

# Community-Associated Methicillin-Resistant *Staphylococcus aureus* Colonization in High-Risk Groups of HIV-Infected Patients

Kyle J. Popovich,<sup>1,2</sup> Kimberly Y. Smith,<sup>1,2</sup> Thana Khawcharoenporn,<sup>1,2</sup> C. J. Thurlow,<sup>1,2</sup> John Lough,<sup>1</sup> Guajira Thomas,<sup>2</sup> Alla Aroutcheva,<sup>1,2</sup> Chad Zawitz,<sup>2,3</sup> Kathleen G. Beavis,<sup>2,4</sup> Robert A. Weinstein,<sup>1,2</sup> and Bala Hota<sup>1,2</sup>

<sup>1</sup>Rush University Medical Center; <sup>2</sup>Stroger Hospital of Cook County; <sup>3</sup>Cermak Health Services, Chicago, Illinois; and <sup>4</sup>University of Illinois at Chicago Medical Center

**Background.** We examined the epidemiology of community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) nasal colonization among 3 groups of human immunodeficiency virus (HIV)-infected and 1 group of HIV-negative outpatients.

**Methods.** We determined prevalence and risk factors associated with MRSA colonization among women, recently incarcerated, and Hispanic HIV-infected patients and HIV-negative patients; isolates were typed by pulsed-field gel electrophoresis. Relative prevalence was calculated using Poisson regression, and logistic regression was used for multivariate analysis.

**Results.** Of 601 patients, 9.3% were colonized with MRSA; 11% of HIV-infected and 4.2% of HIV-negative patients were colonized (relative prevalence, 2.6; 95% confidence interval [CI], 1.12–6.07;  $P = .03$ ). Among HIV-infected patients, recently incarcerated patients had the highest colonization prevalence (15.6%) followed by women (12%); Hispanic patients had the lowest (2.8%). Eighty percent of confirmed MRSA isolates were identified as USA300.

On multivariate analysis, history of incarceration or residence in alternative housing (odds ratio [OR], 2.3; 95% CI, 1.1–4.7;  $P = .03$ ) was associated with MRSA colonization; Hispanic ethnicity was negatively associated (OR, 0.3; 95% CI, .11–.98;  $P = .045$ ). There was a trend (OR, 1.6; 95% CI, .9–3.0;  $P = .097$ ) toward geographic location of residence being associated with colonization. After controlling for incarceration, residence, and geography, HIV status was no longer significantly associated with colonization.

**Conclusions.** The CA-MRSA and HIV epidemics have intersected. Examination of networks of individuals released from incarceration, both HIV positive and negative, is needed to assess the role of social networks in spread of CA-MRSA and inform prevention strategies.

The community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) epidemic has disproportionately affected particular patient groups. While MRSA was once solely the province of healthcare settings,

nontraditional exposures (eg, incarceration [1], type and location of housing [2], participation in athletics [3], sexual behaviors [4], and social and community-based networks [5]) appear to be risk factors for CA-MRSA colonization or infection. In addition, patients infected with human immunodeficiency virus (HIV) appear disproportionately impacted by the CA-MRSA epidemic [5].

In prior work, we found that HIV-infected patients had a >6-fold higher risk of CA-MRSA skin and soft tissue infections (SSTIs) compared with HIV-negative patients [5]. HIV-infected patients have increased *Staphylococcus aureus* colonization [6, 7] and infection, in particular SSTIs [8]. It has been suggested

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Correspondence: Kyle Popovich, MD, Rush University Medical Center, Stroger Hospital of Cook County, 600 S Paulina St, Ste 143, Chicago, IL 60612 (kyle\_popovich@rush.edu).

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that HIV-infected patients may be at increased risk for persistent *S. aureus* colonization [9] and recurrent CA-MRSA SSTIs [10, 11]. In addition, MRSA infections due to multidrug-resistant (MDR) USA300 strains have been observed among men who have sex with men (MSM), many of whom are HIV positive, residing in San Francisco and Boston [4].

