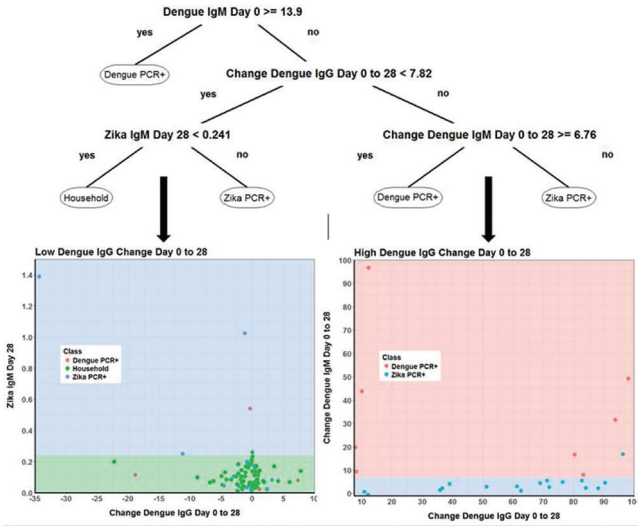
negatives." We fit a statistical decision tree taking as inputs serial serology measurements and outputting a predicted disease category. Funded in part by the NCI Contract No. HHSN261200800001E. Funded in part by the Mexican Ministry of Health.

Results. As of March 2018, we have 32 subjects in the Zika PCR+ group, 32 in the Dengue PCR+ group, and 68 in the household group. Our decision tree (Figure 1) achieved PPV of at least 90% on all three disease categories, while maintaining sensitivity above 50%. The highest PPV achieved by the kit manufacturer recommended cutoffs while maintaining a sensitivity of at least 10% on Zika PCR+ subjects is 30/114 (26%), and for Dengue PCR+ subjects is 21/30 (70%).

Conclusion. Using serology data in a statistical decision tree improves the PPV exhibited by the kit manufacturer recommendations while still maintaining respectable sensitivity. Physicians in regions with co-circulating flaviviruses should be aware of the pitfalls of using only RT-PCR or using pre-established commercial cutoffs in the serology kits for diagnosis.



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

2082. Using a Commercially Available Assay Measuring Cytomegalovirus (CMV)-Specific CD4+ and CD8+ T-Cell Immunity by Intracellular Cytokine Staining to Predict Clinically Significant CMV Events

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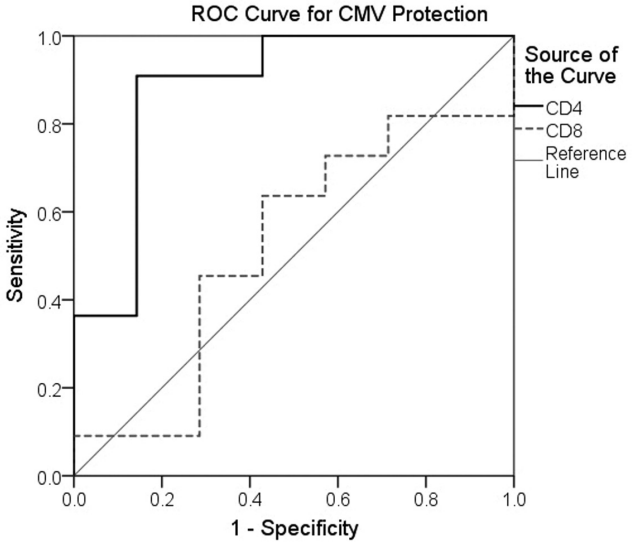
Background. Cytomegalovirus (CMV) infection is a common opportunistic infection associated with significant morbidity, mortality, and risk of allograft loss. Early detection of viremia and initiation of treatment prior to disease progression is paramount. Alternatively, in the absence of treatment, many patients also control CMV infection, including low-level viremia, without progressing to disease. Thus, many treatment decisions (e.g., viremia thresholds to initiate treatment) are not currently well-defined. Given the excessive toxicities and costs of antiviral therapy, there is growing interest in assays that measure CMV-specific T-cell immunity (TCI), which may predict protection against infection. The Viracor® CMV T-cell Immunity Panel (CMV-TCIP) uses flow cytometry and intracellular cytokine staining (ICS) to measure % of CMV-specific CD4+ and CD8+ T-cells. Other currently available TCI commercial assays measure only aggregate (CD4+ and CD8+) or CD8+ immune responses only.

Methods. We included patients who had CMV-TCIP results at Rhode Island Hospital (January 2016–February 2018) and who subsequently had at least one additional assessment for CMV viremia. CMV events were defined as rising viremia prompting initiation of treatment and were captured after the most recent CMV-TCIP result. We built CMV-protection relative-operating curves (ROC) for % of CD4+ and CD8+ CMV-specific T-cells.

Results. We analyzed 17 samples from 13 patients: 10 were SOT (eight kidney, two heart) recipients (seven CMV R+, three D+/R–); two had hematologic malignancies; one other was immunosuppressed (prednisone, infliximab) for autoimmune colitis. Four additional samples were excluded because of CD4+ or CD8+ ICS background positivity. The CMV-protection ROC AUC was significant for % of CMV-specific CD4+ but not CD8+ T-cells (Figure 1). At a cut-off of 0.26% CMV-specific CD4+ T-cells, PPV was 90% (95% CI 71–100%), and NPV was 86% (95% CI 60–100%). In 14 of 17 cases (82%), the CMV-TCIP result was useful in guiding management.

