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Original Article

The impact of an intervention to reduce dispersal from wastewater drain sites on carbapenem-resistant *Pseudomonas aeruginosa* colonization and bloodstream infection on a hematopoietic cell transplant and hematologic malignancy unit

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Abstract

Objective: To evaluate the impact of an intervention to limit dispersal from wastewater drain (WWD) sites on meropenem-nonsusceptible *Pseudomonas aeruginosa* patient and environmental colonization and bloodstream infection (BSI) on a hematopoietic cell transplant (HCT) and hematologic malignancy (HM) unit.

Design: This quasi-experimental study included pre/postintervention point-prevalence surveys in July 2019 and June 2020, respectively. The retrospective cohort included HCT/HM patients with *P. aeruginosa* BSI between 2012 and 2022.

Setting: Adult HCT/HM unit at an academic center.

Participants: This study included consenting HCT/HM patients on the unit at the time of the point-prevalence surveys. HCT/HM patients with *P. aeruginosa* BSI between 2012 and 2022.

Methods: A quality improvement intervention targeting WWD sites was conceived and implemented on a HCT/HM unit. Pre and postintervention colonization samples were obtained from patients and environmental sites, cultivated on selective media, then characterized by susceptibility testing. Whole-genome sequencing and phylogenetic analysis were performed on select isolates. The impact of the intervention on colonization and BSI was evaluated, as was relatedness among isolates.

Results: Although colonization of WWD sites with meropenem-nonsusceptible *P. aeruginosa* was widespread before and after this intervention, we observed a substantial decline in patient colonization (prevalence rate ratio, 0.35; 95% confidence interval [CI], 0.04–3.12) and BSI (incidence rate ratio, 0.67; 95% CI, 0.31–1.42) after the intervention. Among 3 predominant sequence types (ST-111, ST-446, and ST-308), there was striking genetic conservation within groups and among environmental colonization, patient colonization, and BSI isolates.

Conclusions: An intervention targeting WWD sites on a HCT/HM unit had a meaningful impact on meropenem-nonsusceptible *P. aeruginosa* patient colonization and BSI.

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Pseudomonas aeruginosa is a significant cause of morbidity and mortality among hematopoietic cell transplant (HCT) recipients and patients with hematologic malignancy (HM).[1–3] Colonization represents a critical first step in the development of invasive disease.[4–10] An estimated 30%–50% of patients on HCT/HM units and intensive care units (ICUs) become colonized with *P. aeruginosa* during hospitalization.[7–9,11] Studies on HCT/HM units have demonstrated genetic relatedness among isolates from patients and the environment.[9,12–14] Hospital wastewater drain (WWD) sites are increasingly recognized as important reservoirs of *P. aeruginosa* amplification, propagation and transmission,[13,15–20] and several studies have provided insight on mechanisms of dissemination from sink and drain sites.[21,22]

To date, strategies to mitigate pathogen acquisition from WWD sites are nonstandardized and are often impractical, costly, and

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ultimately unsuccessful.[2,17,20,23–25] The Centers for Disease Control and the Society for Healthcare Epidemiology of America have recently proposed interventions to decrease dissemination of multidrug-resistant (MDR) organisms from WWD sites,[26,27] though effectiveness remains to be determined, particularly in vulnerable populations.

Since at least 2012, there has been a sustained relative predominance of *P. aeruginosa* bloodstream infection (BSI) caused by clusters of closely related meropenem-nonsusceptible isolates among patients admitted to the HCT/HM unit at Oregon Health and Science University (OHSU), despite infrequent use of carbapenems.[28] Carbapenem resistance poses risk for poor outcome in this population, largely attributable to inappropriate empirical therapy, with associated mortality as high as 40%–50%.[1,29,30]

Herein, we report on the impact of an intervention aimed at limiting dispersal of meropenem-nonsusceptible *P. aeruginosa* from WWD sites. Appreciating that outbreaks related to WWD sites are often characterized by low attack rates and long durations between cases,[20] we performed prospective screening of patients and environmental sites to provide a more real-time proxy for efficacy of the intervention. Our primary outcomes were meropenem-nonsusceptible patient colonization and BSI events. We performed whole-genome sequencing (WGS) and phylogenetic analysis on select isolates to determine relatedness among and between colonization and BSI isolates, and we examined the impact of the intervention on meropenem-nonsusceptible BSI isolate sequence type (ST).

Methods

A quality improvement intervention, the "splash zone" intervention, focusing on WWD sites and relying primarily on point-of-care behavioral change with adaptive supports, was conceived by a multidisciplinary group and implemented on our HCT/HM unit (Fig. 1). The work group included infection prevention and control, unit nursing leadership, environmental services, and facilities staff, and a patient representative. The intervention consisted of behavior change, acquisition of patient care equipment, modification of the physical environment, reduction in water flow rate, and development of standard operating procedures for sink cleaning and maintenance. Unit-based compliance with standard work was assessed by audit using Kamishibai cards (Supplementary Fig. 1 online).

