Molecular Characterization of Methicillin-Resistant Staphylococcus aureus Clinical Isolates Obtained from the Rikers Island Jail System from 2009 to 2013

Joshua Tanner, a Ying Lin, b John Kornblum, b Carolyn T. A. Herzig, c,d Rachel Bystritsky, a Anne-Catrin Uhlemann, a Franklin D. Lowy a,e

Department of Medicine, Columbia University, College of Physicians and Surgeons, Division of Infectious Diseases, New York, New York, USA; New York City Department of Health and Mental Hygiene, New York, New York, USA; Columbia University School of Nursing, New York, New York, USA; Department of Epidemiology, Columbia University, New York, New York, USA; Department of Pathology and Cell Biology, Columbia University, College of Physicians and Surgeons, New York, New York, USA

Inmates of Rikers Island jail potentially introduce Staphylococcus aureus into New York State prisons upon transfer. In this study, methicillin-resistant Staphylococcus aureus isolates (n = 452), collected from infected inmates (2009 to 2013), were characterized. spa type t008 was the predominant clone identified, accounting for 82.3% of the isolates, with no evidence of mupirocin or chlorhexidine resistance.

Methicillin-resistant Staphylococcus aureus (MRSA) is a recognized cause of community-associated (CA) skin and soft tissue infections in otherwise healthy individuals (1, 2). These infections have been especially frequent in certain high-risk groups such as military recruits, prison and jail inmates, athletes, and children in daycare (reviewed in reference 1). Common risk factors associated with CA-MRSA include sharing of personal items, superficial abrasions, crowding, limited access to showers, and exposure to others with MRSA infections (3–6).

MRSA infections that occur in correctional facilities (both prisons and jails) are of special concern due to the high risk for outbreaks and the potential for more invasive infections, as well as the risk of recurrent infections among inmates (7, 8). While a prison holds inmates with extended sentences following conviction, jails hold detainees awaiting trial, inmates awaiting sentencing, and inmates that have been given a sentence of ≤1 year. Newly released inmates may introduce epidemic strains of CA-MRSA into the community, while inmates awaiting transfer may transmit their strains to the prison population (8, 9). Thus, jails may serve as an important reservoir and amplification center of epidemic MRSA strains for both the community and prison populations (9).

Outbreaks of CA-MRSA in jails have occurred in different geographic regions of the United States (6, 10). Notably, a MRSA outbreak in 2002 at the Los Angeles County Jail involved 928 inmates (8). We recently reported that the prevalence of MRSA colonization among inmates entering two New York State (NYS) prisons was 10.6% for females and 5.9% for males, far higher than the prevalence of 0.5% to 1.5% reported for the general population (5, 11).

There have been few investigations that describe MRSA clinical isolates from inmates of large jails (12, 13). No such studies have been performed at Rikers Island Correctional Facility (RICF), one of the largest jails in the country. Of note, 46% of inmates under custody in NYS prisons are committed from New York City (NYC), and most inmates committed from NYC are jailed at RICF (see http://www.doccs.ny.gov/Research/Reports/2013/UnderCustody_Report_2013.pdf). We therefore characterized a large collection of MRSA clinical isolates from RICF with the goal of better understanding the contribution of jail transfers to the introduction of MRSA into the prison system. This would be an initial step toward developing strategies to reduce the introduction and spread of MRSA.

According to the NYC Department of Corrections report from October to December 2012 (14), RICF houses roughly 12,700 inmates, including detainees awaiting trial (76.0%), new convicts serving sentences (16.0%), and new convicts awaiting transfer to a state prison facility (8.0%). The average length of stay for an inmate is 54 days; >75.0% of inmates are discharged directly into the community after their release. In 2012, there were >87,000 admissions to and 88,000 discharges from RICF. Most inmates were male (93.0%) and averaged 34 years of age. Approximately 5% of the inmates are HIV positive. Possession and sale of controlled substances are among the most common charges brought against inmates, suggesting a high prevalence of drug use in this population.

Inmates were held in 1 of the 10 facilities on RICF or 1 of the 4 regional jails in Manhattan, the Bronx, Brooklyn, and Queens. Health professionals at RICF identified inmates with MRSA infections. Swabs, with samples collected from suspected infections, were sent to BioReference Laboratories (Elmwood Park, NJ) for culture and susceptibility testing. Between July 2009 and July 2013, all MRSA clinical isolates were sent to the NYC Department of Health and Mental Hygiene (DOHMH) for further analysis, including pulsed-field gel electrophoresis (PFGE). A total of 452 MRSA isolates were collected. Of the 452 isolates, 421 were from different inmates, and of the 31 duplicate samples, 15 were collected within the same week. Although medical information is not available, it is possible that the remaining duplicate samples reflect either recurrent or new infections.

MRSA isolates were reconfirmed as S. aureus by coagulase and protein A testing (Murex Staphaurex, Kent, England). Isolates...
were genotyped by spa sequencing, and SCCmec typing was used to confirm methicillin resistance. All isolates were SCCmec type IV (15, 16).

