Presentation Type:
Poster Presentation - Top Poster Abstract
Subject Category: Molecular Epidemiology
Large-Scale S. aureus Screening with Molecular Epidemiology; the Role of MSSA and Community MRSA in Hospital Transmissions
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Background: The frequency of Staphylococcus aureus transmission in hospitals is unknown: symptomatic infection may occur months after transmission and colonization, and infection prevention efforts rely on indirect measurements, rather than direct detection of transmission events. We implemented a hospital-based S. aureus screening program, combined with whole genome sequencing of S. aureus surveillance and clinical cultures and data extracted from the electronic health record, to identify S. aureus clonal complex-, patient- and location-specific factors associated with S. aureus transmission in our health system. **Methods:** Screening S. aureus cultures were obtained at admission by nasal swab for adults admitted to Medicine, Transplant, Oncology and intensive care, and weekly by swab of nares, axilla and groin for children admitted to intensive care and Oncology at NYU Langone Health in New York City. All methicillin-resistant S. aureus (MRSA) from screening and clinical (blood, wound, sputum) cultures and all methicillin-susceptible S. aureus (MSSA) from screening and blood cultures underwent whole genome sequencing. Isolates from distinct patients with < 2 0 single nucleotide pair differences were considered genetically related. Electronic health data was extracted for descriptive statistics and for spatiotemporal plots to assess plausible transmissions. We used REDCap electronic data capture tools hosted at NYU Grossman School of Medicine and SAS software for data analysis to evaluate S. aureus transmissions between November 2022 and November 2023. **Results:** We analyzed 8,567 S. aureus isolates: including 6,552 screening cultures, 1,008 blood cultures, and 1,007 clinical cultures. We found 424 plausible S. aureus hospital transmissions using sequencing and electronic health data. Screening cultures identified 75% of transmissions that would have otherwise been missed with blood and clinical cultures alone. The majority of positive screening cultures isolated MSSA, but the proportion of transmissions due to MSSA differed by age. In children, MSSA colonization accounted for 62% of transmissions. In adults, only 15% of transmissions were due to MSSA colonization, whereas MRSA colonization accounted for 56% of transmissions. Analysis of adult MRSA isolates by clonal complex found that 45% of transmissions were due to CC8, higher than the 17% among isolates agnostic of transmissions. Emergency departments and the neonatal intensive care unit had the highest number of transmissions. Patients involved in transmissions had longer lengths of stay and frequent hospitalizations. **Conclusions:** A S. aureus screening program, coupled with genome sequencing and electronic health data, can identify patient group, hospital locations and clonal complexes that are at high risk for S. aureus transmissions.

Antimicrobial Stewardship & Healthcare Epidemiology 2024;4(Suppl. S1):s15
doi:10.1017/ash.2024.115

Presentation Type:
Poster Presentation - Top Poster Abstract
Subject Category: Molecular Epidemiology
Capturing MRSA Diversity by Integrating Genomic and Epidemiological Data of Patients and their Spaces
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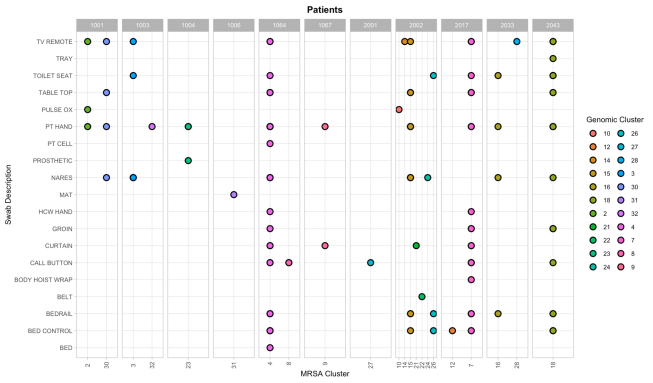

Background: Methicillin-resistant S. aureus (MRSA) is known to cause frequent and severe infections in community living centers, potentially resulting in significant mortality for elderly patients. More research is needed to understand how to utilize genomic and epidemiological data to understand characteristics that may lead to increased transmission. We hypothesized that combining genomic and epidemiological information to sample patients and their environments during long-term stays, we will be able to capture a diverse set of MRSA strains. **Method:** This work included genome sequencing of patient and environmental samples from 11 patients within the VA Ann Arbor Healthcare System from May 4, 2021- November 16, 2022. All 11 patients tested positive for MRSA during their stay (mean days = 31). Patient and environmental samples were taken throughout their stays, screened for MRSA, and whole-genome sequenced. Single nucleotide variants (SNVs) were identified by mapping reads and calling variants against strain-specific reference genomes. We used ape v5.6-2 in R v4.2.2 to analyze and infer evolution, acquisition, and transmission events based on pairwise SNV distances. Genomic clusters were determined using stats v3.6.2, with a SNV distance threshold of 20. **Result:** Samples that were collected from patient bodily sites were able to reveal 20 distinct genomic clusters of MRSA (patient hands: n = 10, nares: n = 7, groin: n = 3). Environmental samples from patient environments also revealed distinct genomic MRSA clusters (tv remote: n = 9, toilet seat and bed rail: n = 6, table top, bed control, and call button: n = 5, bed curtain: n = 4, pulse ox = 2, cell phone, tray, pulse ox, mat, body hoist wrap, and bed: n = 1). **Conclusion:** The identification of various genomic clusters from patients and their environmental reservoirs suggests intrahost variation that can only be captured by using a more holistic approach of integrating epidemiology and genomic sequencing. Developing studies that incorporate genomic data, various environmental sources, and multiple isolates over time within community living centers can increase our understanding of strains that are more likely to transmit, survive on living and non-living surfaces and therefore lead to improved recommendation for infection prevention interventions and drivers of endemicity.
Disclosure: Lona Mody: NIH, VA, CDC, Kahn Foundation; Honoraria: UpToDate; Contracted Research: Nano-Vibronix

Antimicrobial Stewardship & Healthcare Epidemiology 2024;4(Suppl. S1):s15
doi:10.1017/ash.2024.116

Presentation Type:
Poster Presentation - Top Poster Abstract
Subject Category: Pediatrics
Burden of Healthcare-Associated Infections in a Pediatric Intensive Care Setting Before, During, and After the Pandemic
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