Colonization point-prevalence study

We conducted a prospective pre and postintervention point-prevalence survey on a 30-bed adult HCT/HM unit. Institutional review board approval was obtained (no. STUDY00019706). Unit-wide preintervention sampling of consenting patients and their respective rooms was performed on July 22, 2019. Postintervention sampling was performed on June 15, 2020. Following the initial point-prevalence survey, weekly patient sampling was performed through August 2019, both to increase the number of unique patient samples and with intent to follow a subset of patients prospectively for incident colonization.

Demographic and clinical data were extracted from the electronic medical record, including sex, age, race and ethnicity, underlying disease state, transplant status, presence of central venous catheter, hospital length of stay, cumulative days on the HCT/HM unit, and receipt of antipseudomonal antibiotics.

Colonization sampling

Patient colonization cultures were performed by collection of axillary and rectal swabs (BBL CultureSwab EZ swabs, Becton Dickinson, Franklin Lakes, NJ), pooled for each patient for processing and analysis. For the preintervention survey, 7 environmental colonization samples were obtained: main sink drain swab, main sink P-trap fluid, bathroom sink drain swab, bathroom sink P-trap fluid, shower drain swab, shower drain P-trap fluid, and toilet rim swab. For the postintervention survey, 3 swabs were obtained from each room: main sink drain, bathroom sink drain, and toilet. Methods for drain and P-trap sampling are described in the Supplementary Methods (online).

Samples were plated on a Cetrimide agar (Millipore Sigma-Aldrich, St. Louis, MO), a *Pseudomonas*-selective agar. Colonies that were green or yellow in color, suggestive of growth of *Pseudomonas* spp, were isolated, frozen, and subsequently thawed for antibiotic susceptibility testing and for WGS to confirm species identification. Detailed methods for isolate cultivation are described in the Supplementary Methods (online).

Antibiotic susceptibility testing was performed by Kirby-Bauer disk diffusion[31] with levofloxacin (5 mcg) and meropenem (10 μg) discs (BD BBL Sensi Disc Biosciences, Becton Dickinson); interpretation was conducted in accordance with CLSI standards.[32]

Statistical analysis

Pre and postintervention groups were descriptively summarized and compared regarding demographic and clinical characteristics. Colonization prevalence was compared between periods. A sensitivity analysis was performed to compute the prevalence rate ratio (PRR) under scenarios in which "indeterminate" cultures (ie, growth on Cetrimide agar but WGS not performed) were assumed to be positive or negative. Patient and environmental samples that underwent WGS were summarized and compared on *P. aeruginosa* colonization, meropenem susceptibility, and ST group.

BSI study

A qualifying BSI was a *P. aeruginosa* bacteremia that occurred between January 2012 and December 2022 in a HCT recipient or HM patient receiving care at OHSU. The preintervention period was defined as the start of data collection (January 2012) to before the intervention (August 2019). The postintervention period was defined a priori as the point at which 75% unit-wide reliability with the intervention was attained (December 2020) through December 2022. Cases were identified by retrospective review of OHSU's infection control data management software (TheraDoc, Salt Lake City, UT). Only the first BSI within a 1-year period in an individual patient was computed in the analysis. Antimicrobial susceptibility testing on BSI isolates was performed by the OHSU microbiology laboratory with routine clinical care using Vitek 2 (bioMérieux, Marcy-l'Étoile, France).

Statistical analysis

Study participants with a qualifying BSI were descriptively summarized regarding demographic and clinical characteristics. Incidence of BSI in a period was calculated as number of events over that period, divided by estimated time at risk. Estimated time at risk was the total time patients spent on the unit (average daily census in a month multiplied by days in that month). The incidence of meropenem-nonsusceptible BSI was determined in the pre and postintervention periods, and a corresponding incidence rate ratio (IRR) was calculated. To compare the

