RESEARCH BRIEFS

Colonization with *Staphylococcus aureus* and Methicillin-Resistant *S. aureus* among a Sample of Homeless Individuals, Ohio

There is growing consensus that community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) plays an important role in infections both in the community and in the healthcare setting.[1] Risk factors for healthcare-associated MRSA have been well studied, but less is known about the risk for colonization with *S. aureus* or MRSA in the community.

Because they share crowded, often unsanitary living conditions, typically manifest poor underlying health, and have limited access to hygiene facilities and healthcare services, individuals who are homeless may have an increased risk for MRSA colonization. The aim of this study was to investigate the prevalence of *S. aureus* and MRSA colonization among a population of homeless individuals and to determine risk factors for *S. aureus* and MRSA colonization.

A prevalence study was conducted at 3 shelter locations in Columbus, Ohio (a men's emergency shelter, a women's emergency shelter, and a men's long-term shelter), and at a "Homeless Stand-Down," a multiday outreach event for homeless individuals in Cleveland, Ohio. At each site, participants were informed of the study by posters and flyers throughout the facility and self-referred to a private area where the study was conducted.

After providing written informed consent, participants were asked to complete a brief questionnaire on risk factors for *S. aureus* and MRSA colonization, including demographic characteristics, current health status, substance use, recent living arrangements, and hygiene practices. Nasal swab samples were collected from each participant with a dry, cotton-tipped applicator before and after instillation of normal saline (BBL CultureSwab; Becton Dickinson). Specimens were preincubated in a nonselective liquid media (BBL Trypticase Soy Broth, Becton Dickinson) at 37°C for 12 hours, and *S. aureus* was identified using routine microbiologic procedures. *S. aureus* isolates were subcultured on oxacillin resistance screening agar (ORSAB, Oxoid) for the identification of MRSA.

Overall prevalence rates were calculated using the SPSS statistical package, version 14 (SPSS). Assuming a baseline prevalence of 30%, a sample size of 215 was determined to provide a prevalence estimate with a margin of error of 6%. Differences between individuals who tested positive and individuals who tested negative for *S. aureus* and MRSA were compared using χ^2 tests and Student *t* tests. Logistic regression was used to build a model of predictor variables for MRSA colonization with variables that were significant at the $P < .10$ level. The effects of predictor variables were quantified by estimating prevalence odds ratios (ORs) and 95% confidence intervals (CIs).

Seventy-five (34.9%) of 215 participants had positive results for *S. aureus*. Of 71 tested *S. aureus* specimens, 55 (77.5%) were MRSA, for an overall estimate of MRSA colonization prevalence of 25.6%.

Individuals who tested positive for MRSA reported higher frequencies of recent antibiotic use (23.6% vs 12.3%; $P < .04$), history of alcoholism (10.9% vs 4.5%; $P < .08$), and current smoking (85.5% vs 73.1%; $P < .06$) and a lower frequency of having stayed with a friend for at least 1 night in the previous 30 days (5.5% vs 16.0%; $P < .03$), compared with individuals who tested negative for MRSA. Similar results were observed for individuals who tested positive for *S. aureus,* compared with individuals who tested negative for *S. aureus*. Differences in other characteristics did not approach statistical significance (Table).

Results of multivariable logistic regression analysis revealed 3 variables associated with MRSA colonization. In the final multivariable regression model, recent antibiotic use (OR, 2.73 [95% CI, 1.10–6.77]) and history of alcoholism (OR, 5.14 [95% CI, 1.24–21.4]) increased the risk of MRSA infection, whereas living with a friend was protective (OR, 0.18 [95% CI, 0.04–0.72]).

