American Journal of Infection Control 40 (2012) 562-4

Contents lists available at ScienceDirect

American Journal of Infection Control

journal homepage: www.ajicjournal.org

Brief report

Hospital bath basins are frequently contaminated with multidrug-resistant human pathogens

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Key Words:
Hospital-acquired infection
MDR
MDRO
Nosocomial
HAI

The hospital environment is increasingly recognized as a reservoir for hospital-acquired pathogens. During a 44-month study period, a total of 1,103 basins from 88 hospitals in the United States and Canada were sampled. Overall, 62.2% of the basins (at least 1 basin at each hospital) were contaminated with commonly encountered hospital-acquired pathogens.

Hospital-acquired infection (HAI) is the most common complication among hospitalized patients[1] and is among the top 10 leading causes of death in US hospitals.[2] A recent point prevalence study that included 14,414 patients in 1,265 intensive care units (ICUs) from 75 countries found that 51% of patients residing in an ICU at the time of survey were infected, the vast majority with an HAI.[3] The institution of mandatory reporting of HAI rates in some institutions and decreased reimbursement for many HAIs have increased hospitals' motivation to reduce HAI rates in efforts to improve patient safety and clinical care, reduce hospital costs, and improve their reputation.[4] The hospital environment has been increasingly recognized as an important reservoir for nosocomial pathogens and an important factor in the spread of pathogens in hospital settings.[5] Many items commonly used in the routine care of hospitalized patients have been described as reservoirs for and/or vectors in the transmission of pathogens that can lead to nosocomial outbreaks.[5]

Bath basins are commonly used in the care of patients in ICUs, medical-surgical wards, and regular patient wards. The role of bath basins as reservoirs for hospital-acquired pathogens has not been well described, though a small study that sampled 90 bath basins reported a 98% contamination rate.[6] The aim of the present study was to investigate on a large scale in multiple, diverse hospitals the frequency with which bath basins are contaminated with pathogens that commonly lead to nosocomial infections and outbreaks.

METHODS

Study setting and design

This prospective, multicenter trial was conducted between July 2007 and February 2011 in the United States and Canada. Both community and tertiary university-affiliated medical centers participated (Table 1). Local infection preventionists cultured the first 10 basins that they encountered when entering a unit (ie, the convenience sample) using a uniform standardized sampling method. This method involved wiping the entire interior surface of the basin edges, using both sides of a sterile sponge. Each basin was sampled once.

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This study was presented in part at the Society of Critical Care Medicine's 40th Critical Care Congress (abstract 2558), San Diego, California, January 2011 and the Society for Healthcare Epidemiology of America's 21st annual meeting (abstract 4354), Dallas, Texas, April 2011.

Sage Products Inc was responsible for study design, funding of the antimicrobial processing, and recruitment of centers to participate in the study. All culture processing was conducted at an external laboratory; no Sage Products Inc personnel were involved in the processing of cultures or analysis of the results obtained. None of the authors received any financial or other type of support from Sage Products Inc to complete this study.

Conflict of interest: None to report.

doi:10.1016/j.ajic.2011.07.014

Table 1
Distribution of participating hospitals per number of inpatient beds (n = 87)

Hospital size	Inpatient beds	Hospitals in each category
Small	≤200	23
Medium	201-500	47
Medium-large	501-750	14
Large	≥751	3

NOTE. Data on bed number were not available for 1 participating hospital.

At the time of culture, the basins were not visibly contaminated and were considered "clean" and ready for immediate use. Basins from both ICUs and floors were cultured. At all centers participating in the study, basins were rinsed with tap water and soap between uses, in accordance with local infection control policies. No antiseptic agents were used to disinfect the basins between uses. Basins swabbed in the study were supposed to have been stored in a designated spot in the patient room and to have not been shared between patients. On discharge, a basin was either sent out with the patient or discarded. Basins that were shared among different patients (such as those used in some study hospital operating rooms) were excluded from the study. No study basins underwent high-level disinfection or sterilization. No patient information was obtained, and waivers of Institutional Review Board approval were obtained.

