Staphylococcus aureus Oropharyngeal Carriage in a Prison Population

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Throat carriage (42.7%) of *Staphylococcus aureus* exceeded nasal carriage (35.0%) in 2 New York prisons. Methicillin resistance, primarily due to USA300, was high at both sites; 25% of dually colonized inmates had different strains. Strategies to reduce *S. aureus* transmission will need to consider the high frequency of throat colonization.

Recent studies have identified the oropharynx as a potential site of *Staphylococcus aureus* colonization. This colonization may occur in the presence or absence of nasal colonization [1, 2]. Oropharyngeal carriage of *S. aureus* has potentially important ramifications in decolonization strategies for populations at high risk of infection. Topical agents directed at eradication of nasal colonization are not likely to affect throat carriage, and as a result, reservoirs for future infection may persist.

In an earlier report, we found a high rate of nasal methicillin-resistant *S. aureus* (MRSA) carriage in 2 New York prisons [3]. As part of an ongoing investigation of *S. aureus* infection in the prison population, nasal and oropharyngeal swab samples were obtained from study participants at a men's (Sing Sing) and a women's (Bedford Hills) maximum security prison in Westchester, New York. The goal of this study was to further characterize the nature of *S. aureus* carriage and to determine whether oropharyngeal carriage was an important site of colonization in this population known to be at high risk of infection [4].

Received 24 August 2010; accepted 04 January 2011.

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Clinical Infectious Diseases 2011;52(6):775–778

1058-4838/2011/526-0001$37.00
DOI: 10.1093/cid/cir026

The Institutional Review Board of Columbia University and the New York State Department of Correctional Services reviewed and approved this study. At both facilities, the prison administration provided a list of prisoners entering the facility that week. These prisoners, located in the holding area, were privately asked whether they would like to participate and, if agreeable (72.5% at Sing Sing and 77.5% at Bedford Hills), provided written informed consent. Consecutive study participants were then interviewed, and samples from the anterior nares and oropharynx of each inmate were obtained for culture with a rayon-tipped swab (Becton Dickinson). Information collected included demographic characteristics and personal history, such as ethnicity, time spent in the prison system, medical history, and prior living conditions. This information was then verified by review of official prison medical records. Each swab sample was incubated in 6% sodium chloride–supplemented tryptic soy broth (Becton Dickinson) at 35°C overnight, to enrich *S. aureus* selection before being plated onto Mannitol Salt agar (Becton Dickinson) and incubated at 37°C for 48 h. Individual positive colonies were then streaked onto sheep blood agar plates before being confirmed as *S. aureus* with the coagulase and protein A detection kit (Murex StaphAurex) [5].

Positive samples were *spa* typed and compared using Ridom Staph Type software (Ridom GmbH) [6]. Positive methicillin-resistant isolates were staphylococcal chromosomal cassette *mec* typed using multiplex polymerase chain reaction assay, as described elsewhere [7]. Parameters for the Based Upon Repeat Pattern (BURP) clustering in the Ridom StaphType software, using standards determined by Mellman et al [8], were used to further characterize the isolates. Paired inmate samples (ie, from the nose and throat) that were identified as distinct were examined using pulsed-field gel electrophoresis (PFGE) with *Sma*I digest [5] to confirm that they were different. Settings for PFGE were as follows: initial switch time, 1.0 s; final switch time, 30.0 s; included angle, 120°; current, 6.0 V; and run time, 23 h. The buffer temperature was maintained at 12°C [5]. Strains were compared using both the Dice coefficient with a similarity rate of 80% to identify closely related strains (Bionumerics) and the Tenover criteria to examine the number of band differences between the paired strains [5, 9].

The majority of Sing Sing participants were self-described as either black (57.6%) or Latino/Hispanic (30.0%). The vast majority (95.4%) was already in the prison system and was transferred from other prisons for administrative reasons or

placement at a new facility. At Bedford Hills, the majority of prisoners identified themselves as black (40.1%) or white (46.2%). In contrast with the inmates at Sing Sing, they were more likely to be transferred from the jail system (93.3%). Thus, the 2 groups of inmates reflected 2 different stages of incarceration. There were no identifiable differences in the sociodemographic data, including age, ethnicity, and prior residences, when *S. aureus* colonization rates were compared at the 2 prisons (Table 1).

Samples from 312 women and 217 men were collected during an 8-month period (November 2009 through June 2010), with >50% testing positive. There were 185 nasal and 226 oropharyngeal samples positive for *S. aureus*. The overall rate of carriage in the throat (226 [42.7%] of 529) exceeded that in the anterior nares (185 [35.0%] of 529; $P < .01$). The women at Bedford Hills had a lower combined overall nasal and oropharyngeal colonization rate than the men at Sing Sing ($P = .001$).