It is unclear why HIV-infected patients are at increased risk for MRSA. It has been suggested that antibiotic exposure or immune suppression may be factors [7, 12]. However, Shet et al [7] observed increased CA-MRSA colonization and infection among HIV-infected patients with well-controlled disease. Results from a study by Diep et al [4] suggested that factors beyond HIV status, such as having male-to-male sex, can be associated with CA-MRSA. We have found that high-risk groups and community exposures (eg, alternative housing, location of residence, history of incarceration) may interact to facilitate transmission and amplify the CA-MRSA epidemic in the community [5]. HIV-infected women may have an additional increased risk of CA-MRSA due to household exposures (eg, children, crowding in areas of residence, or household contacts with a history of incarceration). In addition, while the literature has suggested a lower prevalence of MRSA colonization among persons of Hispanic ethnicity [13], it is unclear if this association exists among HIV-infected persons.

Incarcerated individuals are another population that has been significantly impacted by the CA-MRSA epidemic, with outbreaks reported in correctional facilities [1] and increased levels of MRSA colonization observed among prison detainees [14] compared with national estimates [15]. Prior work has demonstrated geographic clustering of CA-MRSA SSTIs among HIV-infected patients residing in zip codes that contain high numbers of individuals who were formerly incarcerated [5]. It is unclear what happens to the colonization dynamics of CA-MRSA after incarceration when these individuals have been released into the community, especially among individuals presumably otherwise at increased risk for CA-MRSA such as HIV-infected patients.

Our study objective was to examine the prevalence and epidemiology of CA-MRSA nasal colonization among 3 at-risk groups (recently incarcerated persons, women, and Hispanics) at an outpatient HIV clinic to understand the impact of HIV and associated factors on CA-MRSA risk. We also determined the prevalence of CA-MRSA nasal colonization among HIV-negative individuals in a general medicine clinic at a neighboring institution. We hypothesized that the net effect of community exposure networks (ie, greater carriage of USA300 strains in the community) is changing the epidemiology of MRSA and that it may create a hierarchy of colonization burden among HIV-infected patients.

## METHODS

### Enrollment

#### *Outpatient HIV Clinic*

HIV-infected participants were enrolled from the Ruth M. Rothstein CORE Center, a public HIV clinic with a population of 6000 HIV-infected patients that is affiliated with the Cook County Health and Hospitals System. The CORE Center has several special-focus clinics to facilitate clinical and ancillary care including (1) the Women's Clinic that cares for HIV-infected women, (2) the Bilingual Clinic that cares for HIV patients who are monolingual Spanish speakers of Hispanic ethnicity, and (3) the Continuity Clinic (hereafter referred to as the Recently Incarcerated Clinic [RIC]) that cares for HIV-infected patients who were recently released from jail or prison and are transitioning back to clinic care.

Patients in the Women's Clinic, Bilingual Clinic, and RIC were eligible for enrollment if they were  $\geq 18$  years of age and were not enrolled in the study previously. Nasal surveillance cultures were obtained from enrolled participants, and a questionnaire was administered.

#### *Outpatient General Medicine Clinic*

HIV-negative participants were enrolled from the Rush University Internists Clinic, an outpatient internal medicine clinic affiliated with Rush University Medical Center (RUMC). RUMC is a 679-bed tertiary-care academic medical center. The Rush University Internists Clinic provides primary care to patients in the community near RUMC. Eligible patients were individuals  $\geq 18$  years of age who reported that they were HIV negative. Nasal surveillance cultures were obtained from enrolled participants, and a questionnaire was administered.

### Community Risk Factor Analysis

The questionnaire included details of community-based risk factors because prior studies have suggested that community factors (eg, location and type of residence [2, 5], sexual behavior [4], and incarceration [2, 16]) may be important for predicting CA-MRSA colonization and infection in certain populations. Alternative housing was defined as homelessness or current residence in a shelter, halfway house, substance abuse center, public housing, subsidized housing, supported living, nursing home, or mental health facility. Incarceration history was assessed, as were the exposures one may have within the house such as living with someone who had formerly been incarcerated. Zip codes in Cook County with a high number of individuals who were previously incarcerated (so-called high-risk zip codes [17]) were assessed. For HIV-infected participants, information was collected about CD4 count, trimethoprim-sulfamethoxazole (TMP-SMX) prophylaxis, and antiretroviral therapy. Because individuals on parole or probation were considered a vulnerable patient population by the Institutional

Review Boards at RUMC and Stroger Hospital of Cook County (CCH), we were not permitted to ask these participants about substance use.

