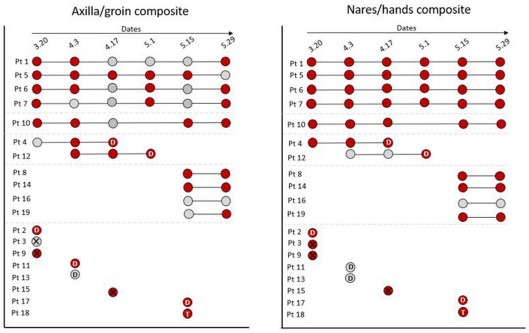
Figure 2. Results of bilateral axilla/groin composite and bilateral nares/hands composite swabs (n=102) using culture-based testing.



Red circles display positive results, and gray circles display negative results. Circles with "D" inside represent patients who were discharged, circles with an "X" inside represent patients who deceased during the study period, and circles with a "T" inside represent patients who were transferred out of the cohort unit.

Figure 3. Venn Diagram showing body site positivity for 48 samples positive using culture-based testing

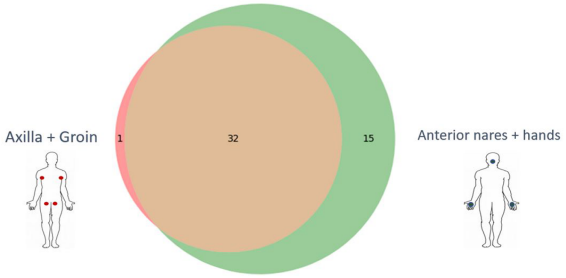
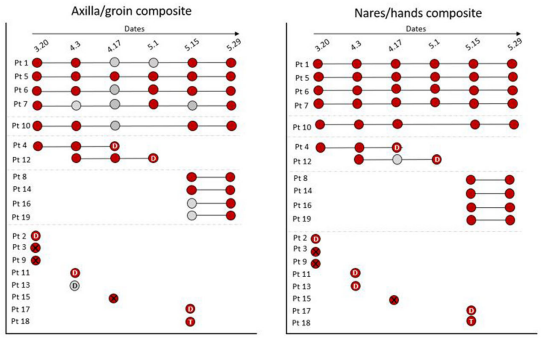


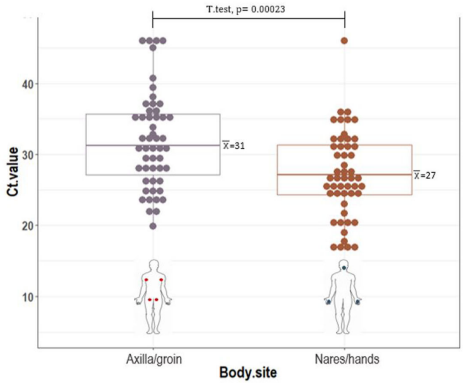
Figure 4. Results of bilateral axilla/groin composite and bilateral nares/hands composite swabs (n=102) using real-time PCR testing.



Red circles display positive results, and gray circles display negative results. Circles with "D" inside represent patients who were discharged, circles with an "X" inside represent patients who deceased, and circles with a "T" inside represent patients who were transferred out of the cohort unit.

methods. **Results:** A total of 102 swabs (51 from each swab type) were collected from 19 patients who were each sampled a median of twice (IQR: 1-5). Among the 102 swabs, 35 of 51 (69%) axilla/groin swabs were positive compared with 45 of 51 (88%) nares/hands swabs using culture (Figure 2). Furthermore, 48 of 51 (94%) swabs were positive by culture for both methods, with 15 positive from the nares/hands and one positive from the axilla/groin (Figure 3). Among 11 patients who were tested ≥2 times with nares/hands swabs, 9/11 (81%) tested positive on all sequential swabs via culture and 10/11 (90%) tested positive via PCR (Ct threshold < 3 6.9). Among the same 11 patients but using the axilla/groin swabs, 3/11 (27%) patients tested positive on all sequential swabs using culture, and 5/11 (45%) tested positive using PCR (Figures 2-4). On average, samples collected from

Figure 5. Ct values of bilateral axilla/groin composite and bilateral nares/hands composite swabs using real-time PCR testing.



