and Laboratory Medicine, Rhode Island Hospital, Providence, Rhode Island, [6]Children's Healthcare of Atlanta, Atlanta, Georgia, [7]Department of Pediatrics, Division of Pediatric Infectious Diseases, University of Utah School of Medicine, Salt Lake City, Utah, [8]Clinical Microbiology, Primary Children's Hospital, Salt Lake City, Utah, [9]Children's Mercy Hospital and Clinics, Kansas City, Missouri, [10]BioFire Diagnostics, LLC, Salt Lake City, Utah, [11]Microbiology Laboratory, Children's Mercy Hospital and Clinics, Kansas City, Missouri

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Background. Early determination of viral etiology among febrile children with suspicion of systemic infection by use of rapid molecular assay could impact patient care. BioFire® FilmArray® Childhood Systemic Infection (CSI) Panel is a non-FDA cleared research use only sample-to-answer PCR-based assay that includes identification of seven viruses from 200 µl of whole blood collected from children suspected of systemic infection. The aim of this prospective multicenter study was to determine the viral diagnostic yield and potential impact of CSI panel on management of pediatric sepsis.

Methods. Children <18 years with suspected systemic infections were prospectively enrolled in emergency rooms at seven healthcare facilities. Febrile children with a clinician order of blood culture for sepsis evaluation were enrolled and additional blood was collected with the standard of care (SOC) blood culture. Blood samples were tested by the CSI Panel on the FilmArray platform. Demographic and laboratory test results from SOC blood, urine and cerebrospinal fluid (CSF) cultures were recorded.

Results. Among 1,022 children enrolled, data for 1,002 was complete. The CSI Panel testing of whole blood detected 203 (20%) viral infections including 14 (7%) with dual/multiple viruses. The median age of children with viral detections (20 months) was significantly lower than children without viral detections (54 months) ($P < 0.01$).The viruses detected were enterovirus (54%), adenovirus (22%), cytomegalovirus (15%), parvovirus B19 (15%) and parechovirus (3%). Herpes simplex virus 1 and 2 were not detected. Among 203 positive and 799 negative viral detections with the CSI Panel, blood culture was positive in 2 (1%) and 24 (3%) children respectively ($P = 0.14$). All CSF bacterial cultures ordered were negative. Urine culture was positive in 7/83 (8.4%) and 31/266 (11.7%) viral positive and negative children respectively ($P = 0.55$).

Conclusion. The CSI Panel detected virus in blood from 20% of febrile children suspected of systemic infection. Concurrent bacterial infection of blood and urine was lower in children that were viral positive vs. negative. Prompt determination of viral etiology using the CSI Panel has the potential to optimize care of children with suspected systemic infection.

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2085. Evaluation of Panther Fusion Flu A/B/RSV, AdV/hMPV/RV and Paraflu Assays for the Detection of Respiratory Viruses in Children

Ferdaus Hassan, PhD; Jordan Crawford, BS; Dithi Banerjee, PhD and Rangaraj Selvarangan, PhD; Children's Mercy, Kansas City, Missouri

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Background. There are many FDA cleared multiplexed respiratory assays available in the United States, ranging from 3 to 20 targets per assay. FilmArray Respiratory Panel (RP) is one of the mega-multiplexed assay, includes 20 targets and results are available in 1 hour. Recently Hologic has received FDA-clearance for several smaller respiratory "Panther Fusion assays" (3–4 targets/assay) and results are available in <3 hours. The aim of this study was to evaluate the performance of three panther fusion multiplexed assays: (i) Flu A/B/RSV assay, (ii) adenovirus/human metapneumovirus/rhinovirus assay, and (iii) paraflu (parainfluenza virus 1–4) assay in comparison to RP assay.

Methods. A total of 194 frozen nasopharyngeal swab samples (from 2016 to 2018) obtained from children aged ≤18 years and previously tested by RP as a routine clinical testing were included in this study. These samples were tested by all three fusion assays. Positive percent agreement (PPA) and negative percent agreement (NPA) of Fusion assays were calculated against RP assay.