This study documents the prevalence of *S. aureus* and MRSA colonization among a population of homeless individuals. Although the *S. aureus* colonization prevalence in this sample is similar to prior population estimates,[2] the prevalence of MRSA colonization (25.6%) was much higher than has been previously reported for individuals in other community settings (1%–2%).[2-5] On the basis of these findings, the rate of MRSA colonization among the homeless may be 10–20 times higher than the rate among the general population. This finding is different from the 2.8% prevalence rate found in a study of the urban poor conducted in San Fransisco in 1999–2000.[6]

The risk factors that were identified for *S. aureus* and MRSA colonization were consistent with those found in other studies. Living with a friend was associated with lower odds for both *S. aureus* and MRSA colonization, and these lower odds may represent less exposure to congregate living situations and relatively better social support and access to hygiene facilities. We were not able to identify specific hygiene-related practices or health conditions that were associated with an increased risk of *S. aureus* or MRSA colonization, such as the frequency of handwashing, showering, or doing laundry.

There are several limitations of the current study. Because we did not determine the genetic subtypes of the isolates, we were unable to control for the effects of shelter-level or community-level MRSA prevalence. Similar to what has been

TABLE. Characteristics of Homeless Individuals in Ohio by *Staphylococcus aureus* and Methicillin-Resistant *S. aureus* (MRSA) Colonization

Characteristic	Sample[a] (n = 215)	With *S. aureus* test results: Positive (n = 75)	With *S. aureus* test results: Negative (n = 140)	P	With MRSA test results: Positive (n = 55)	With MRSA test results: Negative (n = 156)	P
Age, mean ± SD, years	41.7 ± 10.8	41.4 ± 11.8	41.9 ± 10.2		42.1 ± 10.6	40.1 ± 11.2	
Race, proportion (%)							
Black	130/175 (74.3)	44/60 (73.3)	86/115 (74.8)		31/42 (73.8)	96/130 (73.8)	
White	39/175 (22.3)	15/60 (25)	24/115 (20.9)		11/42 (26.2)	28/130 (21.5)	
Other	6/175 (3.4)	1/60 (1.7)	5/115 (4.3)		0/42 (0)	6/130 (4.6)	
Male	165 (77.0)	58 (77.3)	107 (76.0)		41 (74.5)	116 (74.4)	
⩽12th grade education	68 (31.6)	25/67 (37.9)	43/121 (35.5)		21/51 (41.2)	45/132 (34.1)	
Risk factors[b]							
Hospital	23 (10.7)	7 (9.3)	16 (11.5)		6 (10.9)	17 (10.8)	
Emergency department visit	57 (26.5)	24 (32.0)	33 (23.9)		19 (34.5)	37 (23.9)	
Antibiotics	32 (14.9)	16 (21.3)	16 (11.5)	.04	13 (23.6)	19 (12.3)	.04
History of *S. aureus* infection	12 (5.6)	3 (4.0)	9 (6.5)		3 (5.5)	9 (5.8)	
History							
HIV/AIDS	5 (2.3)	1 (1.3)	4 (2.9)		0 (0)	5 (3.2)	
Mental illness	23 (10.7)	13 (17.3)	19 (13.6)		10 (18.2)	22 (14.1)	
Alcoholism	13 (6.0)	7 (9.5)	6 (4.3)		6 (10.9)	7 (4.5)	.08
Hypertension	45 (20.9)	12 (16.0)	33 (23.6)		10 (18.2)	34 (21.8)	
Diabetes	14 (6.5)	7 (9.3)	7 (5.0)		3 (5.5)	10 (6.4)	
Residence,[c] proportion (%)							
With friend	28/215 (13.0)	5/70 (7.1)	23/122 (18.9)	.03	3/51 (5.9)	25/138 (18.1)	.03
Car and/or other	22/215 (10.2)	8/70 (11.4)	14/122 (11.5)		8/51 (15.7)	14/138 (10.1)	
Shelter	133/215 (61.9)	47/70 (67.1)	86/122 (70.5)		34/51 (66.7)	97/138 (70.3)	
Hospital	11/215 (5.1)	6/70 (8.6)	5/122 (4.1)		5/51 (9.8)	6/138 (4.3)	
Group home	14/215 (6.5)	5/70 (7.1)	9/122 (7.4)		3/51 (5.9)	10/138 (7.2)	
Current smoker	163 (75.8)	61 (81.3)	102 (72.9)		47 (85.5)	114 (73.1)	.06
Share cigarettes	112 (52.1)	34/69 (49.3)	51/128 (39.8)		28 (50.9)	83 (53.2)	
Substance use[b]							
Marijuana	59 (27.4)	16/69 (27.4)	39/131 (29.8)		15 (27.3)	42 (26.9)	
Cocaine	31 (14.4)	10/73 (13.7)	21/131 (16.0)		7 (12.7)	23 (14.7)	
Pain medicine	17 (7.9)	6/73 (8.2)	11/131 (8.4)		3 (5.5)	13 (8.3)	
Incarceration[d]	35 (16.3)	10/64 (15.6)	25/119 (21.0)		7 (12.7)	28 (17.9)	
<7 Showers/week	56 (26.0)	25/72 (34.8)	41/137 (29.9)		17 (30.9)	45 (28.8)	