Methicillin-susceptible *S. aureus* (MSSA) oropharyngeal (40.4% Bedford Hills and 46.1% Sing Sing) versus nasal (31.4% Bedford Hills and 40.1% Sing Sing) colonization rates at both facilities were comparable ($P > .05$). MRSA carriage rates at the 2 body sites were also similar. Fifty-nine (11.2%) of 529 participants in our study group were colonized with MRSA at either or both nasal and oropharyngeal sites (Table 1). The rate of MRSA carriage was similar in both nasal and throat samples (28.6% nasal and 21.4% oropharyngeal at Bedford Hills; 17.2% nasal and 15.0% oropharyngeal at Sing Sing). Ten men and 12 women were colonized with MRSA solely in the oropharynx.

Table 1. Description of Inmates and Samples Collected at the 2 Prisons

Characteristic	Bedford Hills ($n = 312$)	Sing-Sing ($n = 217$)
Ethnicity	**Proportion positive for *Staphylococcus aureus* (%)**	**Proportion positive for *S. aureus* (%)**
Black	64/125 (51.2)	82/125 (65.6)
White	78/144 (54.2)	13/19 (68.4)
Latino/Hispanic	19/35 (54.3)	44/65 (67.7)
Other	1/8 (12.5)	5/8 (62.5)
Residence before prison		
Different or same prison	17 (5.4)	207 (95.4)
Jail	291 (93.3)	10 (4.6)
Other (home, apartment, etc.)	4 (1.3)	0 (.0)
Sample site(s) positive for *S. aureus*		
Total individuals colonized at the nares, throat, or both sites	162/312 (51.9)	144/217 (66.4)
Nares	98/312 (31.4)	87/217 (40.1)
Throat	126/312 (40.4)	100/217 (46.1)
Individuals colonized at both nares and throat[a]	62/312 (19.9)	43/217 (19.8)
Same *spa*-type	52 (16.7)	22 (10.1)
Related *spa*-type	1 (.3)	4 (1.8)
Different *spa*-type	9 (2.9)	17 (7.8)
MRSA positive *S. aureus* samples	**Proportion positive for MRSA[b](%)**	**Proportion positive for MRSAb (%)**
Total individuals colonized at the nares or throat	35/162 (21.6)	24/144 (16.7)
Nasal	28/98 (28.6)	15/87 (17.2)
Throat	27/126 (21.4)	15/100 (15.0)
SCC*mec* types[c]		
SCC*mec* I, II, and III	8 (15.4)	2 (6.9)
SCC*mec* IV & V	37 (71.2)	25 (86.2)
Nontypeable	7 (13.5)	2 (6.9)
Most prevalent *spa* types at the 2 prisons		
t-8/eGenomics type 1	8 MSSA*, 23 MRSA	14 MSSA, 13 MRSA
t-2/eGenomics type 2	12 MSSA, 6 MRSA	6 MSSA, 1 MRSA
t-216/eGenomics type	11 MSSA	4 MSSA, 1 MRSA

[a] MSSA, methicillin-susceptible *Staphylococcus aureus*; MRSA, methicillin-resistant *Staphylococcus aureus*.

[b] Dual colonization indicates a difference in *spa* type of the strain isolated from the nasal versus the oropharynx from a single inmate.

[c] Staphylococcal chromosomal cassette (SCC) *mec* types.

One hundred forty-seven different *spa* types were identified. The epidemic strain USA300 (*spa* type t8/eGenomics type 1) was the most prevalent overall, accounting for 14.1% of the positive samples, with 22 of 58 of these isolates being methicillin susceptible [10]. USA300 and strains closely related to USA300 (as defined by BURP analysis of the *spa* types) accounted for 19.4% of all positive samples, again with similar nasal and oropharyngeal colonization rates (5.3% nasal and 4.8% oropharyngeal at Bedford Hills; 4.6% nasal and 4.8% oropharyngeal at Sing-Sing).

A surprising 31 (30%) of 105 individuals who tested positive at both the nasal and oropharyngeal sites had different strains, as defined by their *spa* types, and were classified as dually colonized. Among these were 10 persons colonized with MSSA and MRSA at the 2 sites. Samples from these inmates were compared using the repeat comparison and clustering programs (Ridom Staph Type software) to determine whether the isolates were related. Five individuals with different *spa* types were colonized with related *spa* types as determined by BURP clustering. Six (19.4%) of 31 dually colonized individuals were also MRSA positive. All paired nasal and oropharyngeal isolates identified as different by *spa* typing (n = 26) were further confirmed as unique with use of a separate typing technique, PFGE (Figure 1).

