

Outbreaks in Healthcare:

What are we missing & how can genomics help?

California APIC Coordinating Council (CACC)

August 14, 2026

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Disclosures

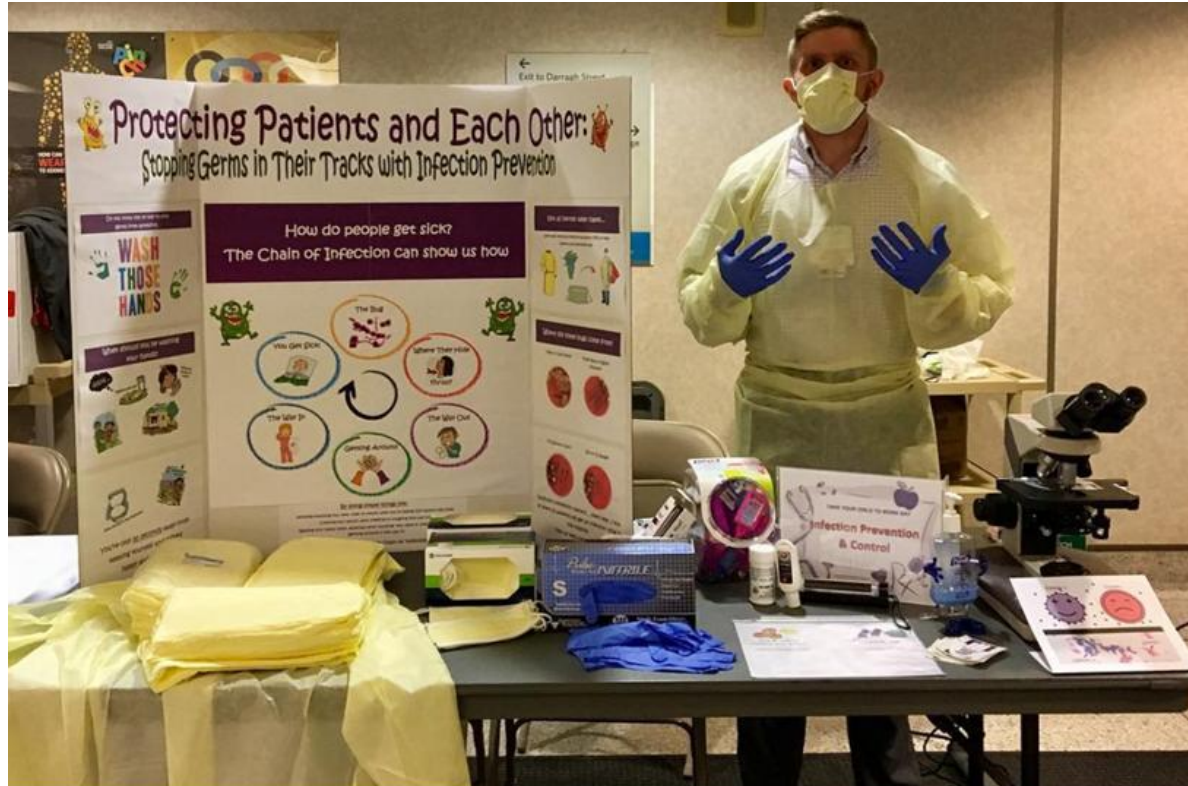
- Next Gen Diagnostics – Consultant
- Society for Healthcare Epidemiology of America (SHEA) – Board of Trustees

Outline

1. Outbreaks - Examples
2. Genomic Surveillance
3. Future Directions



Started as an Infection Preventionist



The outbreak that got me into outbreaks

- Four SOT patients with mucormycosis over 10-months
- Extensive environmental investigation leading towards healthcare linen



NEWS

UPMC: Transplant program shut down as mold investigation continues



BEN SCHMITT | Monday, Sept. 21, 2015 12:00 a.m.

health Life, But Better Fitness Food Sleep Mindfulness Relationships

Emails suggest linens to be 'likely' source in deadly mold outbreak at Pittsburgh hospitals

By Lauren del Valle, CNN

8 minute read · Updated 5:24 PM EDT, Mon April 3, 2017

UPMC, Paris Cleaners Reach Settlement Over Patient Deaths From Fungal Infections

KDKA NEWS

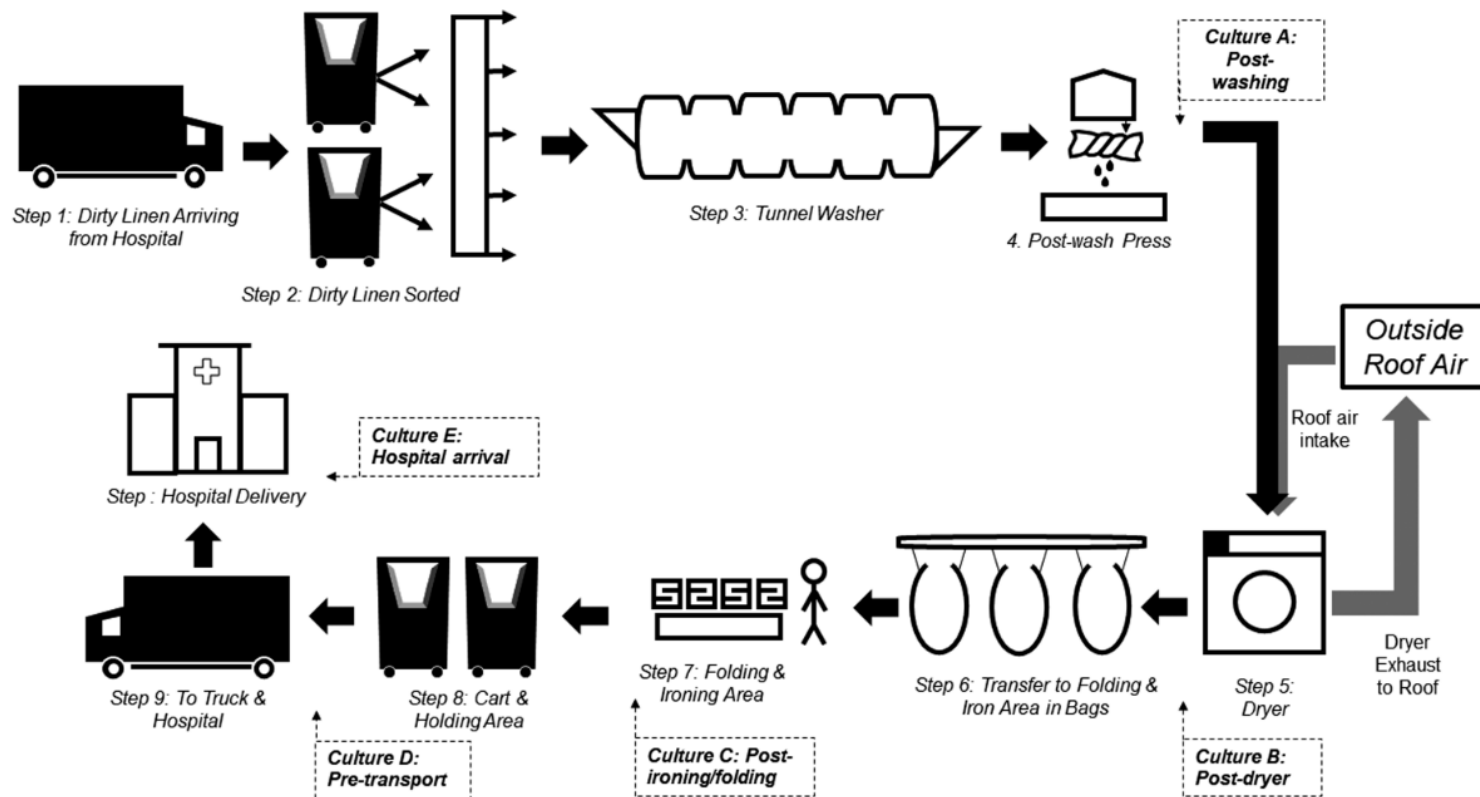
February 13, 2020 / 2:53 PM EST / CBS Pittsburgh



To the facility



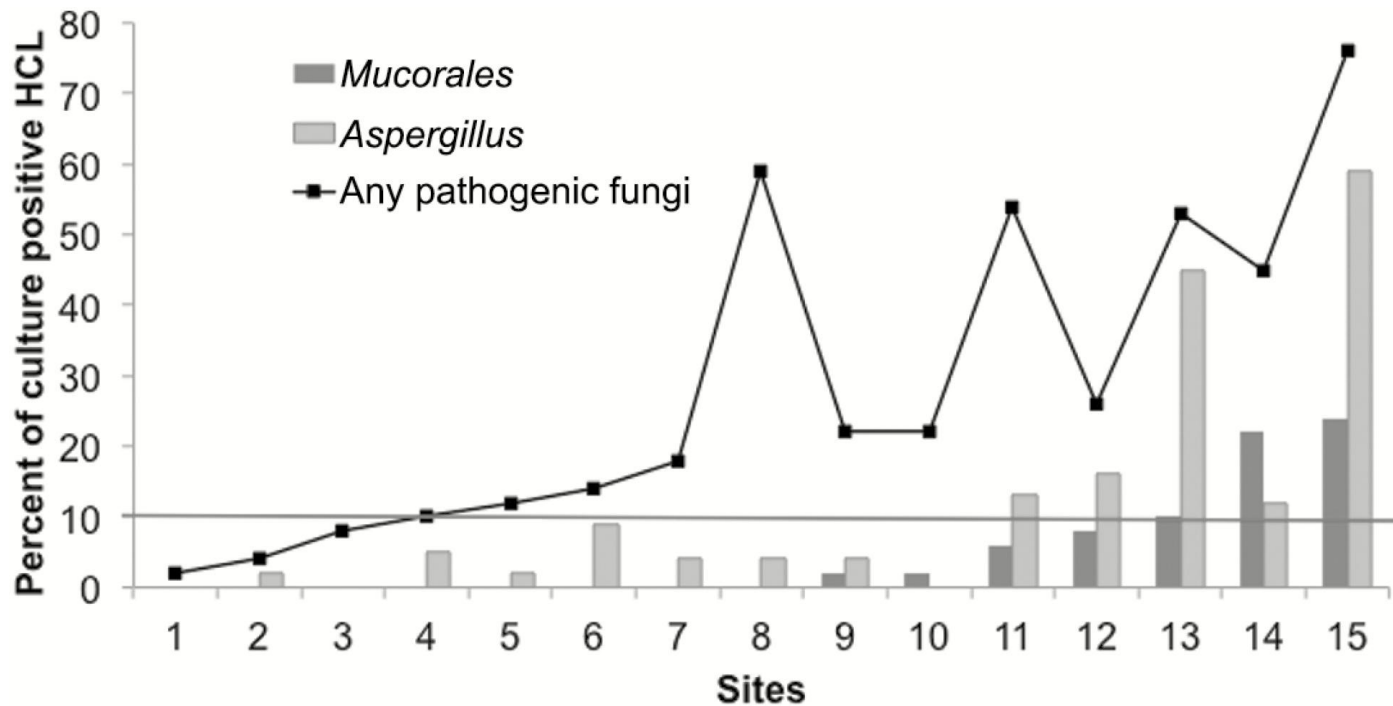
To the facility



To the roof



To other US hospitals



The outbreak that got me into outbreaks

1. In-depth, detailed investigation can reveal clear issues. **You really have to look**
2. Outbreak work doesn't end when the outbreak is over. Share the findings and work with other facilities to help their patients
3. Outbreaks can be preventable – but only if we want to find them

