Contamination of Environmental Surfaces With Staphylococcus aureus in Households With Children Infected With Methicillin-Resistant S aureus

Stephanie A. Fritz, MD, MSCI; Patrick G. Hogan, MPH; Lauren N. Singh, MPH; Ryley M. Thompson; Meghan A. Wallace, BS; Krista Whitney, MD; Duha Al-Zubeidi, MD; Carey-Ann D. Burnham, PhD; Victoria J. Fraser, MD

IMPORTANCE Household environmental surfaces may serve as vectors for the acquisition and spread of methicillin-resistant Staphylococcus aureus (MRSA) among household members, although few studies have evaluated which objects are important reservoirs of MRSA.

OBJECTIVES To determine the prevalence of environmental MRSA contamination in households of children with MRSA infection; define the molecular epidemiology of environmental, pet, and human MRSA strains within households; and identify factors associated with household MRSA contamination.

DESIGN, SETTING, AND PARTICIPANTS Fifty children with active or recent culture-positive community-associated MRSA infection were enrolled from 2012 to 2013 at St Louis Children's Hospital and at community pediatric practices affiliated with the Washington University Pediatric and Adolescent Ambulatory Research Consortium in St Louis, Missouri.

MAIN OUTCOMES AND MEASURES Samples of participants' nares, axillae, and inguinal folds were cultured to detect S aureus colonization. Samples of 21 household environmental surfaces, as well as samples obtained from pet dogs and cats, were cultured. Molecular typing of S aureus strains was performed by repetitive-sequence polymerase chain reaction to determine strain relatedness within households.

RESULTS Methicillin-resistant S aureus was recovered from samples of environmental surfaces in 23 of the 50 households (46%), most frequently from the participant's bed linens (18%), television remote control (16%), and bathroom hand towel (15%). It colonized 12% of dogs and 7% of cats. At least 1 surface was contaminated with a strain type matching the participant's isolate in 20 households (40%). Participants colonized with S aureus had a higher mean (SD) proportion of MRSA-contaminated surfaces (0.15 [0.17]) than noncolonized participants (0.03 [0.06]; mean difference, 0.12 [95% CI, 0.05-0.20]). A greater number of individuals per 1000 ft² (93 m²) were also associated with a higher proportion of MRSA-contaminated surfaces (β = 0.34, P = .03). The frequency of cleaning household surfaces was not associated with S aureus environmental contamination.

CONCLUSIONS AND RELEVANCE Methicillin-resistant S aureus strains concordant with infecting and colonizing strains are present on commonly handled household surfaces, a factor that likely perpetuates MRSA transmission and recurrent disease. Future studies are needed to determine methods to eradicate environmental contamination and prevent MRSA transmission in households.
Over the past decade, strains of methicillin-resistant *Staphylococcus aureus* (MRSA) with enhanced virulence emerged in the community (designated community-associated MRSA), causing a nationwide epidemic of cutaneous and invasive infections in otherwise healthy individuals. Community-associated MRSA poses a major public health challenge, accounting for 2 million infections in the United States annually and resulting in a societal economic burden of $2.7 billion.  

Community-associated MRSA infections cluster within households. Household contacts of children with MRSA infection have a substantially higher prevalence of MRSA colonization and infection compared with the general population. A recent randomized trial determined that decolonization of all household members resulted in a significantly reduced incidence of skin and soft-tissue infections (SSTIs) compared with decolonization of a pediatric index patient alone. Still, during a 12-month period, more than 50% of these index patients experienced recurrent SSTIs, suggesting that other reservoirs of MRSA may perpetuate MRSA transmission and recurrent infection.

Given that *S aureus* survives on inanimate objects for prolonged periods, household environmental surfaces may serve as vectors for the acquisition and spread of MRSA among household members. A case-control study in Manhattan, New York, found that household environments of patients with recent MRSA infections were more likely to be contaminated with MRSA compared with control households. In addition, transmission of MRSA between pets and humans has been proposed, but the directionality is unclear.

To date, few studies have comprehensively evaluated the household environment to determine which environmental surfaces represent MRSA reservoirs. The objectives of our study were to determine the prevalence of environmental MRSA contamination in households of children with MRSA infection; define the molecular epidemiology of environmental, pet, and human MRSA strains within households; and identify factors associated with household MRSA contamination. Ultimately, defining important household MRSA reservoirs will inform future interventions to decrease the burden of MRSA in households and reduce the risk of ongoing transmission and infection.