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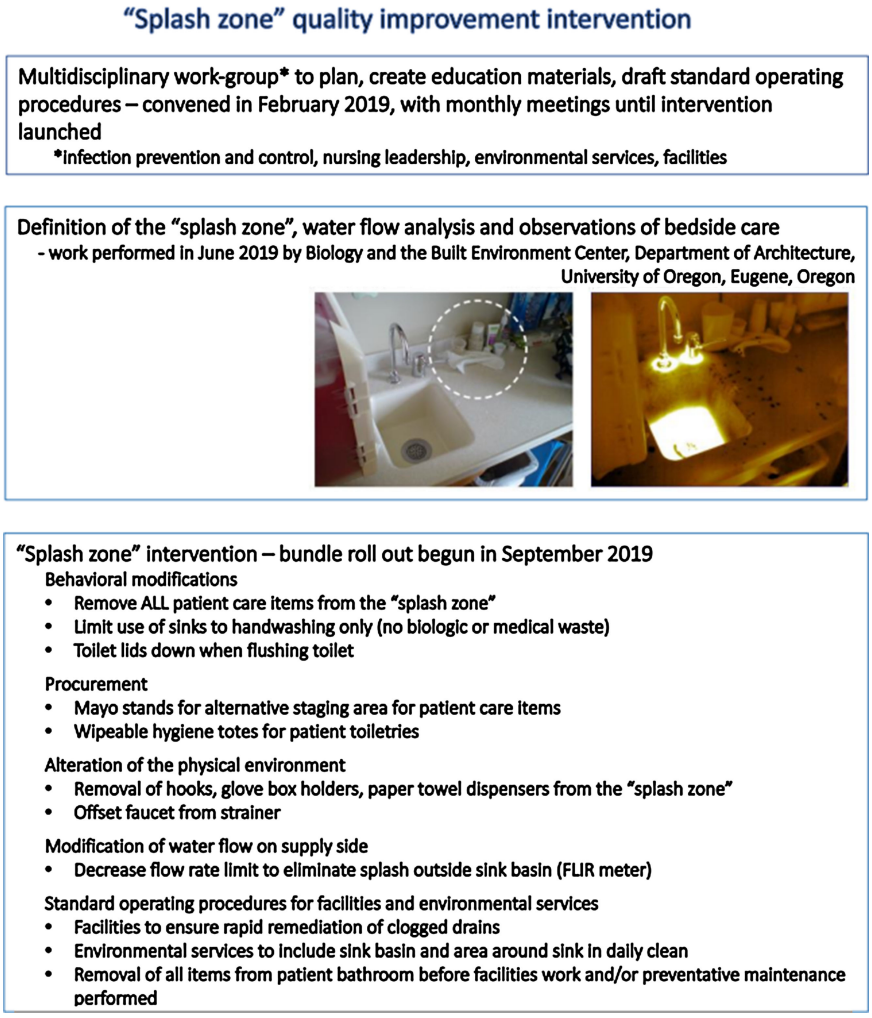

Figure 1. "Splash zone" quality improvement intervention.

incidence of outbreak-associated strains in the presence of BSI isolates not characterized by WGS, a sensitivity analysis was performed to calculate the IRR for each of 2 extreme scenarios. Statistical analyses were conducted using Stata version 15 software (StataCorp, College Station, TX).

Whole-genome sequencing and phylogenetic analysis

WGS was performed on patient and environmental colonization isolates as well as on BSI isolates obtained after October 1, 2016, preferentially on those identified to be meropenem-nonsusceptible. Bacterial DNA preparation, WGS, genome assembly, and ST determination were performed as previously described.[28] Procedures for assessing phylogenetic relatedness are described in the Supplementary Methods (online).

Results

Patient and environmental colonization

The pre and postintervention periods included 27 and 26 patients and their respective rooms. The median time from admission to colonization culture was 8 days in the preintervention and 6.5 days in the postintervention group ($P = .99$). Median days on the unit in the prior year was 19 and 14, respectively ($P = .59$) (Supplementary Table 1 online). Over both study periods, 66% and 74% of patients had received an antipseudomonal antibiotic in the preceding 30 and 60 days, respectively. Just 6% had received a carbapenem in the prior 90 days.

Of 66 patient and environmental colonization isolates cultured on Cetrimide agar submitted for WGS, 76% were confirmed to be *P. aeruginosa*. Whereas 44% of preintervention patient colonization samples yielded growth on Cetrimide agar, only 15% in the postintervention group did ($P = .035$), a roughly 3-fold decrease in colonization prevalence as assessed by selective media (Table 1). Moreover, 19% and 4% of patients in the pre and postintervention point-prevalence surveys, respectively, were confirmed by WGS to be colonized with *P. aeruginosa* (PRR, 0.21; 95% confidence interval [CI], 0.03–1.66). On sensitivity analysis, if the 2 indeterminate samples in the preintervention group were *P. aeruginosa*, the PRR would be 0.15 (95% CI, 0.02–1.12). For patient colonization with meropenem-nonsusceptible *P. aeruginosa*, there was a substantial decline after the intervention from 11% to 4% (PRR, 0.35; 95% CI, 0.04–3.12).