### Laboratory Processing

Nasal swabs were obtained by swabbing both nares using Starplex Scientific Starswab II with Stuart transport media (Fisher Scientific, Thermo Fisher Scientific, Waltham, Massachusetts). Swabs were processed using an enrichment broth (salt-enriched trypticase soy broth) to increase culture sensitivity. Positive broth cultures were inoculated on MRSASelect agar (Bio-Rad, Hercules, California). The identity of colonies with morphologies consistent with MRSA was confirmed by the observation of  $\beta$ -hemolysis on tryptic soy agar plates containing 5% sheep's blood and by positive latex agglutination test (Staphaurex; Remel, Lenexa, Kansas). Methicillin resistance was confirmed by cefoxitin disk testing according to 2009 Clinical Laboratory Standards Institute guidelines.

Genotypic analysis with pulsed-field gel electrophoresis was performed on all confirmed MRSA isolates, with results interpreted as described by McDougal et al [18]. For phenotypic surveillance of CA-MRSA, Microscan was used to determine the antibiotic susceptibility. Double-disk diffusion testing was performed on MRSA isolates that were erythromycin resistant but clindamycin susceptible by Microscan. Disk diffusion was used to determine high-level mupirocin resistance [19].

### Statistical Analysis

Prevalence of CA-MRSA colonization was calculated (number positive/total sampled) for the following groups of participants: (1) HIV-infected participants, (2) participants seen in each clinic at CORE Center, and (3) HIV-negative participants. A comparison was made between participant groups to determine a relative prevalence and to create a hierarchy of colonization burden. Relative prevalence was calculated using Poisson regression.

Analysis was performed using results of surveillance cultures and questionnaires to determine community exposures that may enhance risk for colonization. SAS software version 9.2 (SAS Institute, Cary, North Carolina) was used for statistical analysis. Chi-square analysis was used to examine categorical variables, with the Fisher exact test for small samples, and continuous variables were analyzed with the independent-samples *t* test. The Wilcoxon (Mann-Whitney) test was used to compare the difference between medians. Logistic regression was used for multivariate analysis with MRSA colonization as the outcome variable. Statistically important (ie,  $P < .2$ ) factors on univariate analysis were included in multivariate analysis. Variables were removed using backward elimination of covariates with  $P$  values  $>.15$ . Effect modification was assessed by running models with introduction of product terms and assessing the significance of the interaction term in the resulting

model. We assessed for confounding by determining if the crude and adjusted estimates differed by  $\geq 10\%$ . Goodness of fit of the final model was assessed using the Hosmer-Lemeshow goodness-of-fit test.

The study was approved by the CCH and RUMC institutional review boards, and informed consent was obtained.

## RESULTS

### Characteristics of Study Population

Enrollment occurred from August 2010 through February 2011. A total of 601 participants were enrolled, of whom 458 were HIV infected. The mean age was 45.7 (SD, 11.6) years, and 58% of the study population was female.

Of HIV-infected participants, 208 were from the Women's Clinic, 141 were from the RIC, and 109 were from the Bilingual Clinic; 66% were African American, 26% were Hispanic, and 55% were female. 36% of HIV-infected patients reported a history of a prior SSTI or MRSA infection. 59% of HIV-infected patients had been incarcerated; 47% of these patients were seen outside the RIC. Fifty-one percent of the HIV-infected women reported a history of incarceration that was largely remote (13% had been incarcerated in the prior 6 months).

We enrolled 143 participants who were self-reported to be HIV negative: 77% were African American, and 70% were female. Twenty-five percent of these participants reported a history of SSTI or MRSA infection, and 86% resided in a zip code similar to that reported for HIV participants in the study. Only 10% had been incarcerated. A similar proportion of HIV-infected and HIV-negative participants currently resided in high-risk zip codes ( $P = .98$ ) (Table 1).

### Prevalence of MRSA Colonization

Of 601 participants, 9.3% were colonized with MRSA; 50 of 458 (11%) of HIV participants were colonized compared with 6 of 143 (4.2%) of HIV-negative participants. MRSA colonization among the 4 clinics studied was higher than recent population-based national estimates of nasal MRSA colonization (1.5% in 2003–2004) [15]. The RIC had the highest prevalence of colonization (15.6%), followed by the Women's Clinic (12.2%); the Bilingual Clinic had the lowest prevalence (2.8%) (Table 2).

