Epidemiologic characteristics of health care–associated outbreaks and lessons learned from multiple outbreak investigations with a focus on the usefulness of routine molecular analysis

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Background: Single outbreaks have often been reported in health care settings, but the frequency of outbreaks at a hospital over time has not been described. We examined epidemiologic features of all health care–associated outbreak investigations at an academic hospital during a 5-year period.
Methods: Health care–associated outbreak investigations at an academic hospital (2012-2016) were retrospectively reviewed through data on comprehensive hospital-wide surveillance and pulsed-field gel electrophoresis (PFGE) analysis.
Results: Fifty-one health care–associated outbreaks (annual range, 8-15), including 26 (51%) outbreaks in intensive care units (ICUs), and 263 infected-colonized patients involved in these outbreaks were identified. The frequency of pathogens varied by affected location, specifically multidrug-resistant organisms (20/26 outbreaks, 77% in ICUs vs 2/25 outbreaks, 8% in non-ICUs; $P < .0001$) and gastroenteritis because of *Clostridium difficile*, norovirus, or adenovirus (1/26 outbreaks, 4% in ICUs vs 17/25 outbreaks, 68% in non-ICUs; $P < .0001$). Outbreaks occurred in approximately one-third of all units (37%) with some repeated instances of the same pathogens. Of 16 outbreaks caused by a bacterial pathogen evaluated by PFGE, 12 (75%) included some indistinguishable strains, suggesting person-to-person transmission or a common source.
Conclusions: This study demonstrated epidemiologic characteristics of multiple outbreaks between ICUs and non-ICUs and the value of molecular typing in understanding the epidemiology of health care–associated outbreaks.

Multiple pathogens, including viruses, bacteria, mycobacteria, and fungi, and multiple reservoirs-sources, including health care personnel, patients, visitors, surface environment, medical equipment, air, and water, have been involved in health care–associated outbreaks.[1-5] Health care–associated outbreaks not only may affect patients' morbidity and mortality but also may have severe repercussions in health care operations (eg, ward closure) with the need for time-consuming and potentially expensive interventions.[4]

Single outbreaks caused by a specific pathogen(s) and a source or reservoir have often been reported in hospitals. However, the burden of outbreaks on a hospital over time is still poorly understood. Although there are many publications of outbreak investigations in a single hospital,[4,6] they are likely to be substantially affected by publication bias with larger outbreaks, and those caused by novel reservoirs or routes of transmission, more likely to be published. In addition, concern about health care facility reputation and the risk of legal consequences may interfere with data sharing and obscure the real impact of outbreaks on daily practice in a health care facility.[6,7] To our knowledge, there are no published reports of multiple outbreaks caused by diverse pathogens at an academic medical center and the value of routine molecular typing of pathogens associated with an outbreak over time.

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In this study, we assessed all health care–associated outbreak investigations based on routine practice, examined the value of pulsed-field gel electrophoresis (PFGE) of pathogens involved in outbreaks, and reviewed lessons learned from these multiple investigations at an academic hospital during a 5-year period.

METHODS

This analysis was conducted at an 853-bed tertiary care academic facility with 41 inpatient nursing units. Health care–associated outbreak investigations at our hospital from 2012-2016 were retrospectively reviewed through an institutional health care–associated infection (HAI) database and monthly reports to the hospital infection control committee. Using a laboratory-based pathogen detection system to conduct comprehensive hospital-wide surveillance, outbreak investigations were triggered by an increase in number of infections or pathogens above baseline rate in a unit during a specified period of time; an investigation may also have been triggered by a single case of a rare and epidemiologically important pathogen.[4] In this study, the number of potential health care–associated outbreaks was counted as the number of the corresponding outbreak investigations, including one with only a single case (ie, *Legionella*). Additionally, a health care–associated outbreak identified by molecular typing was defined as (1) cases that overlapped time and space and (2) at least 2 isolates linked by PFGE. Contact tracing associated with exposure investigations of a single patient (eg, varicella, tuberculosis) with a communicable disease were excluded from analysis. Variables in the outbreak investigations included year, duration of outbreak, location, pathogen, presence or absence of HAI, type of specific HAI, number of patients infected-colonized, number of health care personnel involved, presence or absence of PFGE with number of isolates and number of different patterns when PFGE was performed, and brief summary of infection control measures and interventions.