Another Outbreak Story

ERCP endoscope outbreak at UPMC Presbyterian, 2012

- 17 cases over 14-months
 - 12 bloodstream infections
 - 5 deaths
 - Retrospective WGS: related to scope isolate
- Detected early?
 - Prevention of 14 cases, 9 BSIs, 3 deaths



Another Outbreak Story

United States Senate

HEALTH, EDUCATION, LABOR, AND PENSIONS COMMITTEE

Patty Murray, Ranking Member

Preventable Tragedies: Superbugs and How Ineffective Monitoring of Medical Device Safety Fails Patients



Minority Staff Report

January 13, 2016

University of Pittsburgh Medical Center Presbyterian Hospital, Pittsburgh, fall 2012

A few months after Dr. Loeve's report first raised alarms about whether the Olympus closed-channel duodenoscope could be consistently disinfected by following the manufacturer's cleaning instructions, Olympus was contacted by officials at the University of Pittsburgh Medical Center Presbyterian hospital in Pittsburgh, Pennsylvania ("UPMC").⁵¹ In the fall of 2012, UPMC experienced an outbreak of CRE, infecting about 13 patients who had undergone ERCP procedures with Olympus duodenoscopes.⁵² Repeated cultures of one particular duodenoscope by UPMC staff found bacteria in the biopsy and water channels even after the scope had been reprocessed three times.⁵³

After UPMC traced the infections back to the device, Olympus and an outside consulting group, ECRI Institute, evaluated UPMC's reprocessing procedures. ECRI found that UPMC's reprocessing was "consistent with standard practice and manufacturer recommendations."⁵⁴ ECRI told UPMC officials that it could not make a "definitive" assessment about whether "there is a defect within the endoscope that would provide a reservoir for bacteria" because the small crevices in the scope made it impossible for ECRI to fully examine the device.⁵⁵

When Olympus officials raised the possibility that the hospital's Custom Ultrasonics AERs could be at fault, UPMC officials went so far as to purchase an Olympus AER and demonstrated that the use of Olympus' own reprocessing machine did not prevent scopes from remaining contaminated after cleaning.⁵⁶ On December 18, 2012, Olympus filed an MDR with FDA, which documented some of the events at UPMC and the findings of ECRI. This MDR appears to have never been entered into FDA's system.⁵⁷

Another Outbreak Story



Office of Public Affairs
U.S. Department of Justice

PRESS RELEASE

**Olympus Medical Systems Corporation,
Former Senior Executive Plead Guilty to
Distributing Endoscopes After Failing to
File FDA-Required Adverse Event
Reports of Serious Infections**



“It is “not need[ed] to communicate to all the users actively,”
Nishina wrote, because a company assessment of the risk to
patients found it to be “acceptable.””

**Olympus to pay \$85M after
pleading guilty to fraudulently
selling scopes linked to superbug
spread**

By Tina Reed · Dec 10, 2018 5:50pm

Los Angeles Times

Olympus told its U.S. executives no broad warning
about tainted medical scopes was needed, despite
superbug outbreaks

How are healthcare outbreaks detected?

1. Select pathogen monitoring
2. Visual inspection of 'line-lists' of infections
3. Astute clinicians noticing increase of infections
4. Call from the laboratory for unusual findings

INFECTION CONTROL & HOSPITAL EPIDEMIOLOGY APRIL 2016, VOL. 37, NO. 4

CONCISE COMMUNICATION

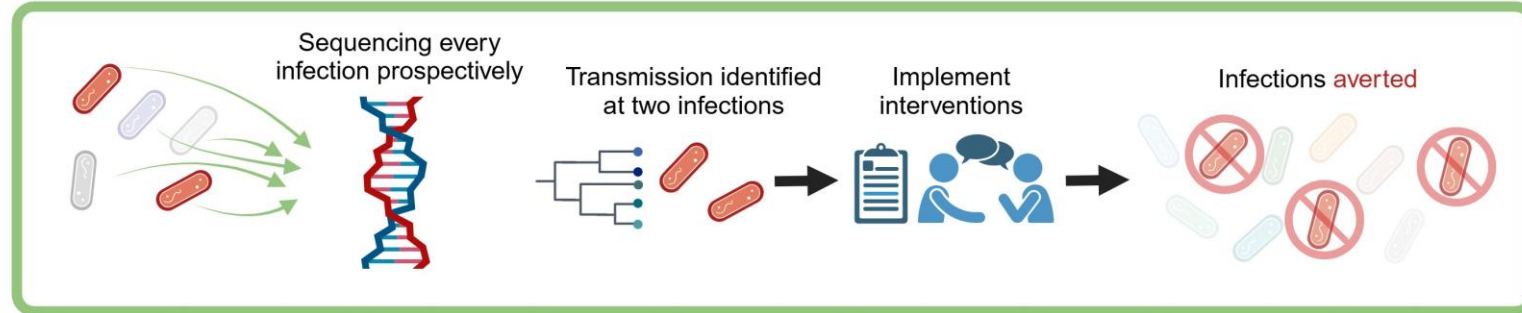
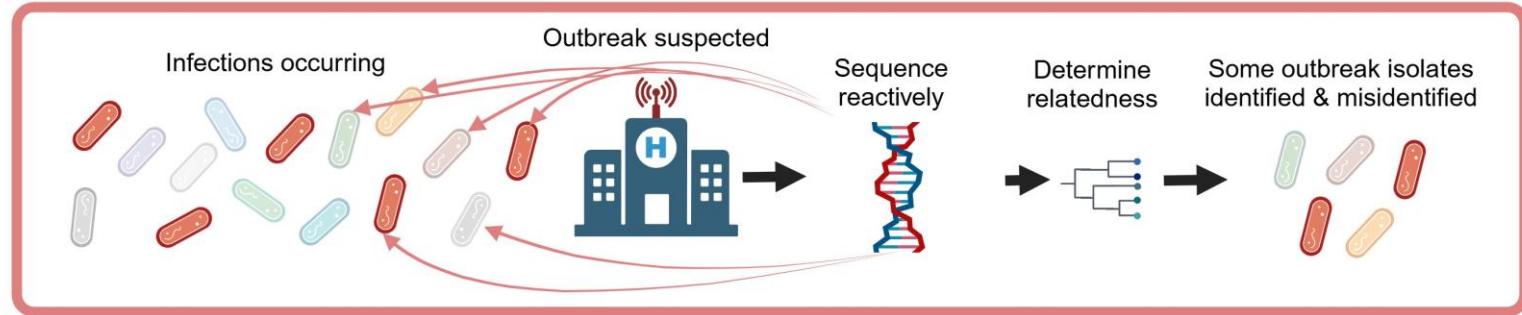
Lack of Comprehensive Outbreak Detection in Hospitals

Meghan A. Baker, MD, ScD;^{1,2} Susan S. Huang, MD, MPH;³ Alyssa R. Letourneau, MD, MPH;⁴ Rebecca E. Kaganov, BA;¹ Jennifer R. Peeples, MPH;⁵ Marci Drees, MD, MS, FACP;⁶ Richard Platt, MD, MSc;¹ Deborah S. Yokoe, MD MPH² for the Centers for Disease Control and Prevention Epicenters Program

CDC
PREVENTION
EPICENTERS
innovative research to protect patients

Whole Genome Sequencing

Reactive Whole Genome Sequencing



Whole Genome Sequencing Surveillance

Outline

1. Outbreaks - Examples
2. Genomic Surveillance
3. Future Directions



Step 1: Retrospective Analysis

Clinical Infectious Diseases

MAJOR ARTICLE



Infectious Diseases Society of America



hiv medicine association



Whole-Genome Sequencing Surveillance and Machine Learning of the Electronic Health Record for Enhanced Healthcare Outbreak Detection