Results. Among 194 samples, 58.0% were from male. Median age was 36 months (IQR 13–72 months). Overall agreement between two assays was 82.5% (95% CI 77.6–88.1). PPA and NPA of Fusion assays for each target was; Flu A-100.0% and 100.0%, Flu B-95.0% and 100.0%, RSV-90.1% and 94.0%, adenovirus-80.0% and 98.2%, hMPV-95.2% and 99.4%, Rhino-79.1% and 95.8%, Parainfluenza virus-100.0 and 100.0%, respectively. There were total 34 discrepant samples. Among these, majority were rhino ($n = 12$), RSV ($n = 12$) and adenovirus ($n = 7$). Of 12 rhinovirus discrepant samples, Fusion assay detected additional seven but missed five samples. For 12 RSV discrepant samples, fusion assay detected 10 more RSV but missed two. Fusion assay missed four adenoviruses and detected additional three samples. All discrepant samples, especially rhinovirus positive samples need further investigation since RP detects both rhinovirus and enterovirus, whereas the Fusion assay detects rhinovirus only.

Conclusion. Performance of fusion Flu A/B/RSV and Paraflu assays were comparable with RP assays. Fusion AdV/hMPV/RV assay had the highest discrepancy with RP assay. Overall, Panther fusion respiratory assays provide the opportunity to customize testing with smaller respiratory panels at a reduced cost.

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

2086. Perils of CMV PCR Primer/Probe Design: Emergence of Mutations in Clinical Samples from Two Pediatric Patients

Amy Leber, PhD[1,2]; Douglas Salamon, MB(ASCP)SV[2]; Monica I. Ardura, DO, MSCS[3] and Huanyu Wang, PhD[2]; [1]The Ohio State University, Columbus, Ohio, [2]Department of Laboratory Medicine, Nationwide Children's Hospital, Columbus, Ohio, [3]Pediatrics, Infectious Diseases and Immunology, Host Defense Program, The Ohio State University and Nationwide Children's Hospital, Columbus, Ohio

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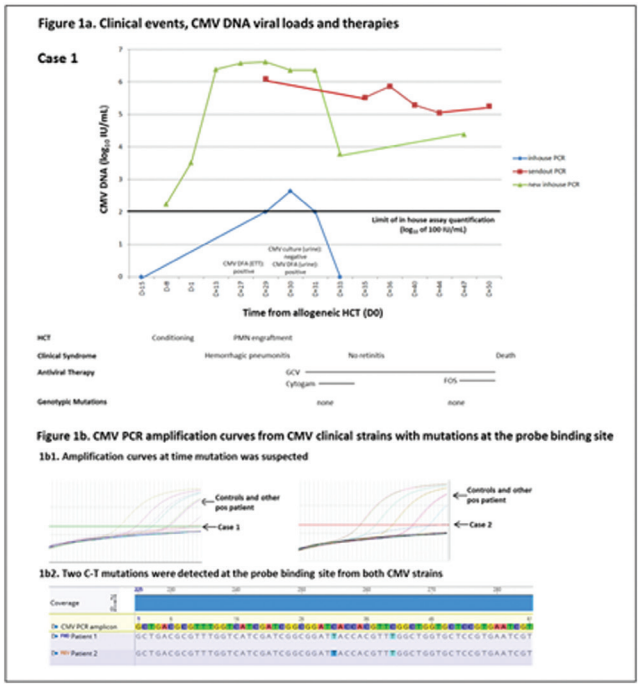
Background. Detection of CMV by PCR is the preferred method for both diagnosing infection and monitoring therapy. The design of CMV PCR depends on analysis of all available nucleic acid sequences to maximize performance. We describe two patients in whom our in-house CMV PCR was falsely negative (FN) due to two recently emerged mutations in the DNA polymerase gene.

Methods. In-house CMV PCR targeting a specific 61 bp fragment of the polymerase gene (*UL54*) has been in use in our lab since 2003. Confirmatory CMV PCR was sent to a reference lab which uses PCR targeting *US9* gene.

