***Background.*** Kawasaki disease(KD) is a medium-vessel vasculitis with a predilection for coronary arteries and is of unknown etiology. KD is responsible for the majority of acquired pediatric cardiovascular disease in the industrialized world, and is associated with development of coronary artery aneurysms in approximately 25% of untreated patients. Epidemiologic, pathologic, and clinical characteristics of KD display notable overlap with common pediatric viral illnesses, leading some to hypothesize that a viral infection is the inciting agent for KD.

***Methods.*** We investigated viral exposure history in KD patients by utilizing a recently developed technique to profile sera against the known human virome in an unbiased manner. We collected sera during the acute (pretreatment) and subacute phases of illness from 35 patients meeting clinical diagnostic criteria for KD, preferentially selecting patients with coronary involvement and/or late presentation. Control samples included healthy children and patients with known viral infections. Using phage immunoprecipitation sequencing(PhIP-seq), the sera were screened against a phage display library expressing epitopes that cover the complete reference protein sequences of the known 206 viruses with human tropism.

***Results.*** The mean patient age was 4.6 years(range 0.4–16.9) and mean day of illness at acute sample collection was 14.5 days(range 5 to 32). A majority of patients demonstrated coronary artery changes during the course of their illness(22/35, 62%). Sera from patients with KD demonstrated patterns of viral infection to common pediatric viruses with similar signal intensity and distribution to healthy control children. Interestingly, one patient demonstrated a strong signal to parvovirus B19. She presented on Illness Day 29 with periungual peeling and severe hip arthritis, and her initial KD course with 14 days of fever and 4/5 clinical criteria was missed.

***Conclusion.*** Although sera obtained early in the disease course could have missed a titer rise, we conclude that patients with KD do not exhibit unique serologic evidence of infection to known viruses or a viral exposure history that differs from age-similar healthy children.

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**2306. Familial and Environmental Impact on Colonization with Antibiotic-resistant Organisms in the Neonatal Intensive Care Unit**

Patrick Reich, MD[1]; Mary Boyle, MSN[1]; Melanie Sullivan, BS, MT[1]; Patrick G. Hogan, MPH[1]; Ryley Thompson, MCSE[1]; Carol Muenks, BA[1]; Colleen Kennedy, BA, BS[1]; Meghan Wallace, BS[2]; Carey-Ann D. Burnham, PhD[2] and Stephanie Fritz, MD, MSCI[1]; [1]Pediatric Infectious Diseases, Washington University School of Medicine, Saint Louis, Missouri, [2]Pathology and Immunology, Washington University School of Medicine, St. Louis, Missouri

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***Background.*** Colonization with antibiotic-resistant organisms (AROs), including methicillin-resistant *S. aureus* (MRSA), places neonatal intensive care unit (NICU) patients at increased risk for infection. Infants are routinely screened for MRSA colonization, but reservoirs for ARO acquisition in the NICU are poorly understood.

***Methods.*** Infants with known MRSA nasal colonization and a control group of infants with negative MRSA screening swabs, and their parents, were enrolled in a prospective cohort study. Weekly swabs were obtained to identify AROs from 4 infant body sites, 3 parental body sites, and 5 high-touch environmental surfaces in the NICU. Culture-based methods were used to identify AROs.

***Results.*** Samples were collected 1–14 times (median 7) from 11 MRSA-colonized infants, 7 control infants, 17 mothers, and 9 fathers. Of MRSA-colonized infants, 9 (82%) were colonized with MRSA in the nares, 6 (55%) in the umbilicus, 8 (73%) in the inguinal folds, and 6 (55%) in the rectum over the study period. Six (55%) MRSA-colonized infants had persistent colonization (i.e., 3 consecutive positive samplings) despite receiving decolonization measures. One (14%) control infant was colonized with MRSA during longitudinal sampling. Sixteen (89%) infants were colonized with ceftriaxone-non-susceptible Gram-negative bacteria. Of 110 *Enterobacteriaceae* isolates recovered from infants, 22% were non-susceptible to gentamicin, 80% to ceftazidime, 33% to cefepime, 2% to meropenem, and 56% to ceftolozane/tazobactam. Six (33%) infants were colonized with *Pseudomonas* species and 2 (11%) infants were colonized with *Acinetobacter*species. An ARO was recovered at least once from the environment for 13 (72%) infants and from a parent for 13 (72%) infants. Twelve (67%) infants and an environmental surface, and 11 (61%) infants and a parent, were colonized with the same ARO at some point. An environmental surface was colonized with MRSA for 9 (82%) MRSA-colonized infants compared with 3 (43%) controls ($P$ = 0.14). A parent was colonized with MRSA for 9 (82%) MRSA-colonized infants compared with 1 (14%) control ($P$ = 0.01).

***Conclusion.*** Extranasal body sites, parents, and environmental surfaces serve as potential reservoirs of ARO acquisition and transmission in NICU infants.