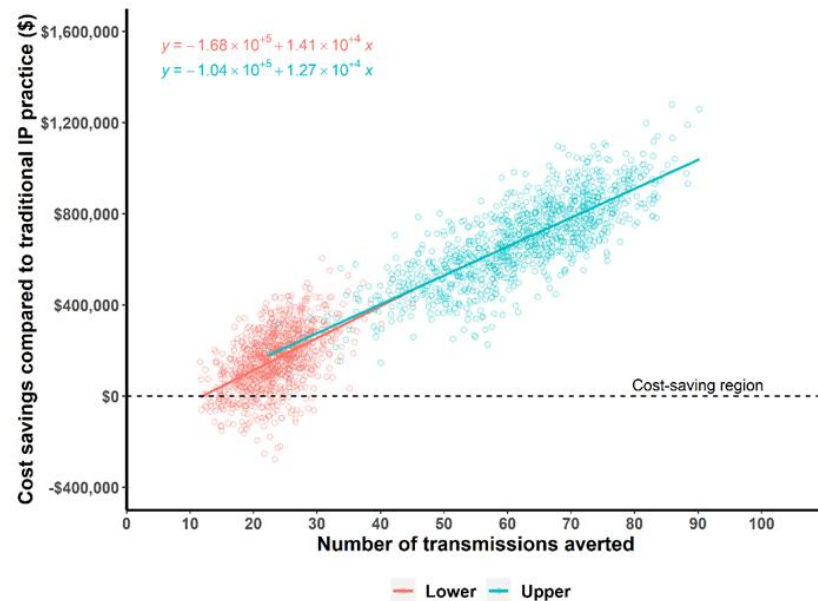
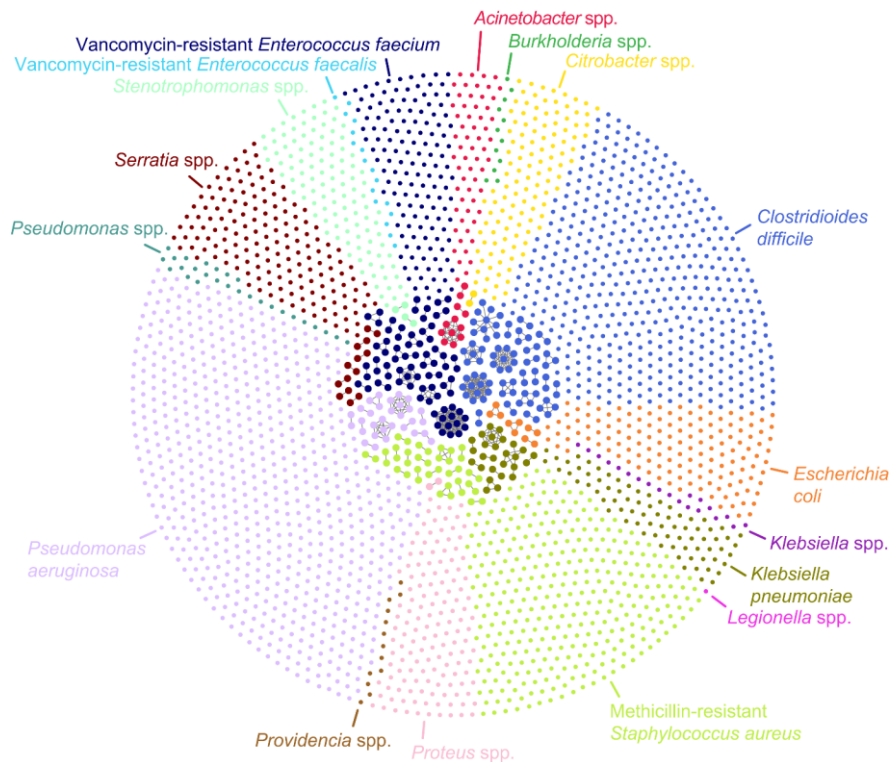
Alexander J. Sundermann,^{1,2,3} Jieshi Chen,⁴ Praveen Kumar,⁵ Ashley M. Ayres,⁶ Shu-Ting Cho,² Chinelo Ezeonwuka,^{1,2} Marissa P. Griffith,^{1,2} James K. Miller,⁴ Mustapha M. Mustapha,^{1,2} A. William Pasculle,⁷ Melissa I. Saul,⁸ Kathleen A. Shutt,^{1,2} Vatsala Srinivasa,^{1,2} Kady Waggle,^{1,2} Daniel J. Snyder,⁹ Vaughn S. Cooper,⁹ Daria Van Tyne,² Graham M. Snyder,^{2,6} Jane W. Marsh,^{1,2} Artur Dubrawski,⁴ Mark S. Roberts,^{5,8} and Lee H. Harrison,^{1,2,3}

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Pitt / UPMC Retrospective Analysis



Notable Outbreak: VRE & IR

Clinical Infectious Diseases

MAJOR ARTICLE



Outbreak of Vancomycin-resistant *Enterococcus faecium* in Interventional Radiology: Detection Through Whole-genome Sequencing-based Surveillance

Alexander J. Sundermann,^{1,2} Ahmed Babiker,^{1,3} Jane W. Marsh,^{1,3} Kathleen A. Shutt,^{1,3} Mustapha M. Mustapha,^{1,3} Anthony W. Pasculle,⁴ Chinelo Ezeonwuka,^{1,3} Melissa I. Saul,¹ Marissa P. Pacey,^{1,3} Daria Van Tyne,³ Ashley M. Ayres,² Vaughn S. Cooper,⁵ Graham M. Snyder,^{2,3} and Lee H. Harrison^{1,3}

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Isolates and Procedures

Table 1. Clinical and Epidemiologic Characteristics of 10 Case Patients With Vancomycin-resistant Enterococci Infection

Patient	Admit Day ^a	IR Procedure Day ^a	Culture Day ^a	Specimen Source	Days From IR to Culture	IR Procedure(s)	Contrast Used?	Staff Group	Charlson Comorbidity Index	Other Organisms Isolated From Same Specimen
1	3	0	22	Jackson-Pratt drainage	22	Angiogram, chemoembolization of hepatocellular carcinoma	Yes	A	8	None
2	36	15	36	Pancreatic tissue	21	Venogram, angioplasty with central line placement	Yes	A	1	<i>Candida dubliniensis</i>
3	68	48	68	Blood	20	Cholangiogram, biliary catheter exchange	Yes	A	4	None
4	170	NA	170	Blood	NA	None ^b	NA	NA	6	None
5	177	184	188	Biliary pigtail	4	Cholangiogram, biliary catheter exchange	Yes	A	10	<i>Klebsiella pneumoniae</i> , <i>Hafnia alvei</i> , <i>Candida tropicalis</i> , <i>Candida glabrata</i>
6	187	187	199	Blood	12	Cerebral arteriogram	Yes	B	5	<i>Candida parapsilosis</i>
7	195	196	204	Lower abdominal	8	Celiac and mesenteric arteriogram	Yes	A	7	<i>Escherichia coli</i> , <i>Pseudomonas aeruginosa</i>
8	187	203	206	Urine	3	GJ tube replacement	Yes	A	5	None
9	243	249	251	Hepatic fluid	2	Cholangiogram	Yes	A	7	<i>Klebsiella variicola</i> , <i>Staphylococcus epidermidis</i>
10	260	241	260	Blood	19	Lower extremity angiogram	Yes	A	7	None

Abbreviations: GJ, gastrostomy-jejunostomy; IR, interventional radiology; NA, not applicable.

^aDays are calculated as the number of days since the IR procedure day of patient 1.

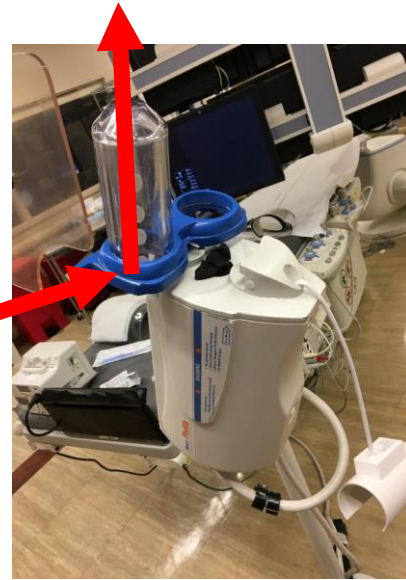
^bThis patient had no IR exposure and had a vancomycin-resistant enterococci (VRE) isolate with substantial genomic differences compared to the VRE genomes from the other 9 patients (see text).

IR Outbreak: Investigation



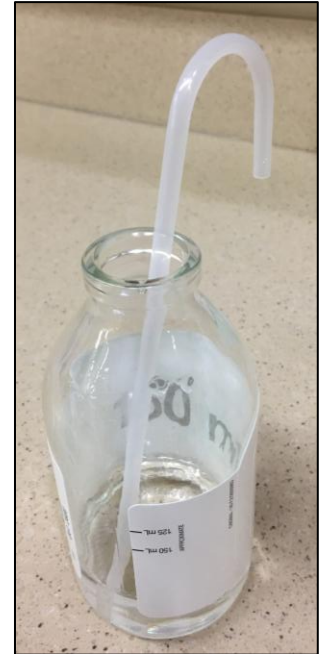
Automatic Contrast Injectors

- Uses disposable/sterile syringe and the automatic injector
- Loaded into the injector



Loading t

st Injector:

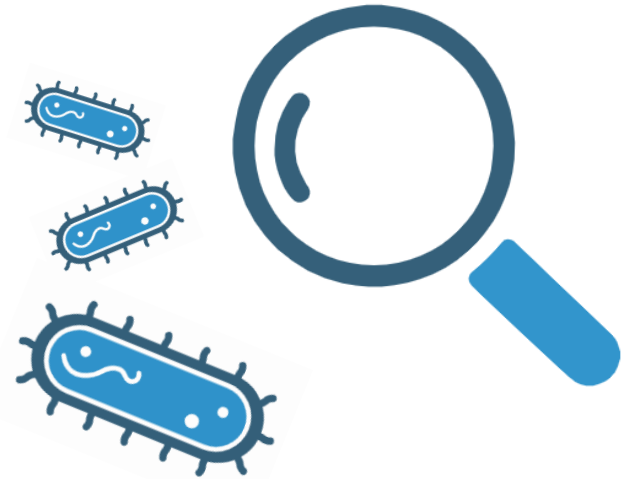


Findings?

Retrospective Analysis

Outbreaks Detected by Traditional IP

- 15 requests for suspected and potentially actionable outbreaks involving 133 patients
- Only 5 (3.8%) patients from 2 clusters genetically related!



Retrospective Analysis

Are transmitted infections reported to NHSN?

- UPMC data 2016-2018
- 44.4% met definition for any NHSN HAI

Infection Control & Hospital Epidemiology (2023), 1–3
doi:10.1017/ice.2023.52



Concise Communication

Sensitivity of National Healthcare Safety Network definitions to capture healthcare-associated transmission identified by whole-genome sequencing surveillance

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Table 1. Infection Sources Determined to be Part of an Outbreak by WGS Surveillance and Not Hospital-Onset by NHSN

Isolate Source	Total	Present on Admission	Did Not Meet Criteria
Respiratory	29	5	24
Urine	29	14	15
Wound	22	15	7
Stool	17	17	0
Blood	13	13	0
Total	110	64 (58.2%)	46 (42%)

Step 2: Real-time Analysis

Clinical Infectious Diseases

MAJOR ARTICLE



OXFORD

Real-Time Genomic Surveillance for Enhanced Healthcare Outbreak Detection and Control: Clinical and Economic Impact

Alexander J. Sundermann,^{1,2,Ⓢ} Praveen Kumar,^{3,Ⓢ} Marissa P. Griffith,^{1,4} Kady D. Waggle,^{1,4} Vatsala Rangachar Srinivasa,^{1,2,4,Ⓢ} Nathan Raabe,^{1,2,4,Ⓢ} Emma G. Mills,⁴ Hunter Coyle,^{1,Ⓢ} Deena Ereifej,^{1,5} Hannah M. Creager,^{6,7} Ashley Ayres,⁵ Daria Van Tyne,^{4,Ⓢ} Lora Lee Pless,^{1,4} Graham M. Snyder,^{4,5,Ⓢ} Mark Roberts,³ and Lee H. Harrison^{1,2,4}

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Real-time Analysis: Implementation