Comprehensive hospital-wide surveillance for all HAIs, including all sites defined by the Centers for Disease Control and Prevention, was conducted through a chart review of each patient in accordance with the Centers for Disease Control and Prevention criteria.[8] Our HAI surveillance included components of laboratory reports of positive culture results, results of serologic testing or molecular-based diagnostic tests, clinical reports of infections, morbidity and mortality conferences, and autopsies. HAIs are classified into one of the following 5 major infections with 14 specific infection sites: bloodstream infections, urinary tract infections, respiratory tract infections (pneumonia and lower respiratory tract infections), surgical site infections, and other type of HAIs (gastrointestinal infections; eye, ear, nose, throat, or mouth infections; skin and soft-tissue infections; cardiovascular system infections; bone and joint infections; central nervous system infections; reproductive tract infections; and systemic infections). All surveillance data of HAIs and outbreak investigations during the study period were entered into an electronic database. This study was approved by the Institutional Review Board of University of North Carolina at Chapel Hill.

PFGE was performed for selected bacterial pathogens based on likelihood of an epidemiologic link (eg, >3 pathogens overlapping in time and location). We reviewed all PFGE analyses performed during the study period. Environmental sampling of the hospital and hand sampling of health care personnel depended on ongoing situation of an outbreak or type of pathogen.

Statistical analyses were performed by 2-tailed Fisher test using JMP 11 (Statistical Analysis System, Cary, NC); $P \leq .05$ was considered to be statistically significant.

RESULTS

Fifty-one health care–associated outbreaks (annual range, 8-15), including 26 (51%) outbreaks in ICUs and 25 (49%) outbreaks in non-ICUs, were identified during the study period. The annual number of outbreaks was almost constant except for 2015 with an increase in gastroenteritis, whereas epidemiologic features (eg, pathogen type) in these outbreaks substantially differed by year (Fig 1). Outbreaks occurred in 15 units (36.6% of all 41 inpatient units). Of the 26 outbreaks in ICUs, 12 (46.2%) and 7 (26.9%) occurred in the burn ICU and the neonatal ICU, respectively. Of the 25 outbreaks in non-ICUs, 6 (24%) occurred in the bone marrow transplant unit. An outbreak of *Stenotrophomonas maltophilia* involved multiple nursing units. Overall, 30 (58.8%) outbreaks were terminated within 1 month, whereas 4 (7.8%) continued for >6 months (ie, 1 methicillin-resistant *Staphylococcus aureus* [MRSA] outbreak in the neonatal ICU, 1 carbapenem-resistant *Enterobacteriaceae* [CRE] outbreak in the burn ICU, 2 multidrug-resistant *Pseudomonas* outbreaks in the burn ICU). The frequency of outbreaks sustained over 2 months was significantly higher in ICUs than in non-ICUs (Table 1), and the burn ICU accounted for 52.6% (10/19) of these prolonged outbreaks in ICUs.

The frequency of pathogens varied greatly by affected location, specifically multidrug-resistant organisms (MDROs) in ICUs (MRSA, CRE, and multidrug-resistant *Pseudomonas aeruginosa*) and gastroenteritis in non-ICUs (*Clostridium difficile*, norovirus, and adenovirus) (Fig 2, Table 1). Of 34 bacterial outbreaks, an MDRO (22 outbreaks, 64.7%) was the most frequent, followed by *C difficile* (7 outbreaks, 20.6%). Eleven viral outbreaks included 7 (63.6%) norovirus gastroenteritis, 2 adenovirus gastroenteritis, 1 enterovirus meningitis, and 1 influenza respiratory infection, whereas 75% of all fungal outbreaks (3/4) were caused by *Rhizopus* spp. A pseudo-outbreak of *Ralstonia insidiosa* via a contaminated sonicator occurred in a laboratory during the study period. The frequency of outbreaks of repeated pathogens at the same location was 63%, and outbreaks in ICUs significantly tended to reoccur more commonly than those in non-ICUs (Table 1).