Results. *Case 1:* 4 months F with familial hemophagocytic lymphohistiocytosis (homozygous *PRF1*) underwent 10/10 MUD BMT (CMVD+/R–). Plasma CMV was not detected on admission and monitoring was performed weekly. She developed respiratory failure, intubated on D+13 with hemorrhagic respiratory secretions. Repeat PCR of tracheal secretions and plasma detected CMV on D+33, prompting ganciclovir and cytogam. She developed refractory hypoxemia and asystolic cardiac arrest on D+51 (Figure 1a). *Case 2*: Thirty-two-week F born via C-section for fetal distress noted to have SGA, microcephaly, thrombocytopenia and hyperbilirubinemia at birth, concerning for congenital CMV; urine CMV + (Ct 43.18). Repeat urine and blood PCRs on Day 5 of life were indeterminate. Given initial CMV detection and clinical stigmata, ganciclovir was started. Close analysis in Case 1 of the amplification curve (Figure 1b1) on the 21st sample submitted lead us to sequence the amplicon region and to discover two mutations (C-T) in the probe binding site affecting the sensitivity of UL54 PCR(Figure 1b2). These previous FNs delayed CMV diagnosis and the start of antivirals. For Case 2, the distinct curve was noted on the first sample and was sent for confirmation, resulting in no adverse clinical implications. We subsequently developed a CMV PCR targeting US9 that can detect these mutations.

Conclusion. Periodic assessment of all available CMV sequences and close review of amplification curves are essential to prevent FN PCR. With conflicting laboratory and clinical data, clinicians with a high suspicion for CMV should question negatives and if appropriate, ask for PCR using an alternate target.



Disclosures. **A. Leber**, Nationwide Children's Hospital: Research Contractor, Research support.

2087. Comparison of Alere™ i Influenza Flu A and B 2 and Cobas® Influenza A/B Nucleic Acid Amplification Tests for Detection of Influenza A/B in Nasopharyngeal Swabs Collected from Children

Neena Kanwar, PhD[1]; Jeffrey Michael, DO[2]; Kathryn Doran, DO[3]; Emily Montgomery, MD[3] and Rangaraj Selvarangan, PhD[4]; [1]Children's Mercy Hospital, Kansas City, Missouri, [2]Emergency Medicine, Children's Mercy Kansas City, Kansas City, Missouri, [3]Children's Mercy Hospital and Clinics, Kansas City, Missouri, [4]Microbiology Laboratory, Children's Mercy Hospital and Clinics, Kansas City, Missouri

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Background. Early diagnosis of influenza virus is critical for patient management and infection control. Both, Alere™ i Influenza A and B two assay (Alere i; Abbott Laboratories) and Cobas® Influenza A/B nucleic acid test (LIAT; Roche Molecular Systems Inc.) are rapid sample-to-answer CLIA waived molecular assays for flu detection. The aim of this study was to compare the performance of these two commercially available flu assays.

Methods. A total of 201 children <18 years were prospectively enrolled from January to April 2018. Subjects with a physician's test order of Flu test were considered eligible for study participation. Nasopharyngeal swab specimens were obtained after consenting the subjects. Aliquots made were frozen for testing on different diagnostic platforms per manufacturer's instructions. CDC Flu A/B PCR was used as a reference method to evaluate the performance of the two platforms.

Results. Among the 201 specimens tested, CDC PCR detected Flu A/B in 107 samples (Flu A: 73, Flu B: 36; Dual flu A/B positive: 2), while Alere i assay detected 102 samples (Flu A: 69, Flu B: 37; dual flu A/B positive: 4; invalid rate: 1/201–0.5%) and LIAT assay detected 112 samples (Flu A: 74, Flu B: 38; invalid rate: 11/201–5.5%). The overall sensitivities for Alere i vs. LIAT (95.3% vs. 100%) and specificities (100% vs. 94.7%) were comparable. Alere i assay missed five samples detected by CDC PCR at high Ct values of 33.81 (range 31.75–36.04). Standard of care BD Veritor™ Flu A/B antigen test (BD) had a sensitivity and specificity of 77.6% (68.3–84.8) and 98.9% (93.3–99.9).