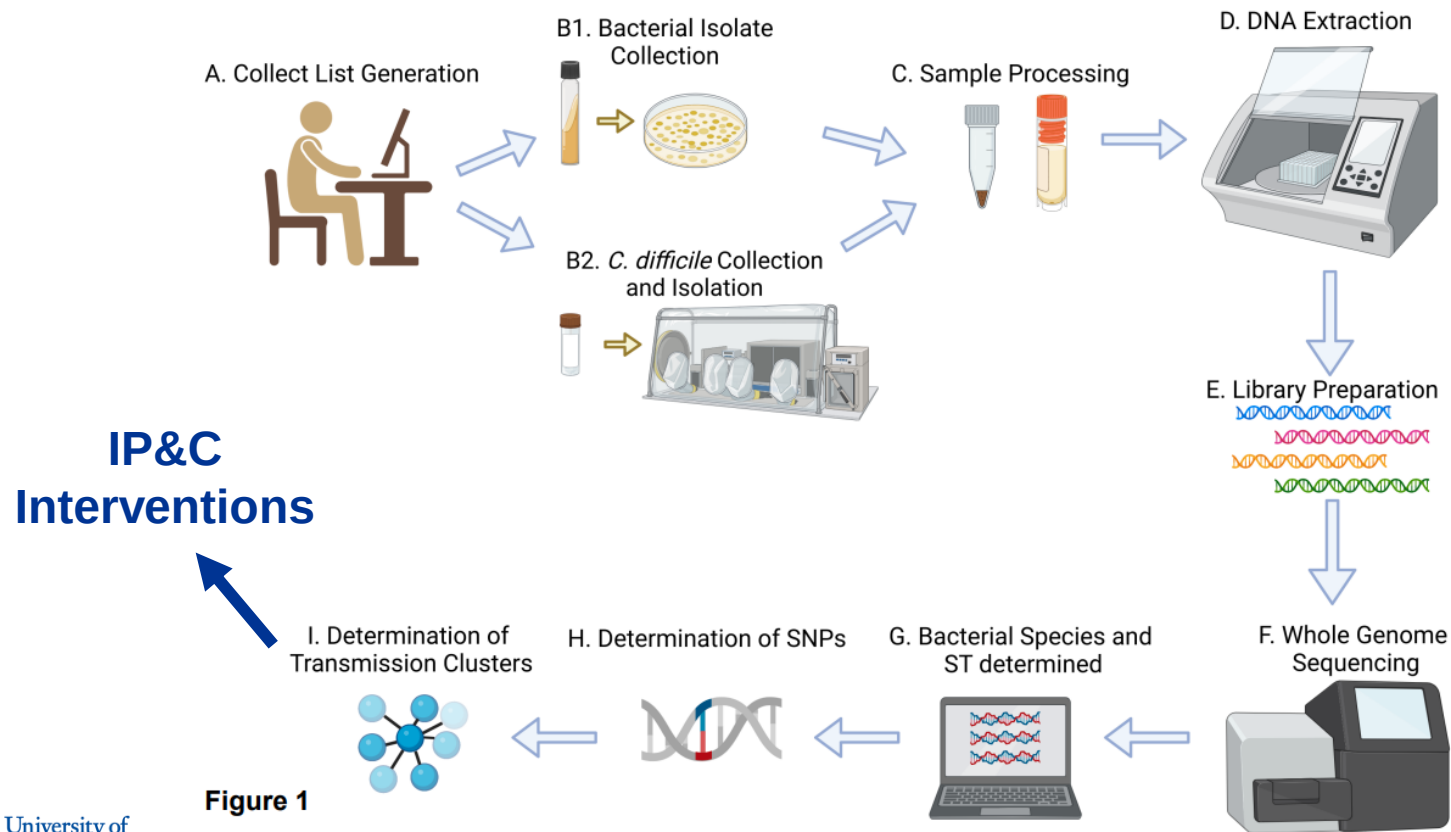


Figure 1

Real-time Analysis: UPitt cost

Table 2. Weekly cost estimates per sample (March 2022–February 2025).

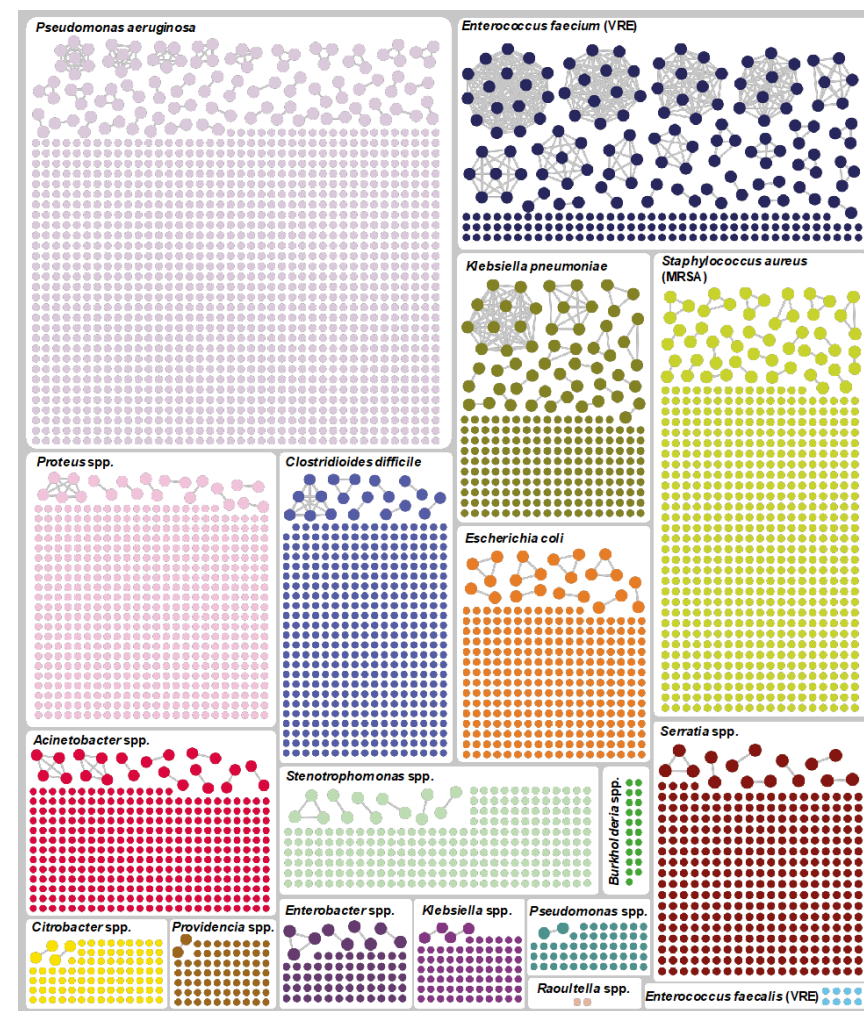
	Phase 1: March 2022 – July 2024					Phase 2: July 2024 – February 2025				
Method	MiSeq Cost	<u>NextSeq550 Cost</u>			Commercial Lab 1 Sequencing Cost [#]	NextSeq 1000 Cost	<u>Commercial Lab 2 (NovaSeq X Plus) Cost</u>			Commercial Lab 1 Sequencing Cost [#]
	32 samples	48 samples	60* samples	96 samples	≤32 samples	72 samples	80* samples	96 samples	192 samples	≤32 samples
Sample Processing	\$2.25	\$2.25	\$2.25	\$2.25	\$2.25	\$2.25	\$2.25	\$2.25	\$2.25	\$2.25
DNA Extraction & Quantification	\$9.35	\$8.66	\$8.39	\$7.98	\$9.35	\$8.21	\$8.11	\$7.98	\$7.98	\$9.35
Library Preparation	\$22.54	\$21.78	\$21.47	\$21.01	\$75	\$21.26	\$21.16	\$21.01	\$21.01	\$65
Sequencing Kit (Flow Cell)	\$58.47	\$43.13	\$34.50	\$21.56		\$13.89	\$14.65	\$12.21	\$6.10	
LABORATORY COST PER SAMPLE	\$92.61	\$75.82	\$66.61	\$52.80	\$86.60	\$45.61	\$46.17	\$43.45	\$37.34	\$76.60
Personnel										
-laboratory technician, 90% effort (\$970/week)	\$30.31	\$20.21	\$16.17	\$10.10	\$30.31	\$13.47	\$12.13	\$10.10	\$5.05	\$30.31
-bioinformatician, 50% effort (\$524/week)	\$16.38	\$10.92	\$8.73	\$5.46	\$16.38	\$7.28	\$6.55	\$5.46	\$2.73	\$16.38
TOTAL COST PER SAMPLE	\$139.30	\$106.95	\$91.51	\$68.36	\$133.29	\$66.36	\$64.85	\$59.01	\$45.12	\$123.29

[#]used for comparison only. not included in calculations for averages:

Real-time Analysis

- Initiated November 2021
- At 2-years (Nov 21-23)
 - 4,723 isolates sequenced, 3,921 unique
 - 476 (12.1%) related in 172 clusters
 - Median TAT 15 days
 - Sufficient for bacterial outbreaks!

Still sequencing today!



Real-time Analysis

Notable outbreaks:

- 9 endoscope clusters at **2 patients**
- Shared ventilators
- Multiple clusters from outside facilities
 - SNF, LTAC
- Pseudo-outbreak autopsy
- Eye drop outbreak

The Journal of Infectious Diseases

BRIEF REPORT

Two Artificial Tears Outbreak-Associated Cases of Extensively Drug-Resistant *Pseudomonas aeruginosa* Detected Through Whole Genome

Sequencing–E

Alexander J. Sundermann,^{1,2}
Marissa P. Griffith,^{1,2,3} Kady I.
Graham M. Snyder,^{2,4} Lee H.

