number of primer sets required to detect all IMP genes was subsequently found by iterative deduction. The predicted primer sets were tested against 7 IMP producing bacterial isolates (IMP-1, 4, 7, 8, 18, 19, and 27 from *Serratia, Enterobacteriaceae, Pseudomonas,* and *Klebsiella spp.*). and one synthesized gene of IMP-35. These isolates were chosen to represent the full genetic spectrum of the IMP family. The remaining 40 genes were evaluated based on gene sequences obtained from GenBank.

**Results.** The in silico analysis showed 6 primer sets were needed to detect all known IMP genes. PCR amplification of template DNA isolated from the 8 strains showed that primer sets 1 and 4 could detect all 8 IMP isolates while the remaining 4 sets (2, 3, 5, 6) had distinct amplification patterns that could be used together to identify a specific IMP gene group. Effectiveness of these primer sets in IMP identification was demonstrated by testing a clinical isolate containing an unidentified carbapenem resistant bacterium. The IMP-27 gene was identified by PCR amplification using the IMP-specific primers designed and confirmed by sequence analysis.

**Conclusion.** A bioinformatic approach can be used to create an assay for bacterial resistance. The assay developed with this approach can detect and classify all known IMP metallo-β-lactamase genes in carbapenem resistant Gram-negative bacteria. Such information could aid in guiding treatment and evaluating the epidemiology of IMP-producing bacteria.

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2022. **Quantiferon conversions and reversions among HIV patients on antiretroviral therapy.**

Andrea L. Covington, MD1; Prakash Shrestha, MD1-2; Ana Fuentes Arzola, MD, MPH1; Christopher R. Frei, PharmD, MS1; and Jose Cadena Zuñiga, MD1-2, UT Medicine, San Antonio, Texas, South Texas Veterans Health Care System, San Antonio, Texas

**Session:** 234. Diagnostics – Bacterial Identification and Resistance

**Background.** Tuberculosis (TB) remains a major global public health problem. Recent guidelines recommend screening of high-risk patients for latent TB infection, with the preferential use of interferon-gamma release assays (IGRA) over PPD. However, there are several reports of reversions and conversion of Quantiferon TB tests (QFT).

**Methods.** The primary aim of this retrospective review among HIV positive patients, >18 years of age, performed from January 2011 to April 2017, was to measure the occurrence of QFT conversions (negative to positive) and reversions (positive to negative) during routine clinical care. Continuous variables will be presented as mean, standard deviation. Categorical variables will be presented as the number and percentage of subjects in each category.

**Results.** There were a total of 381 cases, with an average age of 52.8 (±12) years of age. From those 249 patients had at least one QFT performed during the study period and 98 patients had 2 or more tests. 196 had a PPD test performed. From the patients that were initially QFT negative (N = 100), 7 converted to positive. There were a total of 10 patients who’s QFT was positive and were retested, and from those 7 reversed to negative (see Table 1). Most cases that reversed were considered to be low positives (5 of 6 from those within initial values available).

There were 21 patients had a history of positive PPD and 16 of those had negative QFT.

**Conclusion.** Reversions were common among HIV positive patients with high CD counts. Most reversions occurred with initial low positive QFT results. Providers should consider retesting among patients with QFT conversion and no history of TB exposure in low-risk settings. Future studies must be done to confirm these findings.

| Age | CD4 at (+) QFT | VL with (+) QFT | QTF TB Ag minus Nil value | CD4 at time QFT reversion | VL at the QFT | Antiretroviral therapy/ Latent-TB infection treatment |
|-----|---------------|-----------------|--------------------------|--------------------------|---------------|-----------------------------------------------|
| 56  | 1131 | 21.9 | +/: 2.96 | 877 | 42.1 | Yes/Yes |
| 66  | 502 | <20 | +/: 0.16 | 565 | <20 | Yes/Yes |
| 70  | Not done | <20 | +/: 1.63 | Not done | <20 | Yes/Yes |
| 61  | 424 | <20 | +/: 1.04 | 364 | <20 | Yes/Yes |
| 76  | Not done | <20 | +/: 1.07 | 307 | <20 | Yes/No |
| 56  | 249 | <20 | +/: 1.07 | 664 | <20 | Yes/No |
| 44  | 763 | 38.3 | +/: 1.06 | 664 | <20 | Yes/No |

*TB antigen minus Nil value between 0.35 and 2.0 is a low positive result.

