	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.

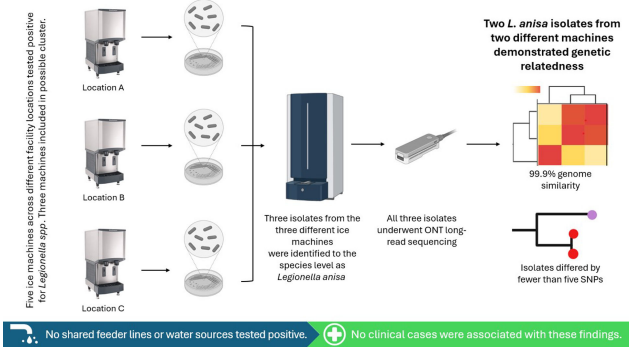
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Presentation Type:
Poster Presentation
Subject Category: Molecular Epidemiology

Utilization of Analytics Software and Whole Genome Sequencing to Identify an Environmental Legionella Cluster‡

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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-



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time implementation of WGS for Infection Control that can be deployed with minimal investment in nearly any clinical setting.

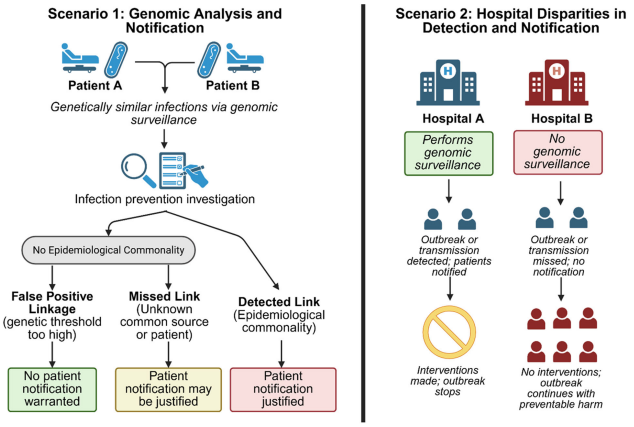
Antimicrobial Stewardship & Healthcare Epidemiology 2026;6(Suppl. S1):s143–s144
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Presentation Type:
Poster Presentation
Subject Category: Molecular Epidemiology
Pathogen Genomic Surveillance in Healthcare: Emerging Ethical Dilemmas in Outbreak Detection and Patient Notification‡

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Background: Genomic surveillance detects healthcare-associated outbreaks that are often missed by traditional methods, offering substantial benefits for infection prevention. However, its use introduces complex ethical dilemmas regarding patient notification and disparities in outbreak detection between institutions with and without genomic capabilities. **Methods:** We applied the Centers for Disease Control and Prevention's 2020 ethical considerations regarding patient notification and the Ethical Infection Prevention and Control (EIPAC) framework to two hypothetical scenarios involving genomic surveillance programs. Our analysis was informed by qualitative research reporting the types of harm experienced by patients across detected and undetected outbreaks. **Results:** We identified ethical justifications for patient notification when both genomic and epidemiologic evidence suggest transmission, as well as considerations militating for and against notification when epidemiologic evidence supporting genomic findings is absent (Figure). We also demonstrated ethical concerns arising from institutional disparities in genomic capability such that patients in hospitals without genomic surveillance may suffer preventable harm and remain uninformed due to lack of detection. A harms matrix illustrates physical, psychological, and ethical harms depending on detection and disclosure status. **Conclusion:** Hospitals adopting genomic surveillance face new ethical duties to disclose transmission events, while those that do not engage in such surveillance risk perpetuating inequities in patient safety and transparency. National guidance is urgently needed to ensure consistency in notification and promote ethical adoption of genomics. Coordinated frameworks from professional societies should define genetic thresholds warranting disclosure, address disparities in pathogen genomic detection methods, and uphold patient trust in the genomic era.

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Presentation Type:
Poster Presentation
Subject Category: Molecular Epidemiology
Integrating WGS with Epidemiologic Data to Guide Containment in a Multi-Facility CP-CRAB Outbreak — Georgia, Nov 2024–May 2025‡

Diane Yi[1], Michael Anderson[1], Shamta Warang[1], Lynn Reynolds, Sue Milligan[1], Tatyana Kiryutina, Addis Bedada, Steven Woods, Ryan Paradis, Eleen Daley, Gebre Tiga[2], Alexis LaCrue, Arunachalam Ramaiah, Karen Williams[1] and JoAnna Wagner[1]
[1]Georgia Department of Public Health and [2]Georgia Public Health Laboratory

Background: Carbapenemase-producing carbapenem-resistant Acinetobacter baumannii (CP-CRAB) is a highly-transmissible multi-drug-resistant organism. In November 2024, the Georgia Department of Public Health (DPH) identified a multi-facility CP-CRAB outbreak in central Georgia and applied whole-genome sequencing (WGS) to guide containment. **Methods:** During November 2024–May 2025, Georgia and Tennessee Public Health Laboratories confirmed 31 CP-CRAB cases. 24 isolates underwent WGS on Illumina MiSeq; sequences were processed with CDC's PHoeNIx pipeline, and single-nucleotide polymorphism (SNP) heatmaps were generated with Snippy and Python. Epidemiologic data were abstracted from medical records; risk factors and network analyses were conducted using Excel, with case pairs ?10 SNPs prioritized for analysis. **Results:** WGS identified 18 cases in three sub-clusters, plus 2 related and 4 unrelated cases; SNP distances ranged 0–34, with 16/49 (33%) case pairs ?10 SNPs. Facilities included four acute-care hospitals (ACH-1–ACH-4, primary ACH-1), with prior exposures to 3 skilled-nursing facilities (SNFs), 1 ventilated-SNF (vSNF), and 1 long-term ACH (LTACH). Sub-cluster 1 (n = 8; 0–26 SNPs; 12/29 pairs ?10 SNPs) specimen sources included 3 respiratory, 2 urinary, 2 wound, and 1 blood specimens from ACH-1–ACH-4. 6 cases formed 12 ?10-SNP pairs, with collection dates 3–52 days apart; 3/6 cases were admitted to ACH-1 from vSNF with direct overlap, 4/6 had prior exposure to ACH-1, and 2/6 had no epidemiologic links. Prior healthcare exposure and intra-facility (ACH-1) movement were observed among all 6 cases. Sub-cluster 2 (n = 5; 2–22 SNPs; 3/10 ?10) involved 5 ventilated respiratory cases, 4 from ACH-1 and 1 from ACH-2. **Conclusions:** Integrating WGS with epidemiologic data revealed sub-clusters—multiple introductions, distinct transmission pathways, and related cases with wide ranges between collection dates—enabling sub-cluster-specific containment recommendations. These findings informed Georgia's first multi-facility CP-CRAB outbreak investigation, contributing to the development of a multi-facility engagement model that improved interfacility communication and provider awareness of transmission. Routine WGS–epidemiologic integration is critical for targeted containment and coordinated regional response.

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Presentation Type:
Poster Presentation
Subject Category: MRSA/VRE
Clinical Factors and Outcomes of Patients with Hospital Onset MRSA Bacteremia‡

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Background: Hospital onset bacteremia (HOB) due to Methicillin Resistant Staphylococcus aureus (MRSA), defined as a positive blood culture obtained on admission day 4 or later, is associated with increased

‡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.

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