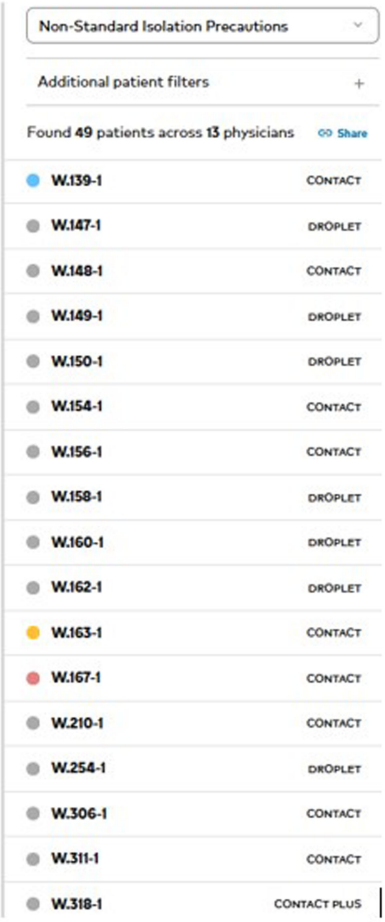
Figure 2. Review Isolation Precautions Patient Level Detail



Figure 3. Patients with Reconciled Isolation



beginning of each shift during daily patient safety rounds including weekends and holidays. **Results:** Tool visuals displayed a patient list to prioritize review of isolation status (Figure 1), patient specific details of mismatch (Figure 2) and reconciled isolation (Figure 3). The average resolution within 24h was 86% (range 79-95%). Charge nurse adoption improved time to isolation, reduced reliance on IP manual processes, improved first time bed assignments and guided nursing patient care assignments. The tool solved for lab "new results" alert gaps to caregivers for MRSA, Candida auris, etc. and provided timely information to care team members unable to access EHR isolation status. Feedback was overwhelmingly positive from users. Short term limitations to reconciliation occurred for patients with clinical conditions warranting isolation pending diagnostic test results (i.e. C. difficile). **Conclusion:** The technology enabler tool brings together various data streams into a single view for patient care teams and leadership to prioritize activities. The tool enabled shared responsibility between nursing and IP for reconciling isolation status, improved communications, driving operational efficiencies and improving safety.

Antimicrobial Stewardship & Healthcare Epidemiology 2026;6(Suppl. S1):s141–s142
doi:10.1017/ash.2026.10658

Presentation Type:
Poster Presentation
Subject Category: Microbiology

Does Chlorhexidine Bathing Contribute to Chlorhexidine Resistance?‡

Rachel Medernach[1], Ellen Gough[1], Mckenzi King[1], Mary Carl Froilan[1], Mackenzie May, Lahari Thotapalli[1], Michael Schoeny[1], Sarah Sansom[2], Erica Hartmann[3] and Mary Hayden[1]
[1]Rush University Medical Center; [2]Rush University and [3]Northwestern University

Background Bacterial resistance to frequently used antimicrobial therapies is a significant threat to human health. Chlorhexidine digluconate (CHG) is a topical antiseptic used to reduce healthcare-associated infections, including those caused by multidrug-resistant organisms. There is concern that exposure to CHG may lead to elevated bacterial CHG minimum inhibitory concentrations (MICs) in healthcare environments where the antiseptic is used. We investigated whether skin bacteria of CHG-exposed patients had elevated CHG MICs compared to patients without CHG exposure. Additionally, we evaluated whether bacteria isolated from environmental surfaces of CHG-exposed patients and from surfaces with detectable concentrations of CHG had higher CHG MICs compared to bacteria isolated from room surfaces without CHG exposure or from surfaces without detectable CHG. Methods We recruited a prospective observational cohort including two patient groups: 15 patients without CHG exposure during hospitalization, and 15 patients with daily CHG bathing for ?14 days prior to enrollment. Informed consent was obtained, and clinical data were recorded. Skin and environmental swab samples were collected using E-swabs and sponge sticks respectively and cultivated on non-selective media (Figure 1). A subset of isolates underwent CHG and antibiotic MIC determination by microbroth dilution. Swab samples of the same locations were collected using pre-moistened sterile water swabs and processed via colorimetric assay. Data were analyzed using multilevel models. Results No significant clinical differences between groups were noted, including in antimicrobial exposure or infection history. 360 unique bacterial isolates were identified, with Staphylococcus epidermidis and Staphylococcus hominis being the most common organisms isolated from all skin and environmental sites (Table 1). CHG MICs were not significantly different across all organisms detected at all sites in exposed versus non-exposed groups (p=0.4) (Table 2). No residual CHG was found on skin or environmental surfaces of the CHG non-exposed group. Residual CHG in the exposed group was most frequently detected on the anterior chest (n=13/15) and bed handle (n=8/15), and levels of residual CHG on body sites were significantly elevated compared to environmental sites (p=<0.0001). Bacteria found where residual CHG was detected on both skin and environmental sites did not have significantly elevated CHG MICs (p=0.21). Conclusion We found no evidence that CHG exposure correlates with elevated CHG MICs of skin or environmental bacteria, suggesting routine CHG use to prevent infections does not contribute to resistance. This study is the first to correlate bacterial