Of the 51 outbreaks, 47 (92.2%) resulted in HAIs. Gastroenteritis (n = 18, 35.3%) was the most common type of infection, followed by pneumonia (n = 9, 17.6%), bloodstream infection (n = 8, 15.7%), and skin and soft-tissue infection (n = 8, 15.7%), whereas there were no HAIs identified in 4 (7.8%) investigations. The type of HAIs differed significantly within or outside an ICU (Table 1). Overall, 263 infected-colonized patients (median, 4; range, 1-20) were involved in health care–associated outbreaks. There was no statistical

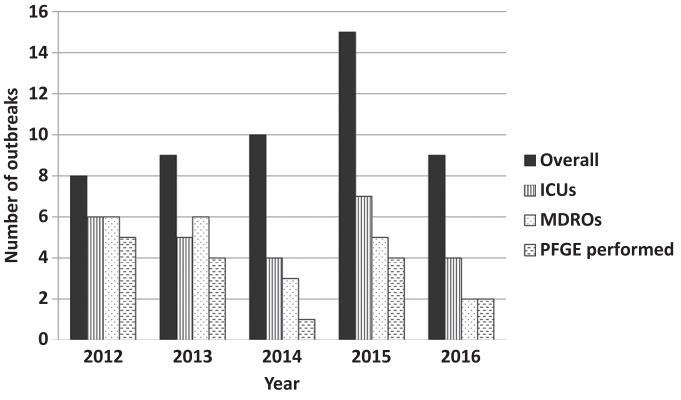

Fig 1. Annual trends in health care–associated outbreak investigations at an academic hospital, 2012-2016. *ICU*, intensive care unit; *MDRO*, multidrug-resistant organism; *PFGE*, pulsed-field gel electrophoresis.

Table 1
Epidemiologic characteristics of health care–associated outbreaks at an academic hospital, 2012-2016

Characteristic	Overall (N = 51)		ICUs (n = 26)		Non-ICUs (n = 25)		ICUs vs non-ICUs
	n	%	n	%	n	%	*P* value*
Duration							
>2 mo	21	41	19	73	2	8	<.0001
Pathogen							
MDRO	22	43	20	77	2	8	<.0001
Clostridium difficile	7	14	0	0	7	28	.0042
Norovirus	7	14	0	0	7	28	.0042
Repeated pathogen at same location	32	63	23	88	9	36	.0001
Infection type							
Any HAI	47	92	23	88	24	96	
Pneumonia	9	18	8	31	1	4	.0238
Lower respiratory tract infection	6	12	6	23	0	0	.0226
Bloodstream infection	8	16	7	27	1	4	.0496
Urinary tract infection	3	6	2	8	1	4	
Surgical site infection	3	6	2	8	1	4	
Gastroenteritis	18	35	1	4	17	68	<.0001
Skin and soft-tissue infection	8	16	7	27	1	4	.0496
Population							
>4 patients involved in an outbreak	29	57	16	62	13	52	
>2 staff involved in an outbreak	9	18	1	4	8	32	.0109
Genotyping							
PFGE performed	16	31	14	54	2	8	.0006
Control measure							
Isolation or cohorting	37	73	18	69	19	76	
Enhanced hand hygiene	20	39	12	46	8	32	
Enhanced cleaning-disinfection	29	57	11	42	18	72	.0483
Modification of care or equipment	21	41	13	50	8	32	
Patient screening or surveillance	14	27	13	50	1	4	.0003
Closure of affected location	7	14	0	0	7	28	.0042
Restriction of work	7	14	0	0	7	28	.0042

HAI, health care–associated infection; *ICU*, intensive care unit; *MDRO*, multidrug-resistant organism; *PFGE*, pulsed-field gel electrophoresis.
*P values are shown only when $P \leq .05$.

difference in the number of patients per outbreak between ICUs and non-ICUs, but health care personnel were significantly more likely to be involved in outbreaks in non-ICU epidemics (Table 1).

Of 16 outbreaks caused by a bacterial pathogen (total of 99 bacteria isolates; median, 4.5; range, 2-20) evaluated by PFGE, including 13 (81.3%) outbreaks caused by an MDRO, 12 (outbreaks demonstrated by PFGE, 75%) included some indistinguishable strains, suggesting person-to-person transmission or a common source, whereas 4 (outbreaks differed by PFGE, 25%) demonstrated only unique strains (Table 2). Of 12 PFGE clonal outbreaks, 11 (91.7%) were implicated in HAIs, whereas there were no HAIs identified during a vancomycin-resistant enterococci outbreak in the 2013 bone marrow transplant unit. All 4 PFGE different outbreaks caused HAIs. PFGE were more frequently performed in ICU outbreaks than in non-ICU outbreaks (Table 1).

