MAJOR ARTICLE

Staphylococcus aureus Colonization and Infection in New York State Prisons

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Methicillin-resistant *Staphylococcus aureus* is increasingly responsible for staphylococcal outbreaks in prison. There is limited information on the source of the outbreak strains, risk factors for infection, and transmission of these strains within a prison. We conducted a survey to determine the prevalence of nasal colonization with *S. aureus* in 2 New York State prisons. *S. aureus* isolates from clinical cultures collected from all New York State prisons during a 6-month period were compared with the colonizing strains. Analyses were conducted to determine whether prison-level characteristics were associated with colonization or infection with *S. aureus*. The colonization rate was 25.5% (124/487); 10.5% of the isolates were methicillin resistant, all were staphylococcal chromosomal cassette (SCC)*mec* type IV, and 61.5% were Panton Valentine leukocidin (PVL) positive. Surprisingly, 21.6% of the methicillin-susceptible isolates were also PVL positive. Of the clinical isolates, 48.3% were methicillin resistant, with 93.1% of the latter being SCC*mec* type IV and 48.3% being PVL positive. The predominant clone was USA 300. Prison-level risk factors for infection included the proportion of inmates with drug offenses, the length of inmate stay, and the jail from which inmates originated. This study suggests that both new and long-term inmates act as sources of *S. aureus* strains, with the more virulent of the latter preferentially being selected as pathogens.

The epidemiology of *Staphylococcus aureus* infections is evolving [1]. Traditionally associated with infections in the health-care setting, antibiotic-resistant *S. aureus* infections increasingly occur in the community [2, 3]. These community-based infections, especially those due to methicillin-resistant *S. aureus* (MRSA), have occurred in such diverse groups as children, Native Americans, members of athletic teams, military recruits, and prison inmates [2–6]. Investigations of the circumstances leading to these infections have primarily focused on outbreaks, and, as a result, there is limited information on the prevalence of staphylococcal colonization and infection among high-risk groups in a nonoutbreak setting. One such high-risk group is prison inmates. Even though numerous staphylococcal outbreaks have been identified in both jails and prisons throughout the United States, there is a paucity of data on the endemic prevalence and transmission dynamics of CA-MRSA among incarcerated populations [7–9]. In particular, there are questions about whether *S. aureus* colonization serves as a prelude to infection, as it does in the health-care setting. In the present study, we collected colonization isolates from 2 prisons and compared the molecular and epidemiological characteristics with those of isolates associated with clinical infections from all New York State (NYS) prisons.

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METHODS

***Collection of anterior nasal-swab cultures to detect carriage of* S. aureus.** A surveillance study of *S. aureus*

nasal carriage was conducted at 2 NYS maximum-security prisons: Bedford Hills and Sing Sing. Bedford Hills houses 792 female prisoners, and Sing Sing houses up to 1741 male prisoners. During several prison visits between October 2005 and April 2006, a convenience sample of nasal-swab cultures for determination of *S. aureus* colonization was collected. Inmates were provided with an informational handout describing the study and were asked whether they were willing to participate. Samples were collected anonymously in the cell blocks, at the infirmary, and in interview rooms. The anterior nares of each inmate were sampled with a cotton-tipped swab (Becton Dickinson Culturette Systems). The study was reviewed and approved by the Columbia University Institutional Review Board and the NYS Department of Correctional Services.

Retrieval of clinical* S. aureus *isolates. Clinical cultures from all NYS prisons were sent to a central commercial microbiology laboratory (Medilabs, Elmwood Park, NJ). Between January and June of 2006, this laboratory sent to our laboratory all cultures positive for *S. aureus.* Cultures were provided without subject identifiers but with a specimen number, the body site from which the culture had been collected (in most instances), and the name of the prison. All duplicate samples from the same inmate (information provided by Medilabs) and all samples that failed to yield *S. aureus* when recultured in the laboratory were eliminated, leaving 60 clinical samples for analysis.

