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1647. Real-Time Metagenomic Sequencing Reveals Discrete Transmission Clusters Within a Hospital-Associated Norovirus Outbreak

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Session: 169. Respiratory and Gastroenteritis Viruses
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Background. Norovirus is the most common cause of acute gastroenteritis in the United States and a major challenge for infection control efforts. The high burden of norovirus in most communities and health care systems makes it difficult to discern viral transmission patterns using traditional epidemiological approaches alone.

Methods. We performed real-time metagenomic sequencing of norovirus isolates from an outbreak among inpatients at Seattle Children's Hospital (SCH). We also sequenced isolates from norovirus cases within the larger University of Washington (UW) Medical System that occurred during and after the outbreak.

Results. Our data showed that the month-long outbreak at SCH was actually characterized by 3 distinct concurrent transmission clusters contained within 3 different hospital units. We were able to report this information to the infection control team at SCH while the outbreak was still in progress. The virus responsible for one of these 3 clusters was genetically stable over a period of 4.5 weeks suggesting serial transmissions from a contaminated fomite, rather than patient to patient transmission. After cases meeting the epidemiological definition for hospital-acquired had ceased, we demonstrated that the virus from one of the 3 outbreak clusters continued to be transmitted to other patients within the SCH medical system. Finally, we showed that one of the patients who acquired norovirus during the outbreak developed a chronic infection with viral shedding documented up until the time of the patient's death, 8 months after the outbreak.

Conclusion. These results demonstrate the value of using metagenomics as an adjunct to traditional epidemiologic techniques in the setting of a hospital-associated norovirus outbreak. Real-time metagenomic sequencing elucidated viral transmission patterns within the outbreak while it was still in progress and follow-up sequencing revealed further infections due to an outbreak-associated viral strain even after the outbreak was thought to be over. Given this potential, metagenomic analyses represent an invaluable, largely untapped resource for improving our understanding of and reducing adverse effects from viral outbreaks.

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1648. Incidence of Norovirus and Rotavirus From Multisite Active Surveillance in Veteran's Affairs Hospitals, December 2016–February 2018: Results From the SUPERNOVA Network

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Background. Viruses are frequently implicated in acute gastroenteritis (AGE) outbreaks, yet the endemic burden of norovirus and rotavirus disease in adult populations is not well characterized. In 2016, we implemented a multisite AGE surveillance platform capturing cases and controls in 4 VA hospitals (Atlanta, Bronx, Houston, and Los Angeles), collectively serving >320,000 patients annually.

Methods. Inpatient AGE cases and age- and time-matched controls were identified through prospective screening of admissions via standardized case definitions. Outpatient cases were passively identified using stool samples submitted for routine clinical microbiological diagnostics. Samples were tested with the FilmArray Gastrointestinal Panel, followed by genotyping of virus positives. Incidence was estimated using population denominators of unique patients served annually by site.

Results. From December 1, 2016 to February 28, 2018, 875 cases (496 inpatients, 379 outpatients), and 374 controls were enrolled. Norovirus and rotavirus prevalence was highest among outpatient AGE cases (11.6% and 2.9%, respectively) followed by inpatient cases (3.4% and 1.6%, respectively); few controls were positive (norovirus, 1.3%; rotavirus, 0%). Norovirus-associated inpatient incidence was 15.2 per 100,000 population (range by site: 10.7–19.9/100,000) and rotavirus-associated inpatient incidence was 7.5 per 100,000 population (range by site: 0–12.8/100,000). The predominant norovirus genotype was GII.P16-GII.4 Sydney (50%), and rotavirus genotype was G12P[8] (83%). Norovirus was detected every calendar month and peaked in December–January, while rotavirus peaked in April. Nine deaths were documented among AGE inpatient cases, including one norovirus-associated death.

Conclusion. Implementation of a multisite AGE surveillance platform captured a wide spectrum of illness for norovirus and rotavirus in US Veterans including outpatient visits, inpatient hospitalizations, and one norovirus-associated death. Norovirus was the leading viral pathogen and was detected year-round. Ongoing surveillance using this platform will allow for further characterization of the pathogen distribution and associated AGE disease burden in adults.

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1659. Variation in Identifying Sepsis and Organ Dysfunction Using Administrative Versus Clinical Data and Impact on Hospital Outcome Comparisons

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Background. Administrative claims data are commonly used for sepsis surveillance, research, and quality improvement. However, variations in diagnosis, documentation, and coding practices may confound efforts to benchmark hospital sepsis outcomes using claims data.

Methods. We evaluated the sensitivity of claims data for sepsis and organ dysfunction relative to clinical data from the electronic health records of 193 US hospitals. Sepsis was defined clinically using markers of presumed infection (blood cultures and antibiotic administrations) and concurrent organ dysfunction. Organ dysfunction was measured using laboratory data (acute kidney injury, thrombocytopenia, hepatic injury), vasopressor administrations (shock), or mechanical ventilation (respiratory failure). Correlations between hospitals' sepsis incidence and mortality rates by claims (using "explicit" ICD-9-CM codes for severe sepsis or septic shock) versus clinical data were measured by the Pearson correlation coefficient (r) and relative hospital rankings using either data source were compared. All estimates were reliability-adjusted to account for random variation using hierarchical logistic regression modeling.

Results. The study cohort included 4.3 million adult hospitalizations in 2013 or 2014. The sensitivity of hospitals' claims data for sepsis and organ dysfunction was low and variable: median sensitivity 30% (range 5–54%) for sepsis, 66% (range 26–84%) for acute kidney injury, 39% (range 16–60%) for thrombocytopenia, 36% (range 29–44%) for hepatic injury, and 66% (range 29–84%) for shock (Figure 1). There was only moderate correlation between claims and clinical data for hospitals' sepsis incidence ($r = 0.64$) and mortality rates ($r = 0.61$), and relative hospital rankings for sepsis mortality differed substantially using either method (Figure 2). Of 48 (46%) hospitals, 22 ranked in the lowest sepsis mortality quartile by claims shifted to higher mortality quartiles using clinical data.

Conclusion. Variation in the completeness and accuracy of claims data for identifying sepsis and organ dysfunction limits their use for comparing hospital sepsis rates and outcomes. Sepsis surveillance using objective clinical data may facilitate more meaningful hospital comparisons.