Conclusion. The diagnostic performance for Alere™ i and LIAT flu assays were found comparable. Both molecular assays had >17% higher sensitivity than BD veritor antigen test. LIAT assay was found to be more sensitive than Alere i whereas Alere i had greater specificity than LIAT.

Table 1: Alere i and LIAT assay results vs. CDC Flu A/B PCR PCR

Assay	Target	True Positive	False-positive	True Negative	False Negative	Sensitivity % (Range)	Specificity % (Range)
Alere i	Flu A	68	1	127	5	93.2 (84.1–97.5)	99.2 (95.1–100.0)
	Flu B	35	2	163	1	97.2 (83.8–99.9)	98.8 (95.2–99.8)
	Overall	102	0	94	5	95.3 (88.9–98.3)	100 (95.1–100)
LIAT	Flu A	73	1	127	0	100 (93.8–100)	99.2 (95.1–100.0)
	Flu B	34	4	161	2	94.4 (80.0–99.0)	97.6 (93.5–99.2)
	Overall	107	5	89	0	100 (95.7–100)	94.7 (87.5–98.0)

Disclosures. **N. Kanwar**, Alere Inc.: Collaborator, Research grant. **R. Selvarangan**, Abbott Diagnostics: Investigator, Research grant.

2088. Association Between Implementation of Prevention Practices and CLABSI Incidence: A National Survey

Debby Ben David, MD[1]; Azza Vaturi, MA[1]; Ester Solter, MA[1]; Elizabeth Temkin, PhD[2]; Yehuda Carmeli, MD, MPH[1,3] and Mitchell J. Schwaber, MD[1]; [1]National Center for Infection Control, Tel Aviv, Israel, [2]Division of Epidemiology, Tel Aviv Sourasky Medical Center, Tel Aviv, Israel, [3]National Center Antibiotic Resistance, Ministry of Health, Israel, Tel Aviv, Israel

Session: 234. Healthcare Epidemiology: Device-associated HAIs
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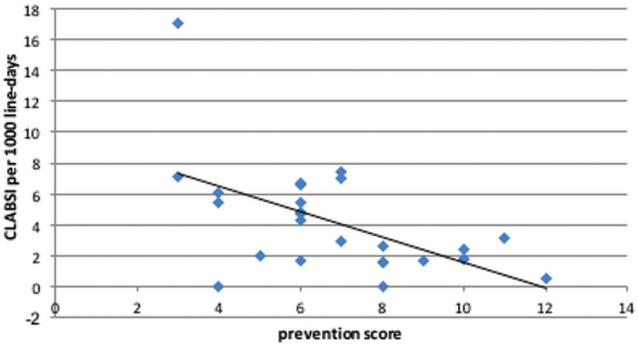
Background. Central-line-associated bloodstream infections comprise 35% of acquired BSI in Israeli intensive care units (ICUs). In 2012, an ongoing national intervention was initiated, including insertion and maintenance bundles, education, outcome surveillance and feedback on CLABSI rates. Following the intervention, a significant decrease in both total BSI and CLABSI rates were observed. However; CLABSI rates remained high in some units. The aims of the study were: (1) to assess the association between hospitals' implementation of prevention practices and CLABSI incidence in general ICUs and (2) to identify which prevention practices were most important for reducing CLABSI incidence.

Methods. A national, prospective surveillance program was implemented in 2012. Since May 2016, monthly individual data replaced prior aggregated reports. The data includes all positive blood cultures, admission and discharge dates, signs/symptoms and diagnostic procedures dates and presence of central lines. In June 2017, an online survey assessing infection prevention practices in general ICUs was sent to all acute care hospitals. Based on the results of the survey, a 14-element prevention score was created that included presence of unit champions, periodic educational sessions, insertion and maintenance practices, and conducting of routine audits. The association between the prevention score and CLABSI rates during the first 6 months of 2017 was assessed using the Spearman correlation test. Negative binomial regression was used to calculate incident rate ratio.

