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, 88.9–96.1), 57.1% positive predictive value (95% CI, 39.5–73.1) and 95.9% negative predictive value (95% CI, 92.8–97.9). Of 18 isolates, bla_oxa-48 was the most common carbapenemase gene (17 isolates; 94.4%), followed by bla_OXA (7 isolates; 38.9%). A combination of blad_vel, and bla_VIM was detected in 6 isolates (33.3%). There were 7 (38.8%) colonization 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 were the most common carbapenemases in our institute. This diagnostic test may be used 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
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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 increase 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-vs.-based prediction with phenotypic susceptibility methods was 99.1% with a sensitivity, specificity, PPV, NPV of 99.6, 99.5, and 98.3%, respectively. Specific concordance for MRSA isolates was 98.8% with a sensitivity, specificity, PPV, NPV of 98, 99, 97, and 98.5% (Table 1), while concordance for VRE isolates was 99.3%, with a sensitivity, specificity, PPV and NPV of 99.6, 98.1, 99.1, and 97.2% (Table 2).

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

Table 1: MRSA WGS and phenotypic resistance concordance

| Antibiotic | Total Number of isolates with both WGS and phenotypic susceptibility | Resistance to WGS No (%) | Resistance by disc Difficult (N%) | Concordance with Diff Difficult (%) | Sensitivity (%) | Specificity (%) | PPV (%) | NPV (%) |
|------------|------------------------------------------------------------------|--------------------------|----------------------------------|------------------------------------|----------------|----------------|--------|--------|
| Meropenem  | 108                                                                | 108 (100)                | 100 (100)                        | 100 (%)                            | 100            | 100            | 100    | 100    |
| Ciprofloxacin| 108                                                                | 98 (90.0)                | 83 (86.4)                        | 90 (%)                             | 95             | 92             | 98.5   | 94.6   |
| Daptomycin | 132                                                                | 132 (100)                | 100 (100)                        | 100 (%)                            | 100            | 100            | 100    | 100    |
| Teicoplanin| 132                                                                | 132 (100)                | 100 (100)                        | 100 (%)                            | 100            | 100            | 100    | 100    |
| Tobramycin | 197                                                                | 197 (100)                | 100 (100)                        | 100 (%)                            | 100            | 100            | 100    | 100    |
| Gentamicin | 197                                                                | 191 (96.9)               | 91 (92.1)                        | 96 (%)                             | 91             | 92             | 98.9   | 95.6   |
| Amikacin   | 197                                                                | 197 (100)                | 100 (100)                        | 100 (%)                            | 100            | 100            | 100    | 100    |
| Vancomycin| 208                                                                | 208 (100)                | 208 (100)                        | 100 (%)                            | 100            | 100            | 100    | 100    |

*With the additional step of examining for prior resistance in bloodstream gene concordance, specificity, sensitivity, NPV and PPV was 100%.

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2066. Accelerated Detection of Carbenapenem Resistance Mechanisms in Enterobacteriaceae by MALDI-TOF Mass Spectrometry Using the Direct-on-Target Microdroplet Growth Assay (DOT-MGA)
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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 test (MALDI-TOF MS) using 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 as carbapenemase detection were analyzed. Synergy between carbapenem and carbapenemase inhibitors (phenylboronic acid, aminophenylboronic acid, clavulanic acid, 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 adherent to the target were 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.

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2067. Novel Methodology for Same-Day Antimicrobial Susceptibility Testing on VITEK 2 for Gram-Negative Rod Bacteremia
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Background. Bloodstream infections with Gram-negative rods are potentially fatal and treated with 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 (VITEK2, bioMérieux) for same-day susceptibility testing directly from clinical specimens.

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