Hand sampling from health care personnel was conducted in a prolonged investigation of MRSA in a neonatal ICU which revealed that health care personnel hands at times carried the outbreak strain, suggesting deficiencies in hand hygiene compliance. Environmental sampling was performed in 3 investigations during the 5-year period. Outbreak 1 (with air sampling) involved invasive cutaneous *Rhizopus* infections among immunocompromised patients in the ICU because of contaminated laundry carts.[9] Outbreak 2 (with water sampling) involved susceptible *P aeruginosa* surgical site infections in a neurosurgical ICU; all 4 patients had *P aeruginosa* strains indistinguishable with those isolated from a sink aerator within the ICU. Outbreak 3 (with water sampling) involved nontuberculosis mycobacteria skin infection at a dermatology clinic; *Mycobacterium mucogenicum* was isolated from a water sample, but multiple different nontuberculous mycobacteria species (2 cases of *Mycobacterium chelonae* and 2 cases of *Mycobacterium abscessus*) were involved in the outbreak, and our investigation did not reveal a possible environmental source.

Infection control measures varied for each outbreak, and multiple measures were often implemented simultaneously. The most frequent enhanced infection control measure implemented was isolation or cohorting (n = 37, 72.5%), followed by enhanced cleaning-disinfection (eg, disinfection with bleach) (n = 29, 56.9%), modification of care or equipment (n = 21, 41.2%), and enhanced hand hygiene education (n = 20, 39.2%) (Table 1). Importantly, 7 (13.7%) outbreak investigations led to closure of the affected location (norovirus: n = 4, other gastroenteritis: n = 1, influenza: n = 1, and vancomycin-resistant enterococci: n = 1) and restriction of health care personnel working off the affected unit (norovirus: n = 6 and *C difficile*: n = 1). Besides enhanced cleaning-disinfection, a ultraviolet-C (UV-C) device was used for terminal disinfection in 3 outbreaks (5.9%) because of vancomycin-resistant enterococci, *C difficile*, or norovirus. Affected locations in non-ICUs were more frequently closed to new admissions as part of enhanced infection prevention efforts because patients in non-ICUs were commonly mobile and pathogens causing these outbreaks (eg, norovirus, *C difficile*, influenza) tended to be spread from person-to-person.

DISCUSSION

This study characterized the epidemiology of multiple outbreaks over time at a single academic hospital. We have previously described at our hospital substantial reductions in overall HAIs, especially HAIs in ICUs, through comprehensive hospital-wide surveillance (2001-2012).[10] On the other hand, there were still substantial numbers of outbreak investigations during the study period (2012-2016); however, the data do not exist to assess how this compares with other similar facilities. MDROs were the most frequent pathogen in health care–associated outbreaks in this study, and MRSA accounted for half of the MDRO outbreaks. Half of all outbreaks occurred in ICUs, most commonly in the burn ICU and

