conclusion. Screening strategies based on LAMP could fasten discontinuation of unnecessary pre-emptive isolation time for patients at risk and earlier implementation of contact precautions for previously unknown carriers of ESBL or CPE.



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2143. Attempting to Add Clarity to "Indeterminates" on a Deployed Rapid Diagnostic with Antimicrobial Stewardship Program (ASP) Intervention

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Background. Rapid diagnostic testing paired with ASP intervention optimizes therapy and improves outcomes but few data guide ASP response in the absence of organism identification (ID). We describe the microbiology for organisms unidentified by Accelerate Pheno™ Gram-negative platform (AXDX) in order to inform ASP-provider team communication (PTC).

Methods. Consecutive, non-duplicate inpatient blood cultures with Gram-negative bacilli (GNB) following AXDX implementation at a single university hospital between April 2018 and March 2019 were included. Standard of care (SOC) ID and susceptibility followed AXDX. Clinical Microbiology emailed AXDX results to the ASP in real time; results were released into the EMR paired with telephone PTC or withheld after ASP review. Bloodstream Infections (BSIs) and patient outcomes for organisms labeled no/indeterminate ID by the AXDX were characterized.

Results. AXDX was performed on 351 blood cultures. Among 52 (15%) labeled no/indeterminate ID, SOC methods revealed: *Enterobacteriaceae* (40%; 9 monomicrobial with AXDX targets), anaerobes (21%), non-lactose fermenters (NLFs) other than *Pseudomonas aeruginosa* (21%), and fastidious GNB (10%). Frequent organisms without AXDX targets included: *Raoultella planticola* (4); *Bacteroides fragilis*, *Cupriavidus* spp., *Haemophilus* spp., *Prevotella* spp., *Providencia* spp., non-*aeruginosa Pseudomonas* spp., *Salmonella* spp. (3 each); *Pasteurella multocida*, *Stenotrophomonas maltophilia* (2 each). BSI sources were most commonly intra-abdominal (21%), central line-associated (17%), or unknown (17%). CLABSIs were associated with immune suppression and/or substance abuse in all but 1 case. BSIs without active empiric therapy included: NDM-producing *Providencia stuartii* SSSI; OXA-48-producing *R. planticola* intraabdominal infection (IAI); *Pandoraea* spp. CLABSI after liver transplant; enteric fever; *B. fragilis*, *Leptotrichia wadei*, and *S. maltophilia*, each of unknown source. In-hospital mortality occurred in 4 of these cases.

Conclusion. When AXDX yields no/indeterminate ID, ASP chart review for possible anaerobic/IAI, unique environmental exposures, and travel history may assist in guiding empiric therapy. GNB with AXDX targets are not excluded.

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2144. Performance of 2019 CLSI Ciprofloxacin Breakpoint Antimicrobial Susceptibility Testing Algorithms for Enterobacteriaceae and *Pseudomonas aeruginosa* Directly from Positive Blood Culture on the Accelerate Pheno™ System

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Background. The Clinical and Laboratory Standards Institute (CLSI) updated fluoroquinolone breakpoints in 2019 in response to evolving resistance and new outcome data. The performance of updated antimicrobial susceptibility testing (AST) algorithms for ciprofloxacin with the 2019 breakpoints for Enterobacteriaceae and *Pseudomonas aeruginosa* was evaluated using the Accelerate Pheno™ system with contrived positive blood culture samples compared with broth microdilution (BMD).

Methods. A total of 294 clinical isolates (100 *P. aeruginosa*, 82 *Klebsiella* spp., 56 *E. coli*, 24 *Citrobacter* spp., 14 *Enterobacter* spp., 15 *Proteus* spp., and 3 *S. marcescens*) were tested with ciprofloxacin. Aliquots of BD BACTEC™ Standard Aerobic media containing healthy donor blood were seeded with 10–100 bacterial cells and incubated until positivity. Aliquots of the positive blood cultures were run using the Accelerate PhenoTest™ BC kit on the Accelerate Pheno™ system according to the manufacturer instructions for use. Results were obtained using an updated ciprofloxacin algorithm and compared with CLSI standard reference BMD. Only samples with valid results with both the Accelerate Pheno™ system and reference BMD were included in analysis. Essential agreement (EA), categorical agreement (CA), very major error (VME), major error (ME) and minor error (mE) rates were calculated using 2019 CLSI breakpoints.

Results. EA and CA for all antimicrobial/organism combinations were >94%. There were 2 MEs (1 *K. pneumoniae*, 1 *C. freundii*) and no VMEs.

Conclusion. Results with the new research use only (RUO) algorithms are very good and meet FDA acceptance criteria for AST performance. These data will be submitted to the FDA for clearance, once FDA recognizes the CLSI breakpoints.

	Ciprofloxacin (2019 breakpoints)		
	Enterobacteriaceae	*P. aeruginosa*	Overall
n	192	95	287
EA	183 (95.3%)	94 (98.9%)	277 (96.5%)
CA	182 (94.8%)	92 (96.8%)	274 (95.5%)
VME	0	0	0
ME	2 (2.2%)	0	2 (1.4%)
mE	8 (4.2%)	3 (3.2%)	11 (3.8%)
S	92	55	147
I	4	7	11
R	96	33	129

Disclosures. **All authors:** No reported disclosures.