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2023. **Attenuated Total Reflectance Fourier Transform Infrared Spectroscopy for Rapid Identification of Non-Fermenting Gram-Negative Bacilli Isolated from Patients with Cystic Fibrosis**

Emilie Vallieres, MD, FRCP1; Caroline Quach, MD, MSc, FRCP12; Liisa Lam, BSc; Fabien Ralla, PhD1; Michele Langella, BSc1; Jacqueline Sedman, PhD1; Martin Raymond Sr., MLT1; Pierre Lebel, MD, FRCP12; and Ashraf Ismail, PhD1.

**Session:** 234. Diagnostics – Bacterial Identification and Resistance

**Background.** Chronic respiratory infections with non-fermenting Gram-negative bacilli are a key feature of cystic fibrosis (CF). For microbiology laboratories, rapid and accurate identification of these bacteria is often challenging and labor intensive. This study was undertaken to evaluate whether attenuated total reflectance Fourier transform infrared (ATR-FTIR) spectroscopy could rapidly discriminate *Pseudomonas aeruginosa* (mucoid and non-mucoid), *Burkholderia cepacia complex, Burkholderia gladioli, Achromobacter* spp. and *Stenotrophomonas maltophilia.*

**Methods.** A total of 263 well-characterized clinical strains isolated from respiratory samples of patients with CF attending the CHU Sainte-Justine CF clinic were included in this study, consisting of 70 *P. aeruginosa,* 83 *Burkholderia* spp., 52 *Achromobacter* spp. and 58 *Stenotrophomonas maltophilia* isolates from the biobank. Isolates were thawed and sub-cultured twice on sheep blood (5%) agar. ATR-FTIR spectral acquisition was performed in triplicate for each isolate. Multivariate statistical analysis of the ATR-FTIR spectra was performed by hierarchical cluster analysis (HCA) and principal component analysis (PCA) in conjunction with the use of a feature selection algorithm.

**Results.** An ATR-FTIR spectral database consisting of 789 spectra of *P. aeruginosa,* *Burkholderia* spp., *Achromobacter* spp. and *Stenotrophomonas maltophilia* was created in this study. Complete discrimination among all four genera as well as among three species within the *B. cepacia complex and B. gladioli* was achieved based on HCA and PCA of the spectra in the database. ATR-FTIR analysis of a validation set consisting of 30 isolates was conducted in parallel with identification by MALDI-TOF mass spectrometry and yielded >95% concordance between the two techniques.

**Conclusion.** ATR-FTIR spectroscopy is a promising tool for rapid, inexpensive and accurate identification of non-fermenting Gram-negative bacilli. Additional work is needed to further expand the spectral database, particularly with mucoid strains.

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2024. **Aminoglycoside Susceptibility Agreement between an Automated System and Broth Microdilution for Carbapenem-resistant Enterobacteriaceae**

Brandon Kulengowski, PharmD, MS1; Matthew Briggs, BS2; Channah Gallagher, BA1; and David S. Burgess, PharmD, FCCP1. 1Pharmacy Practice and Science, University of Kentucky, College of Pharmacy, Lexington, Kentucky; 2Pharmacy Practice and Science, University of Kentucky, Lexington, Kentucky, 3Pharmacy Practice and Sciences, University of Kentucky, Lexington, Kentucky, 4University of Kentucky, College of Pharmacy, Lexington, Kentucky

**Session:** 234. Diagnostics – Bacterial Identification and Resistance

**Background.** CRE are a world-wide public health challenge with extremely limited treatment options. Aminoglycosides have variable susceptibility against these organisms. At our institution, amikacin has been active against these isolates and used as part of a combination regimen for CRE treatment. In this study, we compared the susceptibility results for 3 aminoglycosides between an automated susceptibility system (Phoenix) and broth microdilution (BMD). Aminoglycosides are classified as either intermediate, resistant, or susceptible as defined by CLSI guidelines. The primary CRE was *K. pneumoniae* (46%), followed by *Enterobacter* spp. (32%), and *E. coli* (6%). The categorical agreement ranged 58% (gentamicin) to 68% (tobramycin). Automated susceptibility system provided significantly higher susceptibility from 14% (gentamicin) to 30% (tobramycin and amikacin).