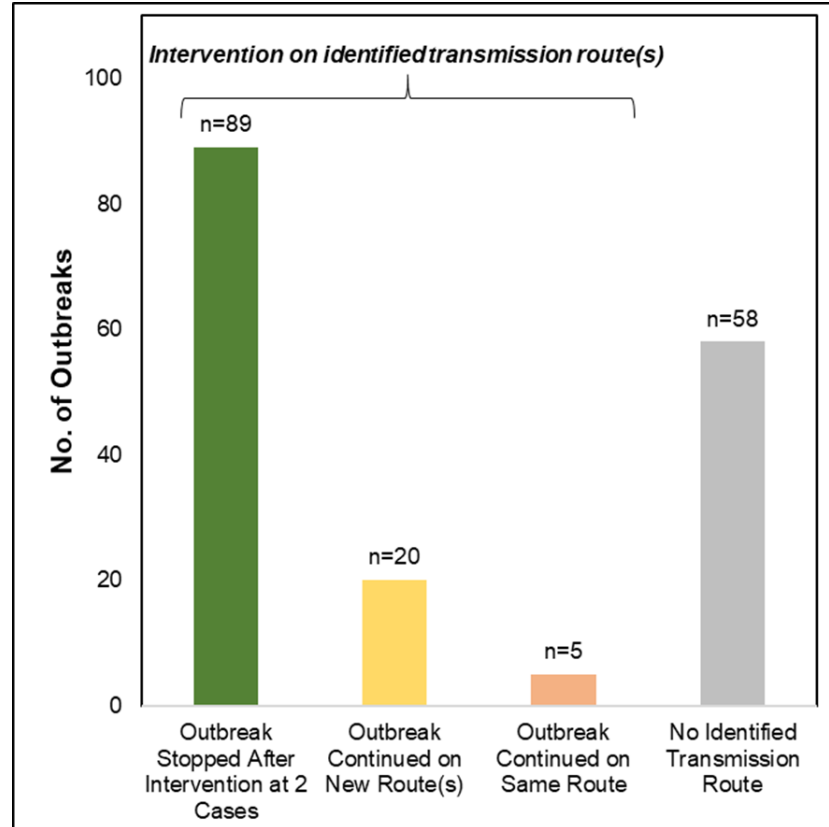
¹Microbial Genomic Epidemiology, University of Pittsburgh; ²Division of Infectious Diseases, University of Pittsburgh; ³Department of Epidemiology, University of Pittsburgh; and ⁴Department of Infectious Diseases, University of Pittsburgh Medical Center–Presbyterian Hospital

Pitt Surveillance System Detected Infection Linked to Eye Drops Months Before Outbreak Declared

September 13, 2023
By: Allison Hydzik

An infectious diseases surveillance system created by [University of Pittsburgh School of Medicine](#) scientists and deployed at a [UPMC](#) hospital successfully flagged cases of a drug-resistant infection spread by eye drops months before national public health officials announced an outbreak.

Findings after Intervention



What did we prevent?

Prevention:

- 62 infections
- 5 deaths

Net cost savings:

- \$695,706

Return on investment:

- 3.2-fold return on investment in sequencing

Bottom line: Saving lives & for every \$1 spent, \$3 saved



Pitt-Developed Outbreak Detection System Saves Lives



4/28/2025

PITTSBURGH – An infectious diseases detection platform developed by [University of Pittsburgh](#) scientists working with [UPMC](#) infection preventionists proved over a two-year trial that it stops outbreaks, saves lives and cuts costs.



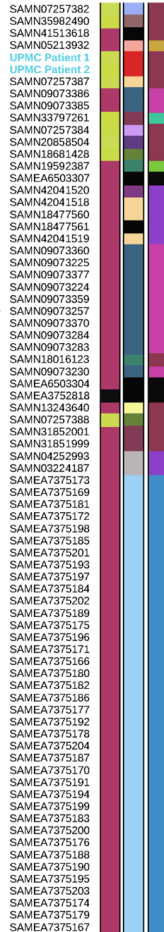
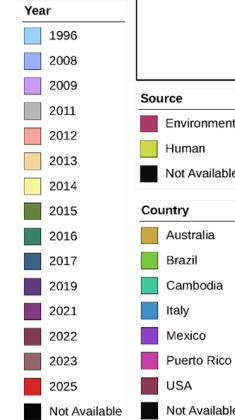
New Outbreaks

2025: 2 transplant patients initially identified as *B. cepacia* complex

1. BSI
2. Pneumonia

- Astute clinician + weekly WGS = *B. sola*
- Investigation supports donor-derived infection with forward transmission

Tree scale: 0.1



Plant Microbiology | Announcement

Draft genome sequence of “*Burkholderia sola*” strains isolated in Mexico

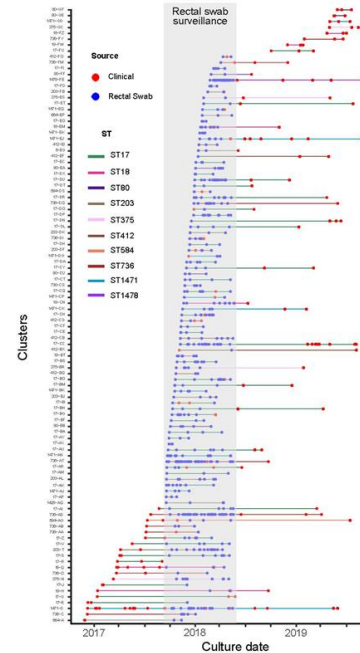
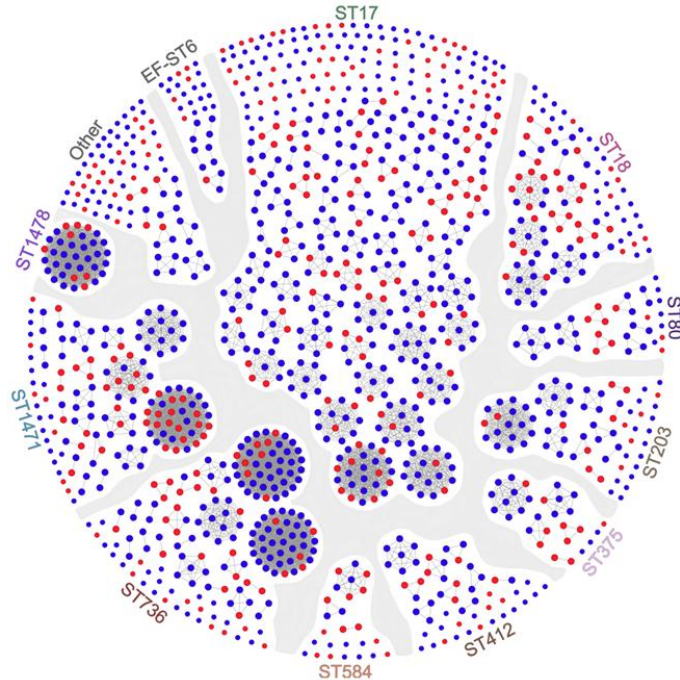
Leslie-Mariana Morales-Ruiz,¹ Violeta Larios-Serrato,² Paulina Estrada-de los Santos¹

AUTHOR AFFILIATIONS See affiliation list on p. 3.

ABSTRACT This study presents the draft genomes of three strains of “*Burkholderia sola*” isolated from *Phaseolus vulgaris* L. trap plants and the rhizosphere of *Coffea arabica* L. in Mexico.

Limitation: Clinical Isolates

Clinical isolates are just the tip of transmission for some pathogens



Other Applications: Respiratory Viruses

Transmission of viruses

- Genomic surveillance for ~2 years at UPMC PUH, SHY, CHP
- 436 specimens, 359 patients
- 14 clusters 36 patients (2-5 patients)

Original Article

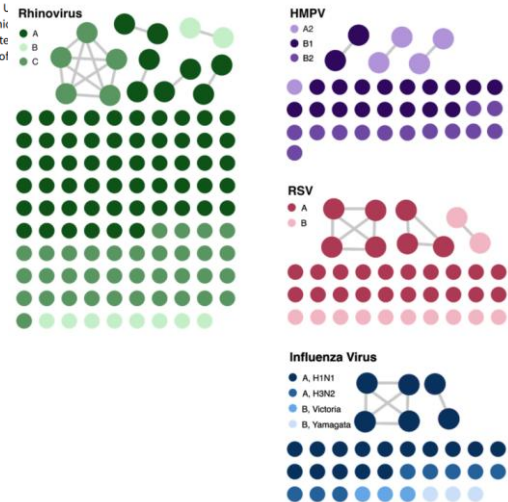
Genomic epidemiology of healthcare-associated respiratory virus infections in Pittsburgh, Pennsylvania, 2018–2020

Vatsala Rangachar Srinivasa MPH^{1,2,3} , Marissa P. Griffith BS^{1,2}, Alexander J. Sundermann DrPH^{1,3}, Emma Mills BS², Nathan J. Raabe MPH^{1,2,3}, Kady D. Waggle MS^{1,2}, Kathleen A. Shutt MS^{1,2} , Tung Phan MD, PhD⁷, Anna F. Wang-Erickson PhD^{3,5,6}, Graham M. Snyder MD, MS^{2,4} , Daria Van Tyne PhD² , Lora Lee Pless PhD^{1,2,*} and Lee H. Harrison MD^{1,2,3,*}

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Vatsala
Rangachar
Srinivasa, PhD



Other Applications: Plasmids

Transmission of plasmids

- 61 NDM isolates across ~5 years
- 6 clusters, 2-28 isolates
- Multi-species involvement, unit location transmission

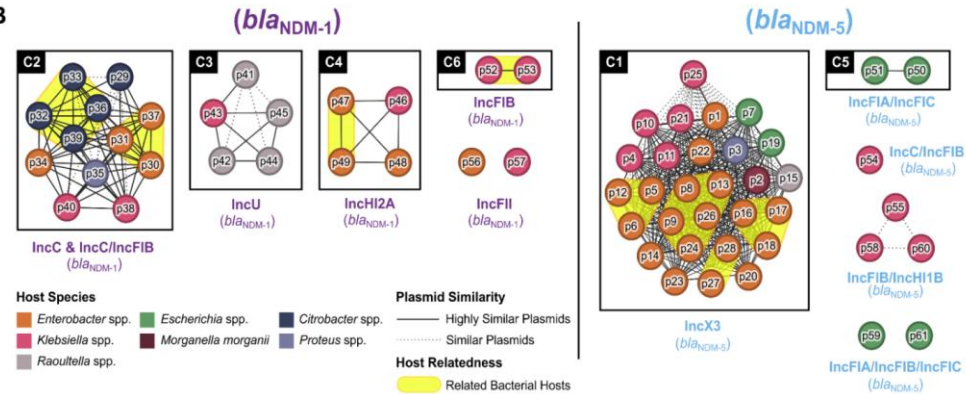
Nathan Raabe, PhD



Genomic epidemiology and transmission dynamics of plasmids carrying New Delhi metallo- β -lactamase (*bla*_{NDM}) at a single hospital system over five years

Nathan J. Raabe, PhD^{1,2,3*}, Emma G. Mills, PhD^{3*}, Sarika Bapat, MPH³, Marissa P. Griffith, BS^{2,3}, Kathleen Shutt, MS², Kady D. Waggle, MS², Alexander J. Sundermann, DrPH^{1,2,3}, Ryan K. Shields, PharmD³, Lora L. Pless, PhD^{2,3}, Graham M. Snyder, MD^{3,4}, Lee H. Harrison, MD^{1,2,3}, Daria Van Tyne, PhD^{3,5}

