Conclusion. Although there was a shift in partnership type towards lower risk partnerships, objective HIV risk behavior remained stable over time. Individuals with higher HIV risk behaviors and risk partnerships had higher TFV-DP levels suggesting maintained strong motivation for PrEP adherence. Thus, recent sexual risk behavior and partnership type may be important predictors of PrEP adherence in MSM.

Disclosures. All authors: No reported disclosures.

883. HIV Antiretroviral Resistance and Transmission in Mother–Infant Pairs Enrolled in a Large Perinatal Study
Nava Yeganeh, MD; Tara Kerin, PhD; Bonnie Ank, BA; Heather Watts, MD; Margaret Camarca, MPH; Esau Joao, MD; Jose Henrique Piloto, MD; Valdélia Veloso, MD, PhD; Yvonne Bryson, MD; Karin Nielsen-Saines, MD, PhD; 1David Geffen School of Medicine at University of California at Los Angeles, Los Angeles, California; 2Office of the Global AIDS Coordinator and Health Diplomacy, Washington, DC; 3Westat, Rockville, Maryland; 4Hospital Federal dos Servidores do Estado, Rio de Janeiro, Brazil; 5Hospital Geral de Nova Iguaçu, Nova Iguaçu and Laboratório de AIDS e Imunologia Molecular, Instituto Oswaldo Cruz, Fundação Oswaldo Cruz; 6Fiocruz, Rio de Janeiro, Brazil; 7Instituto Nacional de Infectologia Evandro Chagas, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil

Session: 93. Preventing and Identifying New HIV Infections
Thursday, October 5, 2017: 2:00 PM

Background. Detection of antiretroviral (ARV) resistance in HIV-infected individuals is not uncommon and may be particularly problematic in HIV-infected pregnant women as it can lead to infant infection with resistant strains. To better evaluate the effect of drug resistance mutations (DRMs) on HIV mother-to-child transmission (MTCT), we determined the prevalence of DRMs in a subset of mother–infant pairs enrolled in a multi-center trial of infant prophylaxis among women not receiving ART during the current pregnancy.

Methods. A case–control design of 1:4 (1 transmitter to 4 nontransmitters) was utilized to evaluate ARV resistance as a predictor of HIV MTCT in specimens obtained from mother–infant pairs. Secondary objectives included identification of potential risk factors associated with the presence of DRMs. Viroseq HIV-1 Genotyping System was performed on mother–infant specimens to assess for mutations that might result in a substantial reduction in drug susceptibility and clinical outcome, as determined by the Stanford HIV Drug Resistance Database.

Results. One hundred and forty infants were infected. Of these, 123 HIV infected mother–infant pairs and 483 of 560 women who did not transmit HIV had aflamilla HIV nucleic acid enabling ARV resistance testing. A wide variety of DRMs were detected (Figure 1). Of 606 women had clinically relevant DRMs; 12 (2%) had 5 or more DRMs against more than 1 ARV class. Among 123 HIV− infected infants, 13 (11%) had clinically relevant DRMs with 3 (2%) harboring DRMs against more than 1 ARV class. Of 13 infants with DRMs, 10 (77%) were infected in utero. In univariate and multivariate analyses, DRMs in mothers were not associated with increased risk of HIV MTCT (AOR 0.79, 95% CI 0.48–1.35). Lipid HIV viral load was the only predictor of MTCT (OR 1.4, 95% CI 1.2–1.6). The presence of DRMs in mothers who transmitted was strongly associated with the presence of DRMs in infants (P < 0.001).

Conclusion. In infected pregnant women without ARV exposure during their current gestation, the presence of pre-existing DRMs with a wide diversity was noted. DRM burden in HIV MTCT. However, if women with DRMs are not virologically suppressed they are likely to transmit resistant mutations even without selective ARV pressure, thus complicitating treatment options.

Disclosures. All authors: No reported disclosures.

884. Missed Opportunities to Initiate Pre-exposure Prophylaxis in South Carolina—2013–2016
Stella Okoye, MD; Man-Huei Chang, MPH; Sharon Weissman, MD; Wayne Hayslett, MD, PhD; Wayne Hayslett, MD, PhD; University of South Carolina School of Medicine, Columbia, South Carolina; 2National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, Centers for Disease Control and Prevention, Atlanta, Georgia; 3Centers for Disease Control and Prevention, Atlanta, Georgia

Session: 93. Preventing and Identifying New HIV Infections
Thursday, October 5, 2017: 2:00 PM

Background. PreP, regular use of antiretroviral medications by HIV-negative individuals to prevent new HIV infections, has not been widely adopted by some young, high risk populations. This study investigated the characteristics and estimated percentage of newly diagnosed HIV-infected individuals in South Carolina (SC) who had visited a health care facility (HCF) while HIV-negative and missed opportunities for initiating PreP.