The results from all environmental colonization sites are presented in Table 2, but our analysis was restricted to sites available in both periods. Room colonization, as assessed by growth on Cetrimide agar from 1 or more sites, was nearly universal: 100% and 96% from the pre and postintervention periods, respectively. Colonization from the main sink drain

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Table 1. Patient Colonization

Variable	Preintervention Period (n=27), No./Total (%)	Postintervention Period (n=26), No./Total (%)	*P* Value[a]
Growth on Cetrimide agar	12/27 (44)	4/26 (15)	.035
Patients with samples submitted for WGS	10/12 (83)[b]	4/4 (100)	. . .
Pseudomonas aeruginosa, confirmed by WGS	5/10 (50)	1/4 (25)	. . .
Patients with confirmed *P. aeruginosa* (total)	5/27 (19)	1/26 (4)	.19
Patients with meropenem-nonsusceptible *P. aeruginosa* (total)	3/27 (11)	1/26 (4)	.61
Sequence type by WGS			. . .
ST-111	1	1	
ST-446	3		
ST-308	1		

Note. WGS, whole-genome sequencing; ST, sequence type.
[a]Fisher exact test.
[b]Multiple attempts at DNA extraction on 2 samples yielded insufficient purity and concentration to allow for WGS.

Table 2. Environmental Colonization

Variable	Preintervention Period (n=27), No. (%)		Postintervention Period (n=26), No. (%)	*P* Value[b]
	All Locations	Restricted Locations[a]		
Colonization of sites in rooms (growth on Cetrimide agar)				
Rooms having ≥1 site with growth on Cetrimide agar	27 (100)	27 (100)	25 (96)	.49
Rooms with growth on Cetrimide agar by specified site				
Main sink drain	25 (93)	25 (93)	10 (38)	<.01
Main sink P-trap	20 (74)	. . .	. . .	. . .
Bathroom sink drain	25 (93)	25 (93)	23 (88)	.67
Bathroom sink P-trap	23 (85)	. . .	. . .	. . .
Shower drain	4 (15)	. . .	. . .	. . .
Shower drain P-trap	12 (44)	. . .	. . .	. . .
Toilet	5 (19)	5 (19)	1 (4)	.19
WGS of samples				
Rooms having ≥1 sample submitted for WGS	23 (85)	17 (63)	11 (42)	.17
Rooms with *Pseudomonas aeruginosa* colonization at any site, confirmed by WGS	20 (87)	15 (88)	10 (91)	1.00
Rooms found to be meropenem-nonsusceptible	17 (85)	12 (80)	9 (90)	.63
Samples submitted for WGS, no.	41	23	11	. . .
Samples with *P. aeruginosa* confirmed by WGS	33 (80)	18 (78)	11 (100)	.15
Meropenem-nonsusceptible	26 (79)	15 (83)	10 (91)	1.00
ST confirmed by WGS, no.	33	18	11	
ST-111	18 (55)	10 (56)	5 (45)	.71
ST-446	8 (24)	5 (28)	2 (18)	.68
ST-308	3 (9)	1 (6)	3 (27)	.14
ST-390	2 (6)	1 (6)	0 (0)	1.00
ST-17	1 (3)	1 (6)	0 (0)	1.00
ST-1337	1 (3)	0 (0)	0 (0)	1.00
ST-298	0 (0)	0 (0)	1 (9)	.38

Note. WGS, whole-genome sequencing; ST, sequence type.
[a]Restricted to room locations measured in postintervention period: main sink drain, bathroom sink drain, and toilet.
[b]Restricted locations only, preintervention vs postintervention period. Fisher exact test.

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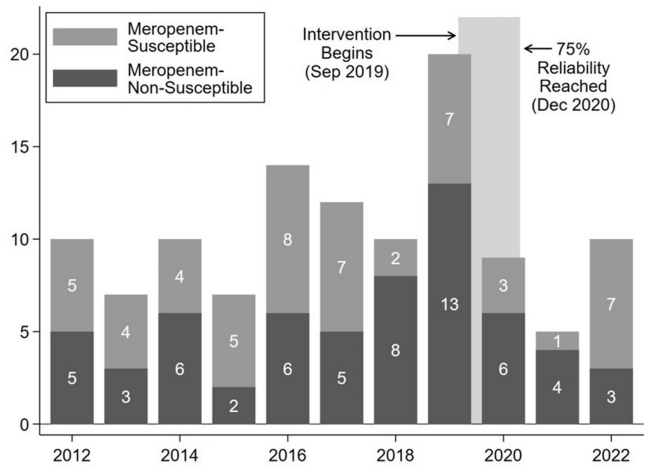

Figure 2. Yearly *P. aeruginosa* bloodstream infection (BSI) events, 2012–2022.

decreased considerably from 93% to 38% ($P < .01$) but not from the bathroom sink drain. Among rooms with 1 or more samples submitted for WGS, most were confirmed to have *P. aeruginosa:* 88% in the preintervention period and 91% in the postintervention period. Among these, 80% and 90% of samples, respectively, were meropenem-nonsusceptible.