### Methods

#### Participant Recruitment

Between January 2012 and February 2013, 50 children with culture-positive active or recent (within the past 2 months) community-associated MRSA infections (48 patients with SSTIs, 1 patient with a retropharyngeal abscess, and 1 patient with bacteremia, myositis, and septic pulmonary emboli) were enrolled in our study. Participants were recruited from St Louis Children’s Hospital (SLCH) and community pediatric practices affiliated with the Washington University Pediatric and Adolescent Ambulatory Research Consortium. Children with nosocomial infections or risk factors for health care-associated infections and those who underwent decolonization (with mupirocin ointment, US Pharmacopeia; chlorhexidine gluconate; or bleach baths) within the past month were excluded. Available MRSA isolates recovered from the site of infection were obtained from the SLCH microbiology laboratory. The Washington University institutional review board and Animal Studies Committee approved the study procedures. Written informed consent was obtained for participants and household pets.

#### Data and Sample Collection

An enrollment visit was conducted in each participant’s home. Study participants received financial compensation for their time and effort. Questionnaires were administered to collect data regarding medical history, prior *S aureus* infections, hygiene practices, activities, household member and pet characteristics, home layout, and cleaning frequency.

Colonization cultures were performed on samples obtained from the anterior nares, axillae, and inguinal folds of each participant (BD ESwab; Becton Dickinson). Nasal samples obtained from indoor pet dogs and cats (BBL CultureSwab Amies liquid, regular aluminum wire; Becton Dickinson) were cultured to detect the presence of *S aureus* colonization. Samples were obtained from 21 environmental surfaces presumed to be frequently handled by multiple household members or possession to play a role in transmission. Standardized operating procedures were developed for each surface to ensure consistency in sampling across all households; the sample collection methods used included the Baird-Parker agar contact plate (Hardy Diagnostics) and the premoistened BD ESwab. The environmental sites tested in the living rooms, bathrooms, kitchens, and bedrooms and the sample collection methods used are listed in Table 1. We instructed participants not to perform any special cleaning measures, and the specific surfaces to be tested were not disclosed prior to enrollment. We obtained samples only from towels and bed linens that had been used but had not been laundered prior to our visit.

#### *S aureus* Isolation, Identification, and Strain-Typing Methods

From human and environmental culture swabs, 100 μL of eluant were inoculated into tryptic soy broth with 6.5% sodium chloride (BBL; Becton Dickinson); pet swabs were placed directly into tryptic soy broth with 6.5% sodium chloride. Broth cultures were incubated overnight at 35°C, and 100 μL of broth were subsequently plated to trypticase soy agar with 5% sheep blood (blood agar plate [BBL; Becton Dickinson]). For environmental culture swabs, in addition to tryptic soy broth overnight incubation, 100 μL of eluant were also inoculated directly to a blood agar plate and incubated overnight. Contact plates were incubated overnight at 35°C, and growth was subcultured to a blood agar plate. Identification of *S aureus* and antibiotic susceptibility testing were performed by use of established procedures.

To determine relatedness of isolates infecting or colonizing the participant, pets, and environmental surfaces, all *S aureus* isolates were analyzed by use of repetitive sequence-based polymerase chain reaction (repPCR) as previously described. Isolates with a similarity index of 95% or higher were considered the same strain. Each distinct repPCR pattern was assigned a numeric “reference strain” designation.
Repetitive sequence–based PCR queries the entire chromosome but is not specific to the mecA gene; thus, an MRSA strain and a methicillin-susceptible S aureus (MSSA) strain could be considered concordant by use of repPCR. All isolates recovered from pets and the reference strain isolates were confirmed as S aureus by matrix-assisted laser desorption ionization-time of flight mass spectrometry using the Vitek MS version 2.0 (bioMérieux). Multiplex PCR assay was also performed as described previously for staphylococcal cassette chromosome mec (SCCmec) characterization of all recovered S aureus strains. Polymerase chain reaction for mecA and mecC was performed on all MSSA isolates that contained SCCmec, using previously described conditions. Methicillin-susceptible S aureus isolates harboring mecA were subjected to additional phenotypic methods: repeat cefoxitin disk diffusion testing, the PBP2a detection assay (Alere), and inoculation to Spectra MRSA selective agar (Remel).

