2171. Phenotypic Correlations for the Presence of CTX-M in Enterobacteriaceae and meca in Staphylococcus aureus using the Verigene® Blood Culture System

Nigo Masayuki, MD; Audrey Wang, PhD; Cesar A. Arias, MD, MSc, PhD, FIDSA; University of Texas in Houston, Houston, Texas; University of Texas Health Science Center, University of Texas Health Science Center, Houston, Texas; CARMIG, UTH ealth and Center for Infectious Diseases, UTH School of Public Health, Houston, Texas; Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogotá, Colombia, Houston, Texas

Session: 243. Bacterial Diagnostics
Saturday, October 5, 2019: 12:15 PM

Background. Rapid identification of antimicrobial resistance markers has the potential to help targeting antimicrobial therapy and enhance efforts for antibiotic stewardship. However, limited data are available to correlate phenotypic and genotypic results for some of these platforms in positive blood cultures (BC). Here, we aimed to evaluate the ability of the Verigene® (VG) Blood Culture System to predict phenotypic susceptibility patterns with the detection of the genes encoding the CTX-M in Enterobacteriaceae and meca in S. aureus (SA) in a large dataset.

Methods. Phenotypic susceptibility and VG results were retrospectively collected between August 2017 and December 2018 from 12 hospitals in Houston, TX. VG testing was performed on only the first isolate was considered in positive predictive BCs. The VG report of the presence of blaCTX-M or meca was correlated with phenotypic susceptibility to ceftriaxone (CTO) (E. coli [EC] and Klebsiella spp.[KL]) or oxacillin (SA), respectively.

Results. We identified a total of 5,937 VG results. The final analysis was performed on 2,356 cases where EC, KL, or SA were identified. Isolates detected KPC and NDM by VG were excluded. 30 EC/KL were missed by VG in polymicrobial bacteria. 7 polymicrobial positive BCs with coagulase-negative staphylococci were mislabeled as MecA positive MSSA. Among isolated detected by VG, there were the high sensitivity and specificity of CTX-M to identify CTO resistance (97.2% and 99.7% in EC and 91.4% and 99.2% in KL). For SA, the sensitivity and specificity of meca were 100% and 99.6% to identify oxacillin resistance. 2 isolates with meca positive by VG were reported as oxacillin-susceptible.

Conclusion. Our results revealed that there is a high correlation between VG and phenotype. For SA, discrepancies between genotype and phenotype seem to be influenced by the presence of other organisms in the sample. Genotypic information seems reliable and should guide targeted therapy in bloodstream infections.

Table. Comparison of CTX-M and CTO in EC and KL, and meca and Oxacillin in SA

|        | Klebsiella pneumoniae | Escherichia coli | Enterobacteriaceae | Pseudomonas and Acinetobacter |
|--------|----------------------|-----------------|---------------------|-------------------------------|
| Sensitivity (%) | 89.58               | 100             | 90.74               | 20.00                         |
| Specificity (%) | 96.55               | 13.67           | 11.67               | 100                           |
| Positive Likelihood ratio | 25.98 (3.97-178.66) | 3.95-34.21     | 13.25               | 0.10 (0.05-0.25)              |
| Negative Likelihood ratio | 0.01               | 0.00            | 0.10                | 100                           |
| Positive predictive value (%) | 63.91              | 81.58           | 100                 | 4.33-48.09                   |
| Negative predictive value (%) | 87.03              | 100             | 96.31               | 43.71                         |

Disclosures. All authors: No reported disclosures.

2172. True Positive of Common Blood Culture Contaminants among Pediatric Hospitals in the United States, 2009–2016

Alicen B. Spaulding, PhD, MPH; David Watson, PhD; Jill Dreyfus, PhD, MPH; Phillip Heaton, PhD; Anupam Kharbanda, MD, MS; Children’s Minnesota Research Institute, Minneapolis, Minnesota; ^Premier, Inc., Charlotte, North Carolina

Session: 243. Bacterial Diagnostics
Saturday, October 5, 2019: 12:15 PM

Background. Distinguishing blood culture (BC) results between common contaminants (CC) and truly pathogenic organisms can be challenging, especially among pediatric patients, but is important for effective clinical care. However, no recent studies have analyzed the true positivity of common BC contaminants in pediatric patients using linked large laboratory data from a large national sample of United States hospitals.

Methods. We conducted a retrospective cohort study among patients ages < 19 using the Premier Healthcare Database (2009–2016), limiting to hospitals reporting ≥ 4 years of BC data and encounters with one of the five most frequent CC among laboratory-conformed BC. True positivity was defined for each CC as a second positive BC within 48 hours among all BCs. A multivariable logistic regression model including all variables significant in univariate analyses was created comparing encounters: (1) with and without a second BC; and (2) second BC positive vs. negative, with corresponding adjusted odds ratios (aOR) and 95% confidence intervals (CI) reported.

