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

Melissa R. Gitman, MD¹; Michael D. Nowak, MD²; Allison Navis, MD¹; Emilia Mia. Sordillo, MD, PhD¹; ¹Icahn School of Medicine at Mount Sinai, New York, New York; ²The Mount Sinai Hospital, New York, New York

Session: 243. Bacterial Diagnostics

Saturday, October 5, 2019: 12:15 PM

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

Session: 243. Bacterial Diagnostics

Saturday, October 5, 2019: 12:15 PM

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 Gramnegative 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.



	Drug sentivity testing		CR GENE +VE		CR GENE -VE	
Organisms	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)	-	-	-	-	-	-