B



Other Applications: VRE Transmission

Emma Mills, PhD



Transmission of VRE

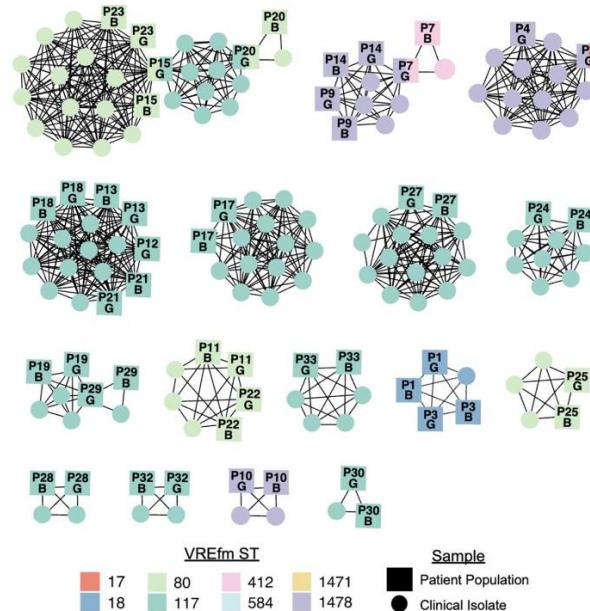
- Limitations of WGS = single isolate
- Patients with VRE in blood and colonized w/ VRE 5 years
- 6 clusters with multi-strain transmission

Culture-enriched metagenomic sequencing reveals within-patient diversity and transmission of vancomycin-resistant *Enterococcus faecium*

[Emma G Mills](#)¹, [Kirsten M Evans](#)¹, [Ava J Dorazio](#)¹, [Kevin M Squires](#)¹, [Alexander J Sundermann](#)^{2,3}, [Madison E Stellfox](#)¹, [Matthew J Culyba](#)^{1,4}, [Ryan K Shields](#)¹, [Daria Van Tyne](#)^{1,4,*}

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PMCID: PMC13015639 PMID: 41891006



Pitt Future Directions

NTM & Other Pathogens

- 13 patients May 2023 and August 2025 *M. abscessus*
- 169 water samples
- 18 positive for genetically linked patient infections

		ClusterA																																		
Type		MYC00116	MYC00244	MYC00232	MYC00117	MYC00270	MYC00246	MYC00248	MYC00252	MYC00286	MYC00375	MYC00114	MYC00234	MYC00361	MYC00128	MYC00323	MYC00379	MYC00391	MYC00377	MYC00245	MYC00376	MYC00249	MYC00285	MYC00296	MYC00269	MYC00233	MYC00282	MYC00334	MYC00392	MYC00250	MYC00001	MYC00292	MYC00342	MYC00406	MYC00003	MYC00135
MYC00116	P	0	0	0	0	0	0	0	0	0	0	1	1	1	1	2	2	2	2	2	2	3	3	3	3	4	4	4	7	8	26	44	65	72	73	74
MYC00244	E	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	1	2	3	3	3	3	3	3	4	4	7	8	25	44	65	72	72	74
MYC00232	P	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	2	2	2	3	3	3	3	4	4	7	8	26	44	65	71	72	74	
MYC00117	P	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	2	2	2	3	3	3	3	4	4	7	8	26	44	65	72	73	73	
MYC00270	E	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	2	2	2	2	3	3	3	4	4	7	8	25	43	64	71	73	71	
MYC00246	P	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	2	2	2	3	3	3	3	4	4	7	8	26	44	65	71	72	74	
MYC00248	P	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	2	2	2	3	3	3	3	4	4	7	8	26	45	66	70	72	74	
MYC00252	P	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	2	2	2	3	3	3	3	4	4	7	8	26	44	65	71	72	74	
MYC00286	E	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	2	2	2	3	3	3	3	4	4	7	8	25	44	65	72	73	73	
MYC00375	E	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	2	2	2	2	2	3	3	3	3	4	4	7	8	26	44	65	71	72	74	
MYC00114	P	1	1	1	1	1	1	1	1	1	1	1	2	2	2	3	3	3	3	3	3	4	4	4	4	5	5	8	9	27	45	66	73	74	74	
MYC00234	P	1	1	1	1	1	1	1	1	1	2	2	2	3	3	3	3	3	3	3	3	4	4	4	4	5	5	8	9	27	45	67	72	72	74	
MYC00361	E	1	1	1	1	1	1	1	1	1	2	2	2	0	0	1	1	1	3	3	3	2	2	4	5	5	8	9	26	45	66	72	73	75		
MYC00128	E	1	1	1	1	1	1	1	1	1	2	2	2	0	0	1	1	1	3	3	3	2	2	4	5	5	8	9	27	45	67	74	73	75		
MYC00323	E	2	1	2	2	2	2	2	2	2	2	3	3	0	1	2	2	2	4	4	4	3	3	5	5	6	4	9	27	46	67	74	75	76		
MYC00379	E	2	2	2	2	2	2	2	2	2	2	3	3	1	1	2	2	2	4	4	4	3	3	5	6	4	9	28	46	67	74	75	76			
MYC00391	P	2	2	2	2	2	2	2	2	2	2	3	3	1	1	2	2	2	4	4	4	3	3	5	6	4	9	28	46	67	73	74	76			
MYC00377	E	2	2	2	2	2	2	2	2	2	2	3	3	3	3	4	4	4	2	4	5	5	5	5	6	6	9	10	28	46	67	74	75	76		
MYC00245	E	2	1	2	2	2	2	2	2	2	2	3	3	3	3	4	4	4	2	4	5	5	5	5	6	6	9	9	28	46	67	73	74	76		
MYC00376	E	2	2	2	2	2	2	2	2	2	2	3	3	3	3	4	4	4	4	4	4	4	5	5	5	6	6	9	10	28	46	67	73	74	76	
MYC00249	P	3	3	3	3	3	3	3	3	4	4	2	2	3	3	3	5	5	4	4	4	6	7	7	5	10	9	29	47	68	74	75	77			
MYC00285	E	3	3	3	3	3	3	3	3	4	4	2	2	3	3	3	5	5	4	4	4	6	7	7	5	10	9	28	47	68	74	75	77			
MYC00296	E	3	3	3	3	3	3	3	3	4	4	2	2	3	3	3	5	5	4	4	4	6	7	7	5	10	9	29	47	70	77	78	77			
MYC00269	E	3	3	3	3	3	3	3	3	4	4	4	4	4	4	5	5	5	5	5	5	6	6	6	6	7	10	11	28	47	68	74	77	78		
MYC00233	P	4	3	3	4	4	4	4	4	5	5	5	5	5	5	6	6	6	7	7	7	6	6	8	7	11	12	30	48	68	75	76	78			
MYC00282	E	4	4	4	3	3	4	4	4	5	5	5	5	5	6	6	6	6	6	6	7	7	7	7	8	8	11	12	29	48	69	76	77	78		
MYC00334	E	4	4	4	4	4	4	4	4	5	5	5	5	5	6	6	6	6	6	6	6	6	6	7	7	8	8	11	10	29	48	69	75	76	78	
MYC00392	P	7	7	7	7	7	7	7	7	8	8	8	8	8	9	9	9	9	9	9	9	10	10	10	10	11	11	15	33	51	72	78	79	81		
MYC00250	P	8	8	8	8	8	8	8	8	8	9	9	9	9	7	7	8	8	10	9	10	9	9	9	11	12	10	15	34	52	73	79	80	82		
MYC00001	P	26	25	26	26	25	26	26	26	25	26	27	27	26	27	27	28	28	28	28	28	29	28	29	28	30	29	33	34	34	25	59	74	76	83	
MYC00292	P	44	44	44	43	44	45	44	44	44	45	45	45	45	46	46	46	46	46	46	47	47	47	47	48	48	51	52	34	64	76	82	97			
MYC00342	P	65	65	65	64	65	66	65	65	65	66	67	67	67	67	67	67	67	67	68	68	70	68	68	69	69	72	73	25	64	117	72	114			
MYC00406	P	72	72	71	72	71	71	70	71	72	71	73	72	72	74	74	74	73	74	73	74	74	77	74	75	76	75	78	79	59	76	117	44	132		
MYC00003	P	73	72	73	73	72	72	73	72	74	72	73	73	75	74	75	74	75	74	75	78	74	76	77	76	79	80	74	82	72	44	83				
MYC00135	P	72	74	74	73	71	74	74	74	73	74	74	74	75	75	76	76	76	76	76	77	77	77	77	78	78	78	81	82	63	97	114	132	83		

Pitt Future Directions

Utilization of AI

- AI-developed tool helps identify transmission routes via electronic health record data mining
- Future research into LLM-guided infection prevention tool for interventions

Infection Control & Hospital Epidemiology (2026), **47**, 170–174
doi:10.1017/ice.2025.10355



Original Article

Artificial intelligence enhances genomic surveillance in healthcare outbreak investigations

Alexander Sundermann DrPH^{1,2,3}, Jieshi Chen MS⁴, Melissa Saul MS⁵, Kathleen Shutt MS^{1,2}, Marissa Griffith BS^{1,2}, Graham Snyder MD^{2,6}, Lora Lee Pless PhD^{1,2}, Artur Dubrawski PhD⁴ and Lee Harrison MD^{1,2,3}

¹Microbial Genomic Epidemiology Laboratory, Center for Genomic Epidemiology, University of Pittsburgh, Pittsburgh, PA, USA, ²Division of Infectious Diseases, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA, ³Department of Epidemiology, School of Public Health, University of Pittsburgh, Pittsburgh, PA, USA, ⁴Anton Laboratory, Carnegie Mellon University, Pittsburgh, Pennsylvania, ⁵Department of Medicine, University of Pittsburgh School of Medicine, Pittsburgh, Pennsylvania and ⁶Department of Pathology, University of Pittsburgh, Pittsburgh, Pennsylvania
doi:10.1017/ice.2018.343



Original Article

Automated data mining of the electronic health record for investigation of healthcare-associated outbreaks

