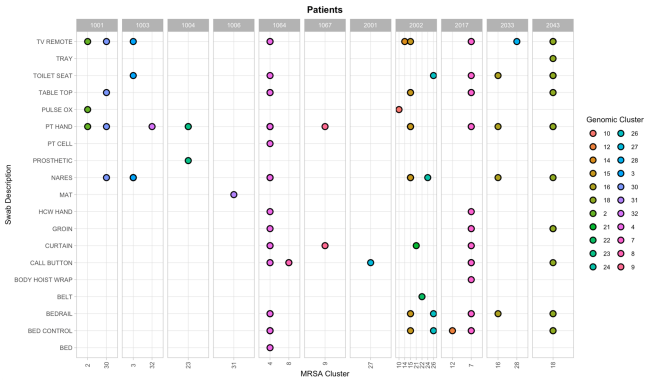
Presentation Type:
Poster Presentation - Top Poster Abstract
Subject Category: Molecular Epidemiology
Large-Scale S. aureus Screening with Molecular Epidemiology; the Role of MSSA and Community MRSA in Hospital Transmissions
Courtney Takats, Emory University; Gregory Putzel, Emory University; Drew Siskin, Emory University; Alejandro Pironti, NYU Langone Medical Center; Bo Shopsin, NYU Langone Medical Center and Sarah Hochman, NYU Langone Health

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
Tasmine Clement, University of Michigan; Kristen Panson, University of Michigan; Marco Cassone, University of Michigan; Ali Mohammed Pirani, University of Michigan; Evan Snitkin, University of Michigan and Lona Mody, University of Michigan, VA Ann Arbor Healthcare System



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
Meghan Engbretson, Children's Hospital of Eastern Ontario; Josh Schaffzin, Children's Hospital of Eastern Ontario; Dayre McNally, Children's Hospital of Eastern Ontario; George Gubb, Children's Hospital of Eastern Ontario and Nisha Thampi, Children's Hospital of Eastern Ontario

Table 1. PICU HAI Incidence, January 2019-November 2023.

Time period	Overall HAI Incidence Per 1,000 patient days	CAUTI (n=21) Per 1,000 catheter days	CLABSI (n=11) Per 1,000 line days	HAVRI (n=18)	ARO (n=6)	CDI (n=3)
				Per 1,000 inpatient days		
Pre-Pandemic	3.66	5.52	1.24	0.92	0.31	0.31
Pandemic	5.3	5.24	2.82	1.49	0.42	0.21
Post-Pandemic	4.56	5.59	0.99	1.74	0.65	0.22

Background: Adult rates of non-COVID-19-related healthcare-associated infection (HAI) initially decreased and subsequently increased during the COVID-19 pandemic. Little is known about pediatric HAI rates during this period. **Methods:** A retrospective review of HAIs was conducted for patients admitted to the intensive care unit (PICU) at a pediatric tertiary care hospital between January 1, 2019 and November 30, 2023. Patients who spent ≥48 hours in the PICU were included. Surgical site infections were excluded. Data were obtained from infection surveillance reports; each HAI was reviewed for validity and attribution based on National Healthcare Safety Network definitions. HAIs were grouped into 3 time periods: pre-pandemic (January 2019-February 2020), pandemic (March 2020- February 2022), and post-pandemic (March 2022-November 2023). Infection rate ratios were calculated for pre-pandemic and post-pandemic periods. **Results:** Among 2,959 PICU patients admitted during the study period, there were 60 HAI events (4.78 per 1,000 patient days). Rates generally remained steady throughout with slight increases and decreases between time periods (Table 1). There was no significant difference in CAUTI, CLABSI, or HAVRI rates noted in the PICU between pre-pandemic and post-pandemic periods despite a significantly higher device utilization ratio in the post-pandemic period for both urinary catheters and central lines (IRR, 0.89; p < 0 .05; 95% CI, 0.82-0.97). The most frequent HAI in all time periods was CAUTI. **Conclusion:** Unlike reports from adult centers, no significant variation between time periods was noted for HAIs in our pediatric center. Despite numerous COVID-19-related changes in infection prevention and control measures and contexts throughout the study period, HAI rates remained stable. This may be due in part to the lower burden of critically ill COVID-19 pediatric patients compared to adult populations. Additionally, this could indicate resiliency and consistency in practice among pediatric providers throughout the pandemic. Further evaluation of pediatric HAIs in the context of the COVID-19 pandemic may reveal practices that could be replicated elsewhere to control HAI rates.

