	Klebsiella pneumoniae	*Escherichia Coli*	*Enerobacteriaceae*	*Pseudomonas and Acinetobacter*
Sensitivity (%) [confidence interval (CI)]	89.58 (77.34-96.53)	100 (36.76-100)	90.74 (79.70-96.92)	20.00 (4.33-48.09)
Specificity % (CI)	96.55 (82.24-99.91)	91.43 (76.94-98.20)	93.15 (84.74-97.74)	100 (71.5-100)
Positive Likelihood ratio (CI)	25.98 (3.78-178.68)	11.67 (3.95-34.42)	13.25 (5.66-31.00)	-
Negative Likelihood ratio (CI)	0.10 (0.05-0.25)	0.00	0.10 (0.04-0.23)	0.8 (0.62-1.03)
Positive predictive value (%)	97.28	63.91	83.58	100
Negative predictive value (%)	87.03	100	96.31	43.71

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

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

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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 persistent positive 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 was identified. Isolates detected KPC and NDM by VG were excluded. 30 EC/KL were missed by VG in polymicrobial bacteremia. 7 polymicrobial positive BCs with coagulase-negative staphyloccocci 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-suscpetible.

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

EC		CTO R (%)	CTO S (%)
CTX-M	+	239 (97.2)	2 (0.2)
	-	7 (0.8)	842 (99.7)
		246	844

KL		CTO R (%)	CTO S (%)
CTX-M	+	64 (91.4)	2 (0.8)
	-	6 (8.5)	255 (99.2)
		70	257

SA		Oxacillin R (%)	Oxacillin S (%)
mecA	+	427 (100)	2 (0.4)
	-	0 (0)	462 (99.6)
		427	464

R, Resistant, S, Susceptible

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

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

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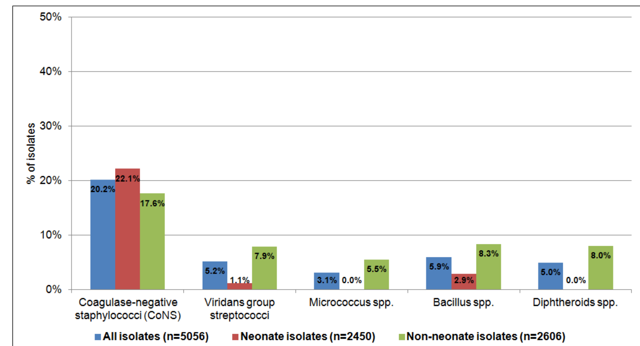
Background. Distinguishing blood culture (BC) results between common contaminants (CC) and truly pathogenic organisms can be challenging, especially among pediatric patients, but is important for effective clinical care. However, no recent studies have analyzed the true positivity of common BC contaminants in pediatric patients using linked 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-confirmed 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 (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.

Figure. True positivity among the top 5 most common contaminants, comparing neonates and non-neonates, among patients less than 19 years of age admitted to one of 140 Premier Healthcare Database hospitals in the United States, 2009-2016.



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

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

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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, rtRCR 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.

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 CPSIT_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 specimens from 13 of 54 outbreak patients tested (Table 1); all 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 intensive care unit admission 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 [a]) results for outbreak patients with rtPCR detection of *C. psittaci*

	Lower Respiratory		Upper Respiratory	Gastrointestinal
Patient	Sputum	Bronchoalveolar lavage	NP Swab	Stool
1	Pos (26)		Neg	
2	Pos (30)		Neg	
3	Pos (30)		Neg	Pos (37)
4	Pos (26)		Neg	
5	Pos (28)		Neg	
6	Pos (27)		Pos (33)	
7	Pos (28)			Pos (32)
8	Pos (30)			Neg
9		Pos (30)		
10		Pos (31)		
11			Neg	Pos (38)
12			Pos (31) [b]	
13				Pos (32)

[a] Average Ct values for triplicate rtPCR tests are shown in parentheses
[b] Second NP collected 3 days later was negative

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

2174. Comparison of the Verigene® and the ePlex® Blood Culture Identification Panels for Gram-Positive and Gram-Negative Bloodstream Infections

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Background. Rapid diagnostic testing for the management of bloodstream infections has become paramount to improving patient outcomes. The primary objective of this study was to assess the differences between 2 FDA approved instruments.

Methods. Retrospective study from August 2018 to April 2019 at the University of Maryland Medical Center. One positive blood culture from each patient was tested using the Verigene® blood culture Gram-positive (BC-GP) or Gram-negative (BC-GN) panels based on the Gram stain and then analyzed using the ePlex® Blood Culture Identification (BCID) Gram-positive (BCID-GP) or Gram-negative (BCID-GN) research-use-only panels and compared with culture results.

Results. The study consisted of 140 positive blood culture bottles. 14 bottles were excluded for a total of 55 GN and 71 GP bottles. Of the 55 GN bottles, 3 had 2 GN rods for a total of 58 GNRs. BCID-GN missed 1 *P. aeruginosa*, 2 *S. maltophilia*, and 1 *E. coli* for a 93% (53/57) positive agreement. The BCID-GN does not detect *A. junii* and therefore it was excluded. BC-GN did not identify 1 *K. pneumoniae* with a 98% (47/48) positive agreement. BC-GN does not include the detection of *S. maltophilia* (4), *Serratia* (4), *Morganella* (1), and *B. fragilis* (1)and these were excluded in the BC-GN analysis. CTX-M was the only resistant marker detected and both panels identified it correctly. 5 samples using the BCID-GN also detected Pan Gram-Positive; 3 grew GP organisms, the other 2 only grew *E. coli*. Of the 71 GP bottles, 3 had two GP bacteria totaling 74 GPs. BCID-GP missed 1 *S. aureus*, 1 invalid, and called an *E. faecalis* that was not identified by the reference method for a 99% (72/73) positive agreement. BC-GP does not detect *Micrococcus* (6) or *E. gallinarum* (1) and missed 1 *S. mitis/oralis* for a 99% (66/67) positive agreement. 18 samples were positive for mecA detected by both panels. 4 samples were vanA/B positive; 1 by BCID-GP was sensitive to vancomycin and not detected by BC-GP. BCID-GP detected 1 sample as Pan Gram-negative although a GNR was not detected.

