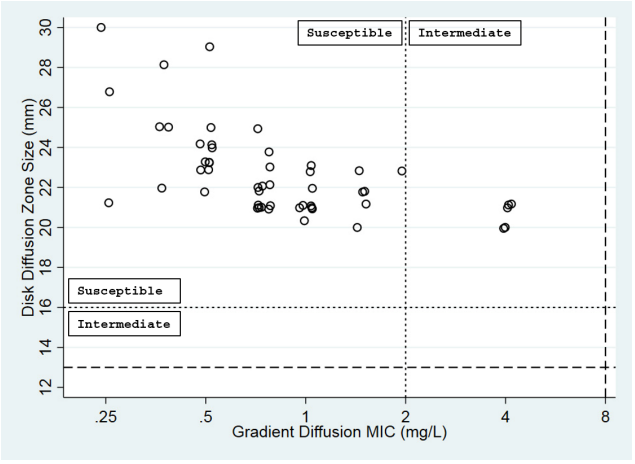
mL) methods according to manufacturer instructions and using FDA clinical breakpoints for interpretation.

Results. 51 isolates were tested: 21 *E. coli*, 9 *P. mirabilis*, 7 *E. cloacae*, 6 *K. pneumoniae*, 3 *K. oxytoca*, 3 *S. marcescens*, 1 *K. aerogenes*, and 1 *C. freundii*. Specimen sites included: 29 blood, 8 urine, 8 soft tissue or bone, 5 intra-abdominal, and 1 sputum. Previous phenotypic AST results demonstrated 19 (37%) were CRE, of which 5 were also gentamicin and tobramycin resistant, and 32 (63%) were tobramycin and gentamicin resistant but carbapenem susceptible. Plazomicin zone diameters and minimal inhibitory concentrations (MIC) for all isolates are shown in the figure (data jittered to show frequency). There was a significant correlation between increased MIC and smaller zone diameters (Pearson coefficient −0.443, $P = 0.001$). However, while all 51 isolates were susceptible by DD breakpoints, only 46 (92%) were susceptible by GD breakpoints. All 5 discordant results were *P. mirabilis* which had an MIC of 4 µg/mL (intermediate) but zone diameters of 20–21 mm (susceptible).

Conclusion. Concordance between plazomicin DD and GD susceptibility was only 92%. All 5 discordant results were *P. mirabilis*. Surveillance studies demonstrate >80% of *P. mirabilis* have MIC of 2–4 mg/L. Given the DD breakpoint is 16 mm, our data suggest DD was overly active in our sample set. Comparison of DD and GD to reference broth microdilution against a larger set of isolates is warranted to determine which method is optimal; however, our data suggest DD may result in categorical errors for *P. mirabilis*.



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2163. Clinical Impact of Inter-site Blood Culture Transport in a Canadian Tertiary Care Center

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Background. The potential delays caused by transport of blood cultures to server laboratories might result in delayed issuance of results for patients with positive blood cultures. In this study, we aimed to determine the clinical impacts of inter-site transport of blood cultures.

Methods. We performed a retrospective cohort study involving cases with positive blood cultures (1 positive blood culture/species/patient/7 days; not deemed as a contaminant) at two sites of a Canadian tertiary care center between January 1, 2018 and December 31, 2018. Blood cultures from the affiliated site were transported to the laboratory of the primary server site. These two sites are located 8 km apart. The following outcomes were studied: the duration between blood culture sampling and issuance of the first report and the duration between blood culture sampling and administration of the first effective antibiotic.

Results. We observed 349 episodes of bacteremia, including 161 in the affiliated site (45.5%) and 193 in the primary server center (54.5%). *Enterobacteriaceae* (n = 151, 43%) and *Staphylococcus aureus* (n = 77, 22%) were the most commonly observed causative bacteria. Median duration for issuance of the first positive report was significantly shorter in the primary server hospital (32.4 h, interquartile range [IQR] 19.8–44.3) than in the affiliated center (37.9 h, IQR 24.1–46.5; $P = 0.004$). The median duration between blood culture sampling and administration of the first effective antibiotic was 2.7 h in the server site (IQR 0.75–15.2) and 2.3 h in the affiliated site (IQR 1–8.45) ($P = 1.0$). Receiving the first effective antibiotic after blood culture sampling required > 60 min in 8/189 patients (4.2%) in the affiliated site and 9/158 patients (5.7%) in the primary server site ($P = 0.3$). The 30-day mortality was 13.8% (26/189) and 8.9% (14/158) at the primary server site and affiliated site, respectively ($P = 0.16$).