BSI study findings

Between January 1, 2012, and December 31, 2022, 128 BSIs were detected in 113 patients. Among them, 68 (53%) of these BSI isolates were meropenem-nonsusceptible. Also, 10 patients had >1 BSI (range, 1–3) within 1 year. Among these patients, only the first event was included. One patient had a second BSI roughly 5 years after the index event, so both were included. Of the 114 qualifying BSIs, 61 (54%) of these BSI isolates were meropenem-nonsusceptible (Fig. 2). On average, 5.5 meropenem-nonsusceptible BSIs were detected per year, and the maximum was 13 in 2019. Meropenem-nonsusceptible BSI incidence decreased 33% from the preintervention period to the postintervention period (IRR, 0.67; 95% CI, 0.31–1.42).

Our institutional neutropenic fever guideline has, since 2012, deemphasized use of carbapenems, with a general decrease in meropenem doses administered over the BSI study period (Supplementary Fig. 2 online). Compared to patients with meropenem-susceptible BSIs, fewer with meropenem-nonsusceptible BSI had ever received meropenem (28% vs 34%; *P* not significant). In the year prior to BSI, a roughly equivalent percentage received meropenem (21% vs 23%) (Supplementary Table 2 online).

Of the 39 BSIs that were present on admission, 30 (77%) of 39 were meropenem-susceptible. Of patients with BSI present on admission and prior stay on the BMT/HM unit, time since last discharge was associated with meropenem susceptibility ($P < .01$, Wilcoxon rank sum): median time from discharge was 5.5 days (IQR, 3–8; maximum, 20; n = 8) for patients with meropenem-nonsusceptible BSI, compared with 54 days (IQR, 10–216; maximum, 1,282; n = 25) for patients with meropenem-susceptible BSI.

Inactivating mutations in the *oprD* gene were observed in a broad sampling of the meropenem-nonsusceptible BSI isolates that were sequenced and included here (unpublished data) and reported in a prior study,[28] with no detection of carbapenemase genes.

WGS and phylogeny

ST-111, ST-446, and ST-308 were the sequence types (STs) identified from patient colonization samples (Table 1), as well as the predominant STs from environmental colonization samples (Table 2). For each patient colonized there was a contemporaneous environmental isolate of the same ST obtained from the corresponding room.

Of 48 ST-111 isolates, only 1 (BSI, October 2019) was widely divergent, differing by >4,500 single-nucleotide variants (SNVs) from any of the other sequences, whereas the remaining 47 differed by 45 or fewer SNVs. This divergent BSI isolate was excluded from subsequent analysis. Phylogenetic trees were constructed from 47 ST-111 sequences, 26 ST-446 sequences, and 9 ST-308 sequences (Fig. 3A–C). We detected considerable genomic conservation within groups. The phylograms depict clustering of relatedness by room and over time for a diversity of isolate sources. For example, the ST-111 phylogram depicts the close relationship of isolates recovered from room 30 patient and multisite environmental colonization sampling in the point-prevalence surveys as well as sequence conservation with and among BSI isolates from patients in room 30 over time. The analysis of within- and between-group differences revealed remarkable similarity among isolates obtained from our institution (Supplementary Fig. 3 online), again suggesting a common source for each ST group.

Superimposing WGS data on BSI incidence over time, we observed striking diminution in the formerly predominant ST-111, ST-308, and ST-446 outbreak strains (Fig. 4). If none of the 6 unknown ST isolates from October 2016 onward (ie, when we began characterizing BSI isolates by WGS) were outbreak-associated strains, the IRR would be 0.057 (95% CI, 0.008–0.419; $P < .01$), representing a 94% decrease. If, in the "worst case" scenario, all unknown ST BSI isolates were outbreak associated, the IRR would be 0.40 (95% CI, 0.17–0.92; $P = .031$), representing a 60% decrease.

Discussion

As reported in several other studies,[2,13,33] we found WWD colonization with *P. aeruginosa*, and specifically meropenem-nonsusceptible strains, to be widespread on our HCT/HM unit. Although it is difficult to discern from a point-prevalence survey whether environmental colonization is the cause or consequence of patient colonization, emerging evidence suggests that the former is frequently the case, specifically for MDR gram-negative bacteria from WWD sites.[34] Limiting transmission from WWD sites to patients should decrease patient colonization but might not influence the degree of environmental colonization. Moreover, we speculated that a decrease in patient colonization would, in turn, decrease BSI events.