Prevalence of MRSA colonization among HIV-infected participants was significantly higher than that for HIV-negative participants (relative prevalence, 2.6; 95% confidence interval [CI], 1.12–6.07;  $P = .03$ ). Among HIV-infected participants, the prevalence in the RIC and Women's Clinic was significantly higher than the prevalence for the Bilingual Clinic (relative prevalence, 5.7; 95% CI, 1.7–18.9;  $P = .005$  and relative prevalence, 4.4; 95% CI, 1.3–14.7;  $P = .015$ , respectively). Among HIV-infected participants, increased prevalence of

**Table 1. Characteristics and Community Exposures of Enrolled Participants by Clinic**

Characteristic	HIV Infected <sup>a</sup>			HIV Negative (n = 143)
	Bilingual Clinic (n = 109)	RIC (n = 141)	Women's Clinic (n = 205)	
<b>Sex</b>				
Male	88 (81)	116 (83)	NA	43 (30)
Female	20 (19)	23 (17)	205 (100)	99 (70)
Age, years, mean (SD)	43 (10.7)	43 (9.2)	45 (8.9)	51 (15.4)
<b>Race/ethnicity</b>				
African American (%)	0	116 (83)	183 (89.3)	110 (77)
Hispanic	108 (99)	3 (2)	8 (3.9)	16 (11)
White	0	20 (14.3)	13 (6.3)	13 (9)
Other	1 (1)	1 (0.7)	1 (0.5)	4 (3)
Prior SSTI or MRSA infection	15 (14)	57 (40)	94 (46)	36 (25)
Live with someone with a history of SSTI or MRSA infection	4 (4)	13 (9)	7 (3)	6 (4)
Tattoos	31 (28)	76 (54)	92 (45)	43 (30)
MSM	34 (52)	33 (40)	NA	0
Sex partners in prior 3 months, mean No. (SD)	1.1 (2.5)	1 (1.4)	0.9 (1.5)	0.7 (0.6)
History of being in jail	23 (21)	138 (98)	99 (48.5)	14 (10)
History of being in prison	8 (7)	105 (74)	55 (27)	5 (4)
Any incarceration history (jail or prison)	24 (22)	141 (100)	101 (49)	15 (10.5)
Incarceration duration (≤6 months)	12 (50)	70 (50)	68 (67)	12 (80)
Time since release from jail or prison, median months (low–high)	60 (2–300)	12 (0.03–420)	48 (0.75–360)	210 (2–540)
Live with someone with a history of incarceration	4 (4)	29 (21)	14 (7)	0
Current residence in high-risk zip code <sup>b</sup>	16 (15)	45 (32)	58 (28)	37 (26)
<b>Current housing type</b>				
House	0	1 (0.7)	18 (9)	53 (37)
Apartment	76 (69.7)	53 (37.6)	107 (52)	82 (57)
Live with family member	28 (25.7)	48 (34)	40 (19.5)	3 (2)
Alternative <sup>c</sup>	5 (4.6)	39 (27.7)	40 (19.5)	5 (4)
Live with children <12 years	28 (26)	22 (16)	50 (24)	38 (27)
<b>CD4 count</b>				
<200	13 (13)	19 (14.8)	44 (24)	NA
200–500	68 (65)	66 (51.6)	77 (42)	
>500	23 (22)	43 (33.6)	62 (34)	
Current TMP-SMX prophylaxis	14 (13)	30 (21)	46 (23)	
Current use or history of TMP-SMX prophylaxis in prior 6 months	24 (22)	35 (25)	55 (27)	
Currently on antiretrovirals	100 (92)	119 (84)	172 (84)	