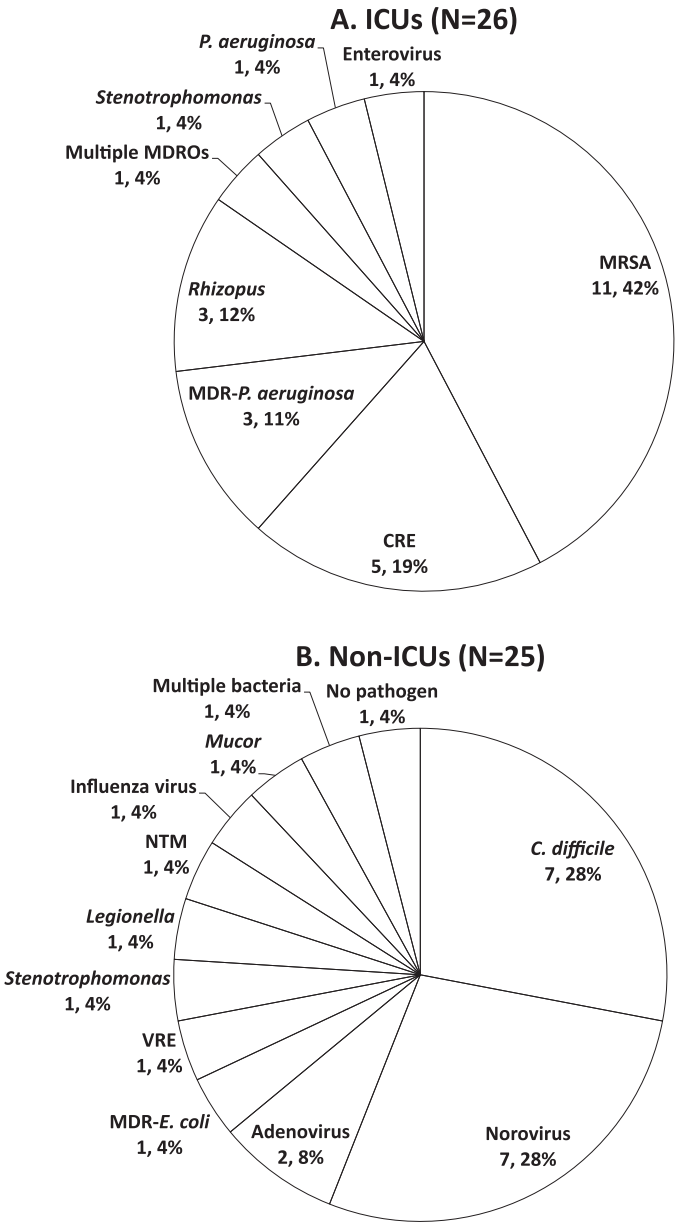

Fig 2. Frequency of pathogens involved in health care–associated outbreak investigations in ICUs (A) and non-ICUs (B) at an academic hospital, 2012-2016. *CRE*, carbapenem-resistant *Enterobacteriaceae*; *ICU*, intensive care unit; *MDR*, multidrug resistant; *MDRO*, multidrug-resistant organism; *MRSA*, methicillin-resistant *Staphylococcus aureus*; *No pathogen*, an investigation for patients with gastrointestinal symptom has not identified a causative pathogen; *NTM*, nontuberculous mycobacteria; *VRE*, vancomycin-resistant enterococci.

neonatal ICU. Importantly, outbreaks occurred in approximately one-third of all units with some repeated instances of the same pathogens, therefore demonstrating the importance of facility-wide comprehensive surveillance for HAIs. Because we perform hospital-wide surveillance, we do not think the distribution of our outbreaks was biased by selective surveillance. We also found significant differences in health care–associated outbreaks between ICUs and non-ICUs. Assessing epidemiologic trends of outbreaks over time can help health care facilities direct surveillance and prevention strategies against health care–associated outbreaks toward these specific types of HAIs, pathogens, and affected locations.

The most common outbreaks in this study were MRSA in the neonatal ICU (n = 6), MDROs in the burn ICU (n = 12), and norovirus in non-ICU units (n = 7). Neonates have immature immune systems and are vulnerable to HAIs, and neonatal ICUs are a high-risk setting for health care–associated outbreaks.[4,11] Severe patients with burn injury are associated with outbreaks of MDRO that can lead to morbidity and mortality in this population and challenges for infection prevention and control.[12-14] In both neonates and burn patients, use of multiple invasive devices and contact with multiple health care personnel are common. Norovirus is a leading cause of gastroenteritis in settings where rotavirus immunization is implemented, and its outbreaks are often associated with genogroup II type 4 strains, posing a major burden in health care facilities.[4,15,16]

C difficile was also an important pathogen associated with outbreaks, especially in a bone marrow transplant unit, and our previous study showed that *C difficile* infection has been our most common health care–associated pathogen in our facility.[10] Leukemia patients were at a higher risk of *C difficile* infection and have been reported to be associated with increased mortality in their cases of *C difficile* infection.[17] Transmission of *C difficile* infection was thought to be predominant in health care settings, and infection prevention efforts were prioritized on symptomatic patients, and the substantial portion of *C difficile* isolates from symptomatic patients was genetically distinguishable by whole-genome sequencing (WGS), suggesting diverse sources of *C difficile*, including asymptomatic patients and environment.[18]

PFGE has been widely used as the gold standard for strain typing[4] and has provided useful information in confirming or refuting epidemiologic links for MDRO outbreak investigations in our study (Table 2). Recognizing outbreak status demonstrated by PFGE can lead to reeducation of health care personnel to enhance infection control measures such as hand hygiene, environmental cleaning-disinfection, and disinfection of shared medical equipment. It may also lead to consideration of a common source or reservoir. Moreover, when initial PFGE results indicate that clinical isolates are indistinguishable, additional sampling (eg, environmental or hand sampling) can be considered.

