(Grant/Research Support) **Samuel Dominguez, MD, PhD**, **BioFire** (Consultant, Research Grant or Support)

685. Comparison of Singleplex qPCR and the Luminex MAGPIX Platform for the Detection of Viral Pathogens

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Session: P-27. Diagnostics: Virology

Background: Various respiratory molecular assays are available, each with different characteristics and advantages that make them uniquely valuable. The objective of this study was to compare rates of viral detection using singleplex and multiplex platforms in a research setting.

Methods: A prospective viral surveillance study was conducted in Davidson County, TN. Infants under one year who presented with fever and/or respiratory symptoms were enrolled from the outpatient, emergency department and inpatient settings. Nasal swabs were collected and tested for influenza A (FluA), influenza B (FluB), human metapneumovirus (MPV), respiratory syncytial virus A and B (RSVA and RSVB), human adenovirus (AdV), parainfluenza 1, 2, 3, and 4 (PIV1-4) and SARS-2-CoV by both singleplex qPCR and the Luminex NxTAG Respiratory Pathogen and NxTAG CoV Extended panels. The rhinovirus/enterovirus, human bocavirus, *Chlamydophila pneumoniae*, *Mycoplasma pneumoniae* and coronavirus HKU1, NL63, 229E and OC43 results from the Luminex panel were excluded because singleplex qPCR was not performed on those targets. For singleplex qPCR results, cycle threshold (Ct) values were used as a surrogate for viral load, with a higher Ct value indicating a lower viral load.

Results: A total of 112 nasal specimens were tested by both singleplex qPCR and Luminex, of which 65 were positive for at least one virus by either platform and 56 had a virus detected on both platforms **(Figure 1).** Seven specimens were positive by singleplex qPCR only and two were positive by Luminex only **(Figure 1).** The targets positive by singleplex qPCR only included FluB, RSVA, AdV and PIV2 and those positive by Luminex only included FluA H1N1 and RSVB **(Figure 2).** Specimens that were positive only on the singleplex assay had a higher average Ct value than those that were positive on both assays, indicating a lower viral load **(Figure 3).**

Figure 1

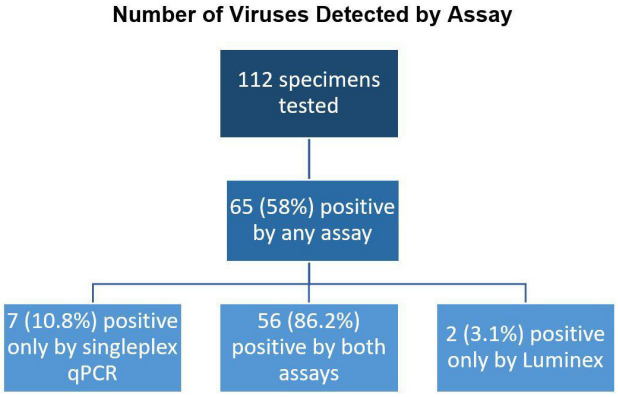


Figure 2

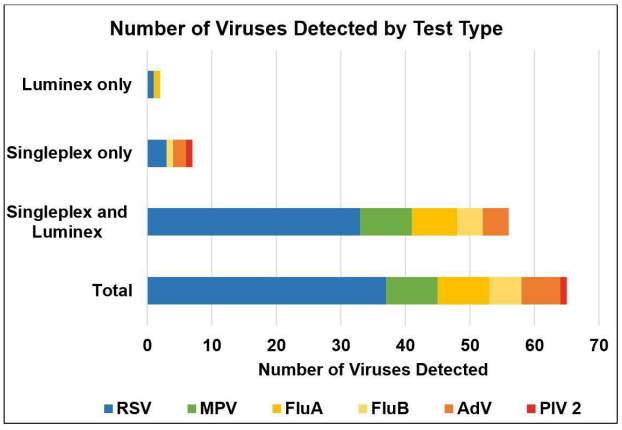
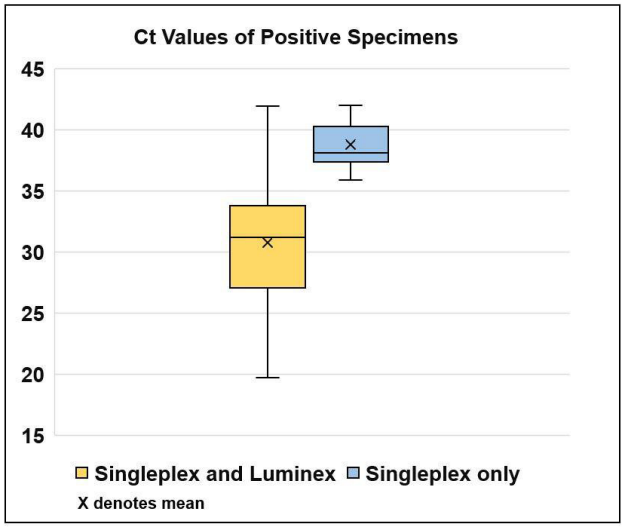