As hypothesized, there was widespread environmental colonization with *P. aeruginosa* after the intervention, with all but 1 room yielding growth from 1 or more locations. Although bathroom sink drain colonization was nearly universal in both periods, there was a significant decrease in main sink drain colonization after the intervention. We speculate this to be a consequence of more stringent use restrictions for the main sink drain, whereas patients continued to use the bathroom sink for hygiene. Patient colonization was infrequent, with a numerical but not statistically significant decrease in the postintervention period.

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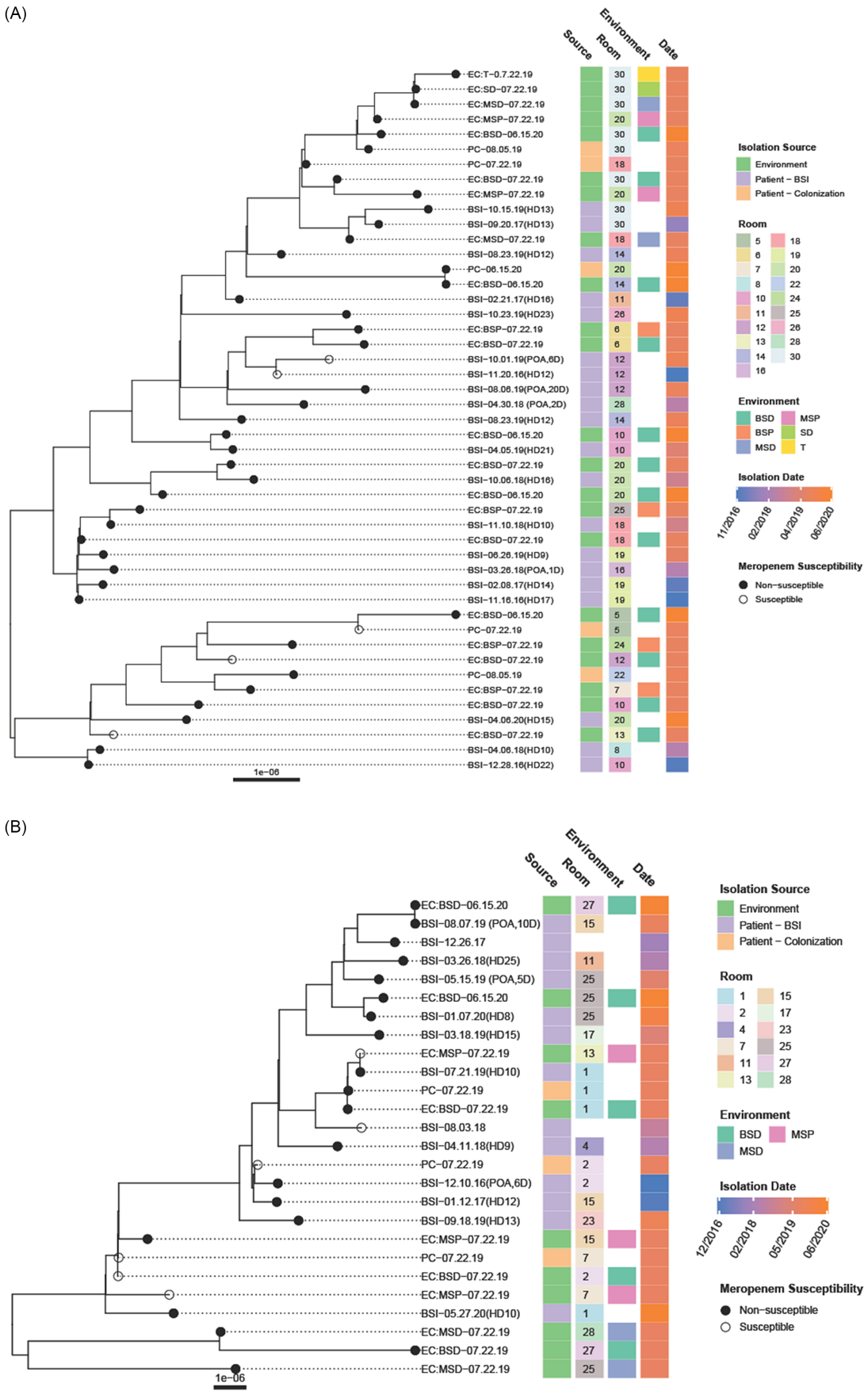

Figure 3. Phylogram of ST-111 isolates (A), ST-446 isolates (B), and ST-308 isolates (C). For bloodstream infection (BSI) isolates, the hospital day (HD) that the BSI occurred on is indicated in parentheses (ie, HD#), and the patient's room on the HCT/HM unit at the time of BSI is denoted. For BSIs that were present on admission (POA), the room on the HCT/HM unit that the patient was in during the most recent proximate HCT/HM unit stay is denoted, provided there was a prior stay on the unit. Note. BSI, bloodstream isolate; BSD, bathroom sink drain; BSP, bathroom sink P-trap; MSD, main sink drain; MSP, main sink P-trap; SD, shower drain; T, toilet rim; HD, hospital day; POA, present on admission.