Microbiologic evaluation of the samples. After incubation in Todd Hewitt broth for 3 h at 37°C, an aliquot from the broth containing bacteria from the nasal-swab cultures was plated onto mannitol salt agar for 48 h at 37°C; the nasal-swab cultures were incubated in broth in order to enhance retrieval of *S. aureus.* In addition, an aliquot of this sample, reflective of the original swab culture, was frozen, at −80°C, for future use if necessary. Positive colonies identified on the mannitol salt agar were then confirmed as *S. aureus* by use of Staphaurex (Remel). All clinical and colonization cultures positive for *S. aureus* were further characterized by staphylococcal chromosomal cassette (SCC)*mec* typing [10, 11] and antibiotic-susceptibility testing performed by the Kirby-Bauer method [12]. Screening for the presence of Panton Valentine leukocidin (PVL) was performed as described elsewhere [13].

All *S. aureus* isolates were further characterized by pulsed-field gel electrophoresis (PFGE) using *Sma*I digestion, as described elsewhere [14]. PFGE profiles were entered into the Bionumerics archival database (version 4; Applied Maths), and the strains were then compared by use of a dendrogram. Closely related strains were defined as showing dendrogram-based similarity that was ⩾70% [15].

Data analysis. Demographic data from the NYS Department of Correctional Services were obtained for 26 NYS prisons that provided clinical ($n = 60$) or surveillance isolates ($n = 487$). Results were presented separately for the clinical isolates and the surveillance isolates, because the latter were obtained only at Bedford Hills and Sing Sing.

Prisons were categorized by security level (maximum or medium). Demographic data for each prison were available at 12 different time points during 12 months that covered the period in which the clinical or surveillance isolates were obtained (2005 calendar year). For each prison, information on inmates' age, race, and drug offenses; the proportion of inmates coming from New York City (Kings, New York County [Manhattan], Queens, Richmond, and Bronx) jails and from NYS jails; and length of inmate stay was averaged over the 12-month period for each prison and then was averaged across prisons, by security level (medium or maximum), as described below.

To summarize the average demographic information across prisons, several steps were taken to analyze the data. For each prison, inmate age was available, in 12 categories ranging from 16 to 65 years. Inmates in the >65-years-old category were excluded because there was no information on that age range. Weighted median age was calculated at each time point by weighting the median of each category by the number of inmates in the category, summing these values over all categories, and then dividing by the total number of inmates in those categories. Data on length of inmate stay also were available, in 10 categories ranging from 0 to >72 months; a length of stay >72 months was coded as 72 months. To determine the proportion of inmates coming from NYC jails versus all other NYS jails, the frequency of inmates from Kings, New York County, Queens, Richmond, and Bronx counties were summed and divided by the total number of inmates in the corresponding prison. To provide the most representative demographic characteristics of the inmates from whom we obtained isolates during the study period, we took advantage of prison demographic data that were presented almost monthly (in some cases bimonthly) during the 12-month period. The average demographic characteristics were calculated by averaging the proportion of inmates with specific characteristics during each of the available 12 time points during the 12-month period. Next, the prison-level demographic averages were averaged over all prisons, by security level (maximum or medium).

To assess potential demographic risk factors associated with the isolation of MRSA in clinical cultures, the prison-level demographic characteristics were collapsed over a 3-month period before the *S. aureus* clinical isolates were obtained. These analyses did not include surveillance isolates or clinical isolates from either Bedford Hills or Sing Sing, because the variability in the time frame during which surveillance was conducted was insufficient to allow assessment of demographic predictors.

To compare the average demographic data for medium-se-

Table 1. Average demographic characteristics of inmates in New York State prisons.

Category[a]	Prison security level	
	Maximum	Medium
Staphylococcus aureus isolates, no.[b]	23	24
Prisons, no.		
Total	9	17
Women's	1	1
Average length of inmate stay, months	24.5	14.5
Average weighted age of inmates, median, years[c]	35.8	33.9
Average proportion of inmates, %		
From New York City jails	60.7	57.1
White	18.9	22.8
Black	51.8	48.1
Hispanic	27.1	27.0
Other race/ethnicity	2.3	2.4
Average total of inmates, no.	1071	1205

[a] Except for age (see footnote c), the averages of the demographic characteristics were calculated by averaging the proportion of inmates in each prison who had each of the specific characteristics during each of the available time points during the 12-month period. The prison-level demographic averages were then averaged over all prisons in each of the security-level categories (i.e., maximum and medium).