Methods. We used a unique person-level identifier to link case reports from the SC enhanced HIV/AIDS Reporting System and records from a statewide all payer HCF database. The HCF data include inpatient (IP), outpatient (OP), and emergency department (ED) visits to SC facilities. Because the Food and Drug Administration approved PrEP in 2012, we analyzed data for individuals diagnosed with HIV during January 2013–September 2016 with initial CD4 count ≥500 cells (recent infection) and HC visits during 2011 through the date of diagnosis. We used the two-tailed chi-square statistics with a significant threshold of P < 0.05 in SAS to investigate the association between presence of a PrEP prescription and patient factors including demographics, behavioral risk, visit setting (IP, OP or ED), frequency of previous visits, and residence at diagnosis.

Results. A total of 785 patients were diagnosed with recent HIV infections (initial CD4 >=500 cell) during January 2013–September 2016. Of these, 504 (64.2%) visited an SC HCF at least once before being diagnosed, 72.4% were males, 52.4% aged <30 years, 54% were men who have sex with men (MSM) or injection drug users (IDU) and 70.2% resided in urban areas. Mean number of HCF visits before HIV diagnosis was 6.6; 64.3% had ED visits; 5.9% had IP visits; and 7.0% had OP visits. Persons of female sex, Black race, younger age and urban residence were more likely to access HCF visit before HIV diagnosis (P < 0.05).

Conclusion. We now know the characteristics and percentage (64.2%) of persons with recent HIV infections captured in two large state-wide databases in SC who missed opportunities to be screened and initiated PreP during visits to HCFs before HIV diagnosis during 2013–2016.

Disclosures. All authors: No reported disclosures.

885. Comparison of Respiratory Pathogen Detections from Routine Hospital Testing and Expanded Systematic Testing from the Minnesota Severe Acute Respiratory Illness Surveillance Program, 2015–2016
Amy Steffens, MPH; Hannah Friedlander, MPH; Kathryn Como-Sabetti, MPH; Dave Broxrud, MD; Sabine Britzdoerfer, BS; Anna Strain, PhD; Carrie Reed, DSc, MPH; Ruth Lynfield, MD, FIDSA; Ashley Fowlkes, MPH; 1Influenza Division, Centers for Disease Control and Prevention, Atlanta, Georgia; 2Minnesota Department of Health, St. Paul, Minnesota; 3Minnesota Department of Health, Minneapolis, Minnesota; 4Public Health Laboratory, Minnesota Department of Health, St. Paul, Minnesota

Session: 94. Respiratory Infection Diagnosis
Thursday, October 5, 2017: 2:00 PM

Background. Hospital testing for respiratory pathogens is nonsystematic, leading to potential missed detection of clinically relevant pathogens. The Minnesota Severe Acute Respiratory Illness (SARI) surveillance program monitors hospitalizations due to acute respiratory illness and conducts systematic testing for respiratory viral pathogens. We assessed viruses detected by the hospital and additional detections identified by expanded testing.

Methods. Residual upper respiratory specimens collected from patients hospitalized for suspected acute respiratory illness for routine diagnostic testing at three hospitals, including one children’s hospital, were submitted to the Minnesota Department of Health (MDH). Specimens were tested for 18 respiratory viruses by RT-PCR. Clinical and hospital test data were collected through medical record review.

Results. From September 2015 to August 2016, 2,351 hospitalized SARI patients were reported, with the following age distribution: 57% <5 years, 13% 5–17 years, 30% ≥18 years. Among all SARI patients, 97% (2,273) had hospital-based, clinician-directed testing for viral pathogens. Viruses were detected among 47% (1,077) of tested patients, among which testing methods included PCR (85%), rapid antigen (13%), and culture (2%); 74% were detected on the day of admission. Most common viruses detected by clinical testing included respiratory syncytial virus (41%), rhinovirus/enterovirus (31%), and influenza (15%) (Figure 1). Systematic RT-PCR testing at MDH identified 1,600 (68%) patients positive for ≥1 respiratory virus, identifying previously unknown detections among 35% (820) of SARI patients (Figure 2). Of 1,272 patients with no virus identified at the hospital, 46% (586) had a viral detection at MDH. Patients aged <18 years were significantly more likely to have an additional pathogen detected by MDH testing than those aged ≥18 years (P < 0.01), including rhinovirus/enterovirus, adenovirus, human metapneumovirus, and coronaviruses.