Statistical Analysis
Data were analyzed using IBM SPSS Statistics 20 for Windows. Risk factors for household environmental S aureus contamination were analyzed by use of the t test, analysis of variance, or linear regression for continuous data and by use of the Fisher exact test for categorical data. When analyzing the frequency of cleaning and household contamination with S aureus, we calculated the Fisher exact test using the Freeman-Halton extension. Relative risks and mean differences (with 95% CIs) were calculated when appropriate for categorical and continuous variables, respectively. All tests for significance were 2 tailed, and P < .05 was considered to be statistically significant.

Urban and rural designations were assigned to participants by geocoding addresses in ArcGIS Desktop 10 (Esri). Data were spatially joined with shapefiles from the 2010 US Census.

Results

Study Population and S aureus Colonization of Participants
Fifty participants with confirmed MRSA infections were enrolled. The median age was 3.0 years (range, 0.6-18.6 years); 58% were male, 64% were white, and 56% had private health insurance (Table 2). The median time from acute infection to study enrollment was 20 days (range, 3-56 days). The median distance between participants’ homes and SLCH was 17.3 miles (27.7 km) (range, 1.2-76.0 miles [1.9-121.6 km]); most participants (84%) lived in urbanized areas (≥50 000 people).

Table 1. Prevalence of Staphylococcus aureus on Household Environmental Surfaces and Sample Collection Methods Used

<table>
<thead>
<tr>
<th>Household Surface or Objecta</th>
<th>Households, No. (%)</th>
<th>With S aureus</th>
<th>With MRSA</th>
<th>With MSSA</th>
<th>Sample Collection Method</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Living room</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TV remote control (n = 49)</td>
<td>13 (27)</td>
<td>8 (16)</td>
<td>5 (10)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Main telephone (n = 50)</td>
<td>10 (20)</td>
<td>6 (12)</td>
<td>4 (8)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Computer keyboard and mouse (n = 45)</td>
<td>8 (18)</td>
<td>4 (9)</td>
<td>4 (9)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Video game controller (n = 38)</td>
<td>9 (24)</td>
<td>4 (11)</td>
<td>5 (13)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td><strong>Bathroom</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sink faucet handle (n = 50)</td>
<td>9 (18)</td>
<td>5 (10)</td>
<td>4 (8)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Hand towel (n = 40)</td>
<td>7 (18)</td>
<td>6 (15)</td>
<td>1 (3)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Participant bath towel (n = 29)</td>
<td>4 (14)</td>
<td>0 (0)</td>
<td>4 (14)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Toilet handle (n = 50)</td>
<td>4 (8)</td>
<td>3 (6)</td>
<td>1 (2)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Door handle (n = 50)</td>
<td>2 (4)</td>
<td>1 (2)</td>
<td>1 (2)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Light switch (n = 50)</td>
<td>12 (24)</td>
<td>5 (10)</td>
<td>7 (14)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Sink (n = 50)</td>
<td>9 (18)</td>
<td>5 (10)</td>
<td>4 (8)</td>
<td>Contact plate</td>
<td></td>
</tr>
<tr>
<td>Bathtub (n = 50)</td>
<td>4 (8)</td>
<td>1 (2)</td>
<td>3 (6)</td>
<td>Contact plate</td>
<td></td>
</tr>
<tr>
<td>Soap bar and dish (n = 32)</td>
<td>2 (6)</td>
<td>2 (6)</td>
<td>0 (0)</td>
<td>Contact plate</td>
<td></td>
</tr>
<tr>
<td>Toilet seat (n = 50)</td>
<td>3 (6)</td>
<td>2 (4)</td>
<td>1 (2)</td>
<td>Contact plate</td>
<td></td>
</tr>
<tr>
<td>Countertop (n = 50)</td>
<td>11 (22)</td>
<td>4 (8)</td>
<td>7 (14)</td>
<td>Contact plate</td>
<td></td>
</tr>
<tr>
<td><strong>Kitchen</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hand towel (n = 36)</td>
<td>6 (17)</td>
<td>3 (8)</td>
<td>3 (8)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Sink faucet handle (n = 50)</td>
<td>3 (6)</td>
<td>2 (4)</td>
<td>1 (2)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Sponge or dish cloth (n = 44)</td>
<td>1 (2)</td>
<td>1 (2)</td>
<td>0 (0)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td>Refrigerator door handle (n = 50)</td>
<td>7 (14)</td>
<td>3 (6)</td>
<td>4 (8)</td>
<td>Contact plate</td>
<td></td>
</tr>
<tr>
<td>Table top (n = 48)</td>
<td>4 (8)</td>
<td>4 (8)</td>
<td>0 (0)</td>
<td>Contact plate</td>
<td></td>
</tr>
<tr>
<td><strong>Bedroom</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Index patient bed sheets and pillowcase (n = 50)</td>
<td>12 (24)</td>
<td>9 (18)</td>
<td>3 (6)</td>
<td>BD ESwab</td>
<td></td>
</tr>
<tr>
<td><strong>Pets</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dogs (n = 26)</td>
<td>6 (23)</td>
<td>3 (12)</td>
<td>3 (12)</td>
<td>Amies liquid swab</td>
<td></td>
</tr>
<tr>
<td>Cats (n = 14)</td>
<td>1 (7)</td>
<td>1 (7)</td>
<td>0 (0)</td>
<td>Amies liquid swab</td>
<td></td>
</tr>
</tbody>
</table>

