June 2017 to December 2017. The automated PCR test was performed directly from respiratory specimens. The results were compared with in-house PCR for detection of carbapenemase genes performed on KP colonies isolated from respiratory specimens as our reference method. Patient and clinical characteristics between patients with CPK and non-CPK were also analyzed.

Results. The prevalence of CPK was 10.6% (18/169 isolates). The automated PCR test had 91.12% accuracy, 66.7% sensitivity (95% CI, 40.9–86.6), 94.0% specificity (95% CI, 88.9–86.6), 57.1% positive predictive value (95% CI, 39.5–73.1) and 95.9% negative predictive value (95% CI, 92.48–97.85). Of 18 isolates, bla_{OXA-48} was the most common carbapenemase gene (17 isolates; 94.4%), followed by bla_{NDM-1} (7 isolates; 38.9%). A combination of bla_{OXA-48} and bla_{NDM-1} was detected in 6 isolates (33.3%). There were 7 (38.8%) colonizations and 11 (61.1%) infections. The significant risk factors for CPK included post-surgery ($P = 0.04$) and prior antibiotics exposure ($P = 0.04$). There was a trend toward higher mortality in patients with CPK albeit not significantly (33% vs. 24.5%, $P = 0.41$).

Conclusion. The automated PCR test has an acceptable accuracy with fair sensitivity for the detection of carbapenemase genes. It is unique that OXA-48 and OXA-48/NDM-1 are the most common carbapenemases in our institute. This diagnostic test may be use for rapid diagnosis or infection control purposes. Exposure to antibiotics associated with colonization or infection with CPK. Patients with CPK had higher mortality.

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2065. Whole Genome Sequencing for Antimicrobial Resistance Prediction in MRSA and VRE: A Real-world Application

Ahmed Babiker, MBBS[1]; Mustapha M. Mustapha, MBBS, PhD[2]; Yohei Doi, MD, PhD[3] and Lee H. Harrison, MD[4]; [1]Division of Infectious Diseases, University of Pittsburgh Medical Center, Pittsburgh, Pennsylvania, [2]Genomic Epidemiology Laboratory, Infectious Diseases Epidemiology Research Unit, University of Pittsburgh, Pittsburgh, Pennsylvania, [3]University of Pittsburgh Medical Center, Pittsburgh, Pennsylvania and [4]Infectious Diseases, University of Pittsburgh, Pittsburgh, Pennsylvania

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Background. The antimicrobial resistance (AMR) crisis represents a serious threat to public health and the healthcare economy. The impact of increasing AMR has resulted in concentrated efforts to increased rapid molecular diagnostics of AMRs. In combination with publicly available web-based AMR databases, whole-genome sequencing (WGS) offers the capacity for detection of antibiotic resistance genes with low turnaround times and is becoming increasingly affordable. Here we sought to examine concordance between WGS-based resistance prediction and phenotypic susceptibility testing results for prospectively collected VRE and MRSA clinical isolates using publicly-available tools.

Methods. MRSA and VRE isolates were prospectively collected and underwent WGS at the University of Pittsburgh Medical Center (UPMC) between December 2016 and December 2017. Antibiotic-resistant gene content was assessed by uploading assembled contigs to ResFinder, NCBI betalactamase and CARD using a BLASTn. search. Routine susceptibility was performed by Microscan™. Concordance between genotypic and phenotypic as well as sensitivity, specificity, positive and negative predictive values methods were calculated for each antibiotic/organism combination, using the phenotypic results as the gold standard. In case of discordance between the methods, repeat susceptibility using disc diffusion results was performed and was then considered to be the gold standard method.

Results. Phenotypic susceptibility testing and WGS results were available for 109 and 105 unique MRSA and VRE isolates, respectively. Out of total of 1,058 isolate/antibiotic combinations overall concordance of WGS-web-based prediction with phenotypic susceptibility methods was 99.1% with a sensitivity, specificity, PPV, NPV of 98, 99.6, 99.5, and 98.3%, respectively. Specific concordance for MRSA isolates was 98.8%. with a sensitivity, specificity, PPV and NPV of 97.6, 99.8, 99.7, and 98.5% (Table 1), while concordance for VRE isolates was 99.3%, with a sensitivity, specificity, PPV and NPV of 98.6, 98.1, 99.1, and 97.2% (Table 2).