PFGE has advantages and disadvantages. PFGE is advantageous to multiple cases by certain pathogen (eg, MDROs), prolonged outbreaks, and outbreaks via environmental source. Disadvantages of PFGE include that the method is labor-intensive, time-consuming, and moderately technically demanding, and PFGE can have discrepancy in reproducibility and interpretation among personnel and facilities.[19] An additional research investigation in our hospital using WGS revealed that CRE outbreaks at the burn ICU, which seemed epidemiologically unlinked, were actually genetically linked over a prolonged period and were driven by multiple mechanisms of resistance transmission among same or different species, affirming other studies that WGS has become a better method for advanced molecular typing in outbreak investigations compared with PFGE.[13,14,19,20]

In a few of our investigations, environmental sampling contributed to identifying a potential reservoir or source of outbreaks. Environmental sampling can be considered in some outbreak investigations but is not routinely recommended, and standard environmental sampling method and interpretation of microbial results is not well established.[21] In our investigations, when outbreaks caused by a dominant strain of a certain pathogen (eg, gram-negative bacteria) among several patients continued for a prolonged time or were considered to be typical of a point source outbreak related to the hospital environment and medical equipment, environmental sampling was performed. In a prolonged outbreak (eg, MRSA), hand sampling of health care personnel was performed to emphasize the importance of hand hygiene.

Most outbreaks in this study were terminated rapidly by enhanced control measures. Unit closure and work restriction severely affect operation of health care facilities, and commonly norovirus

Table 2
Summary of health care–associated outbreaks evaluated by PFGE at an academic hospital, 2012-2016

Location	Duration (mo)	Pathogen	HAI	No. of patients involved	No. of staff involved	No. of isolates on PFGE	No. of different PFGE patterns	Environmental or hand sampling	Control measure in addition to standard practice
Burn ICU	12	MDR *P. aeruginosa*	VAP, LRI	20	0	10	3*	No	Isolation or cohorting, enhanced hand hygiene, enhanced cleaning-disinfection, modification of care or equipment, patient screening or surveillance
Neonatal ICU	4	MRSA	SST	5	0	7	2*	No	Isolation or cohorting, patient screening or surveillance, enhanced hand hygiene, enhanced cleaning-disinfection
BMTU, unit A, unit B	≤1	*Stenotrophomonas maltophilia*	CLABSI	4	0	4	4	No	Not required
Neurosurgical ICU	2	MRSA	RTI	6	0	4	2*	No	Enhanced hand hygiene, modification of care or equipment
Neonatal ICU	2	MRSA	SSI, BSI, conjunctivitis	7	0	2	2	No	Isolation or cohorting, patient screening or surveillance, enhanced hand hygiene, enhanced cleaning-disinfection
BMTU	≤1	VRE	No (colonization)	8	0	8	5*	No	Closure of affected location, isolation or cohorting, enhanced cleaning-disinfection, modification of care or equipment, use of UV-C device
Neonatal ICU	11	MRSA	SST, VAP, BSI	12	29	20	4*	Hand sampling	Isolation or cohorting, patient screening or surveillance, modification of care or equipment, enhanced hand hygiene, enhanced cleaning-disinfection
Neurosurgical ICU	≤1	MRSA	RTI	5	0	5	3*	No	Isolation or cohorting, enhanced hand hygiene, enhanced cleaning-disinfection
Burn ICU	3	CRE (*Enterobacter* sp)	VAP, LRI	4	0	4	1*	No	Enhanced hand hygiene, enhanced cleaning-disinfection
Burn ICU	≤1	MRSA	LRI	3	0	3	3	No	Not required
Burn ICU	2	MRSA	VAE, VAP, CLABSI	4	0	4	3*	No	Isolation or cohorting, enhanced hand hygiene, enhanced cleaning-disinfection
Burn ICU	4	MDROs†	HAIs‡	9	0	2 (MRSA)	2	No	Enhanced hand hygiene, enhanced cleaning-disinfection, isolation or cohorting, modification of care or equipment
Neonatal ICU	3	MRSA	CLABSI, BSI, GI	12	0	8	4*	No	Patient screening or surveillance, isolation or cohorting
Medical ICU	2	*S maltophilia*	VAP	7	0	4	3*	No	Enhanced hand hygiene
Neurosurgical ICU	3	*Pseudomonas aeruginosa* (susceptible)	SSI	4	0	7	4*	Environmental sampling with water sampling	Modification of care or equipment
Burn ICU	3	MRSA	Pneumonia, SST, UTI, BJ	5	0	7	3*	No	Isolation or cohorting, enhanced hand hygiene