Abbreviations: BD, Becton Dickinson; MRSA, methicillin-resistant S aureus; MSSA, methicillin-susceptible S aureus; TV, television.

* Not all objects and surfaces were present in all homes; if present, samples were obtained for testing.

If a landline was not present, a sample of the mobile phone of the participant or the participant’s mother was obtained for testing.

1032 JAMA Pediatrics November 2014 Volume 168, Number 11 jamapediatrics.com

Copyright 2014 American Medical Association. All rights reserved.
Prevalence of *S aureus* in Household Environment and Pets

*S aureus* was recovered from at least 1 environmental surface in 32 participants' households (64%); 8 (16%) exclusively with MRSA, 9 (18%) exclusively with MSSA, and 15 (30%) with MRSA and MSSA recovered from different surfaces. Of households with *S aureus* in the environment, the median number of contaminated surfaces was 3 (range, 1-15). Methicillin-resistant *S aureus* was most frequently recovered from the participants’ bed linens (18%), television remote control (16%), and bathroom hand towel (15%) (Table 1).

Of 26 dogs tested, 6 (23%) were colonized with *S aureus* (3 of 26 [12%] with MRSA), and of 14 cats tested, 1 (7%) was colonized with *S aureus* (specifically MRSA) (Table 1); colonized pets were reportedly in good health. One of the 7 colonized pets (14%), a dog, had an SSTI in the past 6 months, compared with 4 of 33 noncolonized pets (12%), all of which were dogs.

Participant and household characteristics were evaluated as potential risk factors for household environmental contamination with overall *S aureus* and specifically MRSA. Participants colonized with *S aureus* had a higher mean (SD) proportion of *S aureus*-contaminated surfaces (0.24 [0.22]) than noncolonized participants (0.07 [0.10]; mean difference, 0.17 [95% CI, 0.07-0.28]). Participants renting their home had a higher mean (SD) proportion of *S aureus*-contaminated surfaces (0.23 [0.23]) than did participants who own their home (0.09 [0.13]; mean difference, 0.14 [95% CI, 0.02-0.26]). A greater number of individuals per 1000 ft² (93 m²) were also associated with a higher proportion of *S aureus*-contaminated surfaces (β = 0.42, *P* = .006) (Table 3).

Participants colonized with *S aureus* had a higher median (range) proportion of MRSA-contaminated surfaces (0.15 [0.17]) than did noncolonized participants (0.03 [0.06]; mean difference, 0.12 [95% CI, 0.05-0.20]). A greater number of individuals per 1000 ft² (93 m²) were also associated with a higher proportion of MRSA-contaminated surfaces (β = 0.34, *P* = .03) (eTable 1 in the Supplement).

The frequency of cleaning selected environmental surfaces was not associated with overall *S aureus* contamination of those surfaces. Similarly, hot-water washing of bath towels after each use and of bed linens weekly did not correlate with the recovery of *S aureus* from these surfaces (eTable 2 in the Supplement).