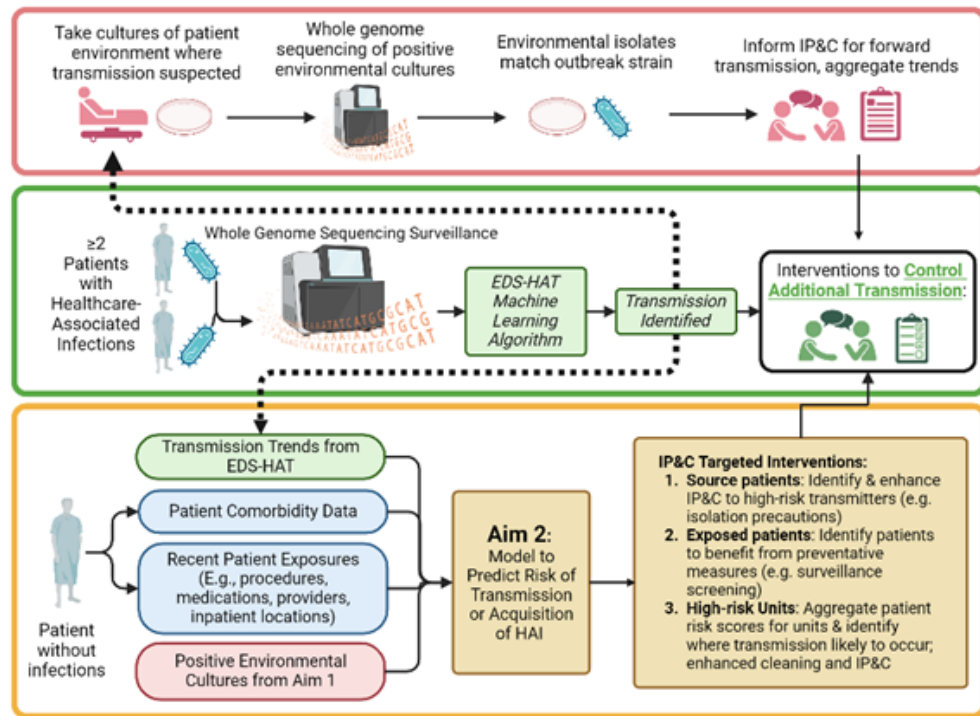
Alexander J. Sundermann MPH, CIC^{1,2}, James K. Miller PhD³, Jane W. Marsh PhD¹, Melissa I. Saul MS⁴, Kathleen A. Shutt MS¹, Marissa Pacey¹, Mustapha M. Mustapha MBBS, PhD¹, Ashley Ayres BS, CIC², A. William Pasculle ScD⁵, Jieshi Chen MS³, Graham M. Snyder MD, SM², Artur W. Dubrawski PhD³ and Lee H. Harrison MD¹

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Pitt Future Directions

Environment & Prediction

- Identifying environmental reservoirs of genomically-detected outbreaks
- Creating risk prediction scores for acquisition of transmitted infections for enhanced interventions



Environment?

The sink splash zone

M.I. Garvey ^{a b c} , N. Williams ^a, A. Gardiner ^a, C. Ruston ^a, M.A.C. Wilkinson ^{a b}, M. Kiernan ^d,
J.T. Walker ^a, E. Holden ^a



What grows in the sink splash zone

Mark I. Garvey ^{1 2} , Robert A. Moran ¹, Martyn A.C. Wilkinson ², Ana D. Sanches Ferreira ¹,
Alyson Gardiner ², Elisabeth Holden ², Alan McNally ¹ 



Pitt Future Directions

Does genomic surveillance work in other settings?

- Step-wedged RCT for effectiveness across multiple hospital settings
- Baseline -> Intervention

Outline

1. Outbreaks - Examples
2. Genomic Surveillance
3. Future Directions



CHOP: *S. aureus* in NICU

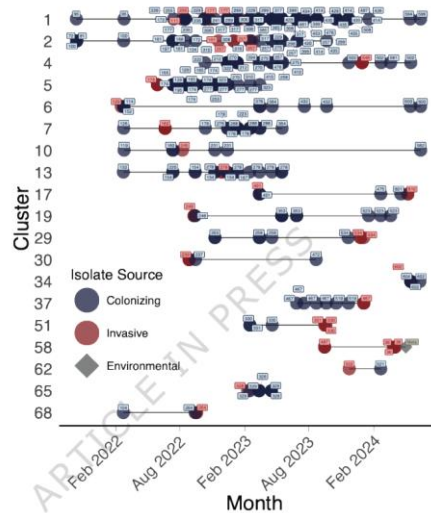
- 3 years of genomic surveillance in NICU
- Colonization + clinical isolates
- 176 babies colonized; 15 BSIs part of an outbreak
- Linked to environment

Article | [Open access](#) | Published: 09 February 2026

Rapid dissemination of *Staphylococcus aureus* in the neonatal intensive care unit is associated with invasive infection

[Qianxuan She](#), [Lakshmi Srinivasan](#), [Erin Theiller](#), [Bianca E. Galis](#), [T'Nia Napper](#), [Andries Feder](#), [Alex Arvanitis](#), [Steven M. Jones](#), [Ericka Hayes](#), [Karen M. Puopolo](#), [Robert N. Baldassano](#), [Michael Z. David](#), [Susan E. Coffin](#), [Kathleen A. Gibbs](#), [Robert F. Potter](#), [Kenneth P. Smith](#), [Rebecca M. Harris](#), [Joseph P. Zackular](#) [✉](#), [Ahmed M. Moustafa](#) [✉](#) & [Paul J. Planet](#) [✉](#)

[Nature Communications](#), Article number: (2026) | [Cite this article](#)



Denmark: multiple species

- 28 months Copenhagen hospital
- 1975/7398 (26.7%) culture-positive hospitalized patients linked to another
- Projected €1.35 million annual savings if intervened

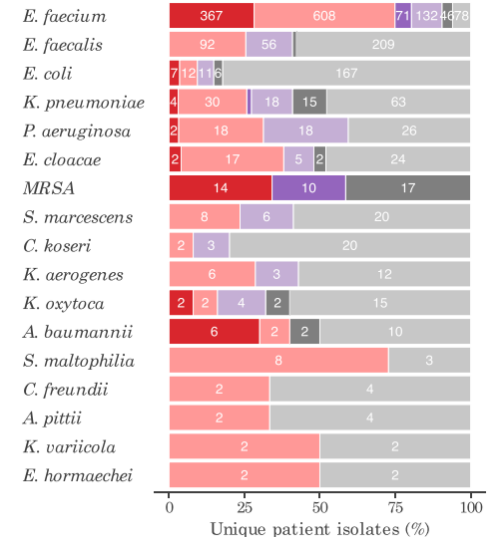
MDRO & Link Type



Original article

Estimating the potential economic and health impact of integrated genomic surveillance in a hospital setting

Frederik Boetius Hertz ^{1,2,†}, Karen Leth Nielsen ^{1,†}, Dmytro Strunin ^{1,†}, Jelena Erdmann ^{4,5,†}, Martin Lucas Jørgensen ³, Theiss Bendixen ³, Roshkan Srinathan ³, Rasmus L. Marvig ⁶, Steen Christian Rasmussen ¹, Asger Nellemann Rasmussen ¹, Christian Salgaard Jensen ¹, Jenny Dahl Knudsen ¹, Susanne Häussler ^{1,4,5,6}



Australia: 3 hospitals

- MRSA, CRAB, VRE, CRE over 4-years at 3 hospitals
- 2,600 isolates - 33% genetically linked among 76 clusters
- Concludes genomic surveillance is feasible and guides targeted interventions that otherwise would have been missed

Clinical Implementation of Routine Whole-genome Sequencing for Hospital Infection Control of Multi-drug Resistant Pathogens

Brian M. Forde,¹ Haakon Bergh,² Thom Cuddihy,¹ Krispin Hajkowitz,³ Trish Hurst,³ E. Geoffrey Playford,⁴ Belinda C. Henderson,⁴ Naomi Runnegar,^{4,5} Julia Clark,^{6,7} Amy V. Jennison,⁸ Susan Moss,⁸ Anna Hume,^{2,3} Hugo Leroux,⁹ Scott A. Beatson,¹⁰ David L. Paterson,^{1,3} and Patrick N. A. Harris^{1,2,9}

Species	Clustered Isolates	No. of Clusters
<i>A. baumannii</i>	18	3
<i>E. coli</i>	249	27
<i>Enterobacter</i> spp. ^a	60	4
<i>K. pneumoniae</i>	67 ^b	7
<i>E. faecium</i>	289	19
<i>S. aureus</i>	149	17

MD Anderson: long-read WGS

Infection Control & Hospital Epidemiology (2025), 46, 129–135
doi:10.1017/ice.2024.202

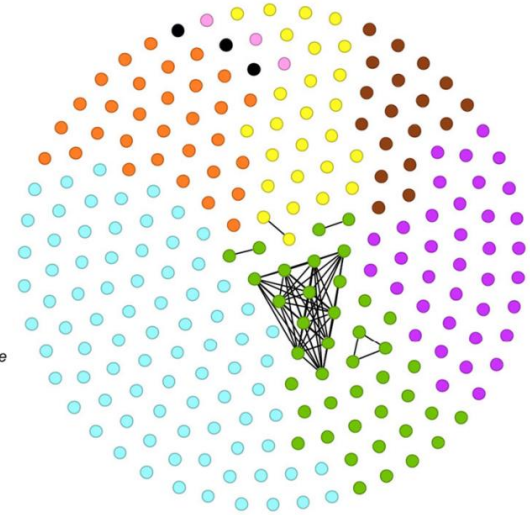
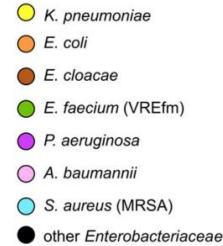


Original Article

Rapid whole genome characterization of antimicrobial-resistant pathogens using long-read sequencing to identify potential healthcare transmission

Chin-Ting Wu MS¹, William C. Shropshire PhD² , Micah M Bhatti MD, PhD³, Sherry Cantu MPH, MT⁴, Israel K Glover BS⁵, Selvalakshmi Selvaraj Anand MS⁶, Xiaojun Liu PhD¹, Awdhesh Kalia PhD¹, Todd J. Treangen PhD^{7,8} , Roy F Chemaly MD^{2,4} and Samuel Shelburne MD, PhD^{2,5}

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Results: Over a six-month period, 242 bacterial isolates from 216 patients were sequenced by a single operator. Compared to the Illumina gold standard, our ONT pipeline achieved a mean identity score of Q60 for assembled genomes, even with a coverage rate as low as 40×. The mean time from initiating DNA extraction to complete analysis was 2 days (IQR 2–3.25 days). We identified five potential transmission clusters comprising 21 isolates (8.7% of sequenced strains). Integrating ONT with epidemiological data, >70% (15/21) of putative transmission cluster isolates originated from patients with potential healthcare transmission links.

This is all great, but how do we get this at our hospital?

