and 185 isolates (63.8%) from the no isolation period (October–December 2021, January–October 2023), representing 202 unique patients. Patient characteristics and microbiological findings are shown in Table 1. Only 4.3% (7/171) of E. faecalis and 70.5% (84/119) of E. faecium isolates were vancomycin-resistant. Long-read WGS revealed no clustering between the isolation and no isolation periods. (Figure 1A and B); however, a dominant E. faecium ST117 cluster was seen, while E. faecalis showed greater diversity (Figure 1C). There were only four pairs of putative transmissions **Conclusion:** The discontinuation of contact isolation precautions at Stanford Hospital did not result in an increase in genetically related Enterococci or genetically related vanA plasmids among patients with Enterococcal bacteremia.

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doi:10.1017/ash.2025.230

Table 1. Patient Characteristics and Microbiological Data During Isolation and No Isolation Periods

	Isolation	No Isolation	*P* value*
Isolates (%)	105 (36.2%)	185 (63.8%)	
Age (range) years	66 (23 – 102)	67 (19 – 99)	.308
Sex: Female (%)	34 (32.4%)	54 (29.2%)	.569
Immunocompromised (%)	26 (24.8%)	73 (39.5%)	.011
Oncological (%)	21 (20%)	45 (24.3%)	.398
Surgical (%)	25 (23.8%)	59 (31.9%)	.144
LOS days (range)	16 (1 – 475)	23 (1 – 387)	.007
Hospital Onset Bacteremia	46 (43.8%)	85 (45.9%)	.725
Vancomycin exposure	55 (52.4%)	112 (60.5%)	.734
Vancomycin days of therapy	2 (1 – 33)	2.5 (1 – 78)	.176
E. faecalis	61 (58.1%)	110 (59.5%)	.820
Vancomycin-resistant	0 (0%)	7 (6.4%)	.044
Vancomycin exposure	23 (37.7%)	54 (49.1%)	.151
Vancomycin Days of therapy	3 (1 – 33)	2 (1 – 78)	.672
E. faecium	44 (41.9%)	75 (40.5%)	.227
Vancomycin-resistant	32 (72.7%)	52 (69.3%)	.392
Vancomycin exposure	32 (72.7%)	58 (77.3%)	.572
Vancomycin Days of therapy	2 (1 – 27)	3 (1 – 32)	.253

Comparisons between groups were performed using the Mann-Whitney U test for continuous variables and the Z-test for proportions.
Abbreviations: LOS, length of stay.

Figure 1. Long-Read Whole-Genome Sequencing Results

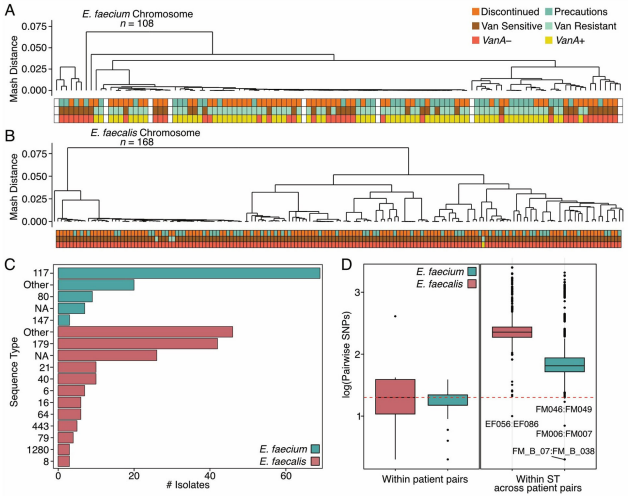
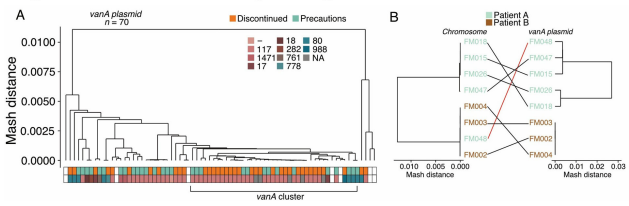


Figure 2. *VanA* Plasmid Sequencing Results



Presentation Type:
Oral Presentation
Subject Category: Molecular Epidemiology

Genomic Epidemiology of Healthcare-Associated Respiratory Virus Infections

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Background: Investigation of transmission of respiratory viruses (RV) in healthcare setting is understudied. To investigate the transmission dynamics of common healthcare-associated RV infections, we performed retrospective whole genome sequencing (WGS) surveillance of rhinovirus, influenza, human metapneumovirus (HMPV), and respiratory syncytial virus (RSV) at one children's and two adult teaching hospitals in the Pittsburgh area. **Methods:** From Jan 2, 2018 to Jan 4, 2020, nasal swab specimens positive for rhinovirus, influenza, HMPV or RSV were collected from patients who had been hospitalized for ≥3 days. Specimens with qPCR Ct values ≤30, HMPV specimens were sequenced using tiled PCR amplicons regardless of their qPCR Ct value. Genomes passed WGS QC if ≥90% of the genome had ≥10× average coverage depth. High-quality genomes were assessed for genetic relatedness using ≤3 single nucleotide polymorphisms (SNPs) as a cut-off. Review of patient health records was performed on all genetically related clusters to identify common epidemiological connections. **Results:** We collected 436 rhinovirus (n = 291), influenza (n = 50), HMPV (n=47) and RSV (n=48) specimens from 360 patients. Of these, 55% (197/360 patients) were from the children's hospital and 45% were from the two adult hospitals. Patients ranged in age from 14 days to 93 years old, 61% were male, and 74% were white. We sequenced 61.2% (178/291) of rhinovirus, 78% (39/50) of influenza, and 92% (44/48) of RSV specimens that met qPCR criteria. Among these, 63.5% (113/178) of rhinovirus, 87% (34/39) of influenza, and 89% (39/44) of RSV genomes passed WGS QC. Additionally, 79% (37/47) of the HMPV genomes passed WGS QC. We identified 13 genetically related clusters (n=5 rhinovirus; n=2 influenza; n=3 RSV; n=3 HMPV) containing 34 patients and ranging in size from 2-5 patients per cluster. We identified common epidemiological links between 56% (19/34) of clustered patients. Of these, 63% (12/19) of patients had a same-unit stay, 11% (2/19) shared a common provider, and 26% (5/19) had overlapping hospital stays. On average, genetically related clusters spanned a duration of 17 days (range: 0–55 days). **Conclusion:** WGS offered valuable insights into RV transmission dynamics in hospitals, which until now have not been rigorously studied. While healthcare-associated RV transmission is common, absence of epidemiological links in 44% of genetically-related cases and the distribution of cluster durations, given the incubation period, highlights the complex transmission dynamics.

Antimicrobial Stewardship & Healthcare Epidemiology 2025;5(Suppl. S2):s32

doi:10.1017/ash.2025.231

Presentation Type:
Oral Presentation
Subject Category: Pediatrics

Reducing MSSA Invasive Infection and Transmission in the NNICU using Whole Genome Sequencing and Environmental Surveillance.

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Background: A Quality Improvement (QI) initiative to reduce invasive Staphylococcus aureus (SA) infections in a level IV neonatal intensive care unit (NICU) successfully eliminated Methicillin-resistant (MRSA) but not Methicillin-susceptible (MSSA) infections. A combination of SA whole genome sequencing (WGS) and environmental culturing helped to better understand the epidemiology of MSSA colonization and infection in the