**Molecular Epidemiology**

The SCCmec types I (n = 4), II (n = 1), III (n = 21), and IV (n = 140) were detected in our sample of 212 *S aureus* isolates. All MRSA isolates (n = 138) contained SCCmec type IV. Twenty-eight of 74 MSSA isolates (38%) possessed SCCmec (eFigure in the Supplement);
Table 3. Potential Risk Factors for Household Contamination With *Staphylococcus aureus*

<table>
<thead>
<tr>
<th>Factor*</th>
<th>Mean (SD) Proportion of Environmental Surfaces Contaminated per Householdb</th>
<th>Mean Difference (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Racec</td>
<td></td>
<td></td>
</tr>
<tr>
<td>African American and multiracial (n = 18)d</td>
<td>0.17 (0.19)</td>
<td>0.05 (−0.06 to 0.15)</td>
</tr>
<tr>
<td>White (n = 32)</td>
<td>0.13 (0.18)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>Health insurance status</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Medicaid (n = 20)</td>
<td>0.16 (0.18)</td>
<td>0.04 (−0.07 to 0.14)</td>
</tr>
<tr>
<td>Private or Tricare (n = 30)</td>
<td>0.13 (0.18)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>Type of home</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Apartment, townhome, or condominium (n = 11)</td>
<td>0.19 (0.24)</td>
<td>0.06 (−0.07 to 0.18)</td>
</tr>
<tr>
<td>House (n = 39)</td>
<td>0.13 (0.16)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>Home ownership status</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rents (n = 18)</td>
<td>0.23 (0.23)</td>
<td>0.14 (0.02-0.26)</td>
</tr>
<tr>
<td>Owns (n = 32)</td>
<td>0.09 (0.13)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>Urban/rural statuse</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Urbanized area (n = 42)</td>
<td>0.16 (0.19)</td>
<td>0.12 (−0.10 to 0.15)</td>
</tr>
<tr>
<td>Urban cluster (n = 5)</td>
<td>0.10 (0.15)</td>
<td>0.06 (−0.16 to 0.29)</td>
</tr>
<tr>
<td>Rural (n = 3)</td>
<td>0.04 (0.06)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>Household member vs no household member within age groupf</td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤3 y (n = 35)</td>
<td>0.15 (0.20) vs 0.14 (0.14)</td>
<td>0.01 (−0.10 to 0.13)</td>
</tr>
<tr>
<td>4-10 y (n = 28)</td>
<td>0.16 (0.17) vs 0.12 (0.20)</td>
<td>0.04 (−0.06 to 0.15)</td>
</tr>
<tr>
<td>11-17 y (n = 17)</td>
<td>0.13 (0.15) vs 0.15 (0.20)</td>
<td>−0.02 (−0.13 to 0.09)</td>
</tr>
<tr>
<td>18-34 y (n = 33)</td>
<td>0.16 (0.20) vs 0.12 (0.14)</td>
<td>0.03 (−0.08 to 0.15)</td>
</tr>
<tr>
<td>≥35 y (n = 30)</td>
<td>0.11 (0.15) vs 0.19 (0.22)</td>
<td>−0.08 (−0.19 to 0.04)</td>
</tr>
<tr>
<td>Pet dog or cat present in household</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes (n = 27)</td>
<td>0.17 (0.19)</td>
<td>0.05 (−0.06 to 0.15)</td>
</tr>
<tr>
<td>No (n = 23)</td>
<td>0.12 (0.17)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>Colonization status of participants</td>
<td></td>
<td></td>
</tr>
<tr>
<td>S aureus colonization (n = 21)</td>
<td>0.24 (0.22)</td>
<td>0.17 (0.07-0.28)</td>
</tr>
<tr>
<td>No colonization (n = 29)</td>
<td>0.07 (0.10)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>Any history of S aureus infection in participantg</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes (n = 18)</td>
<td>0.14 (0.19)</td>
<td>−0.01 (−0.12 to 0.10)</td>
</tr>
<tr>
<td>No (n = 32)</td>
<td>0.15 (0.18)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>Any history of S aureus infection in household contact(s)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes (n = 23)</td>
<td>0.15 (0.18)</td>
<td>0.004 (−0.10 to 0.11)</td>
</tr>
<tr>
<td>No (n = 27)</td>
<td>0.14 (0.19)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>SSTI in participant in past yearg</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes (n = 29)</td>
<td>0.17 (0.20)</td>
<td>0.07 (−0.04 to 0.17)</td>
</tr>
<tr>
<td>No (n = 21)</td>
<td>0.10 (0.16)</td>
<td>1 [Reference]</td>
</tr>
<tr>
<td>SSTI in household contact in past year</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes (n = 33)</td>
<td>0.16 (0.20)</td>
<td>0.05 (−0.06 to 0.16)</td>
</tr>
<tr>
<td>No (n = 17)</td>
<td>0.11 (0.13)</td>
<td>1 [Reference]</td>
</tr>
</tbody>
</table>

Abbreviation: SSTI, skin and soft-tissue infection.

