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.

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

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

Session: 232. Diagnostics: Resistance Testing
Saturday, October 6, 2018: 12:30 PM

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

Session: 232. Diagnostics: Resistance Testing
Saturday, October 6, 2018: 12:30 PM

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

Session: 232. Diagnostics: Resistance Testing
Saturday, October 6, 2018: 12:30 PM

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