Microbiology

The sponges used for culturing and all of the microbiological processing were provided by an external central laboratory (Advanced Testing Laboratory, Cincinnati, OH) that was blinded to the origin of samples. Each basin was sampled with a sponge prewetted with 10 mL of buffer. Each sponge was then placed in an individual sterile bag and shipped overnight to the laboratory. All samples were received in the laboratory within 24-36 hours. No transport medium was used. On receipt in the laboratory, approximately 20 mL of trypticase soy broth was introduced into each bag, and each sponge was thoroughly manipulated to release organisms. The sponge and enrichment fluid were incubated for 48 ± 4 hours at 35°C ± 2°C and streaked onto selective/differential agars for isolation of aerobic gram-negative bacilli, *Enterococcus* species, vancomycin-resistant enterococci (VRE), *Staphylococcus aureus*, and methicillin-resistant *S aureus* (MRSA). The aerobic gram-negative bacilli were identified by growth on MacConkey agar and confirmed by Gram stain. Enterococci were initially identified on m-*Enterococcus* agar, then confirmed as gram-positive cocci on Gram stain and by catalase testing (with negative results consistent with identification of enterococci). Enterococci were then streaked onto a brain-heart infusion agar with vancomycin (6 μg/mL) to identify VRE. *S aureus* was screened on a mannitol salt Baird-Parker agar (BD, Heidelberg, Germany), then confirmed as gram-positive cocci on Gram stain. Isolates underwent latex testing (a positive test was consistent with identification of *S aureus*) and were confirmed as coagulase-positive. The *S aureus* isolates were then streaked onto oxacillin resistance screening agar to identify MRSA. All bacteriologic processing was conducted in accordance with Clinical and Laboratory Standards Institute criteria.[7]

RESULTS

During the study period, a total of 1,103 basins were sampled from 88 different hospitals in 27 US states and 4 Canadian provinces. The mean number of basins sampled at each participating hospital was 10 ± 2 (median, 10; range, 2-24). As shown in Table 2, 686 basins (62.2%) were contaminated with 1 or more study pathogens. All hospitals participating in this study had at least 1 basin that was contaminated with 1 or more study pathogens. Gram-negative bacilli were the most frequent type of bacteria isolated, followed by enterococci and *S aureus* (Table 2). Of the 414 *Enterococcus* species isolated, 385 (93%) were VRE, and 36 of the 40 (90%) *S aureus* strains were MRSA. A total of 426 basins (38.6%) were contaminated with a single study pathogen, 243 basins (22%) were contaminated with 2 study pathogens, and 17 basins (1.6%) were contaminated with all 3 study pathogens.

Table 2
Prevalence of isolations of certain pathogens commonly associated with hospital-acquired infections from bath basins

Pathogen	Positive basins (1103 basins sampled)	Positive hospitals (88 hospitals participating)
Any growth*	686 (62.2)	88 (100)
Gram-negative bacilli	495 (44.9)	86 (97.7)
S aureus (n = 40)		
Methicillin-susceptible *S aureus*	4 (0.4)	4 (4.5)
MRSA	36 (3.3)	28 (31.8)
Enterococcus spp (n = 414)		
Vancomycin-susceptible enterococci	29 (2.7)	14 (15.9)
VRE	385 (34.9)	80 (90.9)

NOTE. Data are presented as number (%) of the total number (denominator) listed in the column heading.
*Growth of only any of the following was included: *Enterococcus* spp (not necessarily resistant to vancomycin), *S aureus* (not necessarily resistant to methicillin), or gram-negative bacilli.

DISCUSSION

In this large, prospective study that included rural community and tertiary university-affiliated centers in multiple regions across North America, almost 2/3 of the bath basins studied were found to harbor at least 1 pathogen commonly associated with HAIs. One or more basins were contaminated in all 88 hospitals that participated in this study. These contaminated basins were found in ICUs, medical-surgical wards, and regular non-ICU wards. The specific groups of pathogens identified are not only common causative organisms in HAIs, but also include multidrug-resistant organisms (MDROs), such as VRE and MRSA, which pose particular treatment and management challenges to both clinicians and infection control professionals.

The most common source of contamination of bath basins is likely patients, and basins likely become contaminated during bathing. Basins are also used for incontinence cleanup, indwelling catheter care, and emesis collection. Other potential sources of contamination may include the soap, the soap tray,[8] and the tap water used to wash the patient or clean the basin.[9] In addition, transfer of pathogens can occur when medical equipment or supplies are stored in basins. Regardless of the source of contamination, basins are common reservoirs for bacterial pathogens. Pathogens from the environment can contaminate a basin and contribute to horizontal transmission, regardless of the patient's own flora.[10] The use of basins should be limited to the extent possible, to eliminate a potentially hazardous environmental reservoir for serious nosocomial pathogens. It may be considered ironic that we are "cleaning" patients with a contaminated object. Although some items, such as bed linens, are changed frequently, basins are often not replaced throughout a patient's entire hospital stay.

Basins should be considered as potentially contaminated with nosocomial pathogens, including MDROs. Hand hygiene should be performed after handling basins, and when contact with basins is anticipated, glove use seems prudent. Basins should be approached

and handled in the same manner as patients known to be carriers of MDROs. In addition, medical equipment and supplies should not be stored in basins. Unfortunately, storage of medical equipment in bath basins is a common practice in many hospitals. Any equipment stored in basins should be considered contaminated.

This study has identified bath basins as a reservoir and possible source for the spread of nosocomial MDROs. Detailed molecular investigations of the genetic similarity of strains carried by patients and strains isolated from basins will add validity to the hypothesis that patient-to-patient transmission of pathogens occurs through exposure to contaminated bath basins.

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