* The factors analyzed by linear regression and not included are number of people per 1000 ft² (93 m²), number of colonized pets in home, and distance from medical center.

b The mean number of environmental surfaces per household for which samples were obtained for testing is 19 (range, 16-21).

c Race was self-reported.

d Multiracial participants include African American/white (n = 3), white/American Indian (n = 1), and African American/white/American Indian (n = 1).

e Categorization was based on 2010 US Census Bureau TIGER/Line Shapefiles.33 Urbanized areas and urban clusters are densely settled territories measured at the census tract and census block levels of geography that contain 50 000 or more people or between 2500 and 49 999 people, respectively. All other areas are considered rural.32

f Includesthe participant and their household contacts.

g This does not include the infection that prompted enrollment in our study.
3 of these MSSA isolates carried mecA, which was detected by use of PCR, but methicillin resistance was not detected by additional phenotypic methods. Thus, these isolates appear to possess genetic remnants of mecA that are not expressed.

Among the 212 S. aureus isolates recovered from participants, pets, and household surfaces, 7 distinct strain types were identified by use of repPCR (1 MRSA strain, 3 MSSA strains, and 3 strains comprising both MRSA and MSSA); 1 predominant strain type accounted for 59% of all isolates (eTable 3 in the Supplement). Among 35 MRSA isolates associated with SSTI, 3 distinct strain types were identified. Among 30 S. aureus isolates colonizing participants, 4 distinct strain types were detected. Seven distinct strain types were recovered from household environmental surfaces (140 S. aureus isolates). Among 7 S. aureus isolates colonizing pets, 3 distinct strain types were detected. Two of the 7 overall strain types were recovered only from nonhuman sites (eTable 3 in the Supplement). Among households with 1 or more strains available for typing, the median number of strain types per household was 2 (range, 1-4).

Focusing solely on the 35 participants with an infecting isolate available for typing, we found that 11 (31%) possessed concordant infecting and colonizing strain types, whereas 5 (14%) were colonized with a strain type that was distinct from the infecting strain type. Thirteen of the 35 participants (37%) were infected with a strain type that was identical to at least 1 strain recovered from the household environment. Of 20 participants reporting an SSTI in the year prior to their enrollment infection, 10 (50%) had concordant infecting and environmental strain types, compared with 3 of 15 (20%) participants who did not report an SSTI in the prior year (P = .09).

Of the 50 participants, 14 (28%) were colonized with a strain type that was concordant with an environmental strain. Overall, 20 participants (40%) had a colonizing or infecting strain type concordant with an environmental strain recovered from their household. Environmental surfaces most commonly contaminated with a strain concordant with the participant’s strain included the participants’ bed linens (8 of 41 [20%]), television remote control (8 of 40 [20%]), bathroom light switch (7 of 41 [17%]), bathroom hand towel (5 of 31 [16%]), and bathroom sink (6 of 41 [15%]) (Figure).

Of 3 participants with a baseline colonizing or infecting strain and a colonized pet, 1 participant’s strain was concordant with their pet’s strain. Within that household (with 2 dogs and 1 cat), the 2 dogs were colonized with S. aureus, 1 with a strain type concordant with the participant, and 1 with a strain type discordant from the other dog and the participant. One other household had multiple pets (2 dogs) colonized with S. aureus (with concordant strain types).

**Discussion**

The household environment is an important reservoir for S. aureus contamination. In the present investigation of children with MRSA infection, nearly half of the household environments tested were contaminated with MRSA. Surfaces commonly touched by multiple household members (such as the television remote control or bathroom hand towel) and surfaces with which individuals have prolonged, close contact (such as bed linens) were frequently contaminated with MRSA. Interestingly, surfaces commonly perceived to be contaminated (such as toilet seats and door handles) were not major reservoirs of MRSA.

The present study’s prevalence of MRSA household environmental contamination is concordant with other studies. A case-control study by Uhlemann and colleagues in Manhat-
taneously (sampling 8 household surfaces on average) detected MRSA environmental contamination in significantly more case households (32%) than control households (5%). Methicillin-resistant *S. aureus* was most frequently detected on doorknobs and couches. In a survey by Scott et al. in Boston, Massachusetts, consisting of healthy individuals with a child in diapers and a pet dog or cat, MRSA was recovered in 9 of the 35 homes tested (26%). Among 32 sites tested, prevalent sites of MRSA contamination included kitchen dish towels, faucet handles, and the infant high-chair tray. Household members had no known history of MRSA colonization or infection, and colonization status was unknown.

