resistant organisms may be inhibited by a carbapenem antibiotic until sufficient carbapenemase production has been achieved and traditional AST platforms must wait to make MIC calls. More accurate carbapenem MICs can be determined by implementing a carbapenemase test alongside rapid AST.

**Methods.** We demonstrate a novel, proprietary test to detect carbapenemase production that enables rapid MIC testing for carbapenem antibiotics. The test is performed in parallel with the Sentax next-generation phenotyping (NGP) AST method, enabling rapid, ≤6-hour, accurate MIC determinations. The carbapenemase assay utilizes high concentrations of intact bacteria. After 3 hours of incubation, a fluorescent pH indicator is read spectrophotically. The solution pH is lowered by carbapenemase-mediated imipenem degradation and is indicative of enzyme activity.

**Results.** This assay accurately identifies carbapenemases across multiple enzyme classes and bacterial species. Figure 1 shows the accuracy and speed of NGP AST at determining MICs for representative isolates from the FDA CDC antimicrobial resistance bank compared with results from overnight broth microdilution (BMD). To date, over 100 challenge strains of Enterobacteriaceae, Pseudomonas aeruginosa, and Acinetobacter baumannii have been tested with very few major errors and an average time-to-result of 5.3 hours.

**Conclusion.** By incorporating a rapid, on-board carbapenemase activity assay, the NGP AST platform rapidly delivers accurate carbapenem results. Combined with NGP's comprehensive antibiotic menus, this platform will therefore ensure prompt delivery of personalized antibiotic therapies for all patients, including those infected with MDROs, and enable streamlined antibiotic stewardship coordination.

2160. Performance of the Cepheid Rapid PCR Test for Patient Screening and Association with Efficacy of Svaturoxam. A Novel Anti-Staphylococcus aureus Monoclonal Antibody, During the Phase 2 SATelliteLE study

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**Background.** Patients with lower airway Staphylococcus aureus (SA) colonization are at greater risk (> 20%) of early-onset ventilator-associated pneumonia (VAP). Thus, a rapid test is required to identify patients at risk. Svaturoxam (formerly MEDI6444) is a human monoclonal antibody that neutralizes SA alpha toxin. SAATELLITE, a phase 2 study of safety and efficacy of svaturoxam for reducing the incidence of SA pneumonia (NCT02256320) was conducted and recently completed within the consortium for Combating Bacterial Resistance in Europe. We investigated the performance of a rapid PCR test (Xpert MRA/SA SSTT), Cepheid as a screening tool during the study and the association between SA load and svaturoxam efficacy.

**Methods.** The PCR assay was used to detect SA and methicillin-resistant SA (MRSA) in lower respiratory tract (LRT) samples. Culture was performed on PCR SA+ LRT samples according to local procedures. PCR SA+ subjects were randomized 1:1 for either a single intravenous infusion of 5000 mg svaturoxam (n = 96) or placebo (n = 100) and followed for 190 days post dose. Efficacy of svaturoxam was defined as relative risk reduction (RRR) in incidence of SA pneumonia within 30 days post-dose compared with placebo.

**Results.** 299 (41.5%) out of 720 screened subjects were SA+ by PCR. Of 209 subjects with culture data, there were 162 (77.5%) SA+; 47 (22.5%) SA- and 9 (5.6%) MRSA by culture. Culture results could have been affected by antibiotic use and site variability in limits of detection ranging from 3.3 to 100,000 colony-forming units per mL (CFU/mL). No discordance was noted between PCR and culture for MRSA detection. An inverse linear correlation was observed between the PCR cycle threshold (Ct) values for SA protein A gene (spa) and SA CFU/mL counts from quantitative culture. In subjects with low SA load (Ct ≥ 29; n = 72), svaturoxam provided 66.7% RRR [90% confidence interval (CI): 21.3%, 86.2%] compared with 31.9% RRR [90% CI: 7.5%, 56.8%] in total study population.

**Conclusion.** Cepheid Xpert PCR assay was easy to perform, sensitive and standardized, and provided better sensitivity than conventional culture for detection of SA. Additionally, quantitative PCR Ct output was associated with the efficacy of svaturoxam in reducing SA pneumonia incidence.