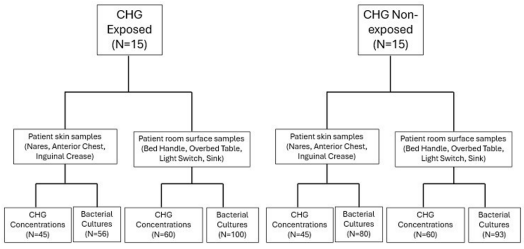


Figure 1: Experimental design. Bacterial culture value (N=) reflects number of unique isolates obtained at each location

‡The abstract titles in this supplement have been corrected since original publication. A notice detailing the changes has been published at https://doi.org/10.1017/ash.2026.10802.

https://doi.org/10.1017/ash.2026.10659 Published online by Cambridge University Press

	CHG Exposed (n=15) (%)	CHG Non-Exposed (n=15) (%)	p-value
Clinical Characteristics			
Age category			0.48
20-30	1	1	
31-40	0	0	
41-50	3	1	
51-60	4	3	
61-70	3	8	
71-80	3	2	
81-90	1	0	
Sex			0.26
Female	7 (47)	11 (73)	
Race			**0.001***
White	10 (67)	1 (7)	
Black or African American	5 (33)	11 (73)	
Other	0	3 (20)	
Ethnicity			1.00
Not Hispanic or Latino	14 (93)	13 (87)	
Hispanic or Latino	1 (7)	2 (13)	
Supplemental oxygen	4 (27)	3 (20)	1.00
IV access	15 (100)	12 (80)	0.20
Antibiotics Prior to Enrollment	7 (47)	3 (20)	0.25
Bed bound	4 (27)	1 (7)	0.33
Urinary incontinence			0.33
Yes	4 (27)	1 (7)	
Stool incontinence			0.04
Yes	5 (33)	0	
Voluntary patient contact with environment			0.48
Yes	13(87)	15 (100)	
No	2 (13)	0	
Indwelling urinary device	2 (13.3)	2 (13.3)	0.33
Fecal management device	0	1 (7)	0.04
Previous MDRO positive			0.17
Yes	5 (33)	1 (7)	

Table 1: Clinical and organism characteristics of enrolled patients. *=significant difference between groups

Species Isolated (n)	Median CHG MIC (µg/mL)	Isolation Source
Acinetobacter junii (1)	2	Environment - Sink
Agrobacterium radiobacter (1)	8	Environment - Sink
Brevundimonas diminuta (1)	8	Environment - Sink
Citrobacter freundii (2)	8	Environment - Sink Skin - Nares
Delftia acidovorans (1)	64	Environment - Sink
Enterobacter cloacae (1)	32	Environment - Sink
Enterococcus faecalis (3)	2	Environment - Bed Handle Skin - Anterior chest, inguinal crease
Enterococcus faecium (5)	2	Environment - Bed Handle, Overbed Table Skin - Anterior chest, inguinal crease
Klebsiella oxytoca (1)	32	Skin - Nares
Klebsiella pneumoniae (3)	16	Environment - Bed Handle, Sink Skin - Inguinal Crease
Proteus mirabilis (1)	32	Skin - Inguinal Crease
Providencia stuartii (1)	128	Skin - Inguinal Crease
Pseudomonas aeruginosa (2)	16	Environment - Sink
Staphylococcus aureus (4)	1	Environment - Overbed table Skin - Nares, Anterior chest
Staphylococcus epidermidis (5)	4	Environment - Sink Skin - Anterior chest, inguinal crease
Staphylococcus hominis (2)	1	Environment - Bed handle Skin - Anterior chest
Staphylococcus salivarius (2)	0.5	Environment - Overbed table Skin - Anterior chest
Staphylococcus simulans (1)	4	Skin - Anterior chest
Stenotrophomonas maltophilia (3)	32	Environment - Sink
Streptococcus pneumoniae (1)	8	Skin - Anterior chest
Streptococcus salivarus (1)	0.5	Skin - Anterior chest