Ridom StaphyType software (version 1.5; Ridom GmbH, Germany) was used to assign spa types and compare isolates (17). There were 42 spa types detected among the 452 isolates. The predominant spa type was t008 (n = 372 [82.3%]), followed by t064 (n = 19 [4.2%]) and t024 (n = 13 [2.9%]) (Fig. 1).

spa types were further grouped by based upon repeat pattern (BURP) clustering using parameters described by Mellmann et al. (18). This analysis yielded three spa clonal clusters (spa-CC). Twenty-one spa types were clustered in spa-CC008, with most connecting directly to the founder t008 and three connecting to a subfounder t1635. Four spa types (n = 9) were clustered in spa-CC686/002, with t686 and t002 as cofounders; three spa types (n = 3) were clustered in spa-CC127, with t127 as founder. One spa type was excluded from analysis (t1784; length, <4 repeats [n = 1]) and 13 spa types were classified as singletons (n = 15).

Isolates were also compared by PFGE using Smal-digested DNA and analyzed using BioNumerics software version 4.00 (Applied Maths). Pairwise similarity scores were calculated by the Dice coefficient (15). USA300 and related types were the dominant clones (n = 416 [92.0%]), followed by USA500 (Iberian strain; n = 17 [3.8%]). Among the USA300 isolates, t008 was the most frequent (n = 362 [87.0%]), followed by t024 (n = 13 [3.1%]) and t622 (n = 6 [1.4%]). Among USA500/Iberian isolates, t064 was the only spa type (n = 17 [100%]). Conversely, 95.4% (n = 355) of t008 isolates were USA300 or related, and 89.5% (n = 17) of t064 isolates were USA500/Iberian related.

Although USA300 was most commonly spa type t008 and USA500 was most commonly t064, two isolates were discordant based on PFGE; they were spa type t064 and USA300. PFGE profiles of the two isolates were compared with PFGE profiles of USA500 and USA300 (Fig. 2). The two discordant isolates shared similarity with both USA300 and USA500 isolates. Screening PCR revealed that both strains lacked the mobile genetic elements Panton-Valentine leukocidin (PVL) (LukS) and arginine catabolic mobile element (ACME), suggesting that they are variants within the sequence type 8 (ST8) lineage as previously described (19, 20, 23). These disparities highlight the limitations of spa and PFGE typing in the characterization of subclones of the ST8 lineage.

ACME was present in 382 (84.5%) of all isolates, 377 of which were USA300 or related (98.7% of ACME-positive isolates). PVL was detected in 416 of all isolates (92.0%), 404 of which were USA300 or related (97.1% of PVL-positive isolates). Both mobile genetic elements were present in 377 isolates (83.4%), while 31 isolates (6.9%) harbored neither element. The ACME- and PVL-negative isolates mainly belonged to USA500 (n = 17), a precursor of USA300, or USA100 (n = 4), a common health care-associated MRSA (21). Although ACME has been infrequently identified in non-USA300 isolates and has been absent in selected USA300 strains, it is in general a reliable marker for USA300 (22).

Screening PCR was also carried out to detect high-level mupirocin resistance (mupA gene) and chlorhexidine resistance (qacA/B gene) as previously described (24). For mupA and qacA/B, a random subset of 86 isolates was tested. No isolates harboring either resistance gene were detected in the tested isolates.

RIFC is one of the largest jails in the country. Due to its size, crowded conditions, and high daily inmate turnover, as well as inmate risk behavior, inmates may introduce strains of MRSA both into the prison system and back into the community (8, 9). RIFC inmates are at especially high risk of both colonization and infection with CA-MRSA and are therefore likely to introduce these strains into the prison system (5).

The goal of this study was to characterize RIFC MRSA isolates as part of an effort to inform future intervention strategies to reduce the high rate of MRSA infections in the NYS prison system. The epidemic CA-MRSA strain USA300 and related isolates accounted for the overwhelming majority of MRSA infections, followed by a smaller subset of USA500 and USA100 isolates. This is in keeping with other studies that found that USA300 accounts for more than half of all CA-MRSA skin and soft tissue infections in the United States (25). Consistent with the predominance of USA300, the mobile elements ACME, PVL, and SCCmec type IV were detected in most isolates. Of interest, USA300 was also the predominant MRSA carriage strain identified among inmates en-
tering two New York State prisons in our earlier study, suggesting a possible role for jails in introducing these strains into the prison system (5).

The high burden of USA300 MRSA infections in the jail system may reflect the accumulated risk groups (i.e., drug users and HIV positive) found in correctional settings (15, 26). We also found a number of infections due to USA500. In other studies, this strain has been found to more frequently colonize and infect individuals with HIV (27, 28). The prevalence of USA500 may therefore reflect the high prevalence of HIV-infected individuals in RICF (14).

Intervention strategies for reducing the number of infections in correctional facilities have primarily involved outbreaks (29). These have generally used an approach that targets individual-level risks. Achieving a reduction in endemic MRSA infections may require alternative institutional strategies. One such approach, “search and destroy,” targets individuals on entry to health care facilities, where those patients or health care personnel colonized with MRSA undergo decolonization (30). To that end, our study found no evidence of resistance to either mupirocin or chlorhexidine, two agents that are often used in MRSA decolonization strategies (31).

CA-MRSA remains a threat in U.S. prisons and jails and thus warrants more study of transmission pathways, as well as prevention strategies. The unusually high proportion of USA300 among RICF MRSA infections raises concerns that this jail may be an epicenter of the dispersal of epidemic USA300 into the prison system and the community at large.

ACKNOWLEDGMENT

This work was supported by the National Institute of Allergy and Infectious Diseases, National Institutes of Health (grant R01AI82536). Anncatrin Uhlemann was supported by NIH grant K08 AI090013.

REFERENCES


Report of MRSA Isolates from Rikers Island Jails

http://jcm.asm.org/ on behalf of guest through download on October 20, 2017.


