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. Sera were collected from patients at different 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 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.

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

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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 for 4 weeks post-birth.

Results. Samples were collected 1–4 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 samples) despite receiving decolonization measures. One (14%) control infant was colonized with MRSA during longitudinal sampling. Sixteen (89%) infants were colonized with Acinetobacter species. Methicillin-resistant Gram-negative species isolated recovered from infants, 22% were non-susceptible to gentamicin, 80% to ceftriaxone-non-susceptible Gram-negative bacteria. Of 110 isolates recovered from infants, 22% were non-susceptible to gentamicin, 80% to ceftriaxone.

Conclusion. Although 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 for 4 weeks post-birth.

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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

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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 visit frequency would be more strongly influenced by behavioral factors rather than environmental factors. This suggests that HA-ILI may be more strongly influenced 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, 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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