nares/hands swabs had lower Ct values (mean=27) compared to axilla/groin swabs (mean=31) (p-value=< 0.001) (Figure 5). **Discussion:** Identifying the swab site with most consistent C. auris detection is important for surveillance purposes. In our study, there were more positives and consistent positivity for nares/hands by both culture and PCR-based methods, as well as lower Ct values, suggesting that these swabs provide more reliable detection of C. auris colonization. Alternative screening methods deserve consideration as CDC continues to explore whether swabbing of other body sites (e.g., nares, hands) would improve accuracy and consistency when identifying colonized patients.

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Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Molecular Epidemiology

Real-time Whole Genome Sequencing Surveillance as an Effective Outbreak Detection and Mitigation Tool

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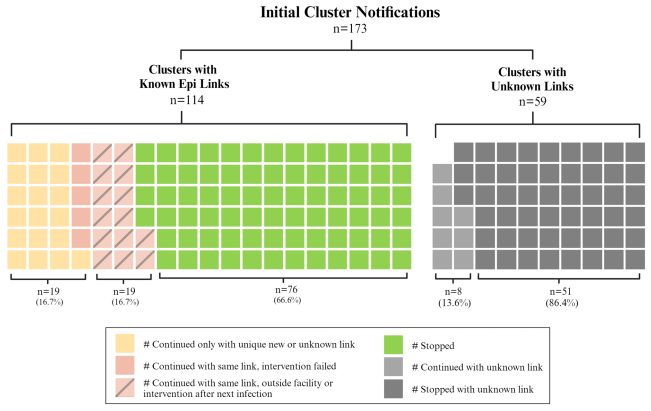
Background: Detection of outbreaks traditionally relies on passive surveillance, and often misidentify or miss outbreaks. Whole genome sequencing (WGS) surveillance has emerged as a proactive measure, enabling early detection of outbreaks and facilitating rapid intervention strategies. WGS surveillance has not been widely studied due to infrastructure, cost, and evidence barriers regarding its impact on reducing healthcare-associated infections (HAIs). This study represents findings from two years of a real-time WGS surveillance program called the Enhanced Detection System for Healthcare-associated Transmission (EDS-HAT). **Methods:** The study was conducted at UPMC Presbyterian hospital, a 694-bed tertiary care center. Patient isolates of select bacterial pathogens were collected and underwent WGS weekly from November 2021 to November 2023. Potential transmission was defined using single-nucleotide polymorphism thresholds (≤15 for all organisms except Clostridioides difficile). Genetically related clusters were reviewed weekly for epidemiological linkages (unit, personnel, or procedural commonalities) and appropriate interventions were initiated by the infection prevention and control team. We described the frequency of genetic relatedness and nature of epidemiological linkages. **Results:** Of 7,051 eligible unique patient organism isolates,



4,723 were deemed healthcare-associated and underwent WGS. EDS-HAT identified 478 (12.2%) isolates genetically related to ≥1 other isolate across 173 clusters. Epidemiological links were found in 278 (58.2%) isolates in 114 clusters, with the majority being unit-based (205 isolates, 71.9%); other epidemiological links included equipment or healthcare workers (32 isolates, 11.5%), external facilities (24 isolates, 8.6%), and shared endoscopes (17 isolates, 6.1%); all endoscope outbreaks were effectively contained at two patients. No epidemiological links could be identified for 200 (41.8%) isolates. Infection prevention initiated 134 interventions in 114 clusters, including 74 (55.2%) general staff notification and education, 25 (18.7%) enhanced cleaning efforts, 23 (17.2%) hand hygiene/personal-protective equipment compliance observations, 9 (6.7%) environmental cultures, and 3 (2.2%) enhanced microbiological surveillance. Following the detection of an epidemiological link and intervention, 94/101 (94.1%) outbreaks were effectively halted on the intervened route (Figure). **Conclusion:** This study demonstrates the feasibility and efficacy of EDS-HAT as an infection prevention tool. Early detection and intervention of outbreaks significantly enhance the capability of healthcare facilities to control and prevent the spread of HAIs. Investment in infrastructure and implementation costs will result in reducing pathogen transmission and improving patient safety in acute care settings.