Conclusion. BothVerigene® and ePlex® GP and GN panels have a high percent positive agreement. Laboratories should take into consideration the epidemiology of their bloodstream infections when deciding on panels for the rapid detection of bloodstream infections.

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

2175. Rapid Detection of Carbapenemase Producing Organisms Directly from Blood Cultures Positive for Gram-Negative Bacilli

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Background. The rapid detection of carbapenemase-producing organisms (CPOs) directly from blood cultures (BC) positive for Gram-negative bacilli (GNB) may accelerate the appropriate treatment of at-risk patients. Our objective was to evaluate the performance of two commercial assays in the rapid detection of CPOs directly from BC positive for GNB.

Methods. BC positive for GNB, taken from patients within the Calgary Health Zone over a 3 month period, were tested for the presence of CPOs with βCARBA® and NG-Test® CARBA 5. A subset of sterile BC samples was seeded with multi-drug-resistant (MDR) GNB. BC were incubated using the Bact-Alert™ system. Positive BC from clinical and seeded samples was tested directly with βCARBA and CARBA 5 from BC pellets processed for direct testing using an ammonium chloride lysis and wash method. Sensitivity, specificity, negative predictive value (NPV) and positive predictive value (PPV) were calculated with 95% confidence intervals for binomial proportions.

Results. 65 samples were tested (30 clinical, 35 seeded). Seeded samples included 1 GES, 4 IMP, 6 KPC, 1 co-producing KPC and NDM, 9 OXA, 4 VIM, 5 NDM, and 5 non-CPO carbapenem-resistant organisms. βCARBA had a sensitivity, specificity, NPV and PPV of 100% (88.4% - 100%), 65.7% (47.8–80.9%), 100%, and 71.4% (61.3%–79.8%), respectively. CARBA 5 had a sensitivity, specificity, NPV and PPV of 90.0% (73.5%–97.9%), 100% (90.0%–100%), 92.1% (80.0%–97.2%), and 100%. When excluding GES, which is known not to be detected by CARBA 5, sensitivity and NPV increased to 93.1% (77.2%–99.2%) and 93.1% (78.0%–98.1%), respectively. False negatives for βCARBA occurred with 1 VIM-1 and IMP-14.

Conclusion. This study demonstrates that the detection of CPOs directly from positive BC can be accurately achieved. βCARBA had excellent sensitivity but suffered from poor specificity. CARBA 5 had good sensitivity and specificity but is unable to detect certain CPOs. Testing positive BC directly using βCARBA and/or CARBA 5 may be useful in rapidly detecting CPOs. Results of direct testing from the CARBA5 assay would quickly identify patients amenable to treatment with avibactam combination compounds.

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

2176. A New Rapid Test for Detection of The Cefazolin Inoculum Effect (CIE) in Methicillin-*Susceptible Staphylococcus aureus* (MSSA)

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Background. Most MSSA harbor one of the four different variants of β-lactamase (BlaZ) (A, B, C and D). The CIE is defined as an MIC >16 μg/mL when a high inoculum (10^7 CFU/mL) is used and depends on the presence of BlaZ. The presence of the CIE has been associated with therapeutic failure in invasive MSSA infections. In some countries of South America, the prevalence of CIE is high, ranging from 36% to 51% (Colombia and Argentina, respectively). Type A BlaZ is most often associated with the CIE due to its high affinity for cefazolin. Here, we developed a rapid test based on the premise that the extracellular form of BlaZ is responsible for the CIE. We aimed to identify invasive MSSA that exhibit the CIE and validate the test in two cohorts of isolates from patients in Colombia and Argentina

Methods. 152 MSSA clinical isolates were collected from Colombia (n = 71) and Argentina (n = 81). We determined MIC at standard and high inoculum. We developed a test using induction of BlaZ with ampicillin (150 μg/mL) for 20 minutes and, using the supernatant for incubation with nitrocefin for 30 min. A change in color from yellow to red was considered positive. MSSA TX0117 (BlaZ +, with the CIE), ATCC 29213 (BlaZ-negative) and ATCC 25923 (BlaZ + lacking the CIE) were used as controls. BlaZ typing of all Argentinian isolates was available by sequencing

Results. A high proportion (43%) of MSSA exhibited the CIE (34% and 52% of Colombian and Argentinian isolates, respectively) by MIC. The rapid test identified 76% of isolates exhibiting the CIE and correctly ruled out all isolates lacking the CIE (sensitivity 80%, specificity 100%). Furthermore, the rapid test detected all isolates with the CIE that harbored Type A BlaZ from Argentina. Conversely, the test failed to identify the CIE in Argentinian isolates that produce type B and C BlaZ. The sensitivity and specificity of the rapid test for the Colombian isolates whose BlaZ type was unknown were 89% and 100%, respectively.