2169. An Algorithm-Based Approach Reduces Overuse of Meningitis/Encephalitis Multiplex PCR Panel

Melissa R. Gitman, MD[1]; Michael D. Nowak, MD[2]; Allison Navis, MD[1]; Emilia Mia. Sordillo, MD, PhD[1]; [1]Icahn School of Medicine at Mount Sinai, New York, New York; [2]The Mount Sinai Hospital, New York, New York

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Background. Syndromic molecular panels enable rapid diagnosis and optimized management of infections with significant morbidity and mortality, but may be overused without clear guidelines. A recent report indicated there was little clinical suspicion of infection in up to 1/3 of cases for which a FILMARRAY® Meningitis/Encephalitis Panel (ME Panel, bioMérieux) was ordered. We recently implemented the ME Panel in our multicenter health system. We assessed ME Panel use for the 6-month period following test implementation.

Methods. A testing algorithm was developed, vetted with our system-wide Infectious Diseases (ID) and Neuro-ID Services, and used as the basis for the education of the Emergency Medicine, Internal Medicine, Hospitalist, Pediatric, and Critical Care Medicine Services. Algorithm elements were embedded in the electronic medical record (EMR). Lab records and EMRs were reviewed for all patients tested by ME Panel or cerebrospinal (CSF) culture. Lab results, baseline demographic and underlying medical history, and results of singleplex viral PCR CSF tests and the multiplex NY State Encephalitis PCR Panel (NYS Panel, Wadsworth Laboratory, Albany, NY) were recorded. ME Panel results were compared with other findings.

Results. 115 ME Panels were performed, with 5 (4%) positives [1 *N.meningitidis,* 1 *H.influenzae*, 1 cytomegalovirus (CMV), 1 Herpes simplex virus type 1 (HSV1), and 1 varicella zoster virus (VZV)]. Other findings were consistent with true infection for the *N. meningitis*, HSV and VZV; the CMV was likely reactivation. Significance of the *H. influenzae* was unclear. There were 830 CSF cultures, with 38 (4%) positive; 5 of the 38 were ME Panel targets. 29 NYS Panels were sent [1 positive each for Human Herpesvirus 6 (HHV6) and Epstein Barr Virus (EBV)]. Finally, 7 singleplex PCRs were positive [5 HSV, 1 CMV and 1 HHV6], including one negative by ME Panel.

Conclusion. We did not find ME Panel overuse; rather, we found several cases for which the ME Panel could have given a more rapid diagnosis. We did identify areas for improvement in test ordering, such as minimizing duplicate testing (e.g., singleplex PCR) A multi-disciplinary approach engaging stakeholders in the lab, ID and Neuro-ID can assist appropriate test utilization and diagnostic stewardship.

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

2170. Xpert Carba-R Assay on Flagged Blood Culture Samples: Clinical Utility in Intensive Care Unit Patients with Gram-Negative Bacteremia

Surendran Rajendran, MD;
Ram Gopalakrishnan, MD, MRCP, AB (Internal Medicine), AB (Infectious Diseases);
Anil Tarigopula, MD, DNB; Sureshkumar Dorairajan, MD, FNB ;
Senthur Nambi Panchatcharam, MD, FNB;
Nandini Sethuraman, MD; Ramasubramanian V, MD, FRCP, DTM&H; Apollo Hospital, Chennai, Tamil Nadu, India

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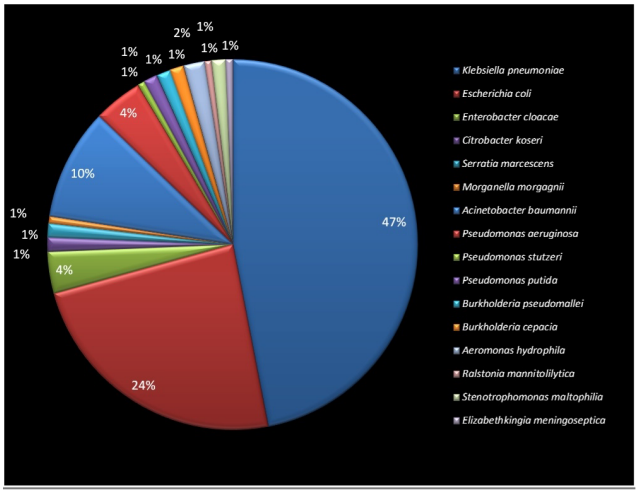
Background. Rapid molecular diagnostics that predict carbapenem resistance (CR) well before the availability of routine drug sensitivity testing (DST) can serve as an antimicrobial stewardship tool in the context of high rates of carbapenem-resistant enterobacteriaceae (CRE).