**Methods.** Gentamicin, tobramycin, and amikacin susceptibility were determined in our academic medical center microbiology laboratory using an automated susceptibility system (Phoenix) and broth microdilution (BMD) according to CLSI guidelines against 120 recent CRE clinical isolates. Categorical agreement was defined between methods as classification of isolates in the same susceptibility category using CLSI breakpoints. Minor, major and very major error rates were calculated for each aminoglycoside.

**Results.** The primary CRE was *K. pneumoniae* (46%), followed by *Enterobacter* spp. (32%), and *E. coli* (6%). The categorical agreement ranged 58% (gentamicin) to 68% (tobramycin). Automated susceptibility system provided significantly higher susceptibility from 14% (gentamicin) to 30% (tobramycin and amikacin).

| Broth Microdilution | Automated Susceptibility System |
|---------------------|---------------------------------|
| Aminoglycoside | %S | MIC<sub>50</sub> | MIC<sub>90</sub> | MIC range | %S | MIC<sub>50</sub> | MIC<sub>90</sub> |
| Amikacin | 63% | 16 | 32 | 1 to ≥128 | 93% | ≥8 | ≤32 |
| Tobramycin | 12% | 16 | ≥128 | ≥2 to ≥128 | 42% | >8 | ≤32 |
| Gentamicin | 17% | 16 | 128 | 0.25 to ≥128 | 31% | >8 | ≤32 |

**Disclosures.** All authors: No reported disclosures.
Methods. A total of 54 pediatric PBC (33 spiked, 21 fresh) were tested within 8 hours of positivity (30 Gram-positive, 20 Gram-negative, 2 yeast, 2 off-panel species). A 0.5 ml aliquot was placed in an Accelerate Pheno™ system which automates sample setup, incubation and reading. Automation minimizes hands-on steps, increasing efficiency, productivity and quality; impacting the rapid identification of pathogens. This system went live in May, 2015.

**Conclusion.** Automated susceptibility system over predicts the true susceptibility of CRE against all 3 aminoglycosides. This could be a major impact on the potential utility of the aminoglycosides especially amikacin for CRE infections.

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2025. Impact of Automation Process on Microbiological Laboratory Efficiency Sauhailereine Suady Barake, MD, MS; Anna Smrcek, MLS, ASCP; Ying Tabak, PhD; Andrew Jasen, MPH; Latha Vankeepuram, MS; David Sellers, RN; and Fatima Levent, MD. **Department of Internal Medicine, Division of Infectious Diseases, Texas Tech University Health Sciences Center, Lubbock, Texas, Clinical Laboratory, University Medical Center, Lubbock, Texas, Clinical Laboratory, University Medical Center, Lubbock, Texas, Becton, Dickinson and Company, Franklin Lakes, New Jersey, Becton Dickinson, Franklin Lakes, New Jersey, Clinical Development, Becton Dickinson, Franklin Lakes, New Jersey, Pediatric University Health System, Lubbock, Texas**

**Session:** 234. Diagnostics - Bacterial Identification and Resistance

**Background.** University Medical Center (UMC) Lubbock made a significant investment to improve the quality and efficiency of the microbiology laboratory by implementing the Becton Dickinson (BD) Kiestra Total Automation Laboratory (TAL) system which automates sample setup, incubation and reading. Automation minimizes hands-on steps, increasing efficiency, productivity and quality; impacting the rapid identification of pathogens. This system went live in May, 2015.

**Methods.** After approval from the Quality Improvement Review Board, a retrospective analysis of electronically captured microbiological data from a BD research database was used to compare pre-installation (January-December 2013) vs. post-installation period (January-October 2016). Twelve common and clinically imical organisms were assessed. The following reporting times were compared: First gram stain, Organism Identification (ID), First antimicrobial susceptibility (AST), and final AST. Reporting time was examined in a 24-hour spectrum divided into day (06:00–12:00), afternoon (12:00–18:00), evening (18:00–21:00) and night (21:00–06:00). Statistical analysis was performed with SAS software version 9.2. Data was analyzed using Chi-squared test. A P value of <0.05 was considered statistically significant.