[b] Information on prison location was unavailable for 3 of the available isolates.

[c] Average weighted median age was computed on the basis of categorical data; the median of each of the age group was multiplied by the number of inmates in that category, and the results was summed and divided by the number of inmates in all age groups. These weighted medians were averaged over 12 time points.

curity versus those for maximum-security prisons, Student's *t* tests for differences in means were used to generate *P* values for differences in average characteristics. To assess molecular differences (i.e., MRSA, PVL, and clonal group [USA 300 vs. other]) between clinical and colonization isolates, χ^2 or Fisher's exact test was used.

We conducted linear regression analyses by prison-security level to assess whether prison-level characteristics were associated with *S. aureus* outcomes among prisons (except Bedford Hills and Sing Sing) providing clinical isolates. Two separate outcomes were examined: (1) the proportion of SCC*mec*-positive isolates (total no. of SCC*mec*-positive isolates/total no. of *S. aureus* clinical isolates) and (2) the proportion of PVL (no. of PVL-positive isolates/total no. of *S. aureus* clinical isolates). Predictor variables included average weighted median inmate age, proportion of inmates in racial categories, average length of inmate stay, proportion of inmates emanating from NYC jails, and proportion of inmates with drug offenses. Results are presented as linear regression slope estimates (β) and SE; surveillance isolates from Bedford Hills and Sing Sing were not analyzed by linear regression analyses, because there was very little variability in the sampling period.

RESULTS

A total of 487 nasal swabs (236 from Bedford Hills and 251 from Sing Sing) were obtained for surveillance. During the same period, 60 unique isolates of *S. aureus* from clinical cultures from 26 NYS prisons were provided. The clinical isolates were collected from the following sites: skin/soft tissue, 41; blood, 5; urine, 2; unknown, 12. Demographic characteristics of inmates in the maximum and medium-security NYS prisons who provided clinical-infection isolates are shown in table 1. During the 12-month period, the average proportion of inmates who were from NYC jails was similar in the maximum- and medium-security prisons (60.7% and 57.1%, respectively [$P = .54$]). The average proportion of white versus black and Hispanic inmates in maximum-security prisons was lower than that in medium-security prisons, but this difference was not significant ($P = .24$). Demographic characteristics of the 2 prisons (Bedford Hills and Sing Sing) over the time period when samples were collected for surveillance cultures are shown in table 2. The average proportion of inmates at Sing Sing who were from NYC jails was higher than that at Bedford Hills (72.2% and 47.7%, respectively [$P < .0001$]). The proportion of inmates who were drug offenders was higher at Bedford Hills than at Sing Sing ($P < .0001$).

The overall *S. aureus* nasal colonization rates for the 2 sur-

Table 2. Average demographic characteristics of inmates in Bedford Hills and Sing Sing (maximum-security prisons).

Category[a]	Prison	
	Bedford Hills ($n = 236$)	Sing Sing ($n = 251$)
Sex	Female	Male
Average length of inmate stay, months	36.5	25.7
Average weighted age of inmates, median, years[b]	34.9	35.4
Average proportion of inmates, %		
From New York City jails	47.7	72.1
With drug offenses	20.9	11.4
White	28.9	12.1
Black	48.9	55.6
Hispanic	20.3	30.1
Other race/ethnicity	2.1	2.4
Average total of inmates, no.	807.1	1737.1

[a] Except for age (see footnote b), the averages of the demographic characteristics were calculated by averaging the proportion of inmates in each prison who had each of the specific characteristics during each of the available time points during the 12-month period. The prison-level demographic averages were then averaged over all prisons in each of the security-level categories (i.e., maximum and medium).