NOTE. Data are no. (%) of people, unless otherwise indicated. There were 215 participants and 211 specimens available for testing. Nonsignificant P values are not listed. SD, standard deviation.

[a] Sample sizes are reduced by missing values for some variables.

[b] In prior 30 days.

[c] Stayed at least 1 night in prior 30 days.

[d] In prior 6 months.

demonstrated in family members of MRSA-colonized individuals,[7,8] it is likely that our sample contained clusters of individuals highly colonized by the same bacterial strains.

Future studies should address *S. aureus* and MRSA colonization in the homeless and other vulnerable populations.[9,10] Identification of specific risk factors and broad intervention to improve the living conditions of high-risk populations may be an important aspect of MRSA prevention control activities. Interventions might include improved individual hygiene, decontamination of colonized individuals, cleaning and improved sanitation of shelters, and coordinated community efforts to address homelessness as a public health problem.

ACKNOWLEDGMENTS

Potential conflicts of interest. All authors report no conflicts of interest relevant to this article.

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Received February 4, 2009; accepted March 11, 2009; electronically published June 30, 2009.

 0899-823X/2009/3008-0016$15.00. DOI: 10.1086/599018

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Pseudobacteremia Outbreak of *Pseudomonas oryzihabitans* in an Emergency Department of a Tertiary Hospital in Korea

Pseudobacteremia is a term used to describe apparent bacteremia that, after careful investigation, is found to be due to a blood culture contaminant.[1] Accurate data on the incidence of pseudobacteremia are difficult to obtain, but in 1977 Weinstein and Stamm suggested that up to 11% of nosocomial outbreaks were pseudoepidemics.[2] Because pseudobacteremia epidemics can be costly and time consuming but also largely are preventable, it is important to recognize this problem.[3] *Pseudomonas oryzihabitans* is the current name for the organism that has been called *Chromobacterium typhiflavum, Flavimonas oryzihabitans,* and CDC group Ve-2.[4] It is an infrequent cause of infection, and in the hospital setting it has been recovered from sink drains and respiratory therapy equipment.[4,5] Central venous catheter–associated bloodstream infection is the most commonly reported infection.[5] We report our experience of an outbreak of pseudobacteremia by *P. oryzihabitans,* presumably arising from faulty aseptic preparation of a blood culture set.