Results. A total of 5056 isolates corresponding to 4915 encounters with a CC were included in this analysis; 3075 (61%) isolates had a second BC within 48 hours. Adjusted odds of a second BC were higher for encounters from urban (aOR: 1.73, 95% CI: 1.31, 2.29) and ≥ 500 bed hospitals (aOR: 1.40, 95% CI: 1.20, 1.63). True positivity was 20.2% for coagulase-negative staphylococci (CoNS), 5.9% for Bacillus spp., 5.2% for Viridans group streptococci, 5.0% for Diphtheroids spp., and 3.1% for Micrococcus spp. True positivity for CoNS was higher among neonates but all other organisms were higher for non-neonates (figure). Adjusted odds of true positivity were higher for encounters with chronic conditions (OR 1.44, 95% CI: 1.13, 1.82), a central line in place (OR: 1.65, 95% CI: 1.30, 2.10), per length of stay day (OR: 1.01, 95% CI: 1.01, 1.01), and with an intensive care unit admission (OR: 1.39, 95% CI: 1.08, 1.77).

Conclusion. True positivity varied substantially by organism, and in most cases was higher among non-neonates. Regional variations for conducting a second BC within 48 hours were found, and more seriously ill patient encounters were more likely to have a common contaminant be pathogenic.

Disclosures. All authors: No reported disclosures.

2173. Detection of Chlamydia psittaci by rtPCR in Outbreak Specimens Tested at CDC—2018

Olivia L. McGovern, PhD, MS; Kelly Shaw, PhD; Christine Szablewski, DVM, MPH; Julie Gabel, DVM, MPH; Caroline Holsinger, DrPH; Skyler Brennan, MPH; Bernard Wolf, MS; Alvaro J. Benitez, BS; Maureen Diaz, PhD, MPH; Kathleen A. Thurnam, MS; Jonas Winchell, PhD; Miwako Kobayashi, MD, MPH; CARMIG, UTH ealth and Center for Infectious Diseases, UTH School of Public Health, Houston, Texas; Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogotá, Colombia, Houston, Texas; University of Texas Health Science Center, University of Texas Health Science Center, Houston, Texas; CARMIG, UTH ealth and Center for Infectious Diseases, UTH School of Public Health, Houston, Texas; Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogotá, Colombia, Houston, Texas

Session: 243. Bacterial Diagnostics
Saturday, October 5, 2019: 12:15 PM

Background. Psittacosis is a respiratory illness caused by Chlamydia psittaci. The most commonly available diagnostic tests are serologic tests, which have low sensitivity and can cross-react with other chlamydial species. Serologic tests also require paired sera collected weeks apart, which is impractical for patient management. Real-time polymerase chain reaction (rtPCR) testing for C. psittaci is rapid, sensitive, and specific. However, rtPCR testing is only available at the CDC Respiratory Diseases Branch laboratory, and appropriate clinical specimen types need to be validated since psittacosis case detection is infrequent. In 2018, the first large psittacosis outbreak in the United States in 30 years occurred, allowing assessment of rtPCR performance among multiple clinical specimen types.

Disclosures. All authors: No reported disclosures.
Methods. rTPCR test positivity rate and turnaround time were determined among 89 specimens tested at CDC from 54 outbreak patients with suspected psittacosis. rTPCR testing was performed on nucleic acid extracted from clinical specimens using oligonucleotides targeting the C. psittaci locus tag CPSTF_RS01985. Clinical information was collected by patient interview and medical record review.

Results. Positivity rates among the most common specimen types were 4.4% (2/46) for nasopharyngeal (NP) swab, 36.4% (8/22) for sputum, and 80.0% (4/5) for stool. Of 21 (24%) specimens with available data, the average time from patient symptom onset to specimen collection was 6 days (range 1–11 days). C. psittaci was detected in 13 of 54 outbreak patients tested and 13 patients had radiographically-confirmed pneumonia, and 7 were rTPCR-positive from a lower respiratory specimen only. Paired sputum and NP swab specimens were tested for 6 patients; C. psittaci was detected in all sputum but only 1 NP swab. The positive NP swab was from a patient requiring intubation and intubation. All results were reported within 1 business day of specimen receipt in the lab.

Conclusion. These data suggest that lower respiratory specimens are more sensitive than NP swabs for rTPCR detection of C. psittaci; stool might be a suitable alternative. Widespread implementation of rTPCR testing using appropriate specimen types could improve psittacosis detection and inform timely public health interventions.

| TABLE 1. Qualitative and cycle threshold (Ct) results for outbreak patients with rTPCR detection of C. psittaci |
|---------------|-----------------|-----------------|-----------------|
| Patient       | Sputum          | Bronchoalveolar | Upper Respiratory | Gastrointestinal |
|---------------|-----------------|-----------------|-----------------|-----------------|
| 1             | Pos (26)        |                 |                 |                 |
| 2             | Pos (30)        |                 |                 |                 |
| 3             | Pos (30)        |                 |                 |                 |
| 4             | Pos (28)        |                 |                 |                 |
| 5             | Pos (28)        |                 |                 |                 |
| 6             | Pos (27)        |                 |                 |                 |
| 7             | Pos (28)        |                 |                 |                 |
| 8             | Pos (30)        |                 |                 |                 |
| 9             | Pos (30)        |                 |                 |                 |
| 10            | Pos (31)        |                 |                 |                 |
| 11            | Neg             |                 |                 |                 |
| 12            | Neg             |                 |                 |                 |
| 13            | Neg             |                 |                 |                 |

Upper Respiratory: Bronchoalveolar Lavage; Lower Respiratory: NP Swab; Gastrointestinal: Stool.