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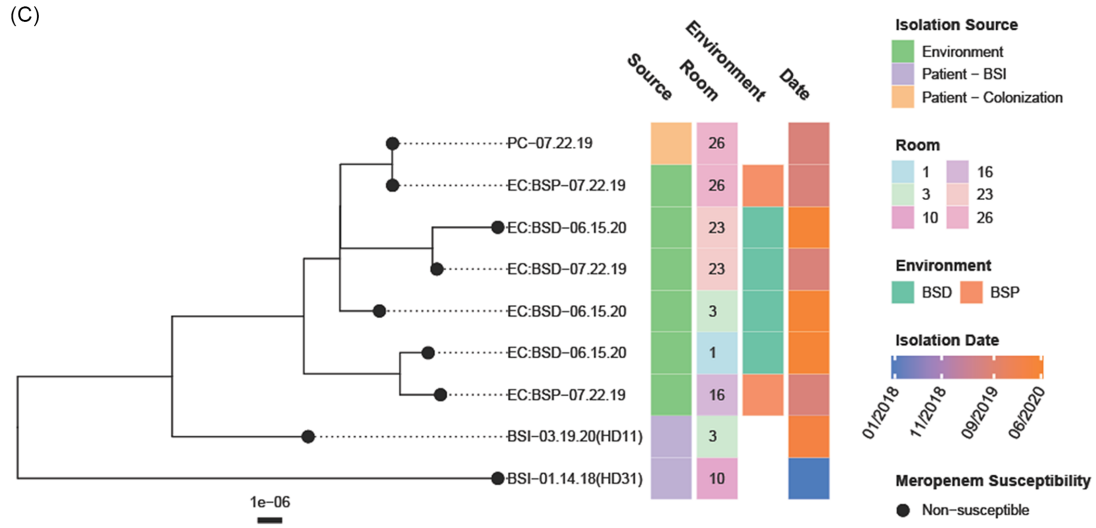

Figure 3. (Continued).

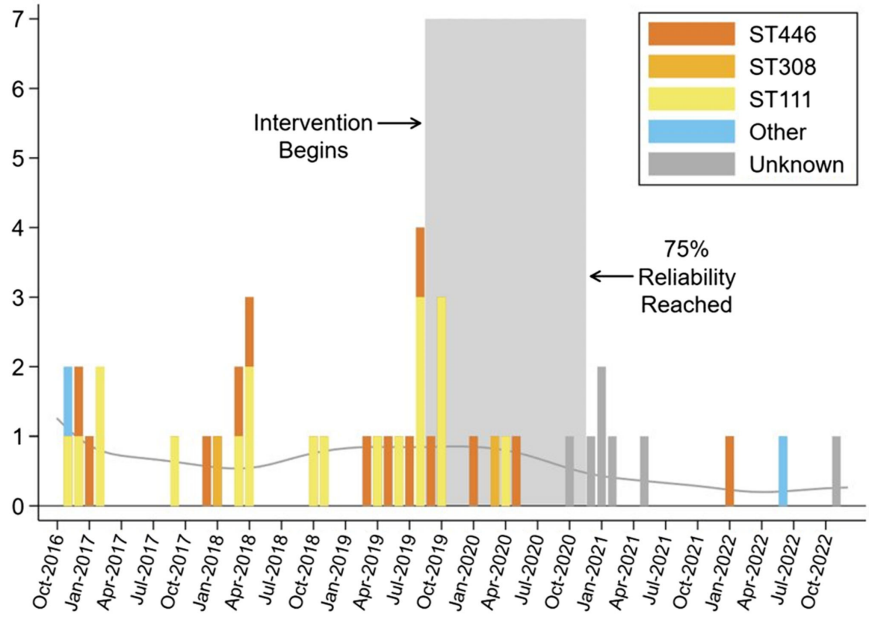

Figure 4. Monthly meropenem-nonsusceptible *P. aeruginosa* BSI events by sequence type, from start of sequencing October 2016 through December 2022.

Meropenem use was not associated with patient colonization with meropenem-nonsusceptible *P. aeruginosa*, again lending support to the hypothesis that acquisition of colonization or infection from an environmental source(s) is the critical and necessary first step.