Results. CLABSI rates in 26 general ICUs varied between 0.0 and 17.0 per 1,000 catheter days. Higher prevention scores were associated with lower CLABSI rates (Spearman's rho = −0.51, $P = 0.01$; Figure 1). Significant lower rates were observed in ICUs that had wards champions (IRR 0.48 CI 95% 0.32–0.73, $P = 0.001$) monitored compliance to preventive insertion measures (IRR 0.36, CI 95% 0.20–0.64, $P = 0.001$), used ultrasound for insertion (IRR 0.48, CI 95% 0.29–0.81, $P = 0.006$) and used simulations for teaching (IRR 0.41, CI 95% 0.24–0.70; $P = 0.001$).

Conclusion. More complete implementation of a multi-faceted intervention was associated with lower CLABSI rates in Israeli ICUs.

FIGURE 1



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

2089. Dwindling Utilization of Central Venous Catheter Tip Cultures: An Analysis of Sampling Trends and Clinical Utility at 128 U.S. Hospitals 2009–2014

Yi Ling Lai, MPH[1]; Jennifer Adjemian, PhD[1,2]; Emily Ricotta, PhD, ScM[1]; Lauren Mathew, MD[3]; Naomi O'Grady, MD, FIDSA[4] and Sameer S. Kadri, MD, MS[3]; [1]Epidemiology Unit, Division of Intramural Research, NIAID, NIH, Bethesda, Maryland, [2]United States Public Health Service, Commissioned Corps, Rockville, Maryland, [3]Critical Care Medicine Department, National Institutes of Health Clinical Center, Bethesda, Maryland, [4]Internal Medicine Consult Service, National Institutes of Health Clinical Center, Bethesda, Maryland

Session: 234. Healthcare Epidemiology: Device-associated HAIs
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Background. The 2009 Infectious Diseases Society of America management guidelines for catheter-related bloodstream infection (CR-BSI) recommend the use of central venous catheter (CVC) tip cultures (TC) to aid in diagnosing CR-BSI. However, reimbursement penalties for CR-BSI and emerging evidence supporting watchful waiting rather than removing CVCs may have impacted sampling tendencies, and as such, the uptake of this recommendation and its clinical utility remain unknown.

Methods. Inpatient encounters with ≥1 orders for CVC TC and blood culture (BC; irrespective of collection site) respectively were identified in the Cerner *Health Facts* electronic health record database. Five-year trends (2009–2014) in TC sampling per 10,000 patients were analyzed and annual percent change (APC) in TC vs. BC sampling were compared. The proportions of (a) TCs with growth of noncontaminant microbial taxa and (b) taxon concordant TC–BC pairs sampled within 2 days of each other were calculated.

Results. Between 2009 and 2014, 18,080 TCs were sampled during 16,092 encounters among 14,844 patients at 128 US hospitals. Over the 5-year period, TC sampling decreased from 22/10,000 patients in 2009 to 8/10,000 patients in 2014 (APC: −14.7% [95% CI −22.3 to −6.4%], $P < 0.01$), representing a five-fold decrease compared with BC sampling (APC: −2.5% [−5.0 to 0%], $P = 0.05$; Figure 1). Only 3,561 (20%) TCs displayed any growth of noncontaminant taxa (Figure 2); the most common taxa isolated from TCs were *S. aureus* (56.5%), Enterobacteriaceae (16%), *Candida* sp. (13%), and *P. aeruginosa* (6%). Of the 3,651 positive TCs, 1,631 (46%) were not accompanied by growth in BCs; *S. aureus* represented 471 (29%) and *Candida* spp. represented 121 (7%) of isolated TC growth. Of the remaining 1,930 (54%) positive TCs that were accompanied by positive BCs, only 874 (45%) displayed species concordance.

Conclusion. The practice of sampling CVC tips for culture is steadily declining at U.S. hospitals. The majority of pathogenic species cultured from CVC tips are either unaccompanied by, or are discordant with, growth in the bloodstream. Barring the isolation of *S. aureus* or *Candida* spp. from CVC tips alone, which may represent opportunities to treat, there appears to be limited clinical utility to TC sampling for diagnosing CR-BSI.