Data are No. (%) of patients, unless otherwise indicated. Data were missing for the following variables, and the resulting denominators were as follows: (1) Bilingual Clinic: sex (n = 108), age (n = 105), sex partners in prior 3 months (n = 107), live with someone with a history of incarceration (n = 106), CD4 count (n = 104), current trimethoprim-sulfamethoxazole (TMP-SMX) prophylaxis (n = 104), and current use or history of TMP-SMX prophylaxis in prior 6 months (n = 107); (2) Recently Incarcerated Clinic: sex (n = 139), race/ethnicity (n = 140), live with someone with a history of incarceration (n = 136), and CD4 count (n = 128); (3) Women's Clinic: age (n = 204), history of being in jail (n = 204), history of being in prison (n = 204), live with someone with a history of incarceration (n = 199), CD4 count (n = 183), current TMP-SMX prophylaxis (n = 202), and current use or history of TMP-SMX prophylaxis in prior 6 months (n = 203); and (4) human immunodeficiency virus (HIV)–negative: sex (n = 142). Variables relating to incarceration only included individuals who reported a history of incarceration. For the men who have sex with men variable, only men who reported sexual activity in the prior year were included, and the resulting denominators are: Bilingual Clinic (n = 65), RIC (n = 83), and HIV-negative (n = 35).

Abbreviations: HIV, human immunodeficiency virus; MRSA, methicillin-resistant *Staphylococcus aureus*; MSM, men who have sex with men; NA, not applicable; RIC, Recently Incarcerated Clinic; SD, standard deviation; SSTI, skin and soft tissue infection; TMP-SMX, trimethoprim-sulfamethoxazole.

<sup>a</sup> Three HIV-infected men were enrolled from the Women's Clinic; for the analysis they were counted with HIV-infected patients but were not identified as being seen in the Women's Clinic. They had the following characteristics: 2 were African American, 1 was Hispanic; 2 had tattoos; 2 had history of being in jail (both had incarceration for ≤6 months and time since incarceration was 12 and 240 months); 2 lived in an apartment, 1 lived in alternative housing; 1 lived with children; ages were 47, 53, and 56; CD4 count was <200, 200–500, and unknown; all were on antiretroviral therapy; 1 was on TMP-SMX currently; and 1 had been on TMP-SMX in the past 6 months.

<sup>b</sup> High-risk zip code was defined as a zip code with high levels of individuals with a history of incarceration [17].

<sup>c</sup> Alternative housing was defined as being homeless or currently residing in a shelter, halfway house, substance abuse center, public housing, subsidized housing, supported living, nursing home, or mental health facility.

**Table 2. Prevalence of Nasal Methicillin-Resistant *Staphylococcus aureus* Colonization and Incarceration Exposure by HIV Status and HIV Clinic**

Population	Sample Size	Prevalence of Incarceration Exposure	Colonization Prevalence	Relative Prevalence	95% CI	P Value
HIV status						
HIV positive	458	59%	11.0%	2.6	1.12–6.07	.03
HIV negative	143	10%	4.2%	Reference		
HIV clinic <sup>a</sup>						
RIC	141	100%	15.6%	5.7	1.7–18.9	.005
Women's Clinic	205	49%	12.2%	4.4	1.3–14.7	.015
Bilingual Clinic	109	22%	2.8%	Reference		

For the comparison of prevalence between human immunodeficiency virus (HIV)-positive and HIV-negative participants, the reference group is HIV-negative participants. For the comparison of prevalence among HIV clinics, the reference group is the Bilingual Clinic. Recently Incarcerated Clinic, clinic caring for HIV patients recently incarcerated; Women's Clinic, clinic caring for HIV-infected women; Bilingual Clinic, clinic caring for HIV patients who are Hispanic.

Abbreviations: CI, confidence interval; HIV, human immunodeficiency virus; RIC, Recently Incarcerated Clinic.

<sup>a</sup> Three HIV-infected men were enrolled from the Women's Clinic; for the analysis they were counted with HIV-infected patients but were not identified as being seen in the Women's Clinic.

incarceration exposure was associated with a higher prevalence of MRSA colonization (Table 2).