[b] Average weighted median age was computed on the basis of categorical data; the median of each of the age group was multiplied by the number of inmates in that category, and the results was summed and divided by the number of inmates in all age groups. These weighted medians were averaged over 12 time points.

veillance site prisons were similar (Sing Sing, 27.5%; Bedford Hills, 23.3%). The MRSA colonization rates at both facilities were higher than those found in the general population [16, 17]. Interestingly, the rate in the women's prison, Bedford Hills, was ~7 times that in the men's prison, Sing Sing (20.0% [11/55] and 2.9% [2/69] [$P = .0026$, by Fisher's exact test]). All of the MRSA colonization isolates from both prisons were SCC*mec* type IV (table 3).

The percentage of MRSA among the isolates from clinical cultures was higher than that among isolates from colonization cultures (48.3% and 10.5%, respectively [$P < .0001$]). Of the MRSA isolates, 48.3% (14/29) were PVL positive. Surprisingly, 32.2% of the methicillin-susceptible *S. aureus* (MSSA) strains were also PVL positive. PVL-positive MSSA and MRSA strains were disproportionately represented among the clinical isolates: overall, 25.8% (32/124) of the colonizing isolates were PVL positive, whereas 40.0% (24/60) of the clinical isolates were PVL positive ($P = .0498$) (table 3). Among the clinical isolates from all NYS prisons, there were 4 from Bedford Hills and 1 from Sing Sing; 4 of these 5 were MRSA.

When 70% similarity was used as the cutoff value, 13 clusters of closely related strains were identified in the total sample (both clinical and colonization isolates) (figure 1; data for colonization isolates are not shown). Isolates from both colonization and clinical cultures were represented in 12 of these 13 clones. All but 5 of the clinical isolates were also present among the surveillance strains. The predominant clone identified in the colonization isolates was USA 300, which was present in 20 of 124 isolates; 14 (70%) of these 20 USA 300 strains were methicillin susceptible. Only 4 of the USA 300 strains were PVL positive (data not shown). USA 300 accounted for 48.3% (29/60) of the clinical isolates. The second largest group was USA 400, with 18 isolates (9 colonization and 9 clinical isolates). A total of 15 of these isolates were methicillin susceptible, and 2 were PVL positive.

When the statistical associations between prison-level characteristics (inmates' average weighted median age, proportion of inmates in race categories, average length of inmate stay, proportion of inmates emanating from NYC jails, and proportion of inmates with drug offenses) and the proportion of PVL- and MRSA-positive isolates were examined in terms of prison-security level, both a higher average age and a higher proportion of inmates from NYC jails who were in medium-security prisons were associated with lower levels of PVL presence among clinical *S. aureus* isolates (age slope, −0.025 [SE, 0.012] [$P = .046$]; NYC-jails slope, −0.806 [SE, 0.346] [$P = .027$]). In maximum-security prisons, a longer length of stay was associated with an increased proportion of PVL presence among *S. aureus* isolates from clinical infections (length-of-stay slope, 0.011 [SE, 0.003] [$P = .003$]).

In medium-security prisons, older age and longer average length of stay were significantly associated with a lower proportion of MRSA infection (older-age slope, −0.037 [SE, 0.010 [$P = .001$]; length-of-stay slope, −0.010 [SE, 0.006] [$P < .130$]). In both maximum- and medium-security prisons, a higher proportion of inmates with drug offenses was associated with a significantly higher proportion of MRSA-positive clinical isolates (maximum security–prison MRSA slope, 3.774 [SE, 0.908] [$P < .001$]; medium security–prison MRSA slope, 1.559 [SE, 0.663] [$P = .025$]). Ethnicity was not a contributing factor in either medium- or maximum-security prisons.

DISCUSSION

In the present study, we investigated *S. aureus* colonization and clinical infection, during a defined time period, in NYS prisons. Surveillance cultures were collected at 2 maximum-security prisons, and culture data for the entire prison system were collected during the same time period. There are a number of interesting observations. The predominant strain, USA 300, was identified in both the colonizing and infecting isolates. Interestingly, these clones, whether methicillin susceptible or methicillin resistant, were preferentially selected as pathogens, accounting for a far higher proportion of the clinical infections than did the other colonizing isolates. This result suggests that

Table 3. Characterization of *Staphylococcus aureus* nasal colonization and clinical isolates from inmates in New York State prisons.