Table 2: Clinically relevant organisms isolated with corresponding median CHG MIC values. Organisms are from both body and environmental sites.

‡The abstract titles in this supplement have been corrected since original publication. A notice detailing the changes has been published at https://doi.org/10.1017/ash.2026.10802.

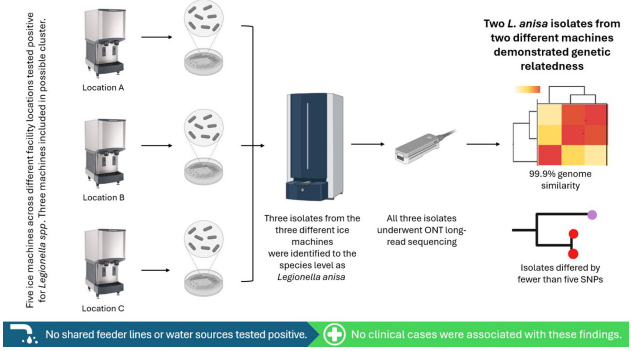
CHG MICs with residual environmental CHG, and to perform colorimetric CHG testing on environmental surfaces.

Antimicrobial Stewardship & Healthcare Epidemiology 2026;6(Suppl. S1):s142–s143
doi:10.1017/ash.2026.10659

Presentation Type:
Poster Presentation
Subject Category: Molecular Epidemiology
Utilization of Analytics Software and Whole Genome Sequencing to Identify an Environmental Legionella Cluster‡

Chin-Ting Wu[1], Guy Handley[2], Kim Cuong T Nguyen-Coleman[1], Noel Ellis[3], William Shropshire[1], Chia-Chi Chang[4], Nadim Ajami, Aaron G Richter, Linette Leadon[3], Matt Berkheiser, Samuel Shelburne[4] and Amy Spallone[2]
[1]The University of Texas MD Anderson Cancer Center; [2]MD Anderson Cancer Center; [3]UT MD Anderson Cancer Center and [4]University of Texas MD Anderson Cancer Center

Background:? Legionella poses a significant threat to immunocompromised oncology patients. To mitigate nosocomial legionellosis, healthcare systems often implement environmental surveillance. At MD Anderson Cancer Center, we combined a shared analytics platform with long-read whole genome sequencing (WGS) to enable detection of genetically related isolates from facility ice machines.? Methods:? A centralized dashboard (Power BI, Microsoft) was developed to monitor environmental Legionella surveillance across the institution and highlight areas with elevated positivity rates. Targeted environmental sampling was conducted to identify potential reservoirs. Given repeated isolation of L. anisa strains, a subset of isolates underwent WGS using the MinION platform (Oxford Nanopore Technologies). Genetic relatedness was assessed using MINTyper for single-nucleotide polymorphism (SNP) calling and Prokka with Roary for pan-genome analysis.? Results:? Environmental sampling of facility water sources revealed five positive Legionella samples from five separate ice machines, three of which grew L. anisa. No shared feeder lines or water sources tested positive. WGS performed by an infection control practitioner and revealed that two L. anisa isolates shared 99.9% genome similarity, differing by fewer than five SNPs, suggesting a common origin or transmission route (Figure 1). No clinical cases were associated with these findings during the investigation.? Conclusion:? A WGS based investigation powered by infection control practitioners without the use of a core genome sequencing facility uncovered potential transmission between geographically separated reservoirs that would have gone unrecognized through conventional methods. WGS also helped exclude a third ice machine from the suspected cluster. These findings led to the development of an updated institutional standard operating procedure (SOP), integrating data visualization and genomic analysis to enable earlier identification of related environmental sources and guide proactive interventions before clinical cases occur. This provides a framework for real-



https://doi.org/10.1017/ash.2026.10659 Published online by Cambridge University Press