Conclusion. In this small, single-center, heterogeneous series, the % of CMV-specific CD4+ T-cells measured by ICS was predictive of protection against CMV. The CMV-TCIP can be a useful, cost-effective test, and merits further validation in larger prospective studies.



Variable	AUC	SE[a]	P-value[b]	95% CI	
				Lower Bound	Upper Bound
CD4	.883	.092	.008	.703	1.000
CD8	.519	.147	.892	.232	.807

a. Standard error under the nonparametric assumption

b. Null hypothesis: true area = 0.5

Figure 1.

Disclosures. **D. Farmakiotis**, Viracor: Consultant and Invited speaker, Consulting fee.

2083. Rapid Diagnosis and Differentiation of Dengue During Peri-monsoon Season in Tropical Resource Limited Facilities

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Background. Dengue is a re-emerging public health problem threatening the tropical developing world, mandating rapid diagnosis and supportive management in the absence of licensed vaccines or anti-dengue therapy. Regions endemic for dengue and related viruses are overwhelmed by the sudden surge of cases during outbreaks. It is difficult to justify confirmatory diagnosis of every case using WHO criteria or differentiate it from other concurrent viral illnesses. The study evaluated a rapid, sensitive and specific diagnostic methodology suitable for dengue outbreaks in resource limited facilities.

Methods. One hundred dengue patients as per WHO Criteria as well as 100 healthy controls from New Delhi, India were included. Samples collected on fifth day on onset of fever were tested by lateral flow immunochromatography (LF-ICT), IgM ELISA and reverse transcriptase polymerase chain reaction (RT-PCR), and results were compared. Diagnostic accuracy indices and Kappa analysis were calculated.

Results. The sensitivity, specificity, positive and negative predictive values (PPV and NPV) of NS1 against RT-PCR was 98.31, 100, 100, and 99.3% and strength of agreement was perfect.

Conclusion. Antigen-based and molecular tests are a better tool for early diagnosis of dengue. The combined LF-ICT kits are highly sensitive, specific, user-friendly, compact, frugal and thus recommended for use in dengue outbreaks, field conditions and as bed side diagnostic tests, for confirmatory dengue diagnosis. Further studies are required to assess their utility in prognosis, surveillance and establishment of guidelines for dengue outbreaks.

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

2084. Prospective, Multi-Center Analysis of a BioFire® FilmArray® Childhood Systemic Infection (CSI) Panel for Detection of Viral Bloodstream Infections in a Pediatric Emergency Department Setting

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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.

Disclosures. **N. Kanwar**, Biofire Diagnostics: Collaborator, Research grant. **J. Dien Bard**, BioFire Diagnostics: Research Contractor, Research support. **A. Leber**, Nationwide Children's Hospital: Research Contractor, Research support. **J. Dunn**, BioFire: Investigator, Research support. **K. C. Chapin**, Biofire: Research Contractor, Research support. **C. A. Rostad**, Biofire Diagnostics: Collaborator, Research support. **A. J. Blaschke**, BioFire Diagnostics, LLC: I have intellectual property licensed to BioFire through the University of Utah, Independent Contractor and Investigator, Consulting fee, Licensing agreement or royalty and Research support. **M. Jones**, BioFire Dx: Employee, Salary. **E. Ott**, BioFire Diagnostics: Employee, Salary. **J. Bastar**, BioFire Diagnostics, LLC.: Employee, Salary. **R. Selvarangan**, BioFire Diagnostics: Investigator and Scientific Advisor, Consulting fee, Research support and Speaker honorarium.

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

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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

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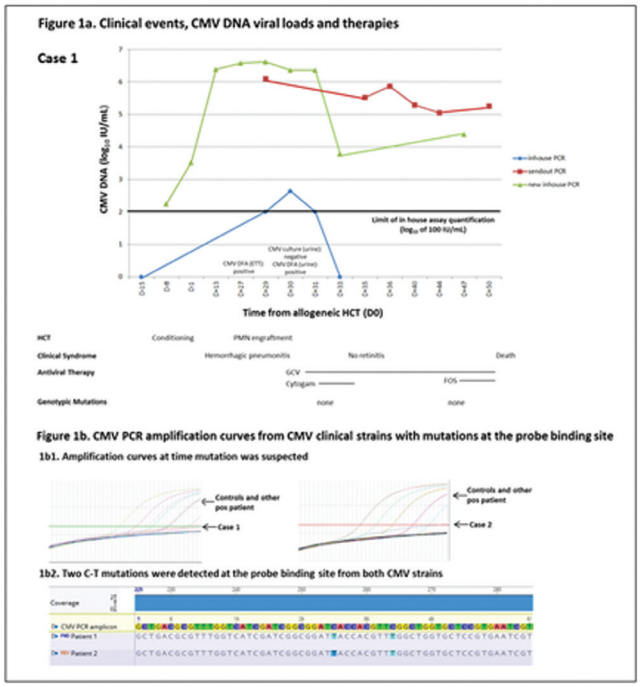
Background. Detection of CMV by PCR is the preferred method for both diagnosing infection and monitoring therapy. The design of CMV PCR depends on analysis of all available nucleic acid sequences to maximize performance. We describe two patients in whom our in-house CMV PCR was falsely negative (FN)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