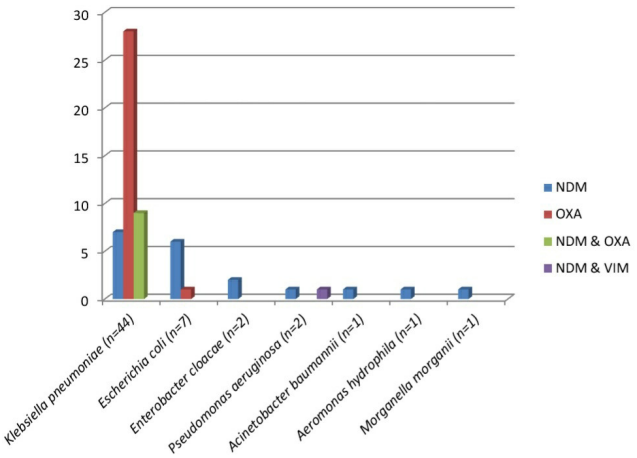
Methods. A retrospective observational study of patients more than 18 years of age on whom Xpert Carba-R (FDA approved for rectal swab specimen) was done on Gram-negative bacteria (GNB) flagged blood culture samples, in a tertiary care Indian intensive care unit between January 2015 and November 2018.

Results. The study included 160 patients who had a median (Sequential Organ Failure Assessment) SOFA score of 16. A total of 164 GNB were isolated with 4 patients having polymicrobial bacteremia. *Klebsiella pneumoniae* and *Escherichia coli* were the predominant isolates (Figure 1). Carba-R was positive in 58/164 (35.36%) samples (Figure 2) and 73/161 isolates (45.34%) were CR (after excluding intrinsic CR organisms) on routine DST. The distribution of CR genes overall was: OXA-48 like (29/58–50%), followed by NDM (19/58–32.7%), followed by OXA-48 and NDM co-expression (9/58–15.51%) and in individual groups as in Figure 3. The sensitivity, specificity, positive likelihood ratio, negative likelihood ratio, positive predictive value (PPV) and negative predictive value (NPV) of Carba-R vs. routine DST were 90.74%, 93.15%, 13.25, 0.10, 83.58% and 96.31% for enterobacteriaceae (Figure 4). The median time to obtaining the Carba-R report was 30 hours 34 minutes vs. 74 hours and 20 minutes for carbapenem resistance on routine DST. Based on the Carba-R report, 9.72% of patients had escalation of antibiotics (e.g., colistin) to cover CR organisms and 27.08% had de-escalation from CR cover that had already been started.

Conclusion. Xpert Carba-R serves as a rapid diagnostic tool for CR Gram-negative bacteremia, particularly hospital-acquired enterobacteriaceae in intensive care units with a high CRE prevalence. It assists in initiating early appropriate therapy and early institution of infection control measures in these patients, as well as in de-escalation of colistin in patients without carbapenem resistance. We recommend that clinicians consider routinely utilizing this test in this setting.