A total of 4 isolates of *P. oryzihabitans* were taken from 4 sets of blood cultures collected from 4 different patients who had visited an emergency room of a tertiary hospital within a 24 hour period. We reviewed the clinical records of each patient and determined that the clinical course was compatible with *P. oryzihabitans* bacteremia. We identified the patients' demographic data and medical history, the reasons for blood culture, the presence of a central venous catheter, the other laboratory tests performed at the same time, and the person who drew the blood. In addition, we reviewed the preparation of the equipment for blood sampling, including the disinfectants and dispenser used; the blood sampling technique; and the laboratory procedures for processing the blood culture, including the culture detection system. Surveillance culture was conducted on samples taken from the environmental surfaces in the emergency department. Culture specimens were also taken from uninoculated blood culture bottles from the current batches, disinfectants for the venipuncture site, cotton balls, and dispensers that might be handled at the time blood cultures were collected. The culture plates were incubated aerobically at 35°C for 48 hours. Four *P. oryzihabitans* isolates were genotypically analyzed with pulsed-field gel electrophoresis (PFGE). Results of the strain typing were interpreted with the Tenover criteria.[6]

The clinical characteristics of the 4 patients are summarized in the Table. Their clinical courses were stable and not compatible with *P. oryzihabitans* bacteremia. None had any type of central venous catheter. The blood sample from each patient had been collected by a different worker, and there was no problem in blood sampling technique. However, the dispensers and disinfectants for the blood culture sets were not

TABLE. Clinical Characteristics of Patients

Patient No.	Sex	Age, years	Body temperature (°C)	Underlying conditions	Final diagnosis	Presence of central venous catheter
1	F	67	39.0	Chronic renal failure, diabetes mellitus, hypertension	Pneumonia[a]	No
2	M	69	38.0	Myeloid metaplasia, myelofibrosis	Common cold	No
3	M	69	38.2	Bladder cancer	Common cold	No
4	M	59	38.7	Drug intoxication	Transient bacteremia after gastric lavage	No

[a] Pneumonia may be caused by methicillin-susceptible *Staphylococcus aureus.*

disposable and were prepared by different registered nurses. The blood culture sets were composed of two blood culture bottles, sterile gloves, a disposable syringe, curved Kelly forceps, and disinfectants for skin cleaning (10% povidone-iodine on a cotton ball and 70% alcohol on a cotton ball) in a simple dressing set. There was no focus of contamination in the processing of the blood cultures. Blood samples were placed in culture bottles (Vital AER or Vital ANA, bioMérieux) and incubated for 24–48 hours; bacteria were identified by standard criteria (ATB, bioMérieux). Antimicrobial susceptibility testing was performed using the API 20E system (bioMérieux). The blood culture detection system was fully automated (involved no manual manipulation). Each patient had a single positive blood culture result and had no microorganism isolated from another site. There were no isolations of microorganisms from the surveillance culture of the environmental surface in the emergency department, the disinfectant dispensers, and the disinfectants in the culture sets except *Alcaligens* spp. isolated from the bottom of the forceps jar. *P. oryzihabitans* was not isolated from environmental samples. PFGE patterns of 4 *P. oryzihabitans* isolates demonstrated that they were genotypically identical.

Pseudobacteremia is usually caused by hospital environmental contaminants, such as coagulase-negative cocci, *Bacillus* spp., *Corynebacterium* spp., *Micrococcus* spp., *Propionibacterium* spp., gram-positive bacilli, or *Clostridium perfringens*.[7,8] *Pseudomonas oryzihabitans* is an infrequent cause of infection and has characteristics similar to those of *P. luteola*, but to our knowledge no report has described a pseudobacteremia outbreak caused by *P. oryzihabitans*. In our cases, the patients did not have a focus of *P. oryzihabitans* bacteremia, and their clinical course was not compatible with bacteremia. The results of PFGE demonstrated the epidemiologic relationship, because the isolates were genotypically identical. Consequently, although we failed to find the *P. oryzihabitans* focus of contamination, we were able to conclude a pseudobacteremia outbreak of *P. oryzihabitans* through the daily monitoring of blood culture results.

ACKNOWLEDGMENTS

Potential conflicts of interest. All authors report no conflicts of interest relevant to this article.

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Received January 5, 2009; accepted February 16, 2009; electronically published June 15, 2009.

 0899-823X/2009/3009-0017$15.00. DOI: 10.1086/598340

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