### Community Risk Factor Analysis

Significant factors associated with MRSA colonization on univariate or bivariate analysis included clinic, race/ethnicity, history of incarceration in jail or prison, HIV status, prior history of a SSTI or MRSA infection, and residence in a high-risk zip code (Table 3). Eighty-seven percent of participants with a history of prior SSTI or MRSA infection did not have MRSA nasal colonization. Thirty-eight percent of HIV-infected and 50% of HIV-negative participants who had MRSA colonization resided in high-risk zip codes. A smaller proportion of Hispanic participants lived in alternative housing (7% HIV infected vs 18% HIV negative,  $P = .0013$ ) or high-risk zip codes (12% HIV infected vs 33% HIV negative,  $P < .001$ ) in comparison to the proportion of African American patients with these exposures. Although recently incarcerated individuals were not asked about illicit drug use, it was not associated with colonization among the remaining study population ( $P = .77$ ).

Of HIV-infected women, 63% who were colonized with MRSA had been formerly incarcerated, whereas 50% who were not colonized had a history of incarceration. Durations of incarceration and time since release from jail or prison were not significantly different between those who were colonized and those who were not. CD4 counts (82% had a CD4 count  $\geq 200$  cells/mL) and receipt of antiretrovirals or TMP-SMX did not differ significantly between those with and without colonization.

Qualitative review of the relationship of alternative housing with incarceration revealed evidence of a strong positive association: 71 (79%) individuals who were living in alternative

housing had been formerly incarcerated. Logistic regression of alternative housing on incarceration revealed a  $>5$ -fold increased odds of incarceration. Therefore, we chose to combine these variables to create a composite variable.

No effect modification was found during model building. However, HIV status appeared to confound the effects of incarceration and ethnicity on MRSA colonization; therefore, HIV status was retained in the final model.

On multivariate analysis, history of incarceration or residence in alternative housing (odds ratio [OR], 2.3; 95% CI, 1.1–4.7;  $P = .03$ ) was significantly associated with MRSA colonization, and Hispanic ethnicity was negatively associated (OR, 0.3; 95% CI, .11–.98;  $P = .045$ ). There was a trend (OR, 1.6; 95% CI, .92–3.0;  $P = .097$ ) toward geographic location of residence being associated with colonization. After controlling for incarceration, residence, and geography, HIV status was no longer significantly associated with MRSA colonization (Table 4).

### Genotypic and Phenotypic Surveillance of CA-MRSA

Pulsed-field gel electrophoresis was performed on all 56 confirmed MRSA isolates. The majority of isolates were USA300 (80%), the predominant CA-MRSA strain in the United States [20]. Remaining isolates were USA500 (8.9%), USA100 (5.4%), and USA1000 (5.4%).

Three USA300 strains exhibited resistance to TMP-SMX. Of these strains, 1 was classified as MDR (ie, resistant to erythromycin, fluoroquinolones, gentamicin, TMP-SMX, and tetracycline). This MDR strain also exhibited high-level mupirocin resistance. No other isolates had high-level mupirocin resistance. The MDR strain was found in an HIV-infected participant in the Women's Clinic who had formerly been incarcerated; she did not live in alternative housing or a high-risk zip code.

**Table 3. Univariate Analysis of Demographics and Community Risk Factors for Nasal Colonization With Methicillin-Resistant *Staphylococcus aureus* Among HIV-Infected and HIV-Negative Outpatients**

Characteristic	MRSA Colonization (n = 56)	No MRSA Colonization (n = 545)	P Value
Sex (n = 597)			.385
Male	20 (36)	230 (42)	
Female	35 (64)	312 (58)	
Age, years, mean (SD) (n = 596)	44.9 (11.5)	45.8 (11.6)	.598
Race/ethnicity (n = 600)			.013
African American	45 (82)	366 (67)	
Hispanic	4 (7)	132 (24)	
White	6 (11)	40 (7)	
Other	0	7 (1)	
Prior SSTI or MRSA infection (n = 601)	26 (46)	176 (32)	.033
Live with someone with a history of SSTI or MRSA infection (n = 601)	4 (7)	26 (5)	.512
Tattoos (n = 601)	27 (48)	217 (40)	.223
MSM (n = 186)	5 (29)	62 (37)	.552
Sex partners in prior 3 months, mean No. (SD) (n = 599)	0.7 (0.7)	0.9 (1.6)	.143
History of being in jail (n = 600)	39 (70)	237 (44)	<.001
History of being in prison (n = 600)	23 (41)	150 (28)	.034
Any incarceration history (jail or prison) (n = 601)	40 (71)	243 (45)	<.001
Incarceration duration (≤6 months) (n = 283)	22 (55)	142 (58)	.683
Time since release from jail or prison, median months (low-high) (n = 283)	24 (0.25–312)	24 (0.03–540)	.651
Live with someone with a history of incarceration (n = 587)	6 (11)	41 (8)	.351
Current residence in a high-risk zip code <sup>a</sup> (n = 601)	22 (39)	134 (25)	.017
Current residence in alternative housing <sup>b</sup> (n = 601)	13 (23)	77 (14)	.070
Live with children <12 years (n = 601)	13 (23)	126 (23)	.987
HIV status (n = 601)	50 (89)	408 (75)	.016
CD4 count (n = 417)			.979
<200	8 (18)	69 (18)	
200–500	23 (52)	189 (51)	
>500	13 (30)	115 (31)	
Current TMP-SMX prophylaxis (n = 450)	10 (20)	81 (21)	.967
Current use or history of TMP-SMX prophylaxis in prior 6 months (n = 454)	13 (26)	103 (26)	.938
Currently on antiretrovirals (n = 458)	41 (82)	353 (87)	.384