Conclusion. Inter-site transport of blood cultures is associated with a significant delay in the issuance of positive blood culture reports. However, this delay does not cause any delay in administration of effective antibiotic therapy because of rapid recognition of sepsis in bacteremia patients. These results are reassuring in the context of increasing microbiology service centralization.

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2164. Activity of Fosfomycin (FOF) and Frequency of Nonsusceptible Inner Colonies During Susceptibility Testing of an International Collection of Clinical *Pseudomonas aeruginosa* (PA) Isolates

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Background. FOF has been used clinically for the treatment of PA infections in the absence of established interpretive criteria. A recent study identified a low frequency of nonsusceptible inner colony mutants during disk diffusion (DD) testing of *Escherichia coli*; however, the frequency of this phenomenon in PA isolates is not well characterized. We sought to determine FOF activity against an international collection of PA isolates and the frequency of inner colony mutants observed during Etest and DD testing.

Methods. Minimal inhibitory concentration (MIC) values were determined for a convenience collection of 109 PA ([70/94] 64.2% MDR) isolates from 4 institutions in the United States and Australia. MIC testing was conducted in duplicate on separate days utilizing agar dilution (AD), broth microdilution (BMD), DD, and Etest as recommended per Clinical and Laboratory Standards Institute (CLSI). CLSI *E.coli* interpretive criteria (≤ 64 mg/L susceptible) were used for MIC interpretations. The proportion of isolates containing inner colonies was determined using DD and Etest. Inner colony mutants were subcultured and retested using BMD with comparison to the parent isolate MICs.

Results. FOF MICs varied widely and ranged from 1024 mg/L with MIC_{50}/MIC_{90} values of 64/256 (AD), 64/512 (Etest), and 64/256 (BMD) mg/L. Using *E. coli* criteria, susceptible/resistant rates were: 60.5/17.4% for AD; 60.5/22.0% for Etest; 86.2/7.3% for DD; and 53.2/17.4% for BMD. Inner colonies were frequently observed in 38.5% and 35.8% of DD and Etest inhibition zones, respectively. After repeat testing, mutant MIC values ranged from 64 to > 1024 mg/L and a majority (85.9%) had MIC values ≥ 512 mg/L.

Conclusion. Observed MIC values of this (64% MDR) collection varied widely with $MIC_{50/90}$ values commonly at or above the *E. coli* susceptibility breakpoint. Inner colony mutants were frequently observed and highly resistant. Whole-genome sequencing is currently underway for a subset of parent/mutant pairs to determine whether specific genetic alterations are attributed to the increased MICs. Based on these results, caution should be warranted in extrapolating *E. coli* breakpoints to other organisms, and treatment of PA with FOF should be further evaluated.

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2165. *Helicobacter pylori* Infections in the Bronx, New York: Whole-Genome Sequencing for Rapid Genotypic Susceptibility Testing

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Background. Susceptibility-guided treatment of *H. pylori* is superior to empiric therapy. We determined the accuracy of whole-genome sequencing (WGS) compared with phenotypic testing using CLSI/EUCAST breakpoints.

Methods. Thirty-three clinical isolates of *H. pylori* cultured from gastric biopsies were sequenced with a coverage range between 40x and 80x using Illumina Miseq platform and the reads were assembled and annotated with PATRIC. Phenotypic susceptibility tests were performed using E-test strips under microaerophilic conditions for 72 hours. Mutations associated with amoxicillin, tetracycline, clarithromycin, levofloxacin, metronidazole and rifampin resistance were examined.