Conclusion. WGS is a reliable predicator of phenotypic resistance for both MRSA and VRE.

Table 1: MRSA WGS and phenotypic resistance concordance

Antibiotic	Total Number isolates with both WGS and phenotypical susceptibility	Resistant by Automated methods n, , (%)	Resistant by Disc Diffusion	Resistant by WGS n, (%)	Concordance of WGS with Disc Diffusion (%)	Sensitivity (%)	Specificity (%)	PPV(%)	NPV(%)
Methicillin	107	107 (100)	105 (98)	105 (98)	100	100	100	100	100
Erythromycin	102	90 (88.2)	89 (87.3)	88 (86)	88	95.7	92.9	98.9	76
Clindamycin	103	35 (33.9)	52 (50.4)	52 (50.4)	99	98.1	100	100	98.1
Tetracycline	107	10 (9.3)	9 (9.1)	9 (9.1)	100	100	100	100	100
Bactrim*	106	6 (5.6)	7 (6.5)	7 (6.5)	99	87.5	100	100	99
Gentamicin	109	2 (1.8)	2 (1.8)	2 (1.8)	100	100	100	100	100
Rifampin*	108	5 (4.5)	3 (2.7)	0	97.2	50	100	100	97.2
Vancomycin	109	0	0	0	100	n/a	n/a	n/a	n/a
Linezolid	108	0	0	0	100%	n/a	n/a	n/a	n/a
Total	742	255	267	263	98.8	97.6	99.8	99.7	98.5

* With the additional step of examining for point mutations in housekeeping genes concordance, specificity, sensitivity, NPV and PPV was 100%

Table 2: VRE WGS and phenotypic resistance concordance

Antibiotic	Total Number isolates with both WGS and phenotypical susceptibility	Resistant by Automated methods, N,(%)	Resistant by Disc Diffusion, N (%)	Resistant by WGS , N (%)	Concordance of WGS with Disc Diffusion (%)	Sensitivity (%)	Specificity (%)	PPV(%)	NPV(%)
Vancomycin	105	105 (100)	102 (96.2)	103 (97.1)	99%	99	100	100	75
Linezolid*	102	3 (2.9)	2 (2.0)	2 (2)	98	50	100	100	98
Erythromycin	60	60 (100)	60 (100)	52 (60)	100	100	100	100	98.1
Tetracycline	49	46 (93.9)	46(93.9)	48 (98)	100	100	60	95.9	100
Total	316	255	210	263	99.3	98.6	98.1	99.1	97.2

* With the additional step of examining for point mutations in housekeeping genes concordance, specificity, sensitivity, NPV and PPV was 100%

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

2066. Accelerated Detection of Carbapenem Resistance Mechanisms in *Enterobacteriaceae* by MALDI-TOF Mass Spectrometry Using the Direct-on-Target Microdroplet Growth Assay (DOT-MGA)

Carlos Correa-Martinez, MD[1]; Evgeny A. Idelevich, MD[1]; Katrin Sparbier, PhD[2]; Markus Kostrzewa, PhD[2] and Karsten Becker, Prof.[1]; [1]Institute of Medical Microbiology, University Hospital Münster, Muenster, Germany, [2]Bruker Daltonik, Bremen, Germany

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Background. The differential identification of carbapenemases relies mostly on molecular techniques. Current phenotypic methods require 18 hours of incubation. We propose a matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS)-based direct-on-target microdroplet growth assay (DOT-MGA) aiming to offer an easy and rapid phenotypic identification of AmpC, KPC, MBL and OXA production.

Methods. Seven well-characterized *Enterobacteriaceae* strains recommended by EUCAST for carbapenemase detection were analyzed. Synergy between meropenem and carbapenemase inhibitors (phenylboronic acid, aminophenylboronic acid, cloxacillin, dipicolinic acid, ethylenediaminetetraacetic acid, and avibactam) and temocillin resistance were determined using a testing panel developed on a 96-spot MALDI-TOF MS target (MBT Biotarget 96, Bruker Daltonics, Germany). Microdroplets (6 µl) containing bacterial suspension and antibiotic or antibiotic/inhibitor in cation-adjusted Mueller–Hinton broth were spotted on the target and incubated for 4 hours at 36°C in a humidity chamber to avoid evaporation. The medium was subsequently removed and MALDI-TOF MS of the cells adhered to the target's surface was performed. The minimum inhibitory concentration (MIC) was considered to be the lowest concentration at which the MALDI Biotyper software yielded no organism identification. Synergy was defined by an eightfold or greater reduction of the meropenem MIC in the presence of an inhibitor. The absence of synergy between meropenem and inhibitors as well as high-level temocillin resistance was considered suggestive of OXA production. Results were processed and interpreted with a computer-based algorithm.