Antimicrobial Stewardship & Healthcare Epidemiology 2024;4(Suppl. S1):s15–s16

doi:10.1017/ash.2024.117

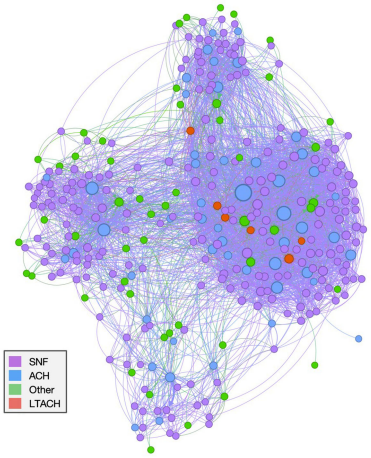


Figure 1. Social Network of 2022 CMS Patient Transfers in Colorado.
This network shows Medicare beneficiary inpatient transfers (edges) between healthcare facilities (nodes), stratified by facility type (node color). SNF, skilled nursing facility. ACH, acute care hospital. Other, facilities not otherwise classified. LTACH, long term acute care hospital.

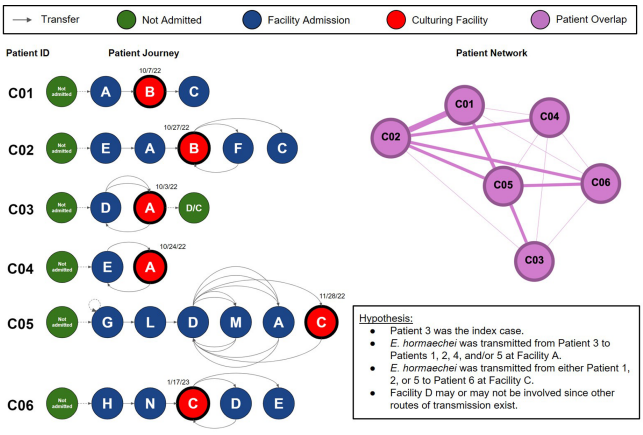


Figure 2. Example of patient journey diagrams coupled with a patient overlap network.
These visualization tools enable public health to identify inpatient overlap and hypothesize where clustered *E. hormaechei* transmission may have occurred based on culture date.

Presentation Type:
Poster Presentation - Top Poster Abstract
Subject Category: Public Health

Public Health Applications of Patient Transfer Networks—Colorado, 2022–2023

Kristen Marshall, CDC, Colorado Department of Public Health and Environment; Karlie Hoetzer, Colorado Department of Public Health and Environment; Jennifer Driscoll, Colorado Department of Public Health and Environment; Braden Bardach, Ascension All Saints Hospital; Janell Nichols, Colorado Department of Public Health; Samuel Baird, Colorado Department of Public Health and Environment; Vishnu Panicker, Colorado Department of Public Health and Environment; Devon Williford, Colorado Department of Public Health and Environment and Christopher Czaja, Colorado Department of Public Health and Environment

Background: During 2021–2023, an increase in Klebsiella pneumoniae carbapenemase producing Enterobacterales species (KPC-CRE) cases occurred among patients admitted to several overlapping healthcare facilities, prompting an investigation by the Colorado Department of Public Health and Environment (CDPHE). We applied social network analysis (SNA) to identify KPC-CRE networks and other multidrug-resistant organism (MDRO) transmission, created a tool for public health prevention planning and for facilities to examine their own patient transfer connectivity, and explored additional public health and emergency preparedness applications. **Methods:** A statewide patient transfer network was created using 2021–2022 Medicare beneficiary data. Subnetworks were isolated from the larger network to examine a cluster of facilities involved in a KPC-CRE outbreak, defined as ≥2 KPC-CRE cases related by whole genome sequencing (WGS). WGS was conducted at the CDPHE State Lab. Highly connected facilities were determined by patient transfers between at least two KPC-CRE testing facilities. Individual patient journeys were constructed using admissions and culture date. SNA was conducted in RStudio; visualizations, network metric calculations, and clustering analysis were conducted using Gephi and ArcGIS software. **Results:** SNA yielded 4,864 direct patient transfers between 326 healthcare facilities (220 skilled nursing facilities, 50 acute care hospitals, 32 critical access hospitals, six long term acute care hospitals, and 18 facilities not previously classified; Figure 1). WGS identified five separate KPC-CRE outbreaks among 14 patients during February 2022–January 2023; 14 patient specimens were collected at four testing facilities. We identified five highly connected facilities in addition to the four testing facilities. Patient journeys allowed us to identify possible locations of KPC-CRE transmission in four of the five outbreaks (Figure 2). CDPHE provided guidance to all involved facilities on admission