Category[a]	Nasal colonization, % (proportion)			Unique clinical-infection isolates, % (proportion)
	Sing Sing (men's prison)	Bedford Hills (women's prison)	Total	
S. aureus positive	27.5 (69/251)	23.3 (55/236)	25.5 (124/487)	100 (60)
MRSA positive/total *S. aureus* positive	2.9 (2/69)	20 (11/55)	10.5 (13/124)	48.3 (29/60)
SCC*mec* type IV/MRSA positive	100 (2/2)	100 (11/11)	100 (13/13)	93.1 (27/29)
PVL-positive MSSA/total MSSA	0 (0/67)	54.5 (24/44)	21.6 (24/111)	32.2 (10/31)
PVL-positive MRSA/total MRSA	0 (0/2)	72.7 (8/11)	61.5 (8/13)	48.3 (14/29)

[a] MRSA, methicillin-resistant *S. aureus;* MSSA, methicillin-sensitive *S. aureus;* PVL, Panton Valentine leukocidin; SCC, staphylococcal chromosomal cassette.

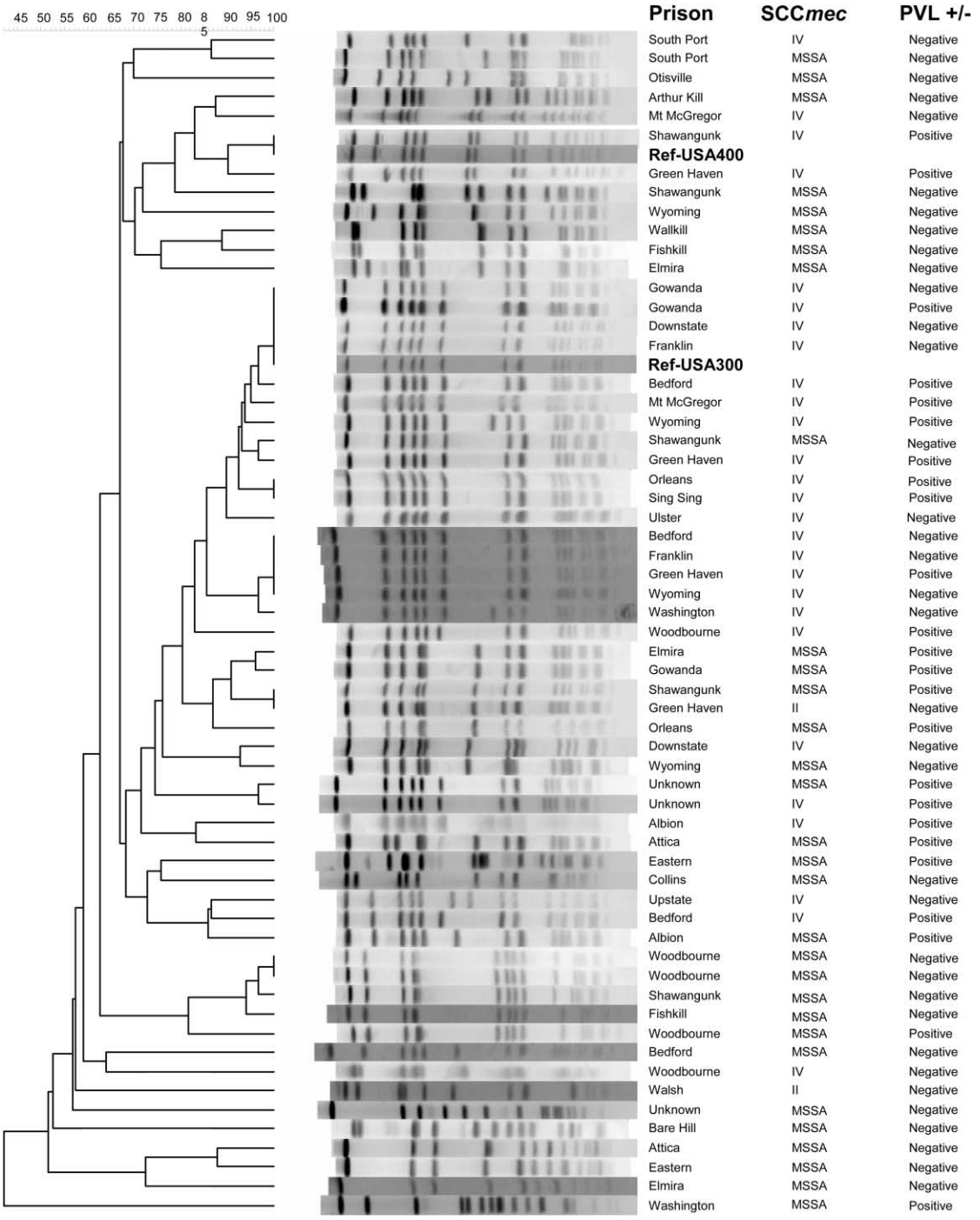

Figure 1. Clinical *Staphylococcus aureus* isolates collected from inmates in New York State prisons during a 6-month period (January–June 2006). The dendrogram of pulsed-field gel electrophoresis (PFGE) profiles depicts the degree of relatedness of the strains. The first, second, and third columns to the right of the gels indicate, respectively, the prison site where the isolate was collected, the staphylococcal chromosomal cassette (SCC)*mec* type (when the strain is methicillin-resistant *S. aureus* positive), and the presence or absence of the Panton Valentine leukocidin (PVL) gene. Representative PFGE profiles for USA 300 and USA 400 are included for comparison. MSSA, methicillin-susceptible *S. aureus*.

these strains are more effective as pathogens than are the other colonizing strains.

PVL-positive strains accounted for a high proportion of the clinical isolates. PVL has been identified as an epidemiologic marker for, if not virulence determinant of, invasive strains of CA-MRSA [18, 19]. Whether PVL is the virulence determinant or a marker for other determinants remains uncertain; there is relatively limited information on carriage versus infection

with PVL-positive strains. The present study provides additional evidence of the ability of these unique CA-MRSA strains to cause invasive disease.

The role that PVL-positive MSSA strains play as community pathogens is also gaining increased attention. In their survey of cutaneous infections treated in emergency departments throughout the United States, Moran et al. [20] reported that 31% of MSSA isolates causing infections were USA 300 and that 42% were PVL positive. MSSA PVL-positive isolates were recently responsible for an outbreak of infections at a Rockland County jail [21]. This outbreak is noteworthy because inmates from this jail are transferred to NYS prisons; inmate transfers may therefore be responsible for the introduction of these strains into the prison system.