Results. After 4 hours, the method was able to correctly detect the foreknown resistance mechanisms of all tested strains (KPC, MBL, OXA, and AmpC), yielding results that agreed with those obtained by performing broth microdilution with 18 hours of incubation.

Conclusion. The DOT-MGA approach allowed easy identification and differentiation of carbapenemase production, delivering reliable results one day earlier than the usual phenotypic methods, thus displaying great potential for the clinical setting.

Disclosures. **E. A. Idelevich**, Bruker Daltonik: Co-inventor of a pending patent, Licensing agreement or royalty and Speaker honorarium. **K. Sparbier**, Bruker Daltonik: Employee, Salary. **M. Kostrzewa**, Bruker Daltonik: Employee, Salary. **K. Becker**, Bruker Daltonik: Co-inventor of a pending patent, Licensing agreement or royalty and Speaker honorarium.

2067. Novel Methodology for Same-Day Antimicrobial Susceptibility Testing on VITEK®2 for Gram-Negative Rod Bacteremia

Catherine Hogan, MD, MSc[1]; Indre Budvytiene, MS, CLS[2]; Nancy Watz, CLS[2] and Niaz Banaei, MD[3]; [1]Department of Pathology, Stanford University School of Medicine, Stanford, California, [2]Clinical Microbiology Laboratory, Stanford University Medical Center, Palo Alto, California, [3]Department of Medicine, Division of Infectious Diseases and Geographic Medicine, Stanford University School of Medicine, Stanford, California

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Background. Bloodstream infections with Gram-negative rods are potentially fatal and require tailored antimicrobial treatment. Optimizing therapy is currently limited by the 1–2 days turnaround time required for antimicrobial susceptibility testing. Novel same-day technologies have been developed but are expensive. Here, we describe and investigate the accuracy of a repurposed existing technology (VITEK®2, bioMérieux) for same-day susceptibility testing directly from positive blood cultures.

Methods. Starting in August 2017, patients with blood cultures positive for Gram-negative rods were prospectively included. In addition, aerobic and anaerobic blood culture bottles were spiked with a standardized inoculum of enteric Gram-negative rods from a repository of frozen samples. Positive blood cultures were processed using

a newly developed protocol based on red blood cell lysis and differential centrifugation of bacteria, followed by VITEK®2 card set-up. VITEK®2 results from the direct method were compared with a reference method (VITEK®2 results using a 24-hour colony).

Results. In the prospective study, a total of 109 nonduplicate samples were collected, with *E. coli* (n = 54) and *Klebsiella pneumoniae* (n = 51) the main pathogens detected. In addition, a total of 52 blood culture bottles were spiked with resistant Gram-negative rods. Overall weighted essential agreement was 98.8%, and categorical agreement was 97.9% between the direct and reference methods. Accurate results were produced for the main antibiotics used to treat enteric Gram-negative bacteremia, including ceftriaxone, piperacillin–tazobactam and meropenem. Mean turnaround time to susceptibility results for *Enterobacteriaceae* in the prospective study was 9.0 (±1.3) hours.

Conclusion. Preliminary data from direct antimicrobial susceptibility testing by VITEK®2 for enteric Gram-negative rod bacteremia suggest this technique is accurate, practical, easily integrated in the laboratory workflow, and substantially cheaper than its competitor technology. The next phase of this study will assess the impact of faster antimicrobial susceptibility turnaround time on patient outcomes and antimicrobial stewardship targets.

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2068. Evaluation of Ceftazidime-Avibactam Disks from Different Commercial Manufacturers for Susceptibility Testing against Meropenem Nonsusceptible Enterobacteriaceae

Lynn-Yao Lin, MS and Ian A. Critchley, PhD[1]; [1]Allergan plc, Irvine, California

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Background. Ceftazidime and avibactam (CAZ-AVI) diffusion disks have been widely used in hospitals and clinical laboratories in the United States for susceptibility testing of infections caused by Enterobacteriaceae and *Pseudomonas aeruginosa.* A few cases of high error rates and overcalling of resistance in some carbapenem-resistant Enterobacteriaceae (CRE) isolates have been reported. The purpose of this study was to evaluate the performance of CAZ-AVI diffusion disks made by two manufacturers in comparison with that of the standard broth microdilution (BMD) method for susceptibility testing against a large collection of CRE.