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2161. Organism-Specific Turn Around Time Improvement in Urinary Specimens as a Result of Microbiological Laboratory Automation

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**Background.** University Medical Center in Lubbock, TX is one of few medical centers in West Texas to utilize Kiestra Total Laboratory Automation (TLA) system since May 2015. The impact on organism-specific turn around time (TAT) in urinary specimens after implementation of TLA was evaluated.**

**Methods.** After approval from the Quality Improvement Review Board, a retrospective analysis of microbiological data from urinary specimens in BD research database was performed. Before vs. after implementation (2013 vs. 2016) TAT was compared. Ten clinically relevant organisms were analyzed. Statistical analysis was performed with SAS software version 9.2. Data were analyzed using Chi-squared test. A P-value of < 0.05 was considered statistically significant.

**Results.** Overall, 2282 specimens from 2013 and 2306 specimens from 2016 were analyzed. Compared with before vs. after implementation of TLA, an overall improvement in TAT was observed (expressed as mean hours for each organism): Enterococcus faecalis (55.2 vs. 38.8), Enterococcus fæces (68.4 vs. 43.8), Escherichia coli (44.2 vs. 41.0), Klebsiella pneumoniae (45.0 vs. 44.0), Proteus mirabilis (44.8 vs. 38.6), Pseudomonas aeruginosa (58.9 vs. 37.7), Staphylococcus aureus (49.2 vs. 36.0), Streptococcus agalactiae (49.2 vs. 31.4), Streptococcus pneumoniae (51.7 vs. 61.8), Streptococcus pyogenes (62.6 vs. 26.6). It was also observed that improvement in TAT was more pronounced for Gram-negative organisms than Gram-positive negative organisms.

**Conclusion.** Automation of microbiology laboratory leads to significant TAT improvement in urinary specimens, making early data availability to clinicians. This improves efficacy as well as supporting earlier antibiotic switch, antimicrobial stewardship and optimal patient care in treating urinary tract infections.

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

2162. Comparison of Plazomicin Disk Diffusion vs. Gradient Diffusion Susceptibility Testing Results Against Drug Resistant Clinical Enterobacteriaceae Isolates

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**Background.** Plazomicin, a novel aminoglycoside, is active against carbapenem-resistant Enterobacteriaceae (EB) and is not inhibited by most aminoglycoside modifying enzymes that affect gentamicin and tobramycin. We investigated the activity of plazomicin against resistant EB clinical isolates and compared disk diffusion (DD) vs. gradient diffusion (GD) results.

**Methods.** EB isolates that were carbapenem resistant and/or resistant to both gentamicin and tobramycin were retrieved from the UW Health Clinical isolate repository. Each isolate was tested against plazomicin using both DD (MAST Group Ltd. plates) and GD (0.12–2 µg) and followed as per OFID 2019:6 (Suppl 2) – 5733.
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, 5 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 carabapenem susceptible. Plasmicin 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 44 mg/L (intermediate) but zone diameters of 20–21 mm (susceptible).

Conclusion. Concordance between plasmicin 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 GD was over 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 laboratory (39.7 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) ($P = 0.1$). 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 8.6% (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 interpretative criteria. A recent study identified a low frequency of nonsusceptible inner colony mutants observed during Etest and DD testing.

Methods. Minimal inhibitory concentration (MIC) values were determined for a convenience collection of 109 PA ($\geq 70/94$; 64.2% MDR) isolates from 4 institutions in the United States and Australia. MIC testing was conducted in duplicate on separate blood culture 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 from the range 304 mg/L with MIC of $\leq 2$ mg/L (intermediate) to 308 mg/L (intermediate) to 1024 mg/L (resistant). Of the 109 isolates, four were phenotypically resistant to amoxicillin: 304 mg/L (AD and BMD), 1024 mg/L (DD), and 1024 mg/L (Etest). The 30-day mortality was 13.8% (26/189) and a majority (85.9%) had MIC values ≥ 512 mg/L.

Conclusion. Observed MIC values of this (64% MDR) collection varied widely with MIC$\text{MIC}_{\text{int}}$ 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 patient/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, ceftriaxone and rifampin resistance were examined.

Results. Of the 33 isolates, two were phenotypically resistant to amoxicillin: one carried a β-lactamase gene ($\beta$LAC,$\beta$LAC) and the other exhibited a point mutation TEM-116. 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 observed during DD testing.

Conclusion. Whole-genome sequencing was commonly at or above the $H. pylori$ susceptibility breakpoint. Inner colony mutants were frequently observed and highly resistant. Whole-genome sequencing is currently underway for a subset of patient/mutant pairs to determine whether specific genetic alterations are attributed to the increased MICs. Based on these results, caution should be warranted in extrapolating $H. pylori$ breakpoints to other organisms, and treatment of PA with FOF should be further evaluated.

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