Results. Of the 33 isolates, two were phenotypically resistant to amoxicillin: one carried a β-lactamase gene ($bla_{TEM-116}$) and the other exhibited a point mutation *pbp2* (A541T). All isolates were tetracycline susceptible phenotypically, but three isolates had point mutations in *16S rRNA* that are associated with resistance (A926G). Clarithromycin results showed a good correlation between methods. Nine clarithromycin-resistant isolates demonstrated point mutations in 23S *rRNA* (A2142G/A2143G). Fifteen isolates were phenotypically resistant to levofloxacin, but resistance mutations were found in only 14 strains (N87I/N87K/D91Y/D91N/D91G/D99N in *gyrA*). We analyzed our strains for the presence of intact genes *rdxA* and *frxA,* either of which convert the prodrug form of metronidazole into the active form. Twenty-four

of 33 isolates were tested phenotypically. We found 3 isolates with truncations in both genes. These isolates had metronidazole MICs >256. The presence of one or both intact genes did not always result in low MICs, indicating that there may be significant point mutations that contribute to resistance. Rifampin was not tested phenotypically, but no mutations in *rpoB* were found. In summary, the correlation of WGS and phenotypic testing was 100% for amoxicillin and clarithromycin, 97% for levofloxacin, 91% for tetracycline ($n = 33$), and 67% for metronidazole ($n = 24$).

Conclusion. WGS provides a detailed analysis of *H. pylori* resistance and a broader analysis of antimicrobials that may be of clinical value. Additional studies are needed for genotypic prediction of metronidazole resistance.

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2166. Performance Study on the New ETEST® Piperacillin/Tazobactam (P/T) MIC Strip

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Background. Piperacillin/Tazobactam combination is a first-line antibiotic and carbapenem sparing option for severe infections due to Enterobacteriaceae, *Pseudomonas aeruginosa* and *Acinetobacter baumannii*. ETEST® strips allow to determine antimicrobial Minimum Inhibitory Concentration (MIC). ETEST® Piperacillin/Tazobactam (Ptc) was developped in 1995 against agar dilution reference method. Since then, resistance to Piperacillin/Tazobactam has been increasing and broth microdilution (BMD) substituted for agar dilution as the reference method. The new ETEST® P/T strip for determining MIC of Enterobacteriaceae, *P. aeruginosa* and *A. baumannii* was developed against BMD using a panel of recent strains well genotypically characterized. The aim of this study was to compare the performance of both strips on a panel of challenging strains harboring different-resistant mechanisms.

Methods. A total of 64 strains were tested using ETEST® P/T, ETEST® PTc and BMD: 48 Enterobacteriaceae including 25 resistant strains and 16 *P. aeruginosa* including 11 resistant strains. The results were analyzed for essential (EA) and category (CA) agreements, minor (mE), major (ME) and very major (VME) error rates using FDA/CLSI 2019 breakpoints (Enterobacteriaceae, *P. aeruginosa*: ≤ 16/4(S); ≥ 128/4(R) µg/mL).

Results. Although the panel of strains was challenging including different resistant mechanisms (acquired penicillinase, high-level cephalosporinase, acquired cephalosporinase, ESBL, carbapenemase), the new ETEST® P/T performance was significantly improved for Enterobacteriaceae with an EA at 92,2% without ME or VME. This improvement was also linked to the easiest reading (significant decrease of micrcolonies in the ellipse zone). For P. aeruginosa, the performance was similar between the two strips but the new ETEST® P/T was better correlated with the BMD and showed an EA of 100%. The results are summarized in the table.

Conclusion. The new ETEST® P/T improved the MIC determination and resistance detection, as well as the reading of MIC end points for the routine use. This study emphasizes the need to check the performance of the antimicrobial susceptibility testing products by testing strains reflecting the current epidemiology.

		% EA	% CA	% mE	% ME	% VME
Enterobacteriaceae	New ETEST® P/T	92.2	82.8	17.2	0	0
	ETEST® PTc	70.3	70.3	20.3	0	23.1
Pseudomonas aeruginosa	New ETEST® P/T	100	87.5	12.5	0	0
	ETEST® PTc	93.8	75	25	0	0

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

2167. Evaluation of Attenuated Total Reflectance Fourier Transform Infrared Spectroscopy for Rapid and Reagent-Free Identification of *Burkholderia* spp.

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Background. *Burkholderia cepacia* complex including *B. gladioli* are opportunistic pathogenic bacteria affecting the immunocompromised population. For prognosis and appropriate treatment, rapid and accurate species identification is particularly important for those diagnosed with cystic fibrosis (CF). Conventional biochemical identification techniques are insensitive and problematic for identifying *Burkholderia* spp., leading to common misidentification or inconclusive results. Recent studies have successfully employed attenuated total reflectance-Fourier transform infrared (ATR-FTIR) spectroscopy for rapid, reagent-free and cost-effective microbial identification. In the present study, identification of *Burkholderia* spp. by this technique is investigated.