Conclusion. Systematic, expanded testing at MDH identified a higher proportion of respiratory pathogens among SARI patients compared with clinical laboratory testing. Additional testing for clinically relevant respiratory pathogens may inform medical decision-making.

Disclosures. All authors approved for publication.

Figure 1.
Disclosures. All authors: No reported disclosures.

886. Pneumococcal Urinary Antigen Testing in US Hospitals: Underutilized and Rarely Acted Upon
Sarah Haessler, MD; Jennifer Schimmel, MD; Pei-Chun Yu, MS; Michael Rothenberg, MD, MPH; Infection Diseases, Baystate Medical Center, Springfield, Massachusetts; 2Quantitative Health Sciences, Cleveland Clinic, Cleveland, Ohio; 3Medicine Institute for Center for Value-Based Care Research, Cleveland Clinic, Cleveland, Ohio

Session: 94. Respiratory Infection Diagnosis
Thursday, October 5, 2017: 2:00 PM

Background. The IDSA guideline for CAP recommends Pneumococcal urinary antigen testing (UAT) in addition to blood and sputum cultures for patients with severe CAP. In controlled settings, UAT is 50–80% sensitive and >90% specific; however, its utility and performance on a large-scale in real-world use has not been assessed. It is unclear whether UAT is clinically useful or whether the results impact prescribing behavior.

Methods. Retrospective cohort study of adult patients admitted with CAP or HCAP from 2010 to 2015 at 170 US hospitals that submit data to Premier. Data and time-stamped administrative and microbiologic data were assessed. Patients with a principal diagnosis of pneumonia, or sepsis with a secondary diagnosis of pneumonia plus a CXR and antibiotics within the first 24 hours were included if they had a UAT plus either a blood or respiratory culture within the first 48 hours of admission.

Results. Of 159,894 eligible pneumonia patients, 24,757 (15.5%) had UAT plus either blood or respiratory cultures performed. Of 1,297 (7%) who had a positive UAT, 457 (25%) also grew *S. pneumoniae* (SP) from blood or respiratory cultures, 1,240 (69%) had negative cultures, and 100 (6%) an organism other than SP, with *S. aureus*, *Pseudomonas* spp., and *E. coli* being the most common pathogens, predominately from respiratory cultures. Among 22,960 patients with a negative UAT, 429 (2%) had a positive blood or respiratory culture for SP and 2,653 (12%) had an organism other than *S. pneumoniae* with either blood or respiratory cultures performed. Of 1,797 (7%) who had a positive UAT and antibiotics within the first 24 hours, were included if they had a UAT plus either a blood or respiratory culture for SP within the first 48 hours of admission.

Conclusion. In a large representative US inpatient database, there was poor concordance between UAT and cultures for SP. A positive UAT decreased the probability of having a non-SP pathogen. Antibiotic de-escalation occurred more often in association with a positive blood culture for SP than for UAT or positive respiratory culture, but occurred in less than half the patients with these markers of pneumococcal pneumonia. Overall, UAT is underutilized and does not appear to have a substantial impact on clinical care.

Disclosures. S. Haessler, AHRQ: Investigator, Research grant; P. C. Yu, AHRQ: Investigator, Research grant; M. Rothenberg, AHRQ: Investigator, Research grant

887. Impact of Procalcitonin Guidance on the Management of Adults Hospitalized with Pneumonia
Thomas Walsh, MD; Briana DiSilvio, MD; Crystal Hammer, MD; Moezullah Beg, MD; Swati Vishwanath, MD; Daniel Speredelozzi, MD; Matthew Moffa, DO; Kurt Hu, MD; Rasha Abdulnassih, MD; Jina Makadia, MD; Rikinder Sandhu, MD; Mosahib Naddour, MD; Noreen Chan-Tompkins, PharmD, BCPS - AQ ID; Tamara Trienski, PharmD; Courtney Watson, MPH; Derek Bremmer, PharmD, BCPS; Allegheny Health Network, Pittsburgh, Pennsylvania

Session: 94. Respiratory Infection Diagnosis
Thursday, October 5, 2017: 2:00 PM

Background. Community-acquired pneumonia and healthcare-associated pneumonia are often treated with prolonged antibiotic therapy. Procalcitonin (PCT) has effectively and safely reduced antibiotic use for pneumonia in controlled studies. However, limited data exist regarding PCT guidance in real-world settings for management of pneumonia.

Methods. A retrospective, preintervention/postintervention quality improvement study was conducted to compare management for patients admitted with pneumonia before and after implementation of PCT guidance at two teaching hospitals in Pittsburgh, Pennsylvania. The preintervention period was March 1, 2014 through October 31, 2014, and the post-intervention period was March 1, 2015 through October 31, 2015.