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**2307. Surveillance for Antimicrobial-resistant Organisms in Infants Transferred to the Neonatal Intensive Care Unit: Trends in Colonization and Practices**

Jennifer Duchon, MDCM, MPH[1,2]; Philip Maykowski, MPH[1,2]; Pamela Good, MD[2]; Sonja Kytomaa, MPH[1]; Patricia DeLaMora, MD[3] and Lisa Saiman, MD, MPH[4,5]; [1]Epidemiology, Mailman School of Public Health, NewYork, New York, [2]Pediatrics, Columbia Presbyterian Medical Center, New York, New York, [3]Pediatrics, Weill Cornell Medical College, New York, New York, [4]Infection Prevention and Control, New York-Presbyterian Hospital, New York, New York, [5]Columbia Presbyterian Medical Center, NewYork, New York

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***Background.*** Infections with antibiotic-resistant organisms (AROs), i.e., methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant enterococci (VRE), and multi-drug-resistant Gram-negative rods (MDR-GNR) among infants hospitalized in the Neonatal Intensive Care Unit (NICU) are associated with mortality and serious morbidities. Implementing appropriate infection control policies may help prevent transmission of AROs. However, the most effective strategies for surveillance of AROs in the NICU are unclear. Prior data collected from infants transferred from outside hospitals to 2 NICUs affiliated with New York-Presbyterian (NYP) Hospital detected low rates of ARO colonization in the first week of life. Thus, in 2013 the strategy of performing surveillance on all transferred infants for AROs was changed to performing targeted surveillance on infants transferred at >7 days of life (DOL). The purpose of this study was to assess this change in surveillance strategy and monitor ARO colonization trends in the NICU.

***Methods.*** Data from all infants transported to the NICUs at NYP from 2007 to 2016 were used. Risk factors for colonization with AROs including demographics and admitting diagnoses were explored using a multivariable binomial mixed model clustered by transferring hospital and controlled for NYP NICU. Trends in ARO colonization over time were assessed using negative binomial regression. Site 1 elected not to adopt the change in surveillance policy, and thus was used as a control.

***Results.*** From 2007 to 2016, 2925 infants were transferred to the NYP NICUs, 1101 at Site 1 and 1824 at Site 2; 2571 (88%) had surveillance for at least 1 ARO. There were 226 positive surveillance cultures in 204 infants (8%): 94 (3.7%) for MRSA, 78 (3%) for VRE and 54 (2%) for MDR-GNR. In the final models, transfer DOL remained a highly significant (OR per day = 1.018, $CI_{95}$ 1.014, 1.022, $P < 0.001$) predictor of colonization with any ARO. There was no significant increase in the incidence of transferred infants colonized with AROs over time in either NICU; this remained true in infants who were < 7 days of life at Site 1.

***Conclusion.*** These data continue to support the rationale for our change in surveillance policy. Further studies should evaluate the effect of this strategy on ARO transmission in the general NICU population.

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**2308. Clinic Characteristics Are not Associated with the Risk of Healthcare-associated Influenza-like Illness (HA-ILI) Among Young Children in Pediatric Primary Care Settings**

Kristen Feemster, MD, MPH, MSHP[1,2,3]; Russell Localio, PhD[4],Heather Griffis, PhD[5]; Folasade Odeniyi, MPH[6]; Robert Grundmeier, MD[7]; Susan Coffin, MD, MPH, FSHEA, FPIDS[8,9] and Joshua Metlay, MD, PhD[10]; [1]Division of Infectious Diseases, Department of Pediatrics, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, [2]Department of Pediatrics, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, Pennsylvania, [3]Policylab and Center for Pediatric Clinical Effectiveness, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, [4]Biostatistics, Epidemiology and Informatics, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, [5]Pediatrics, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, [6]Infectious Diseases, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, [7]General Pediatrics, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, [8]Center for Pediatric Clinical Effectiveness, Pediatric Infectious Diseases Epidemiology and Antimicrobial Stewardship Research Group, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, [9]Department of Pediatrics, Division of Infectious Diseases, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, [10]Medicine, Harvard Medical School, Boston, Massachusetts

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***Background.*** The majority of pediatric healthcare encounters for influenza-like illness (ILI) take place in ambulatory settings where there may be multiple opportunities for respiratory virus transmission. Recent evidence shows that a prior clinic visit increases the risk of ILI among young children. We hypothesized that clinic factors would be associated with the risk of HA-ILI among children < 6 years old after a primary care encounter.

***Methods.*** We conducted a prospective cohort study of a sample of 1308 children presenting to any of the 31 primary care clinics in a large pediatric healthcare network for a non-ILI clinic visit during three consecutive respiratory seasons (2012/13 – 2014/15). HA-ILI cases were defined as any ILI encounter within 8 days after a non-ILI visit. Clinic factors (waiting room patient density or number of ILI encounters at appointment time, time in waiting room, clinic location), sociodemographic and clinical data were obtained electronically and from parent interviews. School attendance (daycare, school or parent) and age (≤2 years and >2 years) were combined to create a 5 category composite variable. Logistic regression models after applying sampling weights evaluated associations between HA-ILI risk and patient age, daycare / school attendance, gender, influenza vaccine receipt and waiting room patient density.

***Results.*** Our cohort included 367 HA-ILI cases and 941 non-cases. The majority (48.6%) were ≤2 years and did not attend school, 52.8% were male, and 18.9% received flu vaccine. Mean clinic patient density was 44.2 patients/1,000 square feet. In multivariable models, only the young age/daycare attendance composite variable was significantly associated with increased HA-ILI risk (OR 2.06, 95% CI 1.48,2.88). No clinic characteristics were associated with HA-ILI risk and risk did not vary by site.

***Conclusion.*** In our cohort of young children, HA-ILI was not associated with the measured clinic characteristics that we hypothesized may increase respiratory virus transmission risk. Instead HA-ILI risk was highest in young daycare attendees who may be more likely to engage in behaviors that increase respiratory virus exposure risk or seek out healthcare services when sick. This suggests that HA-ILI may be more strongly influenced by behavioral factors rather than environmental factors.

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