Figure 3



Conclusion: The multiplex assay identified 89% of the total viruses detected while singleplex qPCR identified 97% of the total viruses detected. Lower viral loads may contribute to false negative results on the multiplex platforms. Future studies with larger sample sizes are needed in order validate our findings.

Disclosures: **Erin Yepsen, BS**, **Sanofi Pasteur** (Grant/Research Support, Research Grant or Support) **Zaid Haddadin, MD**, **CDC** (Grant/Research Support, Research Grant or Support)**Quidel Corporation** (Grant/Research Support, Research Grant or Support)**sanofi pasteur** (Grant/Research Support, Research Grant or Support) **Danielle A. Rankin, MPH, CIC**, **Sanofi Pasteur** (Grant/Research Support, Research Grant or Support) **Natasha B. Halasa, MD, MPH**, **Genentech** (Other Financial or Material Support, I receive an honorarium for lectures - it's a education grant, supported by genetech)**Karius** (Consultant)**Moderna** (Consultant)**Quidel** (Grant/Research Support, Research Grant or Support)**Sanofi** (Grant/Research Support, Research Grant or Support)

686. Elevations in TNFα and IL-18 are Associated with Increased Risk of Probable Cytomegalovirus Tissue Invasive Disease in Solid Organ Transplant Recipients

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Session: P-27. Diagnostics: Virology

Background: Human cytomegalovirus (CMV) continues to cause significant morbidity and mortality in solid organ transplant (SOT) recipients despite prophylaxis. Tissue invasive CMV disease (TI-CMV) can lead to end-organ damage and graft loss. Diagnosing TI-CMV can be challenging as CMV viral load in the blood does not always correlate with episodes of TI-CMV and therefore definitive diagnosis often requires an invasive procedure such as bronchoscopy or colonoscopy. The purpose of this study was to determine if proinflammatory cytokines, including IL-18, are elevated in SOT recipients with probably TI-CMV as a way to identify patients at risk for this severe form of CMV disease.

Methods: The electronic medical record was searched for adult SOT recipients who were tested for CMV via blood qPCR during an 11-month period.Twenty-nine SOT recipients were identified that had episodes of CMV DNAemia without other concomitant infections during this time period. Patients were divided into those that had probable TI-CMV and those with CMV DNAemia alone, by chart review. Inflammatory cytokines (IFNγ, TNFα, IL-1β, IL-2, IL-4, IL-6, IL-8, IL-10, IL-12p70, IL-13, IL-18, and IL-1RA) were measured in residual plasma from these patients using a commercially available multiplex assay for at least two time points during the study period. Wilcoxon-Rank-Sum, logistic regression, and principal component analysis was performed comparing patients with and without probable TI-CMV.

Results: Patients with probable TI-CMV had significantly higher IL-18, TNFα, and IL-1β than patients with CMV DNAemia alone ($p < 0.001$, < 0.001, and < 0.05 respectively). When adjusting for transplant type and CMV recipient serostatus, elevations in TNFα (OR 1.43, 95% CI 1.07-1.92) and IL-18 (OR 2.00, 95% CI 1.06-3.75) were associated with increased odds of having probable TI-CMV. In principal component analysis the combination of CMV viral load, IL-18, TNFa, and IL-1β accounted for 80% of the variance in the data.