Results. A total of 152 and 232 patients were included in the preintervention and postintervention cohorts, respectively. When compared with the preintervention group, the mean duration of therapy decreased (9.9 vs. 6.1 days; *P* < 0.001). More patients received an appropriate duration of ≥7 days or less (26.9% vs. 66.4%; *P* < 0.001). Additionally, mean length of hospital stay decreased in the postintervention group (4.9 vs. 3.5 days; *P* = 0.006). Pneumonia-related 30-day readmission rates (7.2% vs. 4.3%; *P* = 0.59) were unaffected. In the postintervention group, patients with PCT levels ≤0.25 µg/l received shorter mean duration of therapy compared with patients with levels >0.25 µg/l (8.0 vs. 4.6 days; *P* < 0.001) as well as reduced hospital length of stay (3.9 vs. 3.2 days; *P* = 0.02).

Conclusion. In this real-world practice study, PCT guidance led to shorter durations of total antibiotic therapy and abridged inpatient length of stay without affecting hospital readmissions.

Disclosures. All authors: No reported disclosures.

888. Detection of Respiratory Pathogens in Parapneumonic Effusions by Hypothesis-free, Next-Generation Sequencing (NGS)
Krow Ampofo, MD, FIDSA, FFIDIS; 1Andrew Pavia, MD, FIDSA, FSHEA, FFIDIS; 1Xinne J. Blaschke, MD, PhD, FIDSA, FFIDIS; 2Robert Schlaberg, MD, MPH; 1Department of Pediatrics, Division of Pediatric Infectious Diseases, University of Utah School of Medicine, Salt Lake City, Utah; 2Department of Pathology, University of Utah, Salt Lake City, Utah

Session: 94. Respiratory Infection Diagnosis
Thursday, October 5, 2017: 2:00 PM

Background. Species-specific polymerase chain reaction (PCR) testing of pleural fluid (PF) from children with parapneumonic effusion (PPE) has increased pathogen identification in pediatric PPE. However, a pathogen is not detected in 25–35% of cases. Hypothesis-free, next-generation sequencing (NGS) provides a more comprehensive alternative and has led to pathogen detection in PCR-negative samples. However, the utility of NGS in the evaluation of PF from children with PPE is unknown.

Methods. Archived PF (n = 20) from children younger than 18 years with PPE and hospitalized at Primary Children's Hospital, Utah, in 2015 and previously tested by PCR were evaluated. Ten PCR-negative and 10 PCR-positive PF specimens were tested using RNA-seq at an average depth of 7.7 x 10^6 sequencing reads per sample. NGS data were analyzed with Taxonomer. We compared pathogens detected by blood and PF culture, PCR, and NGS.

Results. Overall, compared with blood/PF culture, PF PCR and PF NGS testing of PF increased bacterial identification from 55% (P < 0.05) and 65% (P = 0.003), respectively. Pathogen detection in PF by PCR and NGS were comparable (50 vs. 65%, p = NS) (Table). However, compared with PF PCR, NGS significantly increased detection of *S. pneumoniae* (20% vs. 55%; P < 0.05), with 100% concordance when detected by PCR and culture. Detection of *Fusobacterium spp.* (10 vs. 10%) by PF NGS and PF PCR were comparable. In contrast, there was no detection of *S. pyogenes* (15 vs. 0%) by PF NGS compared with PF PCR.

Conclusion. NGS testing significantly improves bacterial identification and comparable to PF PCR testing, which can help inform antimicrobial selection. However there were differences in detection of *S. pneumoniae* and *S. pyogenes*. Further studies of NGS testing of PF of children with PPE are needed to assess its potential in the evaluation of PPE in children.

Disclosures. A. J. Blaschke, BioFire Diagnostics LLC: Collaborator, Have intellectual property in BioFire Diagnostics through the University of Utah and Investigator, Licensing agreement or royalty and Research support; R. Schlaberg, IdbyDNA: Co-founder, Consultant and Shareholder, Stock

889. Utility and Challenges of a Multi-pathogen Diagnostic Platform for Characterizing Public Health Threats of Severe Acute Respiratory Infections in Six Countries
Jennifer Milucky, MPH and International TAC Working Group; Division of Bacterial Diseases, CDC, Atlanta, GA

Session: 94. Respiratory Infection Diagnosis
Thursday, October 5, 2017: 2:00 PM

Background. Pneumonia causes significant morbidity and mortality worldwide. Comprehensive etiology studies of pneumonia in adults are limited; however, new