The vast majority of clinical infections were caused by the same strains of *S. aureus* that were colonizing inmates in the present study. Carriage of CA-MRSA has been implicated as a risk factor in several of the diverse settings in which outbreaks have occurred, including among military recruits, a group with risks for infection that are similar to those for prison inmates [5]; Ellis et al. [5] found that 38% of military recruits colonized with CA-MRSA developed infections (all were PVL positive), versus only 3% of those colonized with methicillin-susceptible isolates. The role of antecedent nasal colonization as a prelude to clinical infection is less clear in CA infections than in health care–associated infections [4, 5, 22, 23]. This may be due in part to the ability of these strains to colonize other unsampled tissue sites (e.g., vagina, rectum, or skin) [24]; and such sites may play a more important role in community-based infections than in health care–associated infections.

Outbreaks of CA-MRSA infections in prisons have been increasingly reported. Most notable among these have been the large-scale outbreaks reported by Texas prisons, Los Angeles county jails, a Mississippi prison, and the Georgia prison system [6, 25, 26]. The risk factors identified in these outbreaks have reflected the conditions found in other CA-MRSA–outbreak settings and include close contact, compromised skin integrity, and limited access to adequate hygiene.

MRSA-outbreak investigations and cross-sectional studies of inmates in correctional facilities have identified some significant demographic risk factors, including comorbidities, female sex (for staphylococcal colonization), and longer incarceration. The much higher MRSA colonization rates among the female inmates at Bedford Hills than among the male inmates at Sing Sing may have to do with several factors: (1) the greater proportion of women than men with drug-related offenses; (2) differences in referral patterns from NYS jails; and (3) perhaps differences in the nature of physical contact within the prisons. Our earlier review of the literature regarding MRSA in prison populations concluded that there is a need to identify risk factors for MRSA in the prison setting and to better understand the characteristics that influence acquisition and transmission in this setting [27].