**Results.** Overall 14,179 positive results were reported during the study period. Specimens were collected using various types of blood cultures, emergency room, obstetric and outpatient laboratories (35%, 32%, 23%, and 10%, respectively). The most common sources were urine, wound/skin, blood, and respiratory (40%, 25%, 14%, and 10%, respectively). Compared with pre-installation vs. post-installation period, a significant improvement in reporting time was noted: Time to first gram stain (30% vs. 56%), First gram identification (14% vs. 58%), first AST (8% vs. 62%) and final AST (7% vs. 58%) (P < 0.01).

**Conclusion.** Continued microbiology laboratory efficiency efforts lead to significant improvement in reporting time which resulted in improved laboratory efficiency. The single VME and 2 of 3 ME were adjudicated to either insufficient time to labor and reporting during night shift in all measures was noted: Time to first gram stain (30% vs. 56%), First gram organism identification (14% vs. 58%), first AST (8% vs. 62%) and final AST (7% vs. 58%) (P < 0.01).

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

2026. Performance Verification of the Accelerate Pheno® System for Rapid Identification and Antimicrobial Susceptibility Testing from Positive Blood Culture in a Pediatric Population Judy Daly, PhD, plots; Aubrie Holmes, MLS, ASCP; Abby Phillips, MLS, ASCP; Mandy Dickey, MLS, ASCP; Ranae Grand-Pre, MLS, ASCP; E. Kent Korgenski, MS; Andrew Pavia, MD, FIDSA, FSHEA, FPID; Emily Thorell, MD, MSCT; and Anne J. Blaschke, MD, FIDSA, FIDSA, FPID. **Primary Children's Hospital, Salt Lake City, Utah, University of Utah, Salt Lake City, Utah, Department of Pediatrics, Pediatric Clinical Program, University of Utah School of Medicine and Intermountain Healthcare, Salt Lake City, Utah, Department of Pediatrics, Division of Pediatric Infectious Diseases, University of Utah School of Medicine, Salt Lake City, Utah**

**Session:** 234. Diagnostics - Bacterial Identification and Resistance

**Background.** Early targeted antibiotic therapy is crucial when treating pediatric patients with bacteremia. While identification (ID) and antimicrobial susceptibility testing (AST) of bloodstream pathogens are critical to optimizing therapy, convention methods can take days resulting in inappropriate use of broad-spectrum antibiotics. The automated Accelerate Pheno® system (AXDX) provides ID in <90 minutes and AST in <7 hours directly from positive blood culture (PBC), enabling clinicians to optimize antibiotic therapy sooner to improve patient outcomes. In addition, the unique AXDX Monomicrobial call effectively rules out polymicrobial samples by indicating only one bacteria is present in the PBC. This study verifies AXDX performance compared with current laboratory ID and AST methods.

**Methods.** A total of 54 pediatric PBC (33 spiked, 21 fresh) were tested within 8 hours of positivity (30 Gram-positive, 20 Gram-negative, 2 yeast, 2 off-panel species). A 0.5 ml aliquot was placed in an Accelerate Pheno™ system in a clinically significant microbiology laboratory that provides services to inpatient and outpatient locations (35%, 32%, 23%, and 10%, respectively). The most common sources were urine, wound/skin, blood, and respiratory (40%, 25%, 14%, and 10%, respectively). The most common organisms were urin, wound/skin, blood, and respiratory (35%, 32%, 23%, and 10%, respectively). Compared with pre-installation vs. post-installation period, a significant improvement in reporting time was noted: Time to first gram stain (30% vs. 56%), First gram organism identification (14% vs. 58%), first AST (8% vs. 62%) and final AST (7% vs. 58%) (P < 0.01).

**Conclusion.** Continued microbiology laboratory efficiency efforts lead to significant improvement in reporting time which resulted in improved laboratory efficiency. The single VME and 2 of 3 ME were adjudicated to either insufficient time to laboratory reporting during night shift in all measures was noted: Time to first gram stain (30% vs. 56%), First gram organism identification (14% vs. 58%), first AST (8% vs. 62%) and final AST (7% vs. 58%) (P < 0.01).

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