Data are No. (%) of patients for the column, unless otherwise indicated. Data were missing for particular variables, and the resulting number of patients for that variable is listed next to the variable name. CD4 count, antiretroviral use, and trimethoprim-sulfamethoxazole prophylaxis were only included for human immunodeficiency virus–infected patients. Variables relating to incarceration only included individuals who reported a history of incarceration.

Abbreviations: HIV, human immunodeficiency virus; MSM, men who have sex with men; MRSA, methicillin-resistant *Staphylococcus aureus*; SD, standard deviation; SSTI, skin and soft tissue infection; TMP-SMX, trimethoprim-sulfamethoxazole.

<sup>a</sup> High-risk zip code was defined as a zip code with high levels of individuals with a history of incarceration [17].

<sup>b</sup> Alternative housing breakdown: 22 in subsidized housing, 18 in shelters, 14 in substance abuse centers, 11 in public housing, 8 in halfway houses, 8 homeless, 4 in nursing homes or mental health facilities, 3 in supported living, and 2 in other.

## DISCUSSION

The CA-MRSA epidemic has disproportionately affected HIV-infected patients [5]. We have identified at-risk HIV-infected outpatients with high levels of nasal MRSA colonization. Individuals who had been incarcerated, recently or remotely, appear to be at highest risk for CA-MRSA nasal colonization,

while Hispanics have the lowest risk. Among HIV-infected patients, the RIC had nearly a 6-fold higher prevalence in comparison to a Hispanic clinic. HIV-infected women, many of whom had a history of incarceration, also had high levels of nasal colonization.

CD4 count, TMP-SMX prophylaxis, and antiretroviral therapy were not significantly associated with MRSA colonization

**Table 4. Multivariate Analysis of Nasal Methicillin-Resistant *Staphylococcus aureus* Colonization Among HIV-Infected and HIV-Negative Outpatients**

Risk Factor for MRSA Colonization <sup>a,b</sup>	OR	95% CI	P Value
Incarceration history or current residence in alternative housing	2.3	1.09–4.72	.028
Hispanic ethnicity	0.3	.11–.98	.045
Residence in a high-risk zip code <sup>c</sup>	1.6	.92–2.96	.097
HIV status	2	.78–5.38	.146

Abbreviations: CI, confidence interval; HIV, human immunodeficiency virus; MRSA, methicillin-resistant *Staphylococcus aureus*; OR, odds ratio.

<sup>a</sup> Hosmer-Lemeshow goodness-of-fit test ( $P = .98$ ).

<sup>b</sup> Initial variables included in the model were race, ethnicity, sex, HIV status, residence in a high-risk zip code, incarceration history or current residence in alternative housing, and prior skin and soft tissue or MRSA infection.

<sup>c</sup> High-risk zip code was defined as a zip code with high levels of individuals with a history of incarceration [17].

among HIV-infected participants, suggesting that factors beyond immune suppression contribute to the higher colonization prevalence. We have identified community exposures associated with MRSA colonization that could potentially contribute to spread of CA-MRSA. A history of incarceration or residence in alternative housing was significantly associated with CA-MRSA colonization. We found a trend toward residence in a zip code having high levels of individuals who were formerly incarcerated also being associated with colonization. When these community exposures were controlled, HIV status was no longer significantly associated with MRSA colonization. This suggests that community exposures may be more important for predicting MRSA colonization than HIV status in certain populations. In our population, HIV status may be a marker for exposure to high-risk social networks rather than being the major factor contributing to the high colonization and infection burden.