There are no studies of which we are aware that have identified a higher proportion of drug offenders as being a risk factor for MRSA infection at the prison level. Data from the US Department of Justice show that drug use is prevalent prior to incarceration and is often concomitant with the timing of the criminal offense: in 1997, 56.1% of men and 62.4% of women reported drug use during the month prior to the offense, and 32% of men and 40% of women reported drug use at the time of the offense [28]; and, in 2001, a third of released state-prison inmates had been convicted of a drug-related offense [29]. Our finding of a much higher rate of colonization among female inmates than among male inmates is consistent with the results of previous surveys and warrants further evaluation. It is of interest that the women's prison also had a higher proportion of inmates with drug-related offenses, which could explain some of the increased risk of colonization. For the clinical isolates, a higher average proportion of inmates with drug-use offenses in prison was strongly associated, in both medium- and maximum-security prisons, with a higher prevalence of clinical isolates that were MRSA positive. Taken together, these findings suggest that drug use—or the behavioral and/or epidemiological patterns associated with drug use—plays an important role as a potential risk factor among inmates.

In maximum-security prisons, a longer length of inmate stay was associated with an increased proportion of PVL-positive isolates; in medium-security prisons, by contrast, length of inmate stay was negatively associated with MRSA infection. One earlier study had identified longer length of inmate stay as a risk factor for MRSA colonization during outbreaks [8]. It is not clear why the present study found, in medium-security prisons, a converse relationship between length of inmate stay and MRSA infection. In medium-security prisons, younger age was associated with an increase in PVL-positive isolates and in MRSA clinical isolates. It is possible that younger inmates are more susceptible, given that they are newer to the environment, or that they may have more risk factors, such as recent drug use; issues such as larger social networks or different forms of interpersonal contact might also contribute to this finding.

The data of the present study would appear to support 2 hypotheses. The first hypothesis is that inmates enter prison facilities with risk factors that increase the likelihood of colonization and/or infection; antecedent drug use and the potential risks of strain transmission [30], as well as incarceration in particular NYS jails, may contribute to this hypothesis. The second hypothesis is that prolonged incarceration in maximum-security prisons also increases inmates' risk of infection, perhaps because of increased likelihood of close contact with inmates with *S. aureus* infection, especially in light of the prevalence of selected strains in the prison system.

The present study had a number of limitations. The comparison between colonizing isolates and isolates associated with clinical infection was limited because only 2 prisons were included in the study of colonization whereas the clinical isolates were obtained from all NYS prisons. It is of interest, though, that the majority of clinical isolates were represented among the colonization strains. From these data, it is difficult to draw any conclusions regarding the likelihood or risk of clinical infection. The proportion of MRSA among clinical isolates may have been associated with interprison differences in the practice of obtaining clinical cultures, which would clearly affect the relative numbers of isolates obtained from the different prisons. Nevertheless, the clinical isolates provided some insight into the nature of the *S. aureus* isolates associated with clinical infections in the NYS prison system.

Our coding of drug offenses may not have been mutually exclusive, because inmates may have had more than 1 drug offense listed; however, multiple offense classifications would most likely lead to an underestimation of the effects that drug offense has on infection levels. Our data were analyzed at the prison level, and, therefore, it is not possible to infer that prison-level risk factors identified in the present study are also significant risk factors at the individual-inmate level. Last, only approximately half of the inmates approached were willing to volunteer to provide a nasal-swab specimen.

In summary, the present study illustrates both the value of surveillance cultures in determining the prevalence of potentially invasive strains of CA-MRSA in high-risk settings and the ability of these strains to predominate as pathogens. It also demonstrates the potential contribution that antecedent risk factors and incarceration make to the likelihood of infection. Further research is necessary to identify both individual and contextual risk factors for *S. aureus* infection among prison populations.

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