BJ, bone and joint infection; *BMTU*, bone marrow transplant unit; *BSI*, bloodstream infection; *CLABSI*, central line–associated bloodstream infection; *CRE*, carbapenem-resistant *Enterobacteriaceae*; *GI*, gastrointestinal infection; *HAI*, health care–associated infection; *ICU*, intensive care unit; *LRI*, lower respiratory tract infection; *MDR*, multidrug resistant; *MDRO*, multidrug-resistant organism; *MRSA*, methicillin-resistant *Staphylococcus aureus*; *PFGE*, pulsed-field gel electrophoresis; *RTI*, respiratory tract infection; *SSI*, surgical site infection; *SST*, skin and soft-tissue infection. *UTI*, urinary tract infection; *UV-C*, ultraviolet-C; *VAE*, ventilator-associated event; *VAP*, ventilator-associated pneumonia; *VRE*, vancomycin-resistant enterococci.
*PFGE results include at least 2 linked isolates.
†MDROs include MDR *Enterobacter cloacae*, MDR *Proteus mirabilis*, MRSA, CRE, MDR *Acinetobacter*, and MDR *P aeruginosa*.
‡HAIs include VAP and BSI with MRSA, and SST with MDR *P aeruginosa*, but no HAIs with *Escherichia coli*.

outbreaks resulted in these extreme measures.[22] In addition to enhanced environmental cleaning-disinfection, an ultraviolet-C device was used in a few instances. Increasing experimental and clinical evidence for patient room disinfection using an ultraviolet-C device has demonstrated their efficacy against health care–associated pathogens.[23,24]

One limitation is that our analysis was conducted at a single academic hospital and may not be generalizable to other health care facilities. There are no standard criteria for a specific number of cases to define a health care–associated outbreak and compare multiple outbreaks, and there are limited articles reporting in a standardized structure even in published outbreaks.[6] Stone et al proposed the outbreak reports and intervention studies of nosocomial infection statement using a comprehensive checklist and summary table to improve the quality of describing these reports and studies transparently.[25] Reporting outbreaks in a well-organized and transparent manner and sharing lessons learned from outbreak investigations is essential because designing a high quality of outbreak investigations, including randomized controlled trials, is difficult or impossible (ie, most outbreaks were reported by case reports and authors' interest). It is also necessary to devise practical epidemiologic indicators for evaluating an actual status of health care–associated outbreaks that may not have been published in most cases. In our facility, only a few outbreaks which occurred during the study period have been published so far.[9,14] Another limitation is that few investigations determined reservoirs, sources, and transmission routes because most outbreaks were addressed before environmental or hand sampling was implemented and infection control measures were prioritized as a practice.

In conclusion, this study demonstrated significant differences in epidemiologic characteristics of multiple health care–associated outbreaks between ICUs and non-ICUs. Our analysis also provided insight into the usefulness of routine molecular analysis in assessing the transmission of MDROs and understanding the epidemiology of outbreaks. These findings are important to implement appropriate infection prevention strategies against health care–associated outbreaks and avoid prolonged transmission. Further pragmatic approaches and research to improve comparability in descriptions of outbreaks (eg, developing meaningful definition of a health care–associated outbreak, establishing comparable epidemiologic indicators of intra- and intertransmission of pathogens causing an HAI) will be needed.

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