Background. In January 2018, the first case of an OXA-48 carbapenem-resistant Klebsiella pneumoniae (OXA-48 CRKP) was identified in a North Carolina hospital in a patient arriving from Eastern Europe. Over the next year across multiple inpatient adult units, 14 patients had clinical isolates and 2 patients had positive rectal surveillance screens for OXA-48 CRKP.

Methods. Investigation activities to characterize the OXA-48 CRKP epidemiology included: >1000 rectal colonization screens of epidemiologically linked patients, chart reviews of infected and colonized patients, hand hygiene and environmental cleaning observations on affected units, environmental sampling to include endoscopes, sinks and toilets, and molecular analyses (pulsed-field gel electrophoresis and whole-genome sequencing).

Results. Molecular analyses confirmed a clonal outbreak. All environmental cultures including endoscope cultures performed were negative for OXA-48 CRKP. All cases were explained by at least one of three mechanisms: (1) time/space overlap on the same unit (presumed lack of hand hygiene or contamination of shared patient equipment); (2) patient housed in room where previously infected patient was housed (presumed inadequate terminal disinfection/contaminated environment); or (3) a single upper gastrointestinal endoscope. Interventions included surveillance to identify and isolate colonized patients, discharge room cleaning of OXA-48 CRKP patients enhanced by ultraviolet light disinfection, curtain laundering, and discarding unused patient supplies, electronic monitoring and feedback for compliance with hand hygiene cleaning, and use of personal protective equipment. A single endoscope used between multiple OXA-48 CRKP patients with no other known transmission link was quarantined upon identification, sterilized with ethylene oxide, and ultimately placed out of service.

Conclusion. A clonal outbreak of a novel carbapenemase-producing Enterobacteriaceae likely spread via multiple modes of transmission. The investigation was complicated by infrequent identification of colonization among patients epidemiologically linked to known cases. Multiple interventions based on epidemiological links were necessary to halt hospital-wide transmission.

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530. Sequential Screening of High-Risk Patients for Carbapenemase-Producing Enterobacteriaceae Colonization

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Session: 57. H1: MDRO – GNR Prevention

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Background. Early identification of patients colonized with carbapenemase-producing Enterobacteriaceae (CPE) facilitates the implementation of appropriate infection control measures and reduces nosocomial transmission. Sequential screening for CPE colonization of close contacts of known cases to confirm initial negative results is recommended. Fraser Health (FH) expanded sequential screening to patients with recent exposure to other risk factors following the identification of CPE in patients who initially screened negative.

Methods. FH screens patients for CPE who report healthcare outside of Canada or travel to endemic countries within the previous 12 months. Patients remain on contact precautions and are re-screened 7 and 21 days after the last known exposure date. We reviewed CPE cases with foreign healthcare or travel to endemic countries who screened negative on admission but subsequently screened positive within 30 days. Patients with colonization of CPE on a rectal screen post-exposure to a current nosocomial source were excluded. Whole-genome sequencing results were examined to confirm foreign healthcare or travel as the likely source of acquisition. Medical records were reviewed to obtain patient history and clinical details.

Results. Between November 2015 and January 2019, 21 patients had a positive CPE screen within 30 days of a negative screen, with no known CPE exposures during that time. The median time between the last date of known exposure and positive CPE screen was 20 days (range: 7–77 days). Twelve (57%) cases were hospitalized outside of Canada. Eight (38%) reported other foreign healthcare encounters, and 1 (5%) had no reported healthcare outside of Canada but had traveled to an endemic country. Sixteen (71%) cases received antibiotics prior to the positive CPE screen.

Conclusion. Patients with unrecognised CPE colonization are a source for nosocomial transmission. Patients screening negative for CPE with recent exposure to risk factors other than contact with a known case may screen positive at a later date. This may be due to higher colonization levels or antibiotic selection pressures. Consideration should be given to sequential CPE screening of high-risk patients based on the last date of exposure.

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531. Practical and Evidence-Based Considerations for Implementation of Bacterial Whole-Genome Sequencing Within Longitudinal Infection Control Practice

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Background. Whole-genome sequencing (WGS) of bacteria is becoming a routine utility to guide infection control (IC) practice longitudinally and is underexplored. As with any technology adopted in the hospital, the integration of WGS into IC practice must be carefully managed and considered. We qualitatively report an evidence-based implementation workflow that considers WGS to help proactively guide IC professionals during investigation of infectious outbreaks.

Methods. We built upon lessons learned in an ongoing surveillance effort at a tertiary care hospital—utilizing retrospective WGS data within the Philips IntelliSpace Epidemiology system—to understand facilitators and barriers to the use of bacterial WGS longitudinally to inform IC workflow. Our team established a 9-month workgroup to study the practical aspects of implementing WGS in routine IC practice. From expert opinion collected via the workgroup, in addition to evidence from the literature, a workflow guidance document and checklist were codified. New ideas included incorporating education to promote the establishment of an IC triage process.

Results. Facilitators to implementation included ability to display genomic relatedness alongside relevant patient data to enable clinical actionability, ability to pivot time and resources rapidly when infections are a pseudo outbreak (false positive) or missed outbreak (false negative), opportunities for nuanced staff education, and willingness to take the first-of-kind approach. Barriers were considered the key concepts to IC professionals and relevant institutional stakeholders, maintaining sharable notes of active investigations to promote data-sharing practices, and timing and review of relevant interventions into the facility workflow. Strategies to address these issues were developed.

Conclusion. This study provides a novel framework for adaptation of existing IC workflow strategies to leverage the utility of bacterial WGS, and it presents a schema to effectively engage relevant stakeholders, based on an analysis of the unique challenges inherent with IC practice. It also offers an innovative model for the development and implementation of IC workflows to account for, and adapt to, site-specific conditions.

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