Methods. A panel of 110 meropenem nonsusceptible Enterobacteriaceae clinical isolates, including 98 *Klebsiella pneumoniae*, eight *Enterobacter cloacae*, and four *Escherichia coli* were tested using CAZ-AVI (30/20 µg) diffusion disks manufactured by Hardy Diagnostics (Hardy) and BD Biosciences (BD). These isolates harbored various carbapenemase genes including KPC-2, KPC-3, VIM, NDM, OXA, ESBL, and altered OmpK35 and OmpK36. The same isolates were tested for susceptibility to CAZ-AVI by BMD using a custom-made Trek panel. Correlation between minimal inhibitory concentration (MIC) and disk diffusion inhibition zones was assessed based on Clinical and Laboratory Standards Institute (CLSI) breakpoints and error rate analysis.

Results. Overall disk diffusion inhibition zones correlated well with MIC for disks manufactured by both Hardy and BD according to CLSI CAZ-AVI breakpoints (susceptible/resistant): MIC ≤8/4/≥16/4 µg/mL, disk diffusion ≥21/≤20 mm. Error rates were low for the Hardy disks grown on Hardy and BD Mueller–Hinton agar (MHA) with 0.9% very major errors (VME)/1.8% major errors (ME) and 1.8% VME/5.5% ME, respectively. The error rates for BD disks grown on Hardy and BD MHA plates were 1.8% VME/0% ME and 1.8% VME/6.4 ME, respectively. ME rates appeared to be lower when Hardy MHA plates were used for both Hardy and BD disks.

Conclusion. CAZ-AVI (30/20 µg) disks manufactured by Hardy and BD performed well in susceptibility testing against a challenging set of CRE isolates. These data showed good categorical agreement between disk diffusion and BMD methods. Error rates were lowest when Hardy MHA plates were used for both Hardy and BD disks.

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2069. Automation Process Improving Microbiological Laboratory Efficiency

Jacob Nichols, MD[1]; Alanna Emrick, MLS (ASCP)[2]; Carolyn Gonzalez-Ortiz, M (ASCP)[2]; Kristen Fuhrmann, Pharm.D.[3]; Ying Tabak, PhD[4]; Latha Vankeepuram, MS[4]; Stephen Kurtz, MS[4]; David Sellers, RN[5] and Fatma Levent, MD[6]; [1]Internal Medicine, Texas Tech Health Sciences Center, Lubbock, Texas, [2]Clinical Laboratory, University Medical Center, Lubbock, Texas, [3]Pharmacy, University Medical Center, Lubbock, Texas, [4]Becton, Dickinson and Company, Franklin Lakes, New Jersey, [5]Clinical Development, Becton, Dickinson and Company, Franklin Lakes, New Jersey, [6]Pediatrics, Texas Tech Health Sciences Center, Lubbock, Texas

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Background. Automation minimizes hands-on steps and facilitates process improvement in the microbiology laboratory. The impact on the efficiency improvement of the culturing process in an academic regional hospital after implementation of total laboratory automation (TLA) was evaluated.

Methods. After approval from the Quality Improvement Review Board, a retrospective analysis of microbiological data in Becton Dickenson (BD) Clinical Insights Research Database was performed. Then, laboratory process change and reported microbiological results turnaround time (TAT) before and after implementation of the TLA was compared (2013 vs. 2016). Specimens were classified into blood, respiratory, urine, wound and others. Statistical analysis was performed with SAS software version 9.2. The comparison was done using chi-square test for categorical and log-transformed t-test for continuous variables. A P-value of < 0.05 was considered statistically significant.

Results. A total of 9,351 pre-defined common and clinically important positive mono-microbial culture results were included in the organism identification (ID) TAT analysis. The time of the day at which results were reported in 2016 was more evenly distributed throughout a 24-hour period, rather than delaying to the following morning (P < 0.0001). The definitive positive bacterial pathogen identification TAT was significantly shorter across all sources in 2016 compared with 2013 with overall TAT mean (standard deviation) of 56.8 (24.3) hours in 2013 vs. 43.3 (20.8) hours in 2016 (P < 0.0001). The negative results' (n = 58,640) TAT was also shortened in 2016 for all (P < 0.05), except for respiratory and other sources.