Disclosure: Alexander Sundermann: Honoraria - Opgen

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Subject Category: MRSA/VRE

Assessing chlorhexidine resistance in MRSA isolates from hospitals in Cleveland, OH and Detroit, MI

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Background: Methicillin-resistant Staphylococcus aureus (MRSA) is one of the most common causes of procedure-related, skin, and soft-tissue infections. Hospitalized patients who are colonized with MRSA are at a higher risk of developing invasive infections after discharge. Chlorhexidine, an antiseptic/disinfectant, has been used to reduce carriage and prevent infections in these patients. Studies have shown chlorhexidine resistance among MRSA strains. Chlorhexidine resistance is associated with qac genes, which encode multidrug efflux pumps that increase bacterial tolerance to disinfectant agents. The global distribution and prevalence of qacA and qacB genes are highly variable. One study reported that qacA and qacB genes could be found in 0.9% - 83.3% of clinical MRSA isolates worldwide. The goal of this study was to determine the prevalence of chlorhexidine resistance and identify the resistance-associated genes from our MRSA samples using whole genome sequencing (WGS). **Methods:** 474 MRSA samples were obtained from hospitals in Detroit, MI (287) and Cleveland, OH (187). Whole genome sequencing was performed using the NextSeq (Illumina Inc., CA) platform. The sequencing data was analyzed using ResFinder 4.1, a publicly available database that can be used to identify acquired genes and chromosomal mutations mediating antimicrobial resistance. The output was organized into a data sheet to visualize the presence of the genes of interest. **Results:** The qacA gene was present in only one MRSA sample from the Cleveland area hospital. In the samples from Detroit, 14 out of 287 showed disinfectant resistance genes. The qacA, qacB, and qacD were present in 1, 6, and 7 samples, respectively. The prevalence of any qac gene in the Cleveland area samples was 0.5%. Meanwhile, the prevalence of any qac gene in Detroit area samples was 4.9%. Among the 7 samples that have qacD gene, 6 samples have more than one copy of qacD. **Conclusions:** The prevalence of the "qac" gene varied widely based on the origin of the samples. Detroit area samples had more qac genes prevalence than Cleveland area samples. Chlorhexidine is a widely used antiseptic/disinfectant, and it plays a vital role in reducing carriage and preventing infection among hospitalized patients colonized with MRSA. Monitoring and addressing MRSA-reduced susceptibility to chlorhexidine is imperative for maintaining the effectiveness of infection control practices such as decolonization.

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Subject Category: MRSA/VRE

Timesavers: Clinical Decision Support and Automation of MRSA and VRE Deisolation

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Background: Most healthcare facilities in the US apply contact precautions (CP) for patients with methicillin-resistant Staphylococcus aureus (MRSA) or vancomycin-resistant enterococci (VRE) infection and/or colonization. Most individuals with MRSA or VRE colonization will clear over time; however, frontline clinicians rarely evaluate for discontinuation of CP, resulting in increased burden on infection preventionists (IPs). Automation of time- and test-based evaluation using clinical decision support systems (CDSS) embedded in electronic health records (EHR) may increase evaluation and discontinuation of CP when appropriate, while preserving IP resources. **Methods:** This quality improvement initiative was implemented at Mass General Brigham (MGB), an integrated healthcare system, where patients with MRSA or VRE infection/colonization are identified in the EHR with a corresponding "infection status" and CP applied. Following MGB policy (Figure 1), CDSS features included: 1) automated time-based resolution from 2/15/2023-11/13/2023 and 2) automated ordering of screening assays for patients eligible for test-based evaluation from 6/20/2023-11/14/2023 (Figure 2). Counts of CP discontinuation and automated ordering were performed. IPs at one MGB facility performing manual review of patients self-recorded the time spent evaluating for CP discontinuation. Using these time reports, the average time to complete these tasks and the projected time savings were calculated over the implementation period. **Results:** Four IPs recorded the time to review patients for CP discontinuation, including reviewing recent antimicrobial administration, microbiology results, ordering screening test(s), and