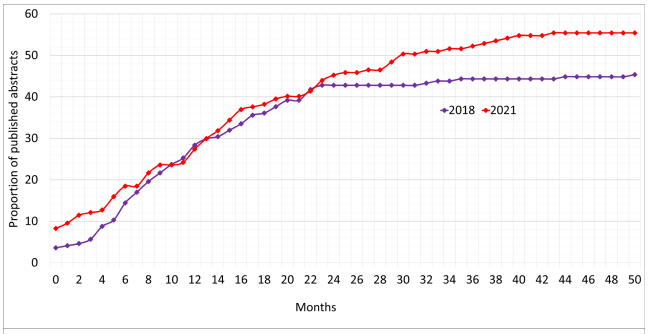

Figure 3: Proportion of abstracts published versus time to publication, SHEA spring 2018 and 2021 conferences

Study, first author, year	Specialty	Meeting and year evaluated	No. published/No. presented (%)
Johnson, 2022 [1]	Infectious Disease	ID Week 2017 & 2018	236/887 (26.6)
Rosmarakis, 2005 [2]	Infectious Disease & Microbiology	ICAAC 1999 & 2000	68/190 (36)
Amarilyo, 2013 [3]	Rheumatology	ACR/ARHP 2006	1270/2149 (59.1)
Fosbøl, 2012 [4]	Cardiology	AHA 2006 to 2008	3921/11365 (34.5)
Gandhi, 2016 [5]	Gastroenterology	ACG 2008	249/791 (31.5)
Baddam, 2018 [6]	Hematology	ASH 2011	327/685 (48)

Figure 4: Comparative studies analyzing abstracts published from infectious disease and various other specialty meetings

Abbreviations: ICAAC, Interscience Conference on Antimicrobial Agents and Chemotherapy; ACR/ARHP, American College of Rheumatology & Association of Rheumatology Health Professionals; AHA, American Heart Association; ACG, American College of Gastroenterology; ASH, American Society of Hematology

DOI
[1] 10.1093/ofid/ofac415
[2] 10.1096/fj.04-3140lfe
[3] 10.1002/acr.21864
[4] 10.1161/circulationaha.112.120535
[5] 10.1159/000450785
[6] 10.1002/ajh.24695

other internal medicine and subspecialty conferences, including IDWeek. **Conclusion:** Approximately half of the abstracts presented were subsequently published as full articles. Collaborative research, involving more authors and authors from different institutions, was associated with a higher publication rate. These findings highlight the strong academic impact of SHEA-presented research. Further research into the barriers to publication is warranted to improve the dissemination of conference abstracts.

Antimicrobial Stewardship & Healthcare Epidemiology 2025;5(Suppl. S2):s28–s29
doi:10.1017/ash.2025.227

Presentation Type:
Oral Presentation
Subject Category: Molecular Epidemiology
Real-time detection of Staphylococcus aureus transmission in hospitals

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Genomic surveillance of Staphylococcus aureus in hospitals usually focuses on clinical infections, missing transmissions from asymptomatic carriers and delaying detection and timely intervention. To address the issue, we performed whole-genome sequencing (WGS) on over 5,000 S. aureus isolates obtained from colonization screens at admission, in addition to standard clinical cultures, at two interconnected urban hospitals. By integrating genomic data with timestamped location information, we identified hundreds of transmissions missed by standard methods. However, nearly 70% of transmissions were detected during readmission after the index case had been discharged. This finding indicates that even with dense genomic sampling, real-time detection remains challenging due to asymptomatic carriage. Therefore, effective monitoring of nosocomial S. aureus transmission will likely require WGS and colonization sampling at both admission and discharge. The data also highlight patient- and strain-specific factors, including methicillin resistance, as predictors of S. aureus spread, which may enable cost-effective, targeted sequencing surveillance strategies.

Antimicrobial Stewardship & Healthcare Epidemiology 2025;5(Suppl. S2):s29
doi:10.1017/ash.2025.228

Presentation Type:
Oral Presentation
Subject Category: Molecular Epidemiology
Lessons from Implementing Wastewater-Based Epidemiological Monitoring in a Northern California Acute Care Hospital, June–July 2024

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Background: Wastewater-based epidemiology has demonstrated effectiveness in monitoring trends of viral infections at the city, state, and national levels. It captures data independent of testing intensity, providing a comprehensive biological sample of pathogens excreted in all secretions, that is unaffected by individual testing behaviors. Traditional healthcare-associated infection surveillance relies on case-based approaches, which can be resource-intensive, prone to misclassification, and may miss patients who are colonized. We aimed to evaluate the feasibility of implementing wastewater-based epidemiology in an acute care hospital for monitoring pathogens relevant to infection prevention and control. **Methods:** In this pilot study, we deployed a Teledyne ISCO 5800™ wastewater autosampler to collect weekly composite 1000 mL samples (15 mL every 151 minutes) from the final Stanford Hospital outflow point before wastewater merged with the community system. Wastewater samples were processed within 48 hours of collection. The solid phase was separated via centrifugation, followed by nucleic acid extraction employing silica-based purification techniques optimized for efficient inhibitor removal. Droplet digital PCR was conducted targeting pathogens previously validated by the WastewaterSCAN program (https://www.wastewaterscan.org/en/pathogens). We compared hospital wastewater nucleic acid concentrations with the number of positive tests/cultures at Stanford Hospital during the same period and with Wastewaterscan community wastewater data. **Results:** We collected three weekly composite samples: Jun 20–26, Jul 10–17, and Jul 18–25. Challenges included the location of the final outflow, and the autosampler's size (132 x 74 x 84 cm and 88.5 kg). The outflow point was situated in a high-traffic area for patients and staff, requiring barricades to ensure safety and prevent interference with sampling equipment. In terms of interpreting results, viral nucleic acid concentrations (e.g., influenza, SARS-CoV-2) appeared to parallel the number of clinical cases and were similar to community wastewater trends (Figure 1). Most antimicrobial resistance genes, including vanA (Figure 2) and carbapenemase genes (KPC, NDM, OXA-48, VIM) (Figure 3), showed limited alignment with clinical cases; however, mecA exhibited some alignment (Figure 2). Hospital wastewater had higher resistance gene concentrations than community wastewater from San Mateo County (Figure 4). **Conclusion:** Continuous collection of hospital wastewater proved challenging, mainly from logistical issues such as equipment size and access limitations. Clinical respiratory virus trends appeared to be reflected in wastewater data. However, trends for antimicrobial resistance genes may be influenced