This study showed continued high *S. aureus* carriage, especially MRSA carriage, in this population known to be at high risk of *S. aureus* infection [3]. The study also began to address when acquisition of carriage might occur. New prison inmates, primarily transferred from jails (Bedford Hills), and prisoners transferred from other New York State correctional facilities (Sing Sing) had high carriage rates. New or prevalent community-based strains therefore appear to be regularly introduced into these facilities by inmates arriving from the community or local jails. Once introduced, the strains may persist and/or be transmitted to other inmates in the prison environment. The transfer of prisoners among different prisons, which occurs on a regular basis, may further contribute to their spread. As in our previous report, the epidemic strain t8/eGenomics type 1 (USA300) was the most prevalent strain found in both MSSA and MRSA isolates, suggesting that it is readily spread in the prison setting [3]. In light of its potential virulence, the basis for the introduction and spread of this strain in the prison system is important.

Our results showing higher throat than nasal carriage of *S. aureus* also confirm earlier observations that the oropharynx is an important reservoir for *S. aureus* [2, 11, 12]. There was no statistically significant difference in colonization rates at the 2 sites for MRSA isolates. This may not always be the case, because other investigators have speculated that, in some settings such as intensive care units, MRSA colonization of the oropharynx may not be as common [13].

Finally, the observation that individuals may be simultaneously colonized with different strains of *S. aureus* is of considerable interest. Nilsson and Ripa [11] noted that 3 of 39 study participants colonized with different strains had persistent carriage of these strains over 25 months. More recently, Hamdan-Partida et al [12], in addition to reporting higher throat than nares colonization in a population of healthy carriers in Mexico, found that a small percentage of dually colonized study participants had different strains in their nares and throat. In the present study, there was a relatively high rate of dually colonized inmates with different strains, suggesting that this type of colonization may be more common than was previously suspected, at least in populations at high risk of infection. These findings were validated using 2 different techniques: *spa* typing and PFGE.

The role of oropharyngeal colonization as a potential reservoir for future infection remains uncertain. Its frequency as a site for colonization raises questions concerning the efficacy of such topical therapies as mupirocin or chlorhexidine as prophylactic regimens. The fact that a significant minority of individuals may be colonized with different strains having different antibiotic susceptibilities, such as persons colonized with both MSSA and MRSA isolates, is also of concern. Future studies will need to address these questions in clinical trials.

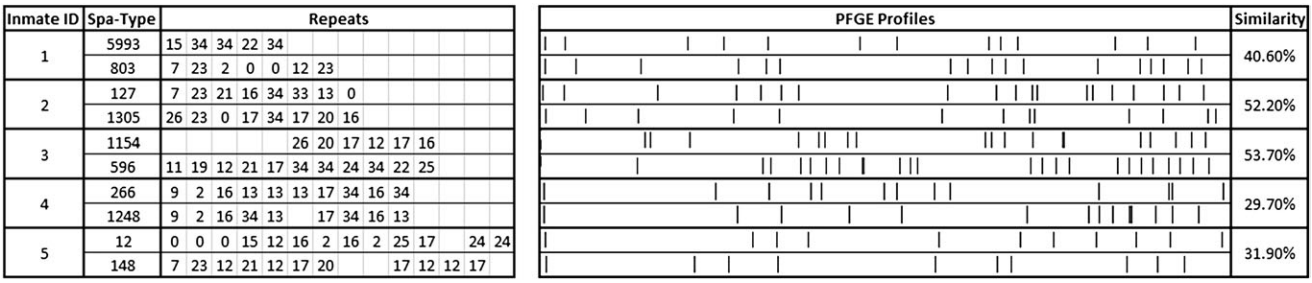

Figure 1. Five representative samples from dually colonized inmates that were chosen to show the differences in the *Staphylococcus aureus* isolate pairs. The *spa* types indicate the assignment of strain type based on the Ridom software. The assignment of the different repeats (allelic profile) and their location for the *spa* types is also provided. The PFGE profiles of the discordant pair are also displayed along with the dendrogram displaying the degree of similarity of the 2 strains. Pairwise similarity scores for the isolates were calculated using the Dice coefficient.

Acknowledgments

We thank Rachel Gordon, Anne-Catrin Uhlemann, Andrew J Lee, Superintendent Philip Heath, Superintendent Sabina Kaplan, Deputy Superintendent Marjorie Byrnes, Deputy Superintendent Kevin Winship, Deputy Superintendent Michael Capra, Dr Maryann Genovese, Dr Lori Goldstein, Dr Denise Sepe, Dr Dana Gage, Dr Bani Choudry, Margaret Franklin, Randi Uszak, Jon Hansen, and Francis Akinyombo.

Financial support. This work was supported by National Institute of Allergy and Infectious Diseases, National Institutes of Health (R01 AI082536).

Potential conflicts of interest. All authors: no conflicts.

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