Phylogenetic analysis of patient and environmental colonization isolates revealed a predominance of ST-111 and ST-446, as did the BSI isolates from patients evaluated in this and a prior study.[28] Although it is challenging to untangle environmental colonization as the source or byproduct of patient colonization or infection, genetic conservation between environmental and patient colonization, in particular when the former preceded the latter, provides evidence that the environment may be the source for at least some, if not many, instances of patient colonization and BSI.

We observed a substantial decrease in meropenem-nonsusceptible *P. aeruginosa* BSIs but not complete elimination. For the first time since 2017, most *P. aeruginosa* BSI isolates were meropenem-susceptible in 2022. The findings that fewer meropenem-nonsusceptible BSI patients than meropenem-susceptible BSI patients received meropenem prior to BSI event and that all but 1 patient with meropenem-nonsusceptible ST-111, ST-446 or ST-308 BSI had current or prior stay on the HCT/HM unit support the hypothesis that colonization and/or infection is acquired from the healthcare environment. Although BSI isolates were not uniformly characterized during the study period, the absence of ST-111 and ST-308 in 2022, despite widespread colonization of environmental sites with these strains in the postintervention period, is

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compelling. The changes we observed were felt to be causally related, in part or on the whole, to the intervention. Given the prolonged nature of the outbreak, several approaches to mitigation were undertaken prior to the intervention, including removal of faucet aerators in 2014, line-care standardization in 2018, and a protocol to decrease shower hose dependent loops in 2018, with no salutatory effect on meropenem-nonsusceptible BSI incidence.

This single-institution study has important limitations. Patient and environmental colonization was assessed in a small sample size, with a numerical but not statistically significant decrease in meropenem-nonsusceptible *P. aeruginosa* patient colonization. Patients on the unit at any given time may not accurately represent the colonization burden. Growth on Cetrimide agar was used as a surrogate for *P. aeruginosa* colonization. Although this selective medium has been used in other studies for this same purpose,[12,21] it was not entirely specific. Due to funding constraints, we were unable to pursue WGS characterization of all isolates. Although several distinct isolates with differing susceptibility phenotypes were cultured from many of the individual WWD sites surveyed, only a fraction were characterized by WGS, and preferentially those identified to be meropenem-nonsusceptible. Other studies have demonstrated the considerable genomic diversity of *P. aeruginosa* colonizing plumbing in the healthcare setting.[14,33] Our data do not comprise a comprehensive analysis of isolates colonizing WWD sites and patients in this study. Rather, our results provide insight regarding relatedness between colonization and BSI on an HCT/HM unit during and following a prolonged meropenem-nonsusceptible *P. aeruginosa* outbreak. Additional sampling and sequencing may inform more robust conclusions regarding relatedness of environmental, patient, and BSI isolates over time and location.

Lastly, our study spanned the coronavirus disease 2019 (COVID-19) pandemic. In alignment with institutional protocols we altered study procedures, and therefore sample collection was limited in the postintervention period. Patients with severe acute respiratory coronavirus virus 2 (SARS-CoV-2) infection were excluded from care on our HCT/HM unit, so it is unlikely that modifications in personal protective equipment use resulted in the changes we observed. However, the direct and indirect impacts of the COVID-19 pandemic are difficult to quantify. Notably, we observed a decrease in meropenem-nonsusceptible *P. aeruginosa* BSI in the face of near-universal increase in healthcare-associated infections nationally, including central-line–associated BSI and MDR infection, during the pandemic.[35,36]

In conclusion, following an intervention to limit transmission from WWD sites, we observed a meaningful decrease in patient colonization with meropenem-nonsusceptible *P. aeruginosa*. Nevertheless, environmental colonization remained widespread. We observed striking genetic conservation within ST groups as well as between environmental colonization, patient colonization, and BSI isolates, supporting our hypothesis that WWD sites are a source for propagation and transmission of meropenem-nonsusceptible *P. aeruginosa*. Over the follow-up period, we observed a substantial decrease in the rate of meropenem-nonsusceptible *P. aeruginosa* BSI events. Notably, in 11 months following completion of the study period, there has been a single meropenem-nonsusceptible *P. aeruginosa* BSI.

Based on initial successes, we adapted and disseminated this intervention to ICUs at our facility. We approached planning for a new oncology tower with situational awareness of WWD sites, ensuring that design features mitigate risk. Going forward, we will evaluate the sustainability of these improvements, with longer-term follow-up of the incidence of meropenem-nonsusceptible *P. aeruginosa* BSI events on our HCT/HM unit, as well as the incidence of infection with other waterborne bacteria on this and other units.

Supplementary material. For supplementary material accompanying this paper visit https://doi.org/10.1017/ice.2023.288

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Conflicts of interest. All authors report no conflicts of interest relevant to this manuscript.

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