Conclusion. Automation facilitates microbiological laboratory efficiency improvement with shorter definitive organism identification TAT across all specimens as well as shorter TAT for negative results with most specimen sources. This information would facilitate earlier, more accurate and appropriate antibiotic choices which in turn improves clinical decision making and enhances optimal patient care.

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2070. Antibiotic Therapy Effects on Enterobacteriaceae Detection Directly from Blood: Pilot Study Implications for Future Clinical Trial Design

Amy Irwin, DNP, MS, RN[1]; Sara Giddins, BS, MT (ASCP)[1]; Irina Yushkevich, MS[1]; Alexiss Jeffers, BA[2]; Michelle Barron, MD[3]; Nancy Madinger, MD[4]; Martin Fuchs, MS[5]; Sungho Kim, PhD[5]; Steven Metzger, BA[6] and Connie Price, MD[7]; [1]Infectious Diseases, Denver Health and Hospital Authority, Denver, Colorado, [2]Infectious Diseases, University of Colorado Denver, Aurora, Colorado, [3]Internal Medicine/Infectious Diseases, University of Colorado Denver, Aurora, Colorado, [4]Infectious Diseases, University of Colorado, Denver, Colorado, [5]Accelerate Diagnostics, Inc., Tucson, Arizona, [6]Research and Development, 3950 S. Country Club Road, Suite 470, Tucson, Arizona, [7]Infectious Diseases, University of Colorado School of Medicine/Denver Health and Hospital, Denver, Colorado

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Background. Detection of bacteremia directly from blood may improve time to clinical diagnosis and initiation of appropriate antibiotic therapy for hospitalized patients. Administration of empiric antibiotic therapy, whether prior to standard of care (SOC) or research study blood collection, adds to challenges in bacterial recovery. Strategies to improve detection were explored in this pilot study to inform future clinical trial design (CTD) on Enterobacteriaceae (ENT) detection directly from blood. One of the objectives was to assess effects of prior antibiotic administration on novel assay performance.

Methods. Confirmed ENT bacteremic (Protocol A (P-A), n = 26), and suspected bacteremic (Protocol B (P-B), n = 25) participants were enrolled into one of two IRB approved protocols after obtaining informed consent. Fresh whole blood (20 mL) was collected within 12 hours of SOC blood culture positivity (P-A) or 20 hours of SOC blood culture collection (P-B), and divided: 10 mL inoculated into a lytic media collection vessel (P-A and B); and 10 mL into a BD BACTEC™ Bottle (P-A) as a control, or an Isolator™ lysis centrifugation tube (P-B) for quantification. For collection vessels, a 3-hour amplification step in lytic growth medium followed by cleanup and concentration steps was employed. Processed samples were tested using an investigational assay for universal bacterial detection on the Accelerate Pheno™ system. Results were analyzed manually and with proprietary software. Descriptive statistics were performed to inform future CTD.

Results. Empiric antibiotic therapy was initiated prior to blood collection in 89% (P-A) and 36% (P-B) of participants. Improved detection sensitivity was achieved in P-B over P-A, when a study sample was obtained prior to empiric antibiotic therapy initiation (Table 1).

Table 1	P-A	P-B
Total samples	26	25
Prior ABT	89%	36%
% positive, n	15%, 5*	24%, 6
SOC BD BACTEC™ Bottle Positive	26	6
SOC BD BACTEC™ Bottle Negative	0	19
BD BACTEC™ Control Positive	4	N/A
Collection Vessel Positive	3	4
Collection Vessel Negative	23	21
Sensitivity	50%	67%
Specificity	96%	100%
*Collection vessel detected 1 positive sample that the BD BACTEC™ bottle control missed.		

Conclusion. Prior antibiotic administration and low bacterial load in clinical samples affects ability to detect ENT directly from blood. Multiple factors are critical to address in future CTD to increase sensitivity of detecting ENT directly from blood including: (1) Targeting study samples prior to antibiotic therapy initiation and (2) Using enzymatic methods to neutralize antibiotics present in the blood.

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