Organisms	Drug sentivity testing		CR GENE +VE		CR GENE –VE	
	Carbapenem Resistant(CR)	Carbapenem Sensitive(CS)	CR	CS	CR	CS
Klebsiella pneumoniae (n=77)	48 (62.33%)	29 (37.66%)	43 (89.58%)	1 (3.4%)	5 (10.41%)	28 (96.5%)
Escherichia coli (n=39)	4 (10.25%)	35 (89.74%)	4 (100%)	3 (8.57%)	0	32 (91.42%)
Enterobacter cloacae (n=6)	2 (33.33%)	4 (66.66%)	2 (100%)	0	0	4 (100%)
Citrobacter koseri (n=2)	0	2	-	-	0	2
Serratia marcescens (n=2)	0	2	-	-	0	2
Morganella morganii (n=1)	0	1	-	1	-	-
Acinetobacter baumannii (n=16)	11 (68.75%)	5 (31.25%)	1 (9.09%)	0	10 (90.9%)	5 (100%)
Pseudomonas aeruginosa (n=7)	4 (57.14%)	3 (42.85%)	2 (50%)	0	2 (50%)	3 (100%)
Pseudomonas stutzeri (n=1)	0	1	-	-	0	1
Pseudomonas putida (n=2)	0	2	-	-	0	2
Burkholderia pseudomallei (n=2)	0	2	-	-	0	2
Burkholderia cepacia (n=2)	2		-	-	2	0
Aeromonas hydrophila (n=3)	2	1	1	0	1	1
Ralstonia mannitolilytica (n=1)	0	1	-	-	0	1
Stenotrophomonas maltophilia (n=2)	-	-	-	-	-	-
Elizabethkingia meningoseptica (n=1)	-	-	-	-	-	-



	Klebsiella pneumoniae	*Escherichia Coli*	*Enterobacteriaceae*	*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

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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[1]; Audrey Wanger, PhD[2];
Cesar A. Arias, MD, MSc, PhD, FIDSA[3]; [1]University of Texas in Houston, Houston, Texas; [2]University of Texas Health Science Center, University of Texas Health Science Center, Houston, Texas; [3]CARMiG, UTHealth and Center for Infectious Diseases, UTHealth School of Public Health, HOU, Texas; [3]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, BOG, COL, Houston, Texas

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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

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

Alicen B. Spaulding, PhD, MPH[1]; David Watson, PhD[1];
Jill Dreyfus, PhD, MPH[2]; Phillip Heaton, PhD[1]; Anupam Kharbanda, MD, MS[1];
[1]Children's Minnesota Research Institute, Minneapolis, Minnesota; [2]Premier, Inc., Charlotte, North Carolina

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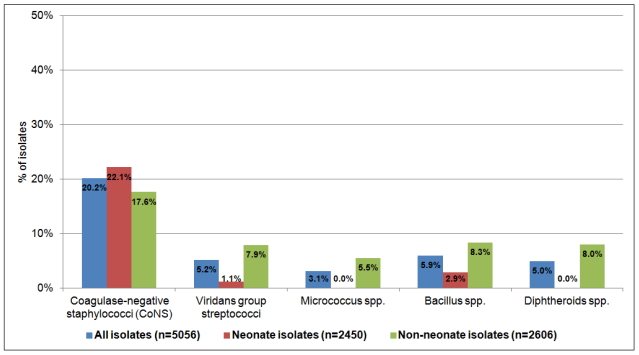
Background. Distinguishing blood culture (BC) results between common contaminants (CC) and truly pathogenic organisms can be challenging, especially among pediatric patients, but is important for effective clinical care. However, no recent studies have analyzed the true positivity of common BC contaminants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



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

Olivia L. McGovern, PhD, MS[1]; Kelly Shaw, PhD[2];
Christine Szablewski, DVM, MPH[3]; Julie Gabel, DVM, MPH[3];
Caroline Holsinger, DrPH[2]; Skyler Brennan, MPH[3]; Bernard Wolff, MS[1];
Alvaro J. Benitez, BS[4]; Maureen Diaz, PhD, MPH[1]; Kathleen A. Thurman, MS[1];
Jonas Winchell, PhD[4]; Miwako Kobayashi, MD, MPH[1]; [1]Centers for Disease Control and Prevention, Atlanta, Georgia; [2]Virginia Department of Health, Richmond, Virginia; [3]Georgia Department of Public Health, Atlanta, Georgia; [4]CDC, Atlanta, Georgia

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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.