Addressing Barriers & Paths Forward



Antimicrobial Agents
and Chemotherapy



8 | Editor's Pick | Genomics and Proteomics | Commentary

Pathogen genomics in healthcare: overcoming barriers to proactive surveillance

Alexander J. Sundermann,^{1,2} Rossana Rosa,³ Patrick N. A. Harris,^{4,5,6} Evan Snitkin,^{7,8} Waleed Javaid,⁹ Nicholas M. Moore,¹⁰ Mary K. Hayden,¹⁰ Krisandra Allen,¹¹ Kyle Rodino,¹² Sharon J. Peacock,¹³ Lilian M. Abbo,^{3,14} Lee H. Harrison^{1,2,15}

AUTHOR AFFILIATIONS See affiliation list on p. 11.

ABSTRACT Pathogen genomic surveillance in healthcare has the potential to enhance patient safety by detecting outbreaks earlier, thereby reducing morbidity and mortality. Despite benefits, there are barriers to adoption, including cost, expertise, and lack of standardized methodologies and incentives. This commentary advocates for 1) investment from healthcare payors, public health, and regulatory bodies and 2) additional research on genomic surveillance for improving patient outcomes and reducing infections. Effective implementation will require strategic investment and cross-sector collaboration.

Evidence: Studies

Author	Year	Pathogen	Duration	Outbreaks or notable findings
Forde et al	2023	Multiple MDR bacteria	4 years	76 clusters
Lee et al	2023	Carbapenemase-producing <i>Enterobacterales</i>	8 years	9 outbreaks, linked to environment
Ludden et al	2021	<i>Escherichia coli</i>	6 months	10 clusters, 20 patients. Both carriage and clinical infection transmission
Miles-Jay et al	2023	<i>Clostridioides difficile</i>	9 months	Low levels of transmission, indicating successful IP&C practice
Sherry et al	2022	Multiple MDR bacteria	15 months	31% acquired MDRO in hospital, directed IP&C interventions
Stribling et al	2023	<i>Pseudomonas aeruginosa</i>	10 years	Protracted outbreak
Sundermann et al	2022	Multiple bacteria	2 years	99 outbreaks, 297 patients
Sundermann et al	2024	Multiple bacteria	2 years	172 outbreaks, 476 patients

Barriers & Paths

TABLE 1 Summary of barrier areas and potential steps forward

Area	Current status for genomic surveillance Considerations		Future directions
Evidence	Multiple studies showing surveillance finds previously unrecognized outbreaks and with interventions can reduce infections and deaths	- Causal evidence in reducing HAIs - Differences in fungal, viral, or bacterial approaches - Cost-effectiveness	- Additional, independent analysis showing benefits and outcomes - Detailed modeling analysis for single centers and broader communities
Financial	Studies showing support for net cost-savings by averted infections	- Different healthcare institution types - In-house versus outsourced capacity - Consistent funding opportunities - Reliable reimbursement model	- Analysis on impact by institution type - Listing of resources available to institutions
Infrastructure	Variability in access and knowledge for genomics	- Necessary equipment and laboratory space - Dedicated staff - Competencies in analysis - Trained infection prevention departments capable of making interventions	- Analysis on optimal practices - Programs to train individuals on analysis and interventions
Methods	No consensus on optimal methodology for genomics	- Consistent methods across multiple centers - Bioinformatic pipeline methods - Identifying genetically related pathogens	Professional society guidance on optimal analysis methods
Legal & Ethical	No guidance or professional society documents on legal, ethical, or regulatory guidelines	- Data security, privacy, and storage - Considerations in patient disclosure equitable access	Discussions and analysis on best practices
Regulatory		- Laboratory certification - Development of billing or reimbursement models	Discussions with regulatory bodies on potential future pathways

Addressing Barriers: Ethics

Infection Control & Hospital Epidemiology (2026), 1–6

doi:[10.1017/ice.2026.10519](https://doi.org/10.1017/ice.2026.10519)



Commentary

Pathogen genomic surveillance in health care: emerging ethical dilemmas in outbreak detection and patient notification

Alexander J. Sundermann DrPH^{1,2,3} , Waleed Javaid MD, MBA, MS⁴  and Lisa Parker PhD^{5,6} 

¹Microbial Genomic Epidemiology Laboratory, Center for Genomic Epidemiology, University of Pittsburgh, Pittsburgh, PA, USA; ²Division of Infectious Diseases, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA; ³Department of Epidemiology, School of Public Health, University of Pittsburgh, Pittsburgh, PA, USA; ⁴Department of Medicine, School of Medicine, West Virginia University, Morgantown, WV, USA; ⁵Center for Research Ethics, University of Pittsburgh, Pittsburgh, PA, USA and ⁶Department of Human Genetics, School of Public Health, University of Pittsburgh, Pittsburgh, PA, USA

OK, how do we pay for it?

- Hospital vs. payer perspective
- Payer-incentivized programs
 - Hospital performs genomic surveillance & intervenes on detected transmission
 - Payer reimburses for genomics pending compliance with interventions and/or reduction of transmission



Spreading Awareness is Key

STAT

OPINION 66 FIRST OPINION

PulseNet identifies and stops foodborne illness outbreaks. Health care needs something similar

Genomic surveillance of health system outbreaks could help curtail their impact

Dec 2024

By Alexander Sundermann Dec. 6, 2024

Sundermann is an assistant professor of epidemiology at the University of Pittsburgh, School of Public Health.

The recently ended Boar's Head listeria outbreak, which has caused 57 infections and nine deaths, is just one of the many foodborne illness incidents that the Centers for Disease Control and Prevention detects each year using its PulseNet system. Many people might not realize the extensive effort behind PulseNet, which systematically collects data on foodborne illnesses from patients across the U.S., performs genomic fingerprinting, and traces outbreaks back to their sources. This network of surveillance has been alerting the public to foodborne outbreaks and recalls for years.



MEDPAGE[®] TODAY

We Can Stop Deadly Hospital Outbreaks -- So Why Aren't We?

— Genomic surveillance can help contain local and nationwide threats

by Alexander Sundermann, DrPH

October 14, 2025 · 4 min read

What We Need Now

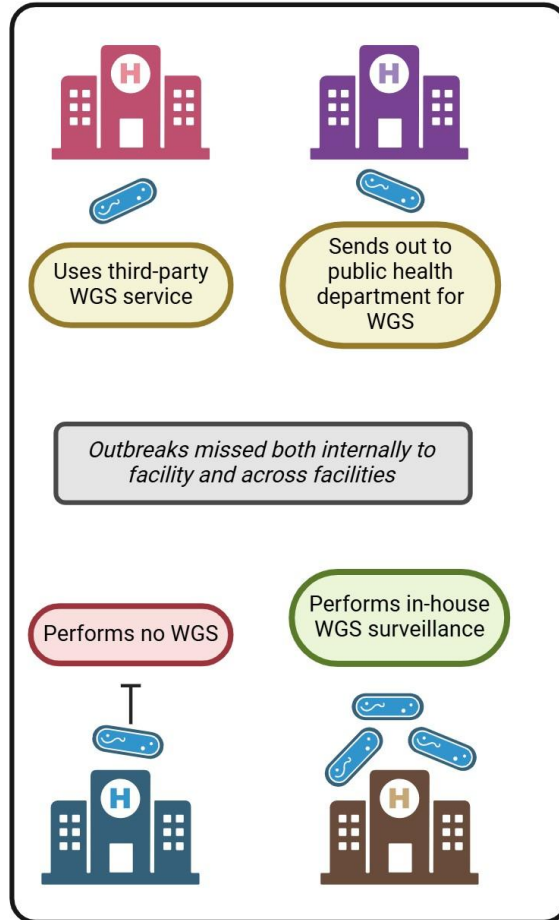
Oct 2025

Hospitals should consider implementing [genomic surveillance](#) as a core part of their infection prevention programs. Regulators should incentivize its use. Patients deserve to be protected by 21st-century tools.

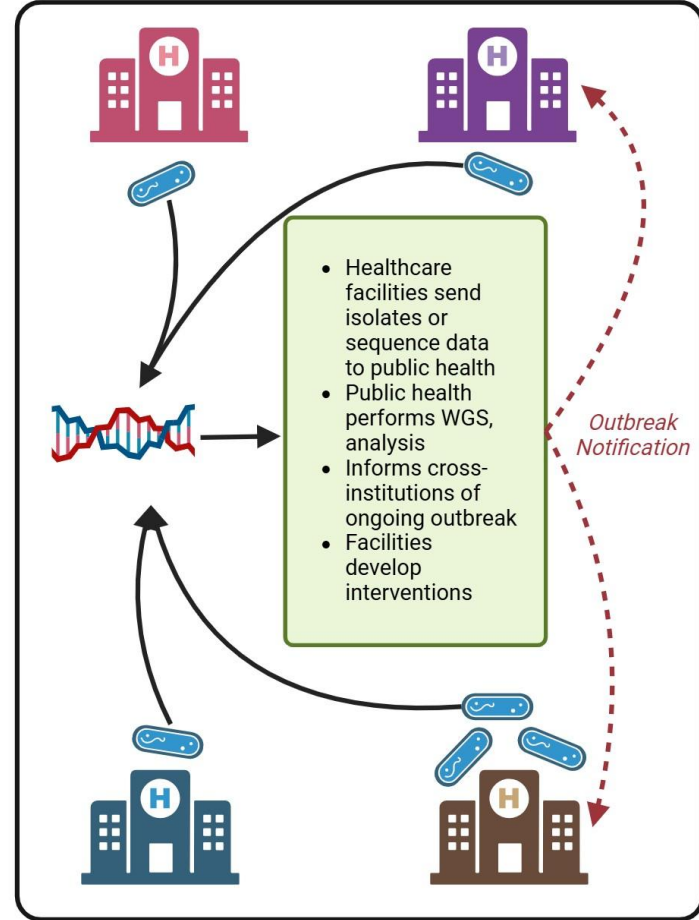
We've seen what happens when we don't look: People like Aaron Young and many others develop preventable infections. National recalls of medication come late. Outbreaks go unnoticed.

But we've also seen what's possible when we do look. And that gives me hope. We can stop hospital outbreaks before they grow. We can save lives. But first, we have to look.

Current State



Ideal State



Harrison Lab

Microbial Genomic Epidemiology Laboratory (MiGEL), Center for Genomic Epidemiology



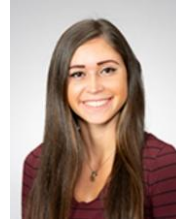
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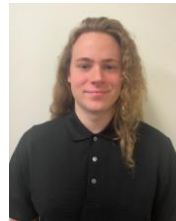
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