nonprescription use was reported by 246 (43%) of 564 individuals, with 91 (16%) reporting nonprescription use within the previous 12 months. Intention to use nonprescription antibiotics was reported by 140 participants (25%). The sensitivity and specificity of prior nonprescription use in the past 12 months to predict the intention to use nonprescription antibiotics in the future were 75.9% (95% CI, 65.3–84.6) and 91.4% (95% CI, 87.8–94.2), respectively. After the Bayes' adjustment, the PPV and NPV of prior use to predict future intention were 74.5% (95% CI, 66.7–80.9) and 92.0% (95% CI, 88.7–94.4) (Table 1). **Conclusions:** These results show that prior nonprescription antibiotic use in the past 12 months predicted the intention to use nonprescription antibiotics in the future (PPV of 75%). As a stewardship effort, we suggest clinicians use a simple question about prior nonprescription antibiotic use in primary-care settings as a screening question for patients at high risk for future nonprescription antibiotic use.

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Poster Presentation - Top Oral Abstract
Subject Category: Molecular Epidemiology

Real-time whole-genome sequencing surveillance for outbreak detection and intervention

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Background: Detecting healthcare-associated transmission and outbreaks often relies on reactive whole-genome sequencing (WGS), which occurs after the suspected transmission has occurred. Additionally, reactive WGS frequently misidentifies transmission and misses transmission when it has occurred. We initiated weekly real-time WGS to detect bacterial transmission and direct infection prevention interventions. We describe our experience after 1 year of real-time WGS surveillance at the University of Pittsburgh Medical Center–Presbyterian Hospital, a large, tertiary-care facility. **Methods:** Weekly WGS surveillance was performed from November 1, 2021, to October 31, 2022. Cultured isolates of select bacterial pathogens from patients who were hospitalized for ≥3 days or had a recent healthcare exposure in the prior 30 days were collected and sequenced. Isolates that were ≤15 single-nucleotide polymorphisms (SNPs) were considered genetically related clusters except for *Clostridioides difficile* (≤2 SNPs). Genetically related clusters were investigated for epidemiological links and interventions to interrupt transmission were implemented at the discretion of the infection prevention team. We analyzed subsequent infections that occurred within an outbreak after an intervention was in place. **Results:** In total, 1,909 isolates were sequenced. Of 1,633 unique patient isolates clustered by sequence type, 74 clusters were identified comprising 210 (12.9%) patient isolates (Table 1). The median time from culture date to sequencing was 14 days (IQR, 5.25). The median cluster size was 2 (IQR, 1) (Table 2). Overall, 118 patient isolates (56.2%) had an epidemiological link to a prior isolate, indicating potential transmission. Of 74 clusters, 66 (89.2%) received infection prevention interventions after notification based upon epidemiological data. The infection prevention team performed 69 total interventions, which included unit education (n = 28), hand hygiene observations (n = 16), enhanced cleaning (n = 16), environmental cultures or removal of endoscope (n = 7), and enhanced microbiology surveillance (n = 2). The 59 subsequent infections after infection prevention notification included 17 (28.8%) with no clear epidemiological link, and 41 (69.5%) with an epidemiological link either to a new transmission route (n = 37) or the same route prior to infection prevention intervention (n = 4). Only 1 (1.7%) subsequent infection within a cluster occurred after an infection prevention intervention from the same potential route, which was a suspected unit-based transmission of vancomycin-resistant *Enterococcus faecium*. **Conclusions:** Real-time WGS was effective at detecting genetically related clusters, finding potential sources, and halting further transmission after interventions by the infection prevention team. Quick turnaround times from patient culture to sequencing and analysis were vital for successful WGS surveillance. Real-time WGS surveillance has the potential to substantially shift the infection prevention paradigm for outbreak detection.

Table 1. Isolates sequenced and clusters detected

Organism	Sequenced	Unique Patient	Clusters	Clustered Isolates (%)
Acinetobacter species	52	50	5	11 (22.0)
Burkholderia species	6	4		
Citrobacter species	30	29		
Clostridioides difficile	100	98	3	8 (8.2)
Enterobacter species	35	34	2	4 (11.8)
Escherichia coli	128	109	5	11 (10.1)
Klebsiella species, not *pneumoniae*	21	21		
Klebsiella pneumoniae, ESBL producing	90	67	6	23 (34.3)
Methicillin-resistant *Staphylococcus aureus*	248	221	9	21 (9.5)
Proteus species	228	189	3	6 (3.2)
Providencia species	24	23		
Pseudomonas aeruginosa	558	438	20	50 (11.4)
Pseudomonas species, not *aeruginosa*	14	14		
Serratia species	153	135	3	6 (4.4)
Stenotrophomonas maltophilia	98	85	1	2 (2.4)
Vancomycin-resistant *Enterococcus faecium*	124	116	17	68 (58.6)
TOTAL	**1909**	**1633**	**74**	**210 (12.9)**

Table 2. Cluster size and distribution by species

Organism	Number of Clusters by Cluster Size (Patients)										
	2	3	4	5	6	7	8	9	10	11	12
Acinetobacter species	4	1									
Clostridioides difficile	2		1								
Enterobacter species	2										
Escherichia coli	4	1									
Klebsiella pneumoniae, ESBL producing	4				1			1			
Methicillin-resistant *Staphylococcus aureus*	6	3									
Proteus species	3										
Pseudomonas aeruginosa	16	1	1	1	1						
Serratia species	3										
Stenotrophomonas maltophilia	1										
Vancomycin-resistant *Enterococcus faecium*	7	5	1			2		1			1

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Subject Category: Outbreaks

Patient and facility characteristics of an NDM-producing *Acinetobacter baumannii* outbreak in California, 2020–2022

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Background: Carbapenem-resistant *Acinetobacter baumannii* (CRAB) are bacteria that cause healthcare-associated infections and outbreaks. Most produce carbapenemases like New Delhi metallo-β-lactamase (NDM), which are more commonly found in carbapenem-resistant Enterobacterales but rarely in CRAB. In 2018, selected laboratories began participating in a public health sentinel surveillance program by routinely submitting CRAB and other antimicrobial-resistant isolates to the AR Laboratory Network for specialized testing. In May 2020, the Antimicrobial Resistance Laboratory Network detected the first NDM-CRAB case in California, triggering an investigation. Initial whole-genome sequencing of subsequent isolates indicated high relatedness. **Methods:** We defined confirmed cases as patients with NDM detected in CRAB isolates and probable cases as NDM detected in a screening swab from a patient epidemiologically linked to a known case(s) with specimens collected during May 2020–September 2022. We defined outbreak facilities as having (1) 1 or more newly identified cases during a point-prevalence survey in response to a known case or (2) at least 2 cases identified within 4 weeks of each other that were epidemiologically linked. We analyzed demographic and specimen characteristics, as well as healthcare exposure history using R Studio version 1.3.959 software. **Results:** Of 230 total patients, 176 (77%) were confirmed and 54 (23%) were probable cases; 150 (65%) were identified