We found that 71% of individuals who were MRSA colonized had formerly been incarcerated. The transmission dynamics of CA-MRSA are unclear once individuals are released from jail or prison into the community. A mathematical model by Hartley et al [21] suggested that the CA-MRSA epidemic may be amplified by institutions, such as correctional facilities, that house high numbers of at-risk individuals and have high rates of release of colonized or infected individuals into the community. It may be necessary to follow individuals after release from correctional facilities to dissect CA-MRSA risk factors and help identify targets for intervention.

Geographic location and type of residence have also been suggested to be associated with CA-MRSA. Diep et al [4] observed a high incidence of MDR USA300 infections in

8 contiguous zip codes in the San Francisco area that had high numbers of MSM residing in them. Hota et al [2] observed uneven geographic distribution of CA-MRSA SSTIs in Cook County, Illinois, with residence in particular public housing complexes being associated with CA-MRSA. We found that 39% of participants who had MRSA colonization resided in high-risk zip codes. In addition, there was significant overlap of individuals who were formerly incarcerated and those who were currently residing in a form of alternative housing. The intersection of populations with high MRSA colonization burden and high-risk environments may serve to facilitate CA-MRSA transmission.

It is unclear why Hispanic ethnicity was negatively associated with MRSA colonization, with the prevalence of colonization among Hispanic HIV-infected participants being lower than that for HIV-negative participants. Others have reported similar findings with both MRSA colonization [13] and SSTIs [2]. We found that a smaller proportion of Hispanic participants in the overall study population lived in alternative housing or high-risk zip codes compared with African American participants. It is unclear if this difference in type or location of residence translated into different community networks and contributed to lower risk of MRSA colonization among Hispanics in our study. As support for a key role of residence, our HIV-negative patients, whose only recognized risk for MRSA colonization was living in high-risk zip codes, had a colonization rate 1.5-fold higher than our Hispanic HIV-infected patients and higher than recent national estimates [15]. A report released from the Bureau of Justice Statistics [22] found that the imprisonment rate for African Americans was higher than that for Hispanics, which was higher than that for whites. We speculate that the low MRSA colonization rate among Hispanics suggests that factors beyond correctional facilities, such as social network exposures and community MRSA colonization burden, may be involved in MRSA colonization risk.

Our study has limitations. First, we relied on the participants' recall of community risk factors, which is subject to recall and reporting bias. Second, we did not assess extranasal colonization, which may be increased among individuals with CA-MRSA colonization [23]. Eighty-seven percent of participants in our study who reported a history of prior SSTI or MRSA infection did not have MRSA colonization in our surveillance, suggesting they either were intermittently colonized, had extranasal colonization, or had "hit and run" CA-MRSA infections [2]. Therefore, we likely underestimated the true colonization burden. Third, we adjusted for effects of confounding in our final model; however, we cannot rule out that residual confounding still exists. For example, some differences between HIV-infected or HIV-negative participants may not have been measured,

which would have confounded our analysis. Finally, while our findings may not be generalizable to non-inner-city patient populations, the concept of community exposures playing a role in CA-MRSA colonization and infection may apply to other populations. In addition, further analysis of the risk in HIV-negative patients with higher incarceration rates is needed to fully understand the independent effect of incarceration on MRSA colonization.

In conclusion, CA-MRSA colonization is high among subgroups of HIV-infected patients, particularly among individuals who have been incarcerated or have high-risk residences. In certain populations, community exposures may be more important for predicting MRSA colonization than HIV status. Social networks may need to be examined for both HIV-positive and HIV-negative individuals following their release from correctional facilities into the community to differentiate community risk factors for CA-MRSA and inform prevention strategies. Because social networks may be contributing to spread of the CA-MRSA epidemic in certain populations, a tool such as social network analysis may be needed to further investigate CA-MRSA spread among at-risk populations.

## Notes

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