In the present study, 40% of participants were colonized or infected with a strain of *S. aureus* that was concordant with a strain type recovered from their household environment. Surfaces frequently contaminated with a strain concordant with a participant’s strain type were again those commonly handled by multiple individuals and the bed linens. In the study by Uhlemann et al., 33% of the cases were infected with a strain type (as determined by spa typing) concordant with a strain recovered from an environmental source. Interestingly, a case’s infecting strain was more likely to be concordant with an environmental strain if it was a recurrent infection rather than a primary infection. This finding further implicates the environment as an important reservoir for ongoing exposure and recurrent infections.

Of 7 distinct *S. aureus* strain types identified by use of repPCR in our study population, 3 were recovered from sites of infection. Isolates recovered from environmental surfaces had the most diversity (7 strain types). These findings suggest that although *S. aureus* may exist on fomites, not all strain types may be well adapted to cause infection. We also evaluated all isolates for the SCCmec element. All MRSA strains possessed the SCCmec type IV element, consistent with contemporary “community-associated” strains. In a study by Miller et al. evaluating the molecular epidemiology of infecting and colonizing strains, most MRSA isolates possessed SCCmec type IV. Interestingly, we detected genetic remnants of SCCmec and mecA in our MSSA isolates. These MSSA isolates possessed diverse SCCmec types—both the contemporary SCCmec type IV and the SCCmec types I, II, and III traditionally associated with healthcare-associated strains. Detection of MSSA isolates with SCCmec genetic remnants has been described indicating the circulation of MSSA strains with a genetic backbone similar to common MRSA strains. Thus, epidemiologic studies should consider the role MSSA plays in the dynamics of *S. aureus* transmission.

Transmission of MRSA between pets and humans has been described previously, although the directionality is unclear. Contact with children is a reported risk factor for the colonization of pets with *S. aureus*. In the present study, 10% of the dogs and cats tested were colonized with MRSA. However, purported risk factors (e.g., the pet’s overall health or recent SSTI) were not significantly associated with colonization. Although the presence of pets was not a risk factor for environmental MRSA contamination in the present study, the survey by Scott et al. demonstrated that cats were significantly associated with MRSA contamination of the household environment. Lastly, in the present study, 1 of 3 participants having an infecting or colonizing strain and a colonized pet carried a strain type concordant with their pet’s strain. Although not based on scientific evidence, some physicians recommend removal of or restricted contact with pets in households with recurrent MRSA infections. Further study of MRSA transmission between pets and owners will inform the management of pets in households with recurrent MRSA infections.

Our study has several limitations. Colonization cultures were not obtained at the time of acute infection; 58% of participants were not colonized at enrollment, which may have resulted from systemic antibiotic administration and temporary eradication of colonization. The infecting isolate was available for only 70% of participants, limiting our analysis of the molecular epidemiology of MRSA strains recovered from samples obtained from participants and household surfaces. We acknowledge that, in an effort to provide “socially acceptable” responses, participants may not have truthfully answered survey questions regarding personal hygiene and the frequency of household cleaning; this may have biased the analysis of their association with the presence of MRSA in the household environment toward the null. Finally, because a prior study rarely detected MRSA in control households, and because our study goal was to specify reservoirs of MRSA contamination in households burdened by MRSA infections (and ultimately targets for intervention), control households were not included.

Important strengths of our study are the wide geographic catchment area (121-mile [194-km] diameter) of our study population and the extensive microbiologic data, culturing 3 anatomic sites of participants, 21 environmental surfaces, and pets. We also performed molecular typing by repPCR and SCCmec typing on all *S. aureus* isolates to classify the recovered strains.

### Conclusions

Although MRSA may persist on environmental surfaces for extended periods of time, current guidelines do not address environmental decontamination of the home. Clinicians often recommend household hygiene measures to patients in an effort to prevent recurrent community-associated MRSA infections. Data such as ours can inform prevention strategies within the household. For example, the recommended laundering in hot water of bath towels after each use and avoiding use of bar soap may not be effective, given the low frequency with which we recovered MRSA isolates from these sources. Additional studies to specify the dynamics of longitudinal MRSA household transmission and to specify effective household decontamination strategies are needed to interrupt the spread of MRSA.
S aureus Contamination of Environmental Surfaces