Methods. A total of 59 isolates belonging to 7 species of *Burkholderia* were included in this study; all these isolates had been well-characterized by VITEK 2, 16S rRNA sequencing, random amplification of polymorphic DNA (*recA* typing) and/or matrix-assisted laser desorption/ionization time of flight mass spectrometry. ATR-FTIR spectra were acquired directly from colonies on 5% blood agar plates.

Results. A spectral database containing ATR-FTIR spectra of over 4300 bacterial isolates, encompassing over 70 genera and 190 species, was updated to include spectra of 39 isolates collected in this study and employed in the identification of the other isolates ($n = 20$). All isolates were correctly identified as *Burkholderia* by a multitier search approach. For *Burkholderia* species identification, spectra belonging to 39 isolates representative of all 7 species were used to construct a spectral database employed to identify the other 20 isolates [*B. anthina* ($n = 2$), *B. gladioli* ($n = 8$), *B. multivorans* ($n = 7$), and *B. vietnamiensis* ($n = 3$)]. Compared with VITEK 2 (30% correct species identification), ATR-FTIR spectroscopy correctly identified all but one isolate, resulting in overall correct species identification of 95%. Prospectively (10 months), 5 of 1100 isolates collected were identified as *Burkholderia* spp. by ATR-FTIR spectroscopy in concordance with VITEK 2.

Conclusion. ATR-FTIR spectroscopy can provide the means of rapid *Burkholderia* spp. identification for appropriate treatment of those diagnosed with CF.

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2168. Comparison of Rapid Diagnostic Tests for Bloodstream Infections Using Desirability of Outcome Ranking Management of Antimicrobial Therapy (DOOR-MAT)

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Background. Rapid diagnostic tests (RDTs) for bloodstream infection (BSIs) are increasingly common. Decisions regarding which RDT to implement remains a clinical challenge given the diversity of organisms and resistance mechanisms detected by different platforms. The desirability of Outcome Ranking Management of Antimicrobial Therapy (DOOR-MAT) has been proposed as a framework to compare RDT platforms but reports of clinical application are lacking. This study compared potential antibiotic decisions based on results of two different RDTs for BSI using DOOR-MAT.

Methods. Retrospective study at University of Maryland Medical Center from August 2018 to April 2019 comparing Verigene® BC (VBC) to GenMark Dx ePlex® BCID for clinical blood cultures. VBC was part of standard of care, ePlex was run on discarded fresh or frozen blood samples. In this theoretical analysis, RDT result and local susceptibility data were applied by two Infectious Diseases pharmacists to make decisions regarding antibiotic selection in a blinded manner. Cohen's Kappa statistic summarized overall agreement. DOOR-MAT, a partial credit scoring system, was applied to decisions based on final organism/susceptibility results (Figure 1). Scores were averaged between reviewers and mean scores compared between RDT systems using the *t*-test. Additionally, a sensitivity analysis with varied point assignment among Gram-negatives (AmpC-producers) was conducted.

Results. 110 clinical isolates were included; 41 Gram-negative, 69 Gram-positive organisms. Overall agreement was 82% for VBC and 83% for ePlex. The average score for VBC was 86.1 (SD 31.3) compared with ePlex 92.9 (SD 22.9), $P = 0.004$. Among Gram-negatives, the average score for VBC was 79.9 (SD 32.1) compared with ePlex 88.1 (SD 28.8), $P = 0.032$. Among GPs the average score for VBC was 89.9 (SD 30.4) compared with ePlex 95.8 (SD 18.3), $P = 0.048$. Sensitivity analysis demonstrated an average score for of 89.9 (SD 30.4) for VBC compared with 95.8 (SD 18.3) for ePlex, $P = 0.27$.

Conclusion. The use of a partial credit scoring system such as the DOOR-MAT allows for comparisons between RDT systems beyond sensitivity and specificity allowing for enhanced clinical interpretation. In this theoretical comparison, the